Integrating Mechanisms into Macroecology

8th Annual Meeting of the Specialist Group for Macroecology of the Ecological Society of Germany, Austria, and Switzerland (GfÖ)

4th - 6th March 2014

Martin Luther University Halle Wittenberg, Institute of Geobotany, Am Kirchtor 1, 06108 Halle (Saale)

Including the satellite workshop

Macroecology Meets IPBES

"Integrating mechanisms into macroecology" is jointly organised by

- the Martin Luther University Halle Wittenberg, Institute of Biology, Department of Geobotany
- the Helmholtz Centre for Environmental Research - UFZ
- the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

"Macroecology meets IPBES" is organized by

- the Biodiversity and Climate Research Centre – BIK-F
- supported by NeFo, the German Network-Forum for Biodiversity Research

Martin Luther University Halle Wittenberg (MLU)

The University of Halle Wittenberg goes back to two universities, one founded 1502 in Wittenberg, the other 1694 in Halle. After closure by Napoleon in 1813, both universities were re-founded in 1817 in Halle. Combining both tradition and future-oriented research, Halle University has a reputation of active promotion of international and interdisciplinary research, evidenced for example by 52 partner universities worldwide, as well as a tight cooperation between Halle University and the Helmholtz Centre of Environmental Research – UFZ. Today, the MLU hosts more than 20.000 students and as a full-range university it offers a broad range of study programmes and research opportunities.

Institute of Biology/ Geobotany

The Department of Geobotany within the Institute of Biology has a long tradition in botanical and ecological research that goes back to its foundation in 1698. The three working groups at the institute cover a broad range of topics including aspects of vegetation ecology, population biology of plants and evolutionary systematics.

Department of Geobotany

Prof. Dr. Helge Bruelheide is professor for vegetation science with experience in several national and international projects on global change effects on biodiversity and ecosystem services in Central Europe and East Asia. He is speaker of the DFG Research Unit 891 (Biodiversity-Ecosystem Functioning, China), co-director of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, has two contributing projects in the DFG Priority Programme 1374 (Biodiversity Exploratories) and participates in the Higrade graduate school of the Helmholtz Centre of Environmental Research – UFZ. Current research fields are vegetation ecology, biodiversity ecosystem functioning relationships, invasion biology and experimental and modelling approaches in plant biogeography.

Department of Plant Ecology

Prof. Dr. Isabell Hensen is professor for plant ecology and since 2010 director of the Institute of Biology and dean of education of the faculty of natural sciences I (Life science). The working group of **Isabell Hensen** is known for basic and applied research across a wide range of plant ecological fields including population ecology, population genetics, biological invasions, and conservation biology. Isabell Hensen's main research centers on the population biology and genetics of South American treeline species as well as on biotic and abiotic factors determining patterns of species regeneration in tropical and subtropical mountain forests.

Department of Systematics & Biodiversity

Prof. Dr. Martin Röser is professor for Systematics & Biodiversity. His working group deals with evolutionary tendencies of morphological and molecular-genetical characters in different plant groups (grasses, Ranunculaceae, Fabaceae, Marantaceae, Zingiberaceae, fungi, lichens, …). They investigate the evolution, phylogeny and spatio-temporal radiation of species, their history of dispersal and speciation process and try to trace the development of characteristics and ecological adaptations.

Herbarium

Prof. Dr. Uwe Braun has long-lasting experience in fungal diversity, systematics and taxonomy worldwide, including tropical and subtropical countries. He worked on various groups of biotrophic microfungi worldwide, but has intimate knowledge of pathogenic leaf fungi in Europe. He is author and co-author of several world monographs of microfungi.

Botanical Gardens

Founded in 1698, the Botanical Garden cultivates approximately 12.000 plant species in an area of 4.5 ha and 3.000 square meters of greenhouses. Among the most important collections are special systematic collections of orchids, bromeliads, carnivorous plants, grass species, *Mammillaria* (Cactaceae), *Echinodorus* (Alismataceae), and *Cryptocoryne* (Araceae). Another focus is the collection of Central Asian plants, especially from Mongolia. These living plants nicely complement the large collection of Mongolian plants in the Herbarium Halle (HAL), which is supposed to be one of the largest collections of Mongolian plants outside Russia and Mongolia.

For further information please visit www.botanik.uni-halle.de

HELMHOLTZ
CENTRE FOR
ENVIRONMENTAL
RESEARCH – UFZ

The Helmholtz Association is dedicated to pursuing the long-term research goals of state and society, and to maintaining and improving the livelihoods of the population. In order to do this, the Helmholtz Association carries out top-level research to identify and explore the major challenges facing society, science and the economy. Its work is divided into six strategic research fields: Energy; Earth and Environment; Health; Key Technologies; Structure of Matter; and Aeronautics, Space and Transport. The Helmholtz Association brings together 18 scientific-technical and biological-medical research centres. With almost 36,000 employees and an annual budget of approximately € 3.8 billion, the Helmholtz Association is Germany's largest scientific organisation. Its work follows in the tradition of the great natural scientist Hermann von Helmholtz (1821-1894).

Helmholtz was one of the last true polymaths and represented a form of natural science that bridged medicine, physics and chemistry. The ophthalmoscope for examining the retina is one of his many developments that are still used (in a modern form) to this day. His research into the conversion of matter led to his formulation of the conservation of energy principle. Helmholtz founded the Imperial Physico-Technical Institute and served as its first Director. The Imperial Physico-Technical Institute was the world's first scientific research centre outside of a university and is therefore a forerunner to the Helmholtz Association.

The Helmholtz Centre for Environmental Research - UFZ was established in 1991 and has more than 1,100 employees in Leipzig, Halle/S. and Magdeburg. As an international competence centre for the environmental sciences, UFZ investigates the complex interactions between mankind and nature under the influence of global change. In close cooperation with decision-makers and stakeholders, scientists at the UFZ develop system solutions to improve the management of complex environmental systems and to tackle environmental issues. For example, we work on the management of water resources, the impacts of land use change on human landscapes and biodiversity, the impacts of chemicals in the environment and on human health as well as adaptation strategies for climate change.

For further information please visit www.ufz.de and www.helmholtz.de

German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

The German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig the first National Centre for Biodiversity Research, is one of six research centers funded by the German Research Foundation (DFG) funded in October 2012. By the end of 2014 the center will encompass more than 100 scientists and staff members.

iDiv, is a hub for international biodiversity science whose central mission is to promote theory-driven synthesis and data-driven theory and connects well-known scientists all over the world, being embedded in a rich scientific landscape in Central Germany with a strong profile in modern biodiversity research. The scientific core of iDiv is formed by five research areas (Theory in Biodiversity Sciences, Ecological Interactions, Evolution and Adaptation, Conservation Biology, and Biodiversity Synthesis).

As a unique feature, a Synthesis Centre for Biodiversity Sciences (sDiv) is integrated in the research environment of iDiv to foster theoretical and synthetic thinking in biodiversity sciences by hosting workshops and funding short-term postdoc and sabbatical positions. The research training group of young biodiversity researchers, iDiv, educates a new generation of scientists in transdisciplinary biodiversity research.

The iDiv research centre is located on the BIO CITY campus in Leipzig a hot spot for life science in the city and jointly hosted by the the University of Leipzig (UL), the Martin Luther University Halle-Wittenberg (MLU), and the Friedrich Schiller University Jena (FSU). The three participating universities are supported by eight non-university institutions: the Helmholtz Centre for Environmental Research (UFZ), Max Planck Institutes for Biogeochemistry (MPI BGC), for Chemical Ecology (MPI CE), and for Evolutionary Anthropology (MPI EVA), the Leibniz Institutes German Collection of Microorganisms and Cell Cultures (DSMZ), of Plant Biochemistry (IPB), the of Plant Genetics and Crop Plant Research (IPK), and Senckenberg Museum of Natural History (SMNG).

For further information please visit www.idiv.de

The mission of the Biodiversity and Climate Research Centre is to carry out internationally outstanding research on the interactions of organismal biodiversity and climate. Using a broad spectrum of state-of-the-art methods from satellite-supported remote sensing of climate, area and ecosystem reactions to advanced genomics and mass spectrometry, the scientists of the centre document and analyse past and present patterns and processes with the goal of providing reliable predictions of future developments.

The Biodiversity and Climate Research Centre integrates the multi-faceted expertise required for the in-depth investigation and management of climate-related biodiversity changes at local, national, European and global levels, including those that are relevant to the environment and health. It thereby contributes to the goals of international agreements at the regional, European and global levels, e.g. the Convention on Biological Diversity (CBD), the United Nations Framework Convention on Climate Change (UNFCCC), the Fauna-Flora-Habitat (EU-FFH) or the Water Framework Policies of the European Union (EU-WRRL).

For further information please visit www.bik-f.de.

The German Network-Forum for Biodiversity Research (NeFo) is the national focal point for scientists, policy-makers and other stakeholders working in the field of biodiversity research and policies. NeFo was set up to improve the information and knowledge exchange both between and within these different stakeholder groups (e.g. between different research disciplines). Our aim is to increase the awareness of the value of biodiversity among policy makers and the society, and the important role scientists play to analyse the drivers of biodiversity change in order to identify solutions for its conservation.

Currently, NeFo has a particular focus on the newly established Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), which had its first plenary in January 2013 (IPBES-1) and the second to be held in December (IPBES-2). NeFo aims at facilitating the involvement of the German biodiversity community in this IPBES process. Our capacity building comprises national and pan-European workshops, provision of information about IPBES and the possibilities for participation. Beyond, we support the German ministries engaged in IPBES by e.g. identifying (scientific) topics relevant for IPBES, feeding in of comments on IPBES documents and representatively attending important IPBES meetings.

Since NeFo initially is a national science-policy interface, our website is primarily in German. However, our team is working internationally interacting intensively with partners on the EU and UN- level. So, we shall be happy to receive your requests.

For further information please visit www.biodiversity.de.

Program

Tuesday, March 4th: Integrating mechanisms into macroecology

08:00 am: Registration opens

09:00 am - 09:30 am: Welcome and introduction

09:30 am - 10:30 am: **Session I - Evolutionary processes (chair: C. Hof)**

Fritz, S.A. et al.: Diversity-environment relationships through time: 20 million years of mammalian diversity dynamics, climatic conditions and biome shifts in the Northern Hemisphere

Dalsgaard, B. et al.: Climate, range-size distribution and specialization in plant-hummingbird networks across the New World

Khaliq, I. et al.: Thermal tolerances of endotherms are phylogenetically conserved, but only in tropics

Wrap-up discussion Session I

10:30 am - 11:00 am: Coffee break

11:00 am - 12:45 pm: **Session II - Dispersal and colonization as divers of distribution patterns (chair: H. Kreft)**

Keith, S.A. & Connolly, S.R.: The role of macroecological processes in the generation and maintenance of Indo-Pacific coral biogeographic provinces

Irl, S.D.H. et al.: Global pattern of treeline elevation on islands

de Carvalho Ximenes, A. & Dahdouh-Guebas, F.: Global spatial dependence of the bioclimatic and environmental variables on the mangrove system

Kisel, Y. et al.: Untangling the drivers of island colonization in flowering plants

Tonkin, J.D. et al.: Dispersal constraints drive colonisation of restored river reaches by benthic invertebrates

Meyer, C. et al.: Setting priorities for overcoming knowledge gaps in species distributions

Wrap-up discussion Session II

12:45 pm - 02:00 pm: Lunch

Program

02:00 pm - 03:45 pm: **Session III - Methods (chairs: I. Kühn & M. Liess)**

Schleuning, M. & Kissling, D.: Bridging scales: ideas for a better integration of the macroecology and community ecology of species interactions

Zurell, D.: Predicting to novel environments: about extrapolating species-environment relationships and demography

Stein, A. et al.: Environmental heterogeneity: a heterogeneous topic and a universal driver of species richness

Beckmann, M., Václavík, T. et al.: glUV: A global UV-B radiation dataset for macroecological studies

Nobis, M.P. & Normand, S.: KISSMig - a simple R-tool to consider limited migration in modeling species distributions

Engler, J.O. et al.: Combining species distribution models with population genetic data: Good for landscape genetics but also good for macroecology?

Wrap-up discussion Session III

03:45 am - 04:15 am: Coffee break

04:15 pm - 05:30 pm: **Session IV - Human-driven processes (chairs: S. Fritz & M. Winter)**

Liess, M.: Macroecological prediction of low-dose pesticide effects based on ecotoxicological mechanisms

Knapp, S. & Klotz, S.: Changes in the phylogenetic composition of a Central European urban flora over three centuries

Bowler, D. et al.: A collaborative project to assess the impacts of climate change on population trends

Lischke, H.: Macroecological studies with spatio-temporal population dynamical models - the example of tree species migration in the Alps under climate change

Wrap-up discussion Session IV

06:30 pm: Conference Dinner at "Zum Mohr" (Burgstraße 72, 06114 Halle)

Program

Wednesday, March 5th: Integrating mechanisms into macroecology

09:00 am - 10:45 pm: **Session V - Neutral vs. trait-based processes (chair: E. Welk)**

Keyel, A.C. et al.: Integrating mechanisms into macroecology using a trait-based, spatially explicit meta-community model

May, F. et al.: Neutral theory and spatial patterns in tropical forests - moving beyond abundance distribution

Schrodt, F. et al.: Functional diversity - ecosystem property relationships across Europe

Pompe, S. et al.: Using ecological and life-history characteristics for projecting species response to climate change

Schweiger, A. et al.: Optimal-sized prey availability shapes global distribution patterns of the Golden Eagle *Aquila chrysaetos*

Sarmento Cabral, J. et al.: Process-based niche models for macroecology

Wrap-up discussion Session V

10:45 am - 11:30 am: Short announcement of the 7th biennial conference of the International Biogeography Society, Coffee break and **poster session with poster presentations by Dengler et al., Filz & Lötters, and Santos et al.**

11:30 am - 11:45 am: **Introduction of working groups on "Integrating mechanisms into macroecology"**

11:45 am - 12:45 pm: Working groups

12:45 pm - 02:00 pm: Lunch

02:00 pm - 03:30 pm: Working groups

03:30 am - 04:00 am: Coffee break

04:00 pm - 04:45 pm: Working groups - time for wrap-up

04:45 pm - 05:30 pm: Working group presentations

Program

Thursday, March 6th: Macroecology meets IPBES

A Nefo satellite workshop at the
8th annual meeting of the GfÖ Macroecology Specialist Group in Halle (Germany)
6 March 2014, 9:00-17:00 h

With the formation of the *Intergovernmental Platform for Biodiversity & Ecosystem Services* (IPBES), the United Nations have acknowledged at an institutional level the challenge to halt the global loss of biodiversity. Crucial for the success of IPBES is the exchange of knowledge between science and policy.

Supported by the Network-Forum for Biodiversity Research Germany (NeFo), our workshop aims to explore how ecological science can contribute to the process of developing IPBES as a successful science-policy platform. In particular, the potential contributions of macroecology with its strengths in global modelling and scenario development will be highlighted. The presentations and discussions will cover a broad range of topics, such as overviews on the IPBES process or on global initiatives of developing the science-policy interface, state-of-the-art approaches of modelling global biodiversity and assessing ecosystem services, and the potential challenges between theory and application, i.e. conservation needs and efforts.

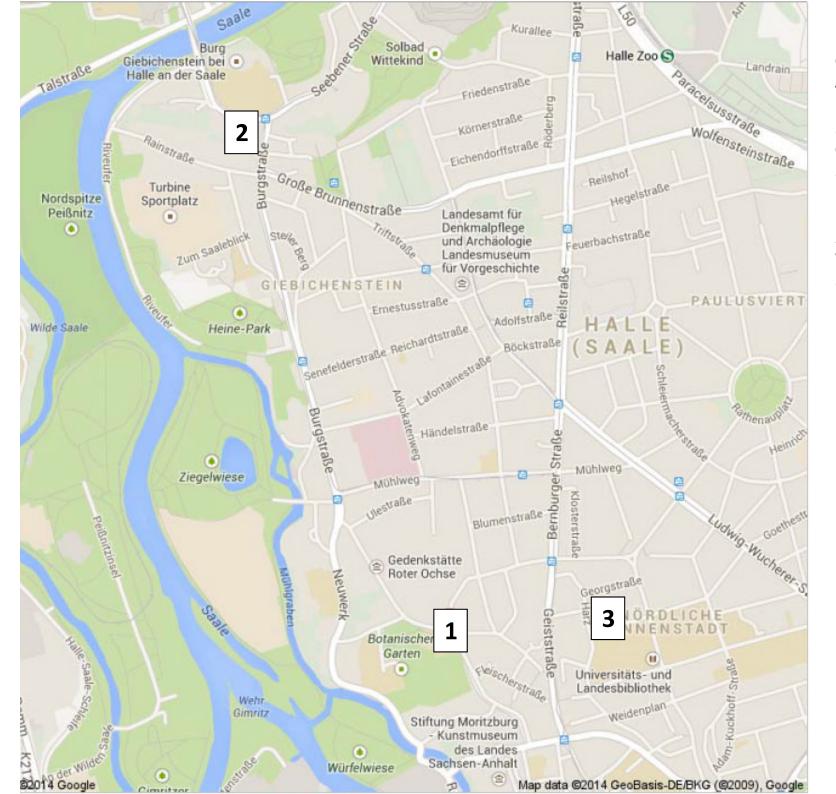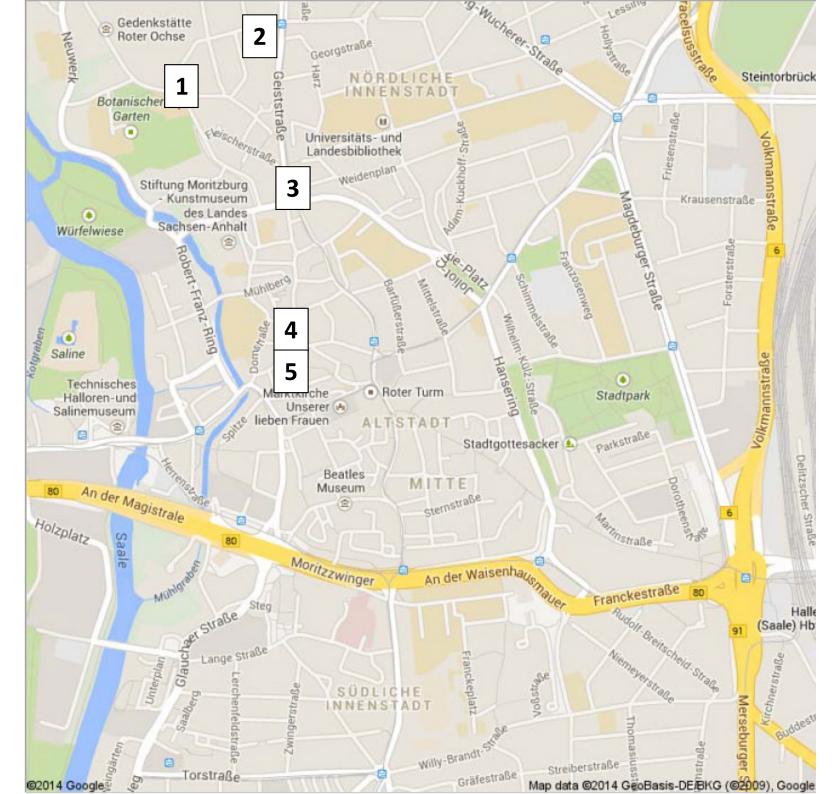|	
9:00	Introduction: Setting the stage (Katrin Böhning-Gaese, BiK-F, Frankfurt)
9:10	Introduction: The IPBES process (Lisa Marquard, Carsten Neßhöver, NeFo/ UFZ, Leipzig)
9:20	Biodiversity data availability and needs (Walter Jetz, Yale University)
9:30	Global biodiversity scenarios (Henrique Pereira, iDiv, Leipzig)
9:40	Discussion of presentation block 1
9:50	Global modelling I: Correlative biodiversity models (Christian Hof, BiK-F, Frankfurt)
10:00	Global modelling II: Ecosystem models (Thomas Hickler, BiK-F, Frankfurt)
10:10	Global modelling III: Global biosphere models (Mike Harfoot, UNEP-WCMC, Cambridge)
10:20	Discussion of presentation block 2
10:30	Coffee break
11:00	Ecosystem services (Felix Eigenbrod, University of Southampton)
11:10	Conservation (Neil Burgess, UNEP-WCMC, Cambridge)

11:20   Discussion of presentation block 3

Program

11:30   Plenum discussion

12:30   Lunch break

13:30   Working groups (seminar rooms)
14:15   Working groups (seminar rooms)

15:00   Coffee break

15:15   Plenum discussion with presentation of working group results

1: Institute of Geobotany:
Conference Venue
Am Kirchtor 1, 06108 Halle

2: „Zum Mohr":
Conference Dinner
2014/03/04
Burgstr. 72, 06114 Halle

3: Harz Mensa:
Workshop-Dinner
2014/03/05
Harz 42, 06108 Halle

1: Institute of Geobotany:
Conference Venue
Am Kirchtor 1, 06108 Halle

2: Berlin Döner:
Cheap Lunch / Fast
Food
Geiststraße 29, 06108
Halle

3: Don't worry be curry:
Cheap Lunch / Fast Food
Universitätsring 12,
06108 Halle

4: Kleine Ulrichstraße:
Several cafés and bars
serving food

5: Ökoase:
Restaurant serving
organic vegetarian food
Kleine Ulrichstraße 2,
06108 Halle

Contact details

If you would like to contact:

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During Conference-Time (04th - 05th March 8:00 am – 06:00 pm):

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Abstracts

Lischke	Macroecological studies with spatio-temporal population dynamical models – the example of tree species migration in the Alps under climate change
May et al.	Neutral theory and spatial patterns in tropical forests – moving beyond abundance distributions
Meyer et al.	Setting priorities for overcoming knowledge gaps in species distributions
Nobis & Normand	KISSMig – a simple R-tool to consider limited migration in modeling species distributions
Pompe et al.	Using ecological and life-history characteristics for projecting species responses to climate change
Santos et al.	Understanding the assembly of island parasitoid faunas through functional diversity
Sarmento Cabral et al.	Process-based niche models for macroecology
Schleuning & Kissling	Bridging scales: ideas for a better integration of the macroecology and community ecology of species interactions
Schrodt et al.	Functional diversity – ecosystem property relationships across Europe
Schweiger et al.	Optimal-sized prey availability shapes global distribution patterns of the Golden Eagle *Aquila chrysaetos*
Stein et al.	Environmental heterogeneity: a heterogeneous topic and a universal driver of species richness
Tonkin et al.	Dispersal constraints drive colonisation of restored river reaches by benthic invertebrates
Zurell	Predicting to novel environments: about extrapolating species-environment relationships and demography

glUV: A global UV-B radiation dataset for macroecological studies

Michael Beckmann, Tomáš Václavík*, Ameur M. Manceur, Lenka Šprtová, Henrik von Wehrden, Erik Welk, Anna F. Cord

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Macroecology has prospered in recent years due in part to the wide array of climatic data that has become available for research. However, important environmental variables are still missing, including spatial datasets on UV-B radiation, an increasingly recognized driver of ecological processes. To fill this gap, we developed a set of global UV-B surfaces (glUV) based on remotely sensed records from NASA's Ozone Monitoring Instrument. Following a similar approach used for the WorldClim and CliMond datasets, we processed daily measurements acquired over a period of eight years into six ecologically meaningful variables with a 15 arc-minute resolution. We correlated our datasets with selected variables of the existing bioclimatic surfaces to test for relations to known gradients and patterns. UV-B surfaces showed a distinct seasonal variance, while the intensity of UV-B radiation decreased towards higher latitudes and was modified by topographic and climatic heterogeneity. UV-B surfaces were correlated with global mean temperature and annual mean radiation data, but exhibited variable spatial associations across the globe. Our dataset provides new climatological information that can be readily used for macroecological analyses. As UV-B is a known driver of numerous biological patterns and processes, our dataset can help us better understand these dynamics in macroecology, biogeography and global change research. The glUV dataset is freely available for download at: http://www.ufz.de/gluv.

A collaborative project to assess the impacts of climate change on population trends

Diana Bowler[1]*, Peter Haase[2,] Ingrid Kröncke[3], Oliver Tackenberg[4], Hans-Günther Bauer[5], Rob Brooker[6], Michael Gerisch[7], Klaus Henle[7], Thomas Hickler[1], Christian Hof[1], Stefan Klotz[8], Ingolf Kühn[8], Silvia Matesanz[9], Hermann Neumann[3], Bob O'Hara[1], David Russell[10], Oliver Schweiger[8], Moritz Sonnewald[11], Stefan Stoll[2], Michael Türkay[11], Fernando Valladares[12], Kok van Herk[13], Karin Voigtländer[10], Eric Welk[14], Katrin Böhning-Gaese[1]

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Understanding variation in species response to climate change will help determine which communities and ecosystems are most at risk. In this project, we are forming a network of data owners with long-term population data sets collected on any taxonomic group in a region of Central Europe. In collaboration with data owners, we investigate the role of species traits (ecology, morphology, physiology, life history) in explaining variation in population trends among species. By comparing the relationship between population trends and traits of a broad range of species, we ask whether there are generalities in how local populations are affected by climate change. We focus on the importance of the thermal niche because it can be expected to mediate the direct impacts of changing temperatures due to climate change. We present results of our analyses of long-term terrestrial, freshwater and marine data sets.

Climate, range-size distribution and specialization in plant-hummingbird networks across the New World

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Quaternary spatio-temporal climate stability is thought to facilitate high degree of endemism and high biotic specialization. Although a link between endemism and biotic specialization is often expected, the idea lack support from empirical evidence. Using data for 57 plant-hummingbird mutualistic networks distributed across the New World and structural equation modeling, we here demonstrate a strong relationship between macroecological patterns of endemism measured as the proportion of range-restricted hummingbird species and community-level biotic specialization. Although degree of specialization and endemism were directly associated with measurements of contemporary and Quaternary climate stability, our structural equation modeling results indicate that endemism explains a considerable amount of unique variation in biotic specialization – more so than the other way around. The results are in accordance with the hypothesized interrelatedness of hotspots of range-restricted species and biotic specialization, and although this partly illustrates the link of these to contemporary and Quaternary climate, it also indicates the unique effect of a shared evolutionary history of coexistent species. This emphasizes the role of range-size distribution processes in shaping biotic specialization.

Global spatial dependence of the bioclimatic and environmental variables on the mangrove ecosystem

Arimatéa de Carvalho Ximenes[1,2]*, Farid Dahdouh-Guebas[1,2]

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Mangroves constitute a wetland forest ecosystem scattered worldwide throughout the tropical and subtropical regions located in coastal environments. This study analyses the spatial dependence of the bioclimatic and environmental of mangroves variables commonly used in species distribution modelling to describe the environment. This study was done using the Geographical Information System (GIS). We used Giri's mangroves map where we could locate the mangroves. We computed 43 environmental variables, including 19 bioclimatic, 22 environmental variables (e.g. salinity, pH, sea surface temperature and others) and geographical coordinates of latitude and longitude, which greatly influence mangroves species distribution. We applied the Self-Organizing Maps (SOM) method because of its properties of dimension reduction, non-linearity, and its capability to provide new insights via geovisualisation tools. We also analysed the datasets using descriptive statistics in the way to understand how environmental variables influence mangroves distribution. The contribution of this work lies in insights into global spatial dependence of environmental variables on the mangrove ecosystems, and in identification of variables for future research. Moreover, we believe this study will improve our knowledge of mangroves and will provide new tools for new paradigms.

Combining species distribution models with population genetic data: Good for Landscape Genetics but also good for Macroecology?

Jan O. Engler[a,b,*], Niko Balkenhol[b], Jan Christian Habel[c] & Dennis Rödder[a]

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[c] *Department of Ecology and Ecosystemmanagement, Technical University Munich, D-85350 Freising-Weihenstephan, Germany*
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Combining species distribution models (SDMs) with genetic data have revealed several insights in the phylogeographic history of many taxa. More recently, studies also started to incorporate SDMs for the analysis of contemporary gene-flow within a landscape genetic context. In this study, we exemplify this approach in combining SDMs with connectivity models using a comparative genetic set derived from three congeneric Skipper butterflies (Hesperidae, *Thymelicus*) with diverging ecological traits. The study reveals strongly diverging landscape responses to gene flow in the three butterflies. In addition to its ecological importance, the combination of SDMs and population genetic data also enables a functional evaluation of species-specific SDM performance. In this sense we could show that SDMs with the highest AUC goodness of fit metric does not necessarily result in the most relevant outcome in terms of gene flow and functional connectivity. We discuss this outcome in the light of the topic of this years meeting – the importance of integrating mechanisms into macroecology. Gene flow as one proximal response of successful exchange between populations should not be neglected when assessing potential impacts on species persistence and distribution against climate change. We call for more research on this topic to bridge the gap between spatial scales and consequently for a more cautious interpretation of macroecological mass-species assessments based solely on the same underlying predictor sets and distributional data.

The Invasion Potential of Pet Herps under Climate Change in Europe

Katharina J. Filz [1,2] & Stefan Lötters [2]

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Biological invasions can occur by multiple pathways and cause worldwide severe ecological and economic disruptions. Pet trade accounts for the majority of herpetological introductions. Today, most amphibian and reptile species intentionally released or unintentionally escaped are not capable of building invasive populations. The main reason might be a climatic mismatch between their original habitat climate and the climatic conditions at the receiving location. Risk assessment allows the identification of non-native species most likely to become invasive and cause damage. In a first step, we asked whether anthropogenic climate change, as predicted for the future, does increase the invasion potential of common pet herp species in Europe by employing species distribution modelling approaches. In a second step, we analyze ecological and life history data to understand factors favouring establishment with the aim to assess the risk of potential invasions of commonly traded pet herps. For most of the 26 amphibian and reptile species observed, species distribution models identified an increase of suitable habitats under climate change in Europe. Potential climatic suitability due to their subtropical origin and their capability to coexist with humans suggest a considerable invasion risk for many species today frequently introduced through pet trade to Europe.

Diversity-environment relationships through time: 20 million years of mammalian diversity dynamics, climatic conditions and biome shifts in the Northern Hemisphere

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The fossil record documents responses of species to past climate change that can provide a long-term perspective for understanding how environmental changes impact biodiversity. Present-day relationships between terrestrial mammalian diversity and environmental conditions are well-established, but the consistency of regional diversity-environment relationships through time has not been tested on large temporal scales. Here, we investigate temporal and spatial variation of fossil mammalian diversity and its relationship to climatic conditions and habitat heterogeneity through the Neogene in North America and Eurasia, and compare patterns to those found for living species. We combine comprehensive databases to compare the five orders Artiodactyla, Carnivora, Perissodactyla, Primates, and Proboscidea at regional and continental scales between 23 and 2 million years ago across the Northern hemisphere. Our results show significant relationships between mammalian fossil diversity and environmental conditions through time and across regions and continents: high total mammalian diversity was consistently related to high precipitation and low habitat heterogeneity, but not to temperature, presumably due to the generally warmer conditions during the early and middle Neogene. Temporal diversity patterns and correlations with environmental conditions differed between the five orders tested. We conclude that the long-term perspective offered by the fossil record can substantially increase our understanding of diversity-environment relationships.

Global pattern of treeline elevation on islands

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Treelines have been an important research focus in ecology and biogeography for decades. Island treelines are suggested to experience specific drivers unique to island ecosystems. We empirically test how the latitude-treeline elevation relationship of islands relate to mainland treeline elevation, and to what extent island treeline patterns are driven by island characteristics and/or latitude. We collected a global dataset (n=87) by applying a stratified design using GoogleEarth to identify island treeline elevations and gather island characteristics. Island treeline elevation followed a hump-shaped distribution with latitude. Treeline elevation decreased from the mainland through continental islands to oceanic islands. The highest island treelines were found in the tropics (vs. mainland maxima in the subtropics). Low species pool and oceanic climates are likely to have negative effects on island treeline elevation. Surprisingly, maximum island elevation was the best single predictor of island treelines, not latitude. Probably, the possibility of range shifts during climatic fluctuations, the summit syndrome and the increasing cloud layer altitude with island elevation are responsible for the maximum islands elevation-effect. Investigating islands in treeline research enables to disentangle the global effect of latitude on treeline elevation from the variation created in continental mountains by continentality or the mass elevation effect.

The role of macroecological processes in the generation and maintenance of Indo-Pacific coral biogeographic provinces

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Indo-Pacific corals are organized into eleven distinct faunal provinces based on large-scale abrupt transitions in the composition and richness of reefs through geographical space. Transitions between provinces, where multiple species reach geographic range limits, are strikingly concordant with plate tectonic boundaries, and to a lesser degree, with environmental conditions and habitat availability. However, correlational approaches are limited in their ability to resolve the underlying processes that generate and maintain this pattern. Therefore, to explicitly test the feasibility that processes hypothesized by Island Biogeographic theory drive the observed distribution of coral species throughout these provinces, we have developed two process-based stochastic simulation models. In the first model, extinction probability is a function of coral reef area, colonization probability is a function of the number of larvae exchanged in a hydrodynamic model, and speciation probability is homogenous throughout the region. We compare this model with an alternative, in which extinction probability is modified to depend, not only on reef area, but also on standing diversity. Preliminary results suggest that island biogeographic processes alone cannot offer a plausible explanation for the observed distributions. In contrast, the diversity-dependent model offers a much more plausible explanation for the underlying processes driving large-scale coral distribution.

Integrating mechanisms into macroecology using a trait-based, spatially explicit meta-community model

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Models can provide a description of patterns and processes. We are developing a meta-community model in order to mechanistically link species' traits and species' responses to environmental change. Our goal is to provide insights into the impacts of changes in land management and climate on biodiversity and ecosystem functioning within a landscape. We are evaluating the model for heuristic conceptual scenarios, for biologically plausible scenarios, and for the specific context of the Biodiversity Exploratories field sites in Germany. Conceptual scenarios are unlikely to match actual biological situations but are useful for testing the model and for understanding ecological concepts in the abstract. Biologically plausible scenarios provide insight into the degree to which the ecological concepts are likely to be observed. Finally, field data is used to evaluate the ability of the model to describe real situations and make informative predictions. Field data may be used to refine the model and may highlight deficiencies in field data and/or in the modeling approach.

Thermal tolerances of endotherms are phylogenetically conserved, but only in the tropics

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Assessments of species responses to climate change require information on species' physiological sensitivity and adaptability to changes in ambient climatic conditions. One of the ways to assess physiological adaptability to climate change is quantifying the phylogenetic signal in species' thermal traits which define their physiological sensitivity. Clades showing higher levels of phylogenetic signal might find it difficult to adapt under climate change. However, closely related species may show similar traits attributed either to common ancestry or to geographic/climatic proximity. To overcome this problem we use a statistical method that jointly estimates phylogenetic and geographic/climatic signals in thermal traits of endotherm species. For birds and mammals, so far such efforts have rarely been made. Here, we investigate the patterns of phylogenetic as well as geographical/climate signals in a large data set of experimentally measured thermal tolerances of birds and mammals. At the global level we found that geography/climate has a stronger influence on thermal traits than phylogeny. When comparing tropical with temperate species, we find stronger phylogenetic signals in all thermal traits in tropical species than in temperate species. These findings provide support for the tropical niche conservatism hypothesis which states that tropical species have a tendency to retain characteristics of their climatic niches over time. This may in turn suggest a lower adaptability to changing climatic conditions in tropical than in temperate species.

Untangling the drivers of island colonization in flowering plants

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Colonization is a fundamental process structuring island biodiversity but until now there has been no large-scale study investigating drivers of island colonization. Here we present first results of a global assessment of island colonization in flowering plants. We compare the colonization success of all 412 terrestrial flowering plant families on more than 400 islands worldwide, and compare the effects on colonization of dispersal- and establishment-related plant traits, distribution-based estimates of plant family environmental "niches", island characteristics, and the level of "niche matching" between islands and plant families. Against expectations, we find that most plant families have colonized at least one oceanic island. Additionally, preliminary results suggest that island colonization is strongly affected by plant families' number of dispersal modes, minimum diaspore size, and range size, by island area and isolation, and by whether islands and families match in "niche" and biogeographic region. These new insights into the filters controlling island colonization may help us to better understand dispersal and biodiversity patterns on islands as well as on mainlands.

Changes in the phylogenetic composition of a Central European urban flora over three centuries

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Urbanisation drives changes in biodiversity. Often concentrating in originally species rich regions, todays' urban areas harbour many species but at the same time threaten natural species assemblages. Spatial studies suggest that the phylogenetic diversity of vascular plants is lower in urban than in rural areas. However, it has not been clarified, yet, whether phylogenetic diversity is lost in the process of urbanisation and whether this is driven by the extinction of native species or the immigration of non-native species. We investigated the phylogenetic composition of a Central European flora exposed to urbanisation using floristic inventories covering 320 years. Based on native species, non-native species, and species that went extinct or that immigrated in the study period, we calculated three measures of phylogenetic diversity: phylogenetic distinctness, mean nearest taxon distance and originality. Native species became increasingly clustered over time, owing to a significant loss of phylogenetic information with the extinction of species. The immigration of neophytes did not buffer this loss. Rather, decreases in mean nearest taxon distance and originality indicate that urbanisation selects for closely related species. Accordingly, urbanisation decreases plant phylogenetic diversity by driving both the extinction of native species and the immigration of non-native species.

Macroecological prediction of low-dose pesticide effects based on ecotoxicological mechanisms

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Low-dose of pesticides may have dramatic effect on Individuals and communities. However, these ecological effects are generally confounded by the multitude of environmental factors and are only getting observable after a considerable time delay. Therefore, a clear link between cause and effect is often difficult to establish on large spatial scales.

This contribution presents an approach on how to establish a link between low-dose of pesticides and community composition. Traits relevant to identify vulnerable species are determined based on existing ecotoxicological knowledge and combined to identify vulnerable communities.
I show how this approach enables to monitor low-dose pesticide effects on all spatial scales. An application for national, continental and global scale is presented. It is discussed on how the approach can also be applied to link the ecological effect of other environmental parameters to community composition.

Macroecological studies with spatio-temporal population dynamical models – the example of tree species migration in the Alps under climate change

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Distribution and dynamics of individuals and species in space are determined by species' traits, population dynamical processes, biotic and spatial interactions, all influenced by environmental and anthropogenic drivers. Bottom-up model approaches and challenges to incorporate these elements will be shortly presented.

As an example for such a modelling approach, I tested the effect of tree species migration on the ability of tree species to follow climate change induced shifts of their potential ranges. I ran simulations until 2100 over Switzerland in 200m resolution with the spatio-temporal forest landscape model TreeMig. The model was adapted to represent roughly current species distributions. Starting from these, I simulated future forest development with different scenarios of a) transient climate change b) land-use change and c) migration (seed dispersal vs. ubiquitous seeds).

The results indicate combined effects of environmental and anthropogenic drivers, migration and species interactions. Biomass decreases, particularly in low elevations, mainly due to extreme drought events. At high elevations, it increases due to rising temperature and by the colonization of abandoned meadows. Species compositions change, drought adapted species become dominant in the lowlands, and most species shift their ranges upwards. Migration delays these upward shifts intermediately; migration delays of dominant species can favor competitors.

Neutral theory and spatial patterns in tropical forests – moving beyond abundance distributions

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The neutral theory of biodiversity provides a hotly debated model of species-rich communities. Despite their simplicity neutral models provided a remarkable fit to observed species abundance distributions and species-area relationships. However, it has not been testes yet, if neutral models are able to predict several spatial patterns, which are provided by fully mapped forest dynamics plots, at the same time. In this study, we address the question, if a neutral model is able to simultaneously predict the species abundance distribution and spatial patterns for large trees on Barro Colorado Island, Panama. For this purpose, we develop a new spatially-explicit model, which consistently includes dispersal limitation at several spatial scales.

We found that in contrast to previous neutral models our model was able to simultaneously reproduce observed species abundance distributions and species-area relationships. However; at the same time the neutral model did not correctly predict the decay of community similarity with distance

We conclude that dispersal limitation and neutral ecological drift can indeed explain important aggregated biodiversity pattern in tropical forests. Considering several spatial patterns simultaneously for model validation and selection offers a promising approach to shed light on the relative importance of different process in the dynamics of species rich communities.

Setting priorities for overcoming knowledge gaps in species distributions

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Gaps and geographical bias in the documentation of global species distributions hamper ecological research and conservation. Cyber-infrastructures that combine multiple data sources such as the *Global Biodiversity Information Facility* (GBIF) or *Map of Life* hold promise for closing these gaps. In view of rapid biodiversity loss and limited funding, we ask: What are priority areas and activities for effectively closing remaining data gaps? We combined 21,170 range maps for amphibians, birds, and mammals with c. 188 million GBIF records to quantify data density and inventory completeness and to test twelve competing hypotheses on their drivers at four spatial grains (resolutions). At the 110 km grain, only 4.2% of grid cells had >80% completeness. This level of completeness was approached over large areas only in North America, Europe and Australia and only at grains of 440 km and coarser, at which resolution that information has limited value for ecological research or conservation. Although completeness differed greatly among biomes and zoogeographical realms, the greatest differences were seen among countries. Tests of twelve hypotheses in a multi-model inference framework (D^2 = 60-78%) revealed that completeness was most strongly limited by proximity to data providers, cooperation of countries with GBIF, and national research funding. To most effectively close remaining data gaps, institution-based mobilization programs should therefore prioritize support for mobilization efforts that target institutions near the identified data gaps. Furthermore, participation of countries with programs like GBIF and alternative, non-institution-based ways of mobilizing species distribution knowledge are key.

KISSMig – a simple R-tool to consider limited migration in modeling species distributions

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Understanding the drivers of species distributions and their dynamics are principal objectives in macroecology and biogeography. Especially the legacy of time-lagged migration in species ranges is important for understanding species distributions. KISSMig is a simple, raster-based, stochastic migration model which generates accessibility maps from areas of origin on top of given suitability maps. KISSMig (a "Keep It Simple and Stupid Migration model") requires no a-priory knowledge on dispersal parameters, which – due to the runtime behavior – can be optimized within the modeling framework. KISSMig has important applications for species distribution models: (i) uncovering the influence of limited migration relative to other drivers, (ii) detection of areas of origin and their importance as sources of migration, (iii) accounting for limited migration in modeling species distributions. Here we introduce KISSMig and use the current distribution and potential glacial refugia of *Quercus cerris* to illustrate its application.

Using ecological and life-history characteristics for projecting species responses to climate change

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Assessing the impact of climate change on range dynamics is difficult in the absence of large-extent distribution data. We developed a novel two-step approach: We modelled the relationship between modelled range loss and gain of 195 plant species under an A1FI climate change scenario up to 2080 and ecological and life history traits using life-form, leaf persistence, ecological strategy, pollen vector, ecological strategy, Ellenberg indicator values, and characteristics derived from species ranges. The resulting coefficients were used to predict climatic sensitivity for 688 plant species for plant species without spatially explicit information. Models predicted a mean range loss of 33±22 % (mean±standard deviation, R^2=0.33) and a mean range gain of 7±8 % (R^2=0.31).

Measures related to species distribution like range size is a consistently significant predictor for range loss and gain estimates. Traits associated with range loss (e.g. life form, number of floristic zones) are not necessarily related to range gain (e.g. Ellenberg indicator of temperature), indicating two distinct ecological processes. Significant interactions between moisture indicator value with life form for range loss, between moisture and temperature indicator values for range gain show that the responses are complex and context dependent. Thus, our results highlight the importance of incorporate trait interaction in models for risk assessment under climate change.

Understanding the assembly of island parasitoid faunas through functional diversity

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Islands can help us understand the patterns and processes occurring in the assembly of communities. We assess the influence of climate, regional and local island characteristics on the global patterns of functional diversity in island parasitoids (Hymenoptera, Braconidae). We also evaluate whether island assemblages deviate from a random functional structure when compared with its species pool, while ascertaining potential mechanisms behind community assembly through species pool-based null models.

We found that overall, climate was the best predictor of island functional diversity, with regional factors being almost negligible. Although functional diversity of many island parasitoid assemblages was similar to that of their regional pool, more than a third of the islands presented functionally clustered assemblages. These islands have particular characteristics and tend to host proportionally more koinobiont species than their species pool. Contrary to previous findings, regional factors were not the main driver of neither functional diversity or the assembly of island faunas. Instead, our results suggest that filters acting during the colonization process may determine the assembly of many island parasitoid faunas, leading to assemblages dominated by species presenting particular ranges of trait values that differ from those of their pool.

Process-based niche models for macroecology

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We present a stochastic model that simulates demography and speciation of multiple competing species in a metabolic framework. We implemented stage-structured populations of species with different traits and habitat requirements that competed for space in hypothetical landscapes (mountains or islands). Surviving communities consisted of species spread heterogeneously within the parameter space, suggesting emerging assembly rules. This was spatially translated into the abundance shift of almost half of the species towards suboptimum conditions and/or incapability to fill their potential range. Moreover, changes in area and isolation were key factors influencing temporal patterns of richness and endemism, with more isolated landscapes having lower richness, but showing more lineages with species radiations and more species per radiation. Turning off competition and metabolic constraints generated unrealistic patterns: unconstrained radiations and survival of few "super plants", respectively. These results indicate a regulatory importance of competition and metabolic constraints for community and landscape diversity patterns. In summary, the explicit simulation of processes at low ecological levels (e.g. populations) of multiple species offers one roadmap to include ecological processes into macroecology and biogeography.

Bridging scales: ideas for a better integration of the macroecology and community ecology of species interactions

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We identify a lack of integration of macroecology and community ecology and seek to address this challenge via a bidirectional integration that allows up-scaling and down-scaling of ecological knowledge across scales. On the one hand, we propose that multi-trait analysis of ecological networks could inform macroecology by identifying functional linkages between species and by quantifying functional diversities of species assemblages across spatial scales. On the other hand, macroecological tools, such as species distribution models, could be used to infer potential future changes in species assemblages in ecological networks. The inclusion of species traits in this modeling framework would allow assessing changes in functional network structure and could be used to identify potential disruptions of functional linkages in ecological communities. A better integration of macroecology and community ecology along these lines might significantly advance our understanding of the drivers and the structural importance of multispecies interactions across spatial scales and could also help to develop more realistic forecasts of changes in biodiversity under climate and land use change.

Functional diversity – ecosystem property relationships across Europe

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Classical biogeography supports the notion that functional diversity (FD) – the range, value and distribution of the functional properties of a biota – is tightly linked to ecosystem functioning. However, limited availability of large-scale data, as well as unclear guidelines on the measures of FD, resulted in many unanswered questions, including the relative influence of different metrics of functional diversity, as well as the spatial patterning of functional diversity on a continental scale. Having access to an extensive database of plant functional traits and species distributions, we aim to answer some of these questions.

We present FD maps of 18 foliar and woody traits of trees across Europe, using the extensive TRY database of plant functional traits (www.try-db.org) and tree distribution maps for 168 tree species sourced from three different sources. In order to emphasize different aspects of FD, including accounting for possible non-linearity of trait correlations and intraspecific trail variability, we apply nine FD indices, correlating them to ecosystem properties using a moving window approach. We explore the effects of different traits and species on the overall variability of FD in European Eco-regions and discuss the spatial patterning of different aspects of FD – ecosystem functioning relationships.

Optimal-sized prey availability shapes global distribution patterns of the Golden Eagle *Aquila chrysaetos*

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The role of environmental settings in shaping species distribution is still one of the major topics in macroecology. The significant effects of abiotic environmental conditions like climate have been shown in numerous studies. However, effects of biotic environmental conditions like food availability are still poorly understood. This even holds true for prominent species like the Golden Eagle *Aquila chrysaetos*, although the role of optimal foraging on species performance has a strong theoretical background in ecology. Here we combined biogeographical information on range margins with biological information about foraging behavior and breeding success of Golden Eagles in a meta-analysis of 67 globally distributed studies. We observed a significant decrease of breeding success and portions of medium-sized, optimal prey species within diets of breeding Golden Eagles towards the species distribution boundaries. Diet breadth and portions of sub-optimal small and large-sized prey species increased, however, towards the distribution edge. Thus, availability of optimal-sized prey species is a crucial driver of foraging behaviour, breeding success and distribution of Golden Eagles on a global scale. However, underlying anthropogenic effects on optimal prey availability have to be studied in more detail to fully understand the link between abiotic and biotic environmental conditions and species distribution patterns.

Keywords: optimal foraging theory, prey biomass, top predators, trophic interactions, spatial distribution patterns.

Environmental heterogeneity: a heterogeneous topic and a universal driver of species richness

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Spatial environmental heterogeneity (EH) is regarded as one of the most important factors governing species richness gradients. It is associated with available niche space, provision of refuges and opportunities for isolation and divergent adaptation and is thus thought to promote species coexistence, persistence, and diversification. The EH–richness relationship has been studied for various taxa, spatial scales and ecological settings, and many different measures have been used to quantify EH. In a systematic literature review including 192 studies and 1148 datasets, we identify more than 160 different EH measures and more than 100 terms related to heterogeneity in land cover, vegetation, climate, soil, and topography. This variability in research and terminology has hampered comparisons among studies, and the extent and generality of positive EH–richness relationships are thus still debated. In a global meta-analysis, we show that the EH–richness relationship for terrestrial plants and animals is significantly positive across EH components, habitat types, and spatial scales, and that vegetation and topographic EH show particularly strong associations with species richness. Our meta-analysis further highlights the pervasive effects of spatial scale in EH–richness research: area constancy, spatial grain and spatial extent emerge as key factors affecting the strength of EH–richness relationships.

Dispersal constraints drive colonisation of restored river reaches by benthic invertebrates

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The species pool in the surrounding river network has recently been identified as a key factor determining colonisation of restored river reaches. Using a comprehensive dataset of 21 river restoration sites and 292 benthic macroinvertebrate sampling sites in the immediate surroundings, we firstly tested the influence of distance to nearest colonist source based on a comparison of river network and Euclidean distances. Secondly, we tested the importance of dispersal distance in relation to several other parameters, such as the number and intensity of barriers along the river network, surrounding species pool occupancy rate, physical characteristics of the restored sites, and habitat restoration techniques used in determining colonisation of commonly-occurring benthic invertebrates. Overall, taxa pool occupancy rate was the most important driver of colonisation likelihood, followed by distance to nearest source, whereas the effect of barriers was minor but significant. Taxa identity had an overriding influence on training boosted regression tree models, but cross validation proved this did not improve the predictive ability. We suggest it is critical to assess regional taxonomic pools and ensure distances between healthy populations are minimised to ensure successful outcomes of habitat restoration projects. These results clearly emphasise the importance of spatial planning for restoration projects.

Predicting to novel environments: about extrapolating species-environment relationships and demography

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Models are important tools in ecological and global change research that enable us to explicitly test hypotheses, to understand complex systems and to predict system response to environmental changes. Many models exist today ranging from simple correlative approaches to complex mechanistic approaches. In my talk, I will present some humble thoughts about extrapolation behaviour of models. Changing or incompletely known species-environment relationships and changing demographic rates may pose problems for making predictions, not only in purely correlative models. Mechanistic models based on first principles may actually provide the means to predict demographic rates bottom up but are often limited in scale and take long to develop. So, what is the best way to go?