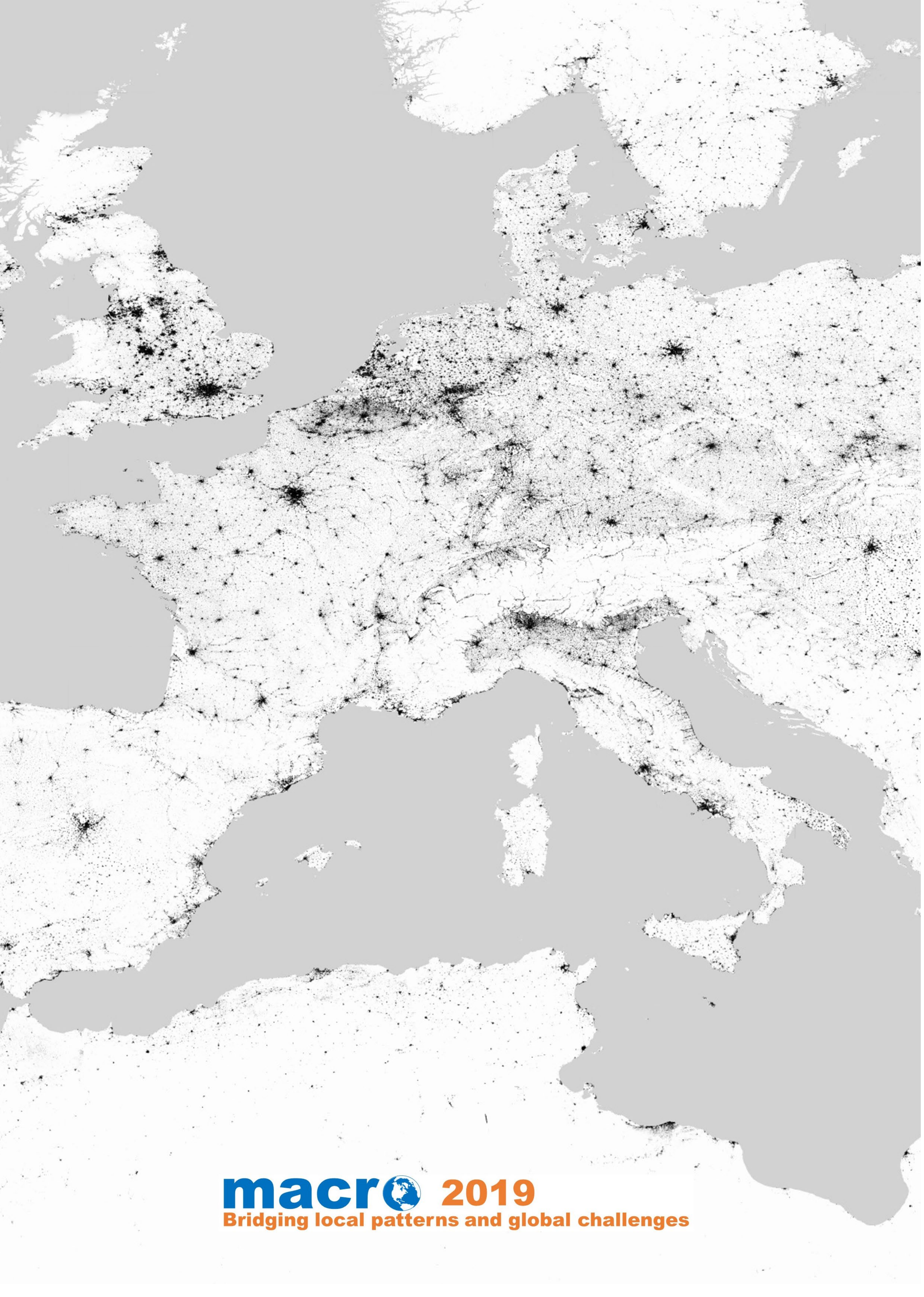


macro 2019

Bridging local patterns and global challenges

macro 2019

Bridging local patterns and global challenges

Dear participants,

Welcome to the macro2019 meeting in the city of Würzburg. The macro2019 will be the 13th annual meeting of the specialist group Macroecology of the Ecological Society of Germany, Austria, and Switzerland (GfÖ). The meeting aims to foster the dialogue between empiricists dealing with local patterns, bioinformaticians, data scientists, theoreticians and modellers, promoting scientific exchange and progress. We received highly interesting submissions for oral and poster presentations covering the diversity of macroecological research from paleontological time series, over studies on elevation gradients to syntheses of global data sets.

We are happy to have you here in Würzburg and hope that you enjoy the macro2019 meeting!

Juliano Sarmento Cabral, Alice Classen, Manuela Engert, Marcell Peters & Martin Wegmann

Information for presenting participants

Talks

Presentations are scheduled to be 15 minutes in total. This includes 12 minutes for presenting and 3 minutes for discussion. You will be signaled the remaining time twice: 3 minutes and 1 minute before the end of the time slot. Please try to keep the time so that we can exactly follow the schedule. Our lecture hall, the room A101 is equipped with a projector, notebook and a laser pointer. There will be a technical assistant helping you with setting up your presentation. **Please note:** you cannot use your own laptop for the presentation! We support the formats PDF and Power Point format. Presentation files can be uploaded at the registration desks which will be opened on Monday from 17:00 – 18:00 in the Würzburg residence before the icebreaker and from Tuesday to Thursday in the room A102. Presentations scheduled for the first session on Tuesday (time slot between 9:15 - 10:30) should hand in their presentations already on Monday. Presentations scheduled for the second session on Tuesday (time slot between 11:00 – 12:45) should upload their presentation until 10:30 latest. All other presenters should upload presentation at the latest by 13:00 if you are presenting in the afternoon (after 14:00), or at 16:00 if you present the following morning.

Posters

The poster session will take place on Tuesday from 18:00 – 20:00. During the poster sessions the authors are required to stand next to their poster, in order to present and discuss the study. The posters must be in A0 format (841 mm by 1189 mm) in portrait format. All posters need to be in place by 16:00 on Tuesday at the latest. More information on attaching the posters will be provided at the information desk in the room A102 (Biocenter).

Internet access

There are two ways to get wireless LAN (WLAN) access:

(1) **eduroam network**: Participants whose institutions are registered for eduroam can have direct access to the eduroam network. Please consult your webpages of your institutional IT for getting access.

(2) **RZUW network**: The university IT provides access to the university network RZUW by using the following data:

Login: macro2019
Password: macro2019
Pre-shared key: Julius-Echter

Venue

The macro2019 meeting starts on Monday with a public talk given in the **Toscana Saal** and an icebreaker in the wine cellar of the **Staatlicher Hofkeller**, both located in the **Würzburg Residence**, an UNESCO World Heritage site in the city center of Würzburg (see below for a map). The main program will take place from Tuesday to Thursday in the **Biocenter** of the University of Würzburg, located at the Hubland Campus in the south-eastern part of the city. The conference dinner will be on Wednesday evening in the **Bürgerspital** in the city center of Würzburg.

Here is a short overview of the meeting locations:

Monday, 16:00 – 17:00, Keynote public talk, **Toscana Saal, Würzburg Residence**

Monday, 17:00 – 20:00, Registration + Icebreaker, **Staatlicher Hofkeller, Würzburg Residence**

Tuesday, 9:00 – 20:00, scientific program, **Biocenter, Hubland Campus**

Wednesday, 08:30 – 18:00, scientific program, **Biocenter, Hubland Campus**

Wednesday, 19:00 – 23:00, conference dinner, **Bürgerspital (in the city center)**

Thursday, 08:30 – 13:00, scientific program, **Biocenter, Hubland Campus**

On Tuesday and Wednesday free lunch will be served at the **Mensateria, Hubland Campus**.

The icebreaker, conference dinner and the lunch on Tuesday and Wednesday (in the Mensateria) are included in the conference fees **when you show your macro2019 name tag to the staff**. Wearing the name tag is, however, obligatory to get the meals for free.

The Biocenter of the University of Würzburg

The Biocenter, where the macro2019 will take place, is part of the Julius-Maximilians-Universität (JMU) Würzburg. The history of the University of Würzburg reaches back as far as 1402. The university was the sixth institution of higher education to be founded in the German-speaking regions of Europe. Many eminent scholars and scientists, fourteen Nobel Laureates among them, have conducted research and taught in Würzburg including, e.g. Wilhelm Conrad Röntgen, who discovered X-rays in Würzburg in 1895, and Klaus von Klitzing, who discovered the Quantum-Hall Effect. Today, Würzburg's university comprises ten faculties with approximately 425 professors and 29,000 students. The Biocenter of the University of Würzburg was founded in 1993 to bring scientists from various faculties but with overlapping biological research topics and methods together under one roof. It is a joint facility of the Faculties of Biology, Chemistry and Pharmacy, and the Faculty of Medicine and currently holds fifteen departments ('chairs') and four core units providing centralized services.

How to get to Würzburg / Würzburg Residence

By plane

From **Frankfurt am Main** airport: Take the ICE train from Frankfurt Flughafen Fernbahnhof to Würzburg Hauptbahnhof (approx. 1.5 hours).

From **Nuremberg** airport: Take subway U2 to Nürnberg Hauptbahnhof. Take the ICE train from Nürnberg Hauptbahnhof to Würzburg Hauptbahnhof (approx. 1 hour).

From Würzburg Hauptbahnhof (central station) to the Würzburg residence you can easily walk in about 15 min (~1.1 km). Alternatively, take the bus 14, direction Gerbrunn and get off at "Mainfranken Theater". From there it is a 3 min walk to the Würzburg residence.

By train

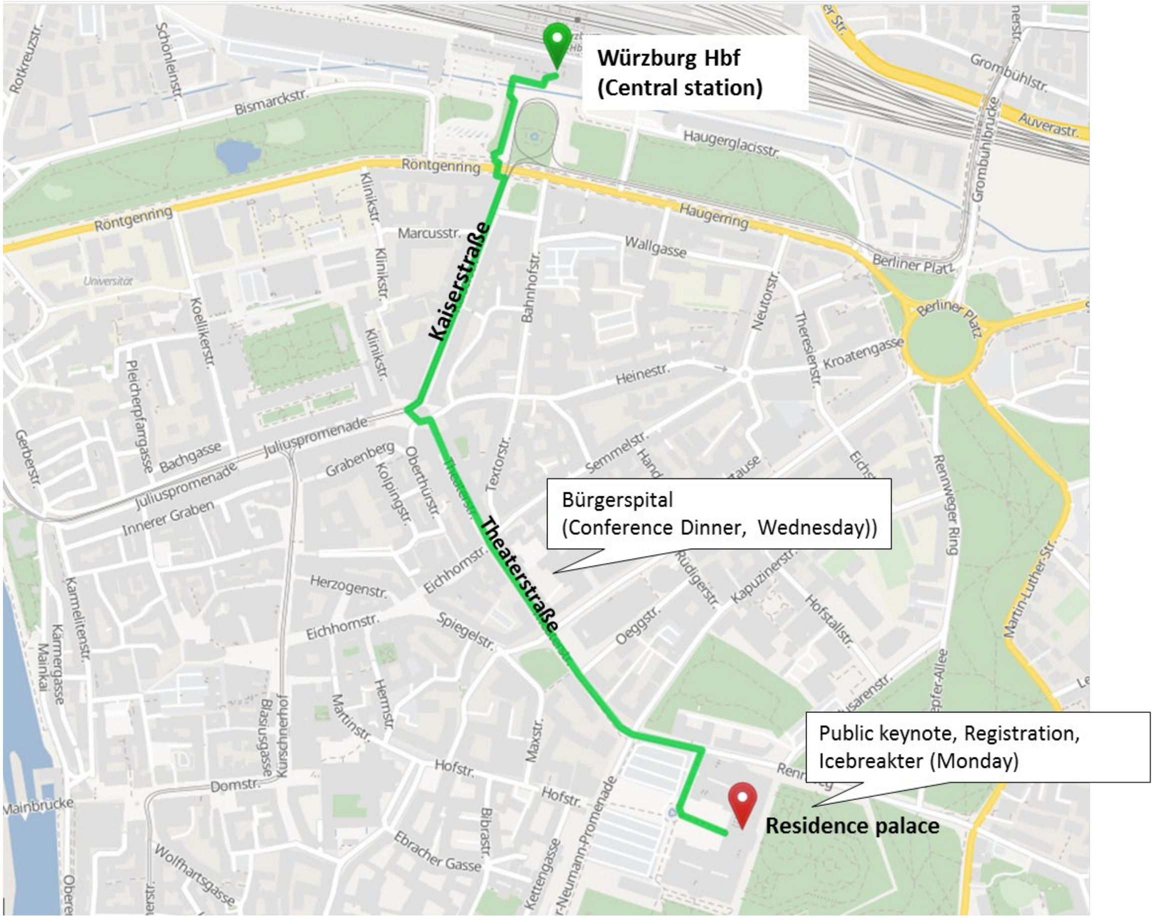
There are several good ICE connections to Würzburg Hauptbahnhof (central station). From Würzburg Hauptbahnhof to the Würzburg residence you can easily walk in about 15 min (~1.1 km). Alternatively, take the bus 14, direction Gerbrunn and get off at "Mainfranken Theater". From there it is a 3 min walk to the Würzburg residence.

By car

Follow your personal route to the Würzburg residence (Residenzplatz 2, 97070 Würzburg).

https://www.google.com/maps/place/Residenz+W%C3%BCrzburg/@49.7927423,9.9391185,15z/data=!4m5!3m4!1s0x0:0xd0ec04fef5adb93f!8m2!3d49.7927423!4d9.9391185

There is a big parking spot in front of the Würzburg residence. Prices are moderate. It is (almost) useless to look for free parking in the vicinity.



Map of the city center of Würzburg showing the train station (Würzburg HBF), the Residence palace, the Bürgerspital and the route you may take to get from the Würzburg HBF to the Würzburg residence (ca. 15 min).

The Residence palace (Würzburg Residence). The macro2019 meeting will start with a public keynote in the Toskanasaal on Monday (11th March 2019) at 16:00 (right entrance). Afterwards there will be the registration (from 17:00) and icebreaker (from 18:00) in the wine cellar of the Staatlicher Hofkeller (left entrance).

How to get to the Biocenter, Hubland Campus

By bus

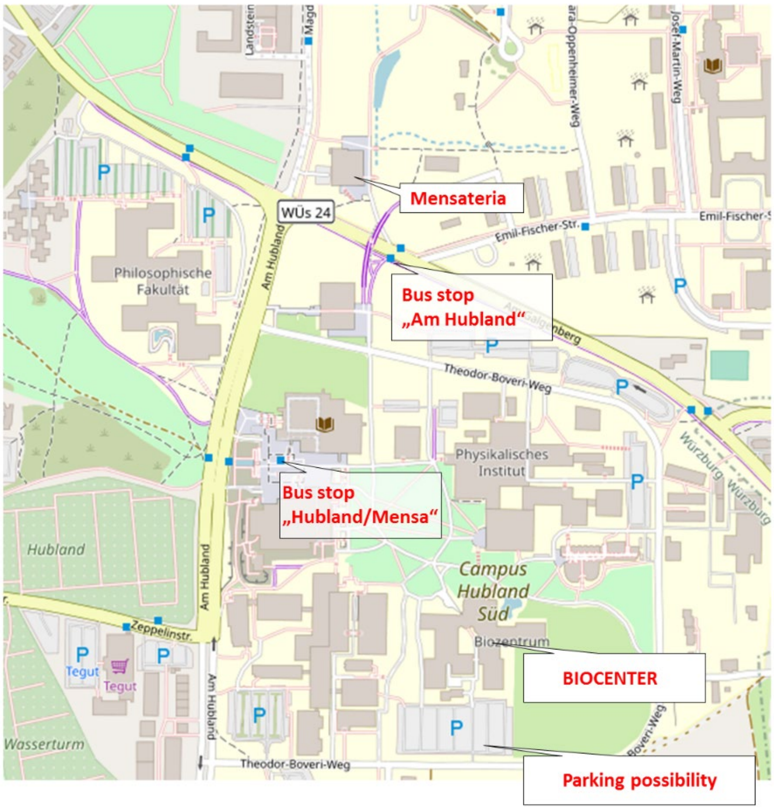
If your hotel is in the city, we recommend to take the bus to the Biocenter, because the Hubland Campus is quite far from the city center (~4 km). There are several buses regularly going up to the Hubland Campus (14, 114, 214, 10). Get off at the stations “Am Hubland” (Line 14) or “Hubland Mensa” (114, 214, 10) and follow the signs to the Macro2019 conference in the Biocenter.

Note: Tickets can be bought on the bus. You need cash money. If you plan to go by bus regularly during the conference, ask for a “6er-Karte” – i.e. you buy 6 tickets at once, which you can use step by step or share with other persons. The tickets must be stamped inside the bus (yellow boxes) every time a journey is made. Price: 11.20€ (in comparison: a single ticket is 2.80€).

By car

Follow your personal route to the Biocenter (Universität Würzburg Biozentrum, Am Hubland, 97074 Würzburg):
https://www.google.com/maps/place/Universit%C3%A4t+W%C3%BCrzburg+Biozentrum/@49.7802647,9.9701358,18z/data=!3m1!4b1!4m5!3m4!1s0x0:0xd95bd7d9cfce1423!8m2!3d49.780263!4d9.97123

There are enough free parking possibilities around the Biocenter (e.g. a big parking slot behind the building). Follow the signs to the Macro2019 conference.



Map of the Hubland Campus (University of Würzburg). The conference takes place in the **Biocenter**. On Tuesday and Wednesday lunch will be served in the **Mensateria**.

How to get to the Bürgerspital (conference dinner)

The conference dinner takes place in the Bürgerspital (Theaterstraße 19, 97070 Würzburg). Coming from the conference, hopp into the **bus** 114 or 214 at “Hubland Mensa” and get off at the station “Mainfranken Theater”. The restaurant is located about 100 m further down the Theaterstraße on the right side.

If you go by **car**, you may park your car in front of the Residence Palace and walk to the restaurant.

Entrance of the Bürgerspital.

Meeting program

Macroecology 2019 Würzburg: Bridging local patterns and global challenges - Detailed Program

Time	Day 1: 11th March	Day 2: 12th March (in Biocenter, University of Würzburg)	Day 3: 13th March (in Biocenter, University of Würzburg)	Day 4: 14th March (in Biocenter, University of Würzburg)
8:30 - 9:00		REGISTRATION	**Maria Dornelas: Detecting and dissecting biodiversity change**	**Alexandre Antonelli: Two hundred years and one billion species sightings in search of Humboldt's vision: Are we there yet?**
9:00 - 9:15		WELCOME		
9:15 - 9:30		**Susanne Fritz**: Seasonal relationships of avian diversity with climate in Australia		
9:30 - 9:45		**Christine S. Sheppard**: Biotic resistance or introduction bias? Immigrant plant performance decreases with residence times over millennia	**Matthias Schleuning**: Coupled species' responses to global change in ecological networks	**Shan Huang**: The complex history behind biodiversity in mountain ranges: New insights from a synthesis of the two old fields of geology and biogeography
9:45 - 10:00		**Niklas Hohmann**: The Necessity of Symmetric Waxing and Waning	**Matthias F. Biber**: Future changes in drivers of avian diversity in Pakistan	**Friederike Gebert**: Climate-mediated changes in the functional composition of dung beetle communities determine rates of dung decomposition along extensive environmental gradients on Mt. Kilimanjaro, Tanzania
10:00 - 10:15		**Ludmilla Figueiredo**: Mechanisms of extincition debt across spatio-temporal scales and ecological levels	**Maria H. Hällfors**: Increased intraspecific temporal aggregation in egg hatching of Finnish birds	**Jimmy Moses**: Nutrient utilization by tropical ant communities along three extensive elevational gradients: a cross-continental comparison
10:15 - 10:30		**Anne Mimet**: Community changes in space and time: Bringing environmental predictability and cmmunitiy specialization in the spotlight	**Damaris Zurell**: Long-distance migratory birds face multiple risks from global change	**Antonia V. Mayr**: Climate and food resources shape species richness and trophic interactions of cavity-nesting Hymenoptera on Mt. Kilimanjaro
10:30 - 11:00		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
11:00 - 11:15		**Holger Kreft**: Functional island biogeography - concepts and prospects	**Christian Hof**: Towards a better understanding of global change impacts on biodiversity by integrating data and approaches across disciplines and scales	**Amanda Taylor**: Global diversity and biogeography of vascular epiphytes
11:15 - 11:30		**Mialy Razanajatovo**: Two global tests of Baker's Law: Plant selfing ability promotes island colonization and naturalization	**Alke Voskamp**: Impacts of climate change on the community compositions and diversity of the world's terrestrial birds under different warming scenarios	**Vladimír Remeš**: Species diversity and vegetation structure drive functional organization of avian communities along a continental-scale latitudinal gradient
11:30 - 11:45		**Elisa Barreto Pereira**: Determinants of global richness and endemism of mammals on islands	**Noëlie Maurel**: Linking local and continental success of alien woody ornamental plants	**David Eichenberg**: Trends in German Plant Distribution – a synthesis study across six decades
11:45 - 12:00		**Dylan Craven**: Interacting abiotic and biotic filters shape woody invasions across spatial scales in the Hawaiian archipelago	**Babak Naimi**: Spatiotemporal changes in the intensity of global land cover fragmentation	**Francesco Maria Sabatini**: Using sPlot - the global vegetation plot database - to explore global patterns of plot-specific plant species pools
12:00 - 12:15		**Yangqing Luo**: The role of pollinator diversity in structuring oceanic island plant assemblages	**Eliane S. Meier and Gisela Lüscher**: Evaluation of agri-envrionment schemes on biodiversity: Analysing local scale data in order to contribute to national strategies	**Jens Mutke:** Trends in the conservation status of the global centres of plant diversity during the last 25 years
12:15 - 12:30		**Iwona Dembicz**: Steppe islands: where island biogeography meets the reality of a severely fragmented habitat	**Laura Antão**: Temperature driven biodiversity redistribution on Earth	**Awards and closing remarks**
12:30 - 12:45		**Dagmar M. Hanz**: Functional diversity of the flora of the Canary Islands	**Aafke M. Schipper**: Implications of three diverging shared socio-economic pathways for terrestrial biodiversity worldwide	Posters (Tuesday evening session):
12:45 - 14:00		LUNCH	LUNCH	Lirong Cai: Global diversity patterns and drivers of plants
14:00 - 14:15		**W. Daniel Kissling**: Using airborne laser scanning to quantify fine-scale habitat structures at macroscales	**Manuel J Steinbauer**: The paleontological legacy in climate-related extinction risk	Alice Claßen: The ADAPT project - Adaptation of alpine pollinators in times of global change
14:15 - 14:30		**Mikael Pontarp**: Linking assembly processes and community patterns - Dynamic models and Approximate Bayesian Computation (ABC)	**John T. Clarke**: Testing for differences in evolutionary dynamics between marine and freshwater environments	Eva Katharina Engelhardt: A framework for analysing cross-taxon biodiversity trends in central Europe
14:30 - 14:45		**Ludwig Leidinger**: Temporal environmental variation interacts with genetic and ecological traits to shape metacommunity composition	**Gregor Mathes**: A novel approach to define evolutionary units in Phanerozoic reefs	Lenka Harmáčková: Foraging specialization and niche overlap in Australian songbirds
14:45 - 15:00		**Carlos Eduardo Arlé**: bRacatus: an R platform to estimate the accuracy and biogeographical status of point-occurrence records	**G. William M. Harrison**: Diversity Dynamics of Bivalves and Brachiopods across the Marine Mesozoic Revolution	Jeroen van Dijk: The extinction-abundance relationship through deep time
15:00 - 15:15		**Laura J. Graham**: Bridging landscape ecology and macroecology: a data aggregation method for environmental heterogeneity	**Sebastian Teichert**: Facilitation of coral reef growth by coralline red algae – patterns during the last 150 million years	Glenda Mendieta-Leiva: EpIG, the epiphyte inventory group database
15:15 - 15:30		**Zsófia Koma**: LiDAR-based species distribution modelling reveals fine-scale habitat associations of wetland birds	**Pascal Abel**: Macroecological patterns in the extinct cephalopod subclass Ammonoidea	Onyedikachi Kingsley Okoye: Domination and invasion of Spartina Alterniflora cordgrass in Yancheng Rare Birds Natural Reserve as sensed by Satellite Remote Sensing from 2003-2018
15:30 - 15:45		**Martha Paola Barajas-Barbosa**: Environmental heterogeneity as a driver of plant diversity on oceanic islands	**Indrė Žliobaitė**: Recent developments in dental ecometric modelling	Ines Pyko: Will arctic reefs disappear with ongoing global change?
15:45 - 16:00		COFFEE BREAK	COFFEE BREAK	Ingmar R. Staude: Range size predicts the risk of local extinction from habitat loss
16:00 - 16:15	**Hannes Taubenböck and Kamran Safi: Space-borne technologies to monitor the transformation of the world and its capabilities for macroecology (Public Keynote in Toscanasaal, the Residence)**			Nina Stilkerich: Trophic network comparison of the Paratethys, Mediterranean Sea and Barents Sea based on ichthyofauna
16:15 - 16:30		**Alexander Zizka**: Improving the reliability of geographic records from biological collections for macroecological research and conservation assessment	MINICOURSES AND DISCUSSIONS	Anna Voulgari-Kokota: Megachilid bees in pollination networks
16:30 - 16:45		**Emilia Jarochowska**: Cryptic diversity along the onshore-offshore gradient: marginal marine environments were a cradle of early vertebrates		Anne Lewerentz: Distribution of functional types of freshwater macrophytes across Bavarian lakes
16:45 - 17:00		**Søren Faurby**: Brain expansion in early hominins explains carnivore extinctions in East Africa		Daniel Vedder: Modelling species invasions on oceanic islands
17:00 - 17:15	REGISTRATION (in Hofkeller, the Residence)	**Giacomo Puglielli**: Contrasting patterns of biomass allocation of woody species to abiotic stress tolerance		Ana Maria Bastidas-Urrutia: Impact of oil palm cultivation on deforestation rate over the last three decades in the southwest of Colombia
17:15 - 17:30		**Thore Engel**: Community weighted means of resource economics traits predict vegetation index in global compilation of grassland plots		Faith Jones: Increasing numbers of rare species in local assemblages are related to more new species entering assemblages
17:30 - 17:45		**Jürgen Dengler**: General patterns of species-area relationships emerging from nearly 5,000 grassland plots		Martina Scacco: Static landscape, uplift availability and energetics of soaring birds across Europe
17:45 - 18:00		**Luis Fernando Marin da Fonte**: Amphibian diversity in the Amazonian floating meadows		Sandra Kehrberger: Emergence of two solitary spring bees advances less strongly with warming temperatures than flowering of an early spring plant
18:00 - 19:00	ICEBREAKER (in Hofkeller, the Residence)	POSTER SESSION		Gergana Daskalova: Population change across Europe's land abandonment hotspots
19:00 - 20:00			CONFERENCE DINNER (until 23:00 - in Bürgerspital)	Carolina Bello: Defaunation affects carbon stock in tropical forests

Legend
- Coffee break
- Lunch
- Registration
- Keynote
- Icebreaker
- Conference Dinner
- Oral presentations
- Poster presentations
- Minicourses, discussions

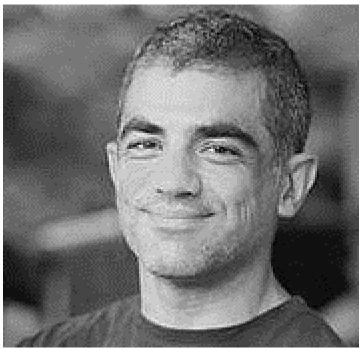
Keynote Speakers

Monday, 11th March 2019 at 16:00-17:00, Toscana Saal, Residence, Public Talk: Space-borne technologies to monitor the transformation of the world and its capabilities for macroecology

Hannes Taubenböck (DLR, Earth Observation Center)

Dr. Hannes Taubenböck leads the team “Modeling and geostatistical analysis” at the German Aerospace Center (DLR). With his team he focuses on the development of methods and applications in the field of urban remote sensing. The works rank from classification approaches to studies on validation to geographical applications. Recently multidisciplinary research became a focus aiming to systematically apply earth observation data for new notions in urban geography.

Kamran Safi (Max Planck Institute for Ornithology)



Dr. Safi's interests lie in understanding the causes and consequences of biological patterns at various scales and from different perspectives, from movement ecology to macro-ecology and macro-evolution. Methodologically, Kamran Safi is deeply interested in combining and fusing data from the wild, using a wide range of sensors deployed on animals, with remote sensing and other sources of information at large spatial and temporal scales. Scaling up from individuals, to collectives, populations, species and species communities, his macro-ecological ambitions are to understand the scale effects associated with extrapolations from individuals to on higher taxonomic levels.

Wednesday, 13th March 2019 at 8:30-9:30, A101, Biocenter, Hubland Campus, University of Würzburg

Maria Dornelas (University of St. Andrews): Detecting and dissecting biodiversity change

Prof. Dr. Dornelas' research focuses on quantifying biodiversity and understanding the processes that shape it. She often works on tropical systems and specifically coral reefs. She combines ecological theory, synthesis of existing data, and fieldwork (preferably in exotic places!) in her research, and most of the research questions she is interested in fall under the disciplines of community ecology, macroecology and biogeography. She tends to work on intermediate spatio-temporal scales (that is communities and networks of communities over time-scales of years to tens of years).

Thursday, 14th March 2019 at 8:30-9:30, A101, Biocenter, Hubland Campus, University of Würzburg

Alexandre Antonelli (Gothenburg Global Biodiversity Centre): Two hundred years and one billion species sightings in search of Humboldt's vision: Are we there yet?

Prof. Dr. Antonelli's lab studies the evolution of biodiversity past, present and future. His studies have focused on elucidating the origins and evolution of the rich biodiversity of tropical regions, with a focus on the Andean and Amazonian regions of South America. His team combines genetic, fossil and distribution data from field surveys and remote sensing for understanding biodiversity patterns and the dynamics of the formation, extinction and migration of species. He is leading the development of approaches for the rapid quantification of biodiversity, by means of high-throughput DNA sequencing and citizen-science observations of species using mobile phones.

Oral presentations

Tuesday, 12th March 2019: Session 1 (9:15-10:30)

Seasonal relationships of avian diversity with climate in Australia

Susanne Fritz[1,2], Juliane Zenner[2], Thomas Müller[1,2] & Katrin Böhning-Gaese[1,2]

[1]Senckenberg Biodiversity & Climate Research Centre (BiK-F), Senckenberg Gesellschaft für Naturforschung, Frankfurt, Germany; [2]Institute of Ecology, Evolution and Diversity, Goethe-University Frankfurt, Germany
eMail: sfritz@senckenberg.de

Aim: Most previous studies of large-scale spatial patterns in avian diversity have concentrated on breeding ranges only, but it is largely unclear how seasonal movements within a year affect the relationship between diversity and climate. Here, we aim to investigate the stability of diversity-climate relationships across seasons given avian movement behaviours such as seasonal migration, nomadism, and smaller-scale movements.

Location: Australia.

Methods: We classified >9 million time-stamped point occurrences for 658 species that were recorded in 'The New Atlas of Australian Birds' between 1998 and 2012 into equal-area grid cells of 100x100km and four seasons. We extracted seasonal climatic data for the same timeframe, and then compared the seasonal relationships of species richness or phylogenetic diversity with climate. Generalized linear models that controlled for spatial autocorrelation were fitted separately for all species and different subsets, i.e. resident, migratory, and nomadic species, to investigate the influence of movement behaviour on diversity-climate relationships.

Results: We expected no seasonal change in spatial diversity patterns for resident birds, so the diversity-climate relationship should change between seasons; expectations for migratory and nomadic species would be the opposite if they tracked their climatic niches through the seasons. In contrast to these expectations, we found that there were seasonal differences in spatial patterns of both species richness and phylogenetic diversity, but also in the relationships of each diversity measure with climate. Differences in spatial patterns and in diversity-climate relationships were larger between the resident, migratory, and nomadic groups than differences within a group between different seasons.

Main conclusions: Our results suggest that there is no single diversity-climate relationship across the year, but that diversity can be driven by different environmental factors in different seasons. To understand the environmental drivers of avian diversity, seasonal climatic effects have to be teased apart for different types of movement behaviour.

Biotic resistance or introduction bias? Immigrant plant performance decreases with residence times over millennia

Christine S. Sheppard[1] & Frank M. Schurr[1]

[1]*Institute of Landscape and Plant Ecology, University of Hohenheim, 70593 Stuttgart, Germany*
eMail: christine.sheppard@uni-hohenheim.de

Aim: Invasions are dynamic processes. Invasive spread causes the geographical range size of alien species to increase with residence time. However, with time native competitors and antagonists can adapt to invaders. This build-up of biotic resistance may eventually limit the invader's performance and reduce its range size. Using a species-for-time approach, we test (1) whether native communities more strongly reduce the fitness of immigrants with longer residence times, and (2) whether the range size of immigrant species shows a unimodal response to residence time.

Location: Germany.

Methods: For 352 plant species of the family Asteraceae with a wide range of minimum residence times in Germany (6-18,000 years), we combined a common-garden experiment with historical and macroecological analyses. In a multi-species experiment, we quantified the effect of native communities on fitness components of 30 annual Asteraceae. For these and other species, we then analysed how current range size depends on minimum residence time and other covariates.

Results: Native communities reduced survival, reproductive output and fitness of Asteraceae. This fitness reduction was stronger for immigrant species with long residence times. We found a unimodal relationship between range size and residence time of Asteraceae in Germany, when including natives that immigrated after the last glaciation.

Main conclusions: Biotic resistance may limit the performance and geographical ranges of immigrant species over long timescales. The initial advantages invaders have over natives thus may not persist over millennia, supporting the concept of an alien-native species continuum defined by gradual changes in eco-evolutionary processes. While our analysis controlled for major ecological, evolutionary and biogeographical factors, it is conceivable that the detected patterns are influenced by additional differences between natives and aliens. Experimental macroecology has great potential to disentangle these processes and predict long-term invasion dynamics.

The necessity of symmetric waxing and waning

Niklas Hohmann[1], Emilia Jarochowska[1]

[1]Institut für Paläoumwelt, Geozentrum Nordbayer, FAU Erlangen-Nürnberg, German
eMail: Niklas.Hohmann@fau.de

Aim: Research has shown that on average, measures of eco-evolutionary success of taxa such as occupancy and diversity show a distinct pattern. This pattern is called "symmetric waxing and waning" and consists of an increase from the origination of the taxon to the middle of the taxon's life span, and a constant decrease from the middle of the taxon's life span to its extinction. We examine whether this can be explained by the procedures used for preprocessing data.

Location: Not Applicable.

Methods: Using results from probability theory, the effects of (1) averaging and (2) the incorporation of knowledge about a priori known origination and extinction times (conditioning) are analysed.

Results: Averaging and conditioning on extinction and origination times necessarily increase symmetry and the difficulty to statistically distinguish processes by means of the trajectories they generate. Symmetric waxing and waning of averaged trajectories of taxa is consistent with many potential scenarios, and does not allow to draw any conclusions about the parameters of the underlying process.

Main conclusions: Data processing introduces mathematically necessary limits on what can and what can not be inferred from data. Symmetric waxing and waning is a pattern generated by such data processing procedures.

Mechanisms of extinction debt across spatio-temporal scales and ecological levels

Ludmilla Figueiredo[1,2], Jochen Krauss[1], Ingolf Steffan-Dewenter[1] & Juliano Sarmento Cabral[2]

[1]Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Am Hubland, 97074, Würzburg, Germany; [2]Ecosystem Modeling, Center for Computational and Theoretical Biology (CCTB), University of Würzburg, Emil-Fischer-Strasse 32, 97074 Würzburg, Germany
eMail: ludmilla.figueiredo@uni-wuerzburg.de

Aim: Extinction debt encompasses the delayed but deterministic extinctions after habitat perturbation. However, environmental perturbations occur across various spatial and temporal scales (e.g. local habitat loss and global warming). Moreover, the relative importance of eco-evolutionary processes varies across scales and levels of ecological organization. Individuals, populations, metapopulations and species should then respond differently to environmental perturbations, delaying extinctions. Therefore, our aim is to identify and summarize general mechanisms putting communities in debt.

Location: Global

Methods: We reviewed recent empirical, theoretical and methodological studies on extinction debts and searched for the proposed mechanistic explanations.

Results: Empirical studies detected debts across ecosystems and taxonomic groups, with estimations ranging from >33% up to 90% of current species richness to be lost in 7-1000 years. Documented causes of delayed extinctions are i) longevity-related traits and ii) slow metapopulation dynamics. Other potential factors that might extend survival time such as microevolutionary dynamics, or delayed extinctions of interaction partners, have been rarely analyzed. Theoretical studies showed that neutral and niche dynamics are both relevant to extinction dynamics. In methodological studies, we found evidence that mechanisms are considerably important for detecting extinction debts.

Main conclusions: Biotic-, abiotic-, mobility- and evolution-related mechanisms and factors are behind the onset of extinction debts and can be summarized in a niche-based framework. Nonetheless, we identify three understudied domains that should be addressed in future research: i) the eco-evolutionary dynamics of relaxation times, ii) the cascading effects of extinction processes and iii) the impact of perturbation regimes on the payment of debts. For their ability to integrate processes happening at different levels of ecological organization (e.g. population, community, metacommunity), we highlight integrative mechanistic models as promising tools to address these gaps and to improve understanding of extinction dynamics. This is particularly necessary considering that perturbations are dynamic and happening at faster rates under ongoing climate and land-use change.

Community changes in space and time: Bringing environmental predictability and community specialization in the spotlight

Anne Mimet [1,2], Ralf Seppelt[1], Henrique Pereira[2], Robert Buitenwerf[3], Brody Sandel[4], Jens-Christian Svenning[3,5], Signe Normand[3]

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Aim: Predicting biodiversity dynamics in our changing world depends on our ability to create frameworks integrating historical, ecological, stochastic and biotic assembly drivers.

Ecological specialization, defined as narrow species niche-breadth, is an important driver of species richness, allowing more species to live together. Specialization is closely dependent on environmental predictability. Taken together, changes in richness and specialization are highly informative of the changes in the state of the communities and of their underlying processes. There, we hypothesize that giving a central place to ecological specialization and environmental predictability in integrative frameworks of community dynamics could allow overcoming some important limitations of existing frameworks. We present the Resource-Predictability framework which enables concomitant predictions of spatio-temporal changes in community richness and specialization in response to environmental changes. We develop the theoretical bases of the framework, show how the framework links the different type of assembly drivers together, and finally demonstrates empirically the predictive power of the framework and its ability to predict community structure in space and time. Finally, we illustrate the usefulness of the framework creating biodiversity baselines and comparing those baselines with the current state of the communities.

Location: USA (maybe Europe)

Methods: We validate the framework using the data of the North-American Breeding Bird Survey over the 70's and the 2000's decades, together with long-term (Holocene) and recent land use and climate data.

Results: Despite a very simple structure, the Resource-Predictability framework is able to explain 72% of the variation in community specialization and 60% of the variation in species richness. Our results demonstrate that the framework can be used to predict communities in any place and time.

Main conclusions: Based on strong theoretical bases, the Resource-Predictability framework could be used as a skeleton for existing integrative frameworks, able to unified the main assembly drivers and provide biodiversity baselines.

Tuesday, 12th March 2019: Session 2 (11:00-12:45)

Functional island biogeography - concepts and prospects

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Summary: Biogeography has learned a lot about the factors shaping species diversity by studying islands. Most analytical models in island biogeography like the Equilibrium Theory of Island Biogeography or the General Dynamic Model are ecologically neutral and treat species as functionally equivalent. This clearly limits our ability to appreciate the full complexity of how ecological, evolutionary and biogeographical forces structure the assembly and diversity of island biota. On the other hand, a huge body of literature exists on traits associated with dispersal and colonization, island syndromes (e.g. derived island woodiness) or convergent trait evolution on different islands. This literature is often natural history driven and so far lacks a coherent conceptual framework. Also, we note a notable disconnect between the currently very successful trait-based focus of functional biogeography on the mainland and its limited application to island biogeography. In this talk, we argue that a trait-based perspective may lead to a better understanding of how island species overcome dispersal, abiotic, and biotic filters and propose functional island biogeography as new subdiscipline of biogeography. We introduce the necessary concepts and showcase them dwelling on different recent case studies.

Two global tests of Baker's Law: Plant selfing ability promotes island colonization and naturalization

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Aim: The current geographic distribution of species largely reflects colonization success after natural long-distance dispersal or introduction by humans. We tested Baker's Law, which refers to the advantage of species with selfing ability to establish beyond their historical range. First, plants with selfing ability should have an advantage when establishing on islands where mates and pollinators are limited. This hypothesis has been challenged by reports of high percentages of dioecious and self-incompatible species on islands that are possibly the result of post-colonization evolution. Second, plants with selfing ability should have an advantage when establishing in non-native regions where mates can be limited, and their usual pollinators do not occur.

Location: Global

Methods: We combined three global databases: one on breeding systems of species, one on island and mainland distributions of native species (GIFT) and one on global naturalization of alien plants (GloNAF). To test whether the colonization of islands is associated with selfing ability (self-compatibility and autofertility), we assigned each of a total of 1,752 angiosperm species as mainland species, island colonists or island endemics, and used multinomial logistic regressions. To test relationships between selfing ability and global naturalization status, we used phylogenetic generalized linear models and path analyses.

Results: Our first test showed that species with high selfing ability were more likely to be island colonist than mainland species. Our second test showed that selfing ability was directly and indirectly associated with global naturalization. Species with high selfing ability were more likely to occupy larger native ranges, which in turn increased their ability to naturalize in new regions to which they were introduced. Selfing ability directly increased the number of regions where a species is naturalized.

Main conclusions: We provide global evidence across angiosperms that high selfing ability fosters island colonization and naturalization.

Determinants of global richness and endemism of mammals on islands

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Aim: Investigate the relationship between islands characteristics and insular biodiversity of terrestrial mammals.

Location: Global

Methods: We used IUCN range maps to estimate native richness and number of single island endemics for 6,309 islands worldwide, after careful inspection and adjustments in the overlap between islands and range polygons. We gathered island physical and bioclimatic characteristics predicted to influence biological diversity from a publicly available database. We fitted Generalized Linear Mixed-effect Models with Poisson-distributed response variables using a log link function and bioregion as random slope effect.

Results: Island area has a positive effect on the diversity of insular mammals, and is proportionally more important for endemism than for richness, especially for non-volant species. Richness is also positively related to island's temperature and connectivity to the mainland during the Last Glacial Maximum, whereas it is negatively related to island distance from the closest mainland. Isolation also explains endemicity, where island's past connectivity is negatively related to species endemism, and current distance from the island to the mainland is negatively related endemism of bats. The effect of island past connectivity on mammalian biodiversity is greater than the effect of current distance, except for species richness of bats.

Main conclusions: In line with island biogeography theory, we found that area and isolation are strong drivers of insular biodiversity. Island past connectivity to the mainland left strong imprints on mammalian biodiversity, resulting in increased richness (except for bats) but decreased endemism. These patterns are expected given the probable increase in species interchange and gene flow between island and mainland with increased connectivity. Flight capacity also influences the importance of past isolation; bats richness is more strongly linked to current than past isolation. These results add to the growing evidence on the importance of past island configuration for current biodiversity patterns, especially for non-volant species.

Interacting abiotic and biotic filters shape woody invasions across spatial scales in the Hawaiian archipelago

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Aim: Here we assess shifts in the importance of abiotic and biotic drivers, and their interactions, on the establishment and dominance of alien woody plants across spatial scales in the Hawaiian archipelago.

Location: Hawaiian archipelago

Methods: We used a database of more than 450 forest plots to examine patterns of woody plant invasions of Hawaiian forests at local (< 1 ha) and regional scales (10,000 ha). We built a phylogeny that we used to calculate phylogenetic distinctiveness of woody alien species as the mean phylogenetic distance to the nearest native species. We also gathered wood density and seed mass data of alien woody species to explain variation in their establishment and dominance. At each spatial scale, we fit phylogenetic multilevel Bayesian models to examine variation in establishment and dominance of woody alien species as a function of biotic and abiotic factors and their interactions.

Results: At the regional scale, we found that the probability of establishment increased with potential evapotranspiration (PET) and that phylogenetically unique alien species were more likely to establish in areas with young soils or low precipitation, while alien species with heavy seeds established well in areas with high precipitation. At the local scale, the establishment of alien species was positively associated with PET, soil age, and the human influence index. However, alien species exhibited different rates of establishment along gradients in precipitation, PET, and soil age that were strongly modulated by species' phylogenetic uniqueness, wood density, and seed mass. Local dominance of alien species also was strongly context dependent; all biotic factors exhibited significant interactions with the human influence index.

Main conclusions: Our results show that where woody alien species occur or where they dominate local communities is contingent upon the joint effects of abiotic and biotic filtering.

The role of pollinator diversity in structuring oceanic island plant assemblages

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Aim: Why plant diversity varies among oceanic islands? Previous studies revealed that climate and other physical characteristics exert significant effects on insular diversity of vascular species, yet the role played by biotic interactions at large spatial scale is less understood. Here, we aimed to examine the effects of pollinator diversity, climate and island characteristics on angiosperm diversity of oceanic islands.

Location: Oceanic islands worldwide.

Methods: We assemble a dataset of main pollinator groups (bee, wasp, butterfly, moth, hawkmoth, beetle, fly, carrion fly, bat, bird, nonflying mammal, others) for a subset of oceanic islands based on literature review and existing databases. Then we explore the effects of pollinator diversity, climate and island characteristics on insular angiosperm diversity with Generalized Linear Mixed Model. We compare performance of models with different sets of predictors to evaluate the significance of pollination in angiosperm diversity.

Results: We assume that pollinator diversity shows significant relationship with insular angiosperm diversity, given the important role of biotic interaction.

Main conclusions: Combining biotic interactions into explaining plant diversity patterns is of great importance to understand and predict ecological processes. Our study will help to improve the understanding that biotic interactions, especially pollinator diversity, have important effects on insular plant assemblages.

Steppe islands: where island biogeography meets the reality of a severely fragmented habitat

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Aim: In southern Ukraine steppe has survived only in nature reserves, loess ravines, old cemeteries and kurgans (tumuli, burial mounds). Kurgans are small, but numerous objects resembling “islands” in “the sea” of arable land. We asked: i) how strongly does vascular plant species richness on kurgans depend on their size and does this relationship differ between steppe specialists and generalist species? ii) Which other factors influence vascular plant species richness on kurgans?

Location: Southern Ukraine

Methods: We recorded species lists and environmental conditions of 112 kurgans. With non-linear regression we analyzed species-area relationships (SARs) for all species and steppe and generalists species separately. Then, we assessed importance of other factors in explaining the residuals of the SAR models using simultaneous autoregressive models and multimodel inference.

Results: Kurgan area had strong influence on species richness of all groups of species, but particularly on richness of steppe specialists. The estimates of slope of the power function (z-values) in the models for total species richness were high for total species richness (0.32), but even higher for steppe species (0.49) and lower for generalist species (0.18). For total species richness and steppe species, the most important predictors in addition to area were steepness of the kurgan (positive), distance to steppe enclave (negative) and precipitation of the warm period (negative). For steppe species also habitat amount index (positive) and the disturbance (negative) were important predictors. For generalist species, the only important predictors were land use in the surrounding (lower when only arable fields) and steepness of a kurgan (positive).

Main conclusions: Our results indicate that kurgans are habitat islands only for steppe habitat specialists. For this group of species, area and isolation are important predictors of species richness, what is in accordance with the theory of island biogeography, while also local factors play a role.

Functional diversity of the flora of the Canary Islands

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Aim: Plant traits that determine under which environmental conditions plants can survive and reproduce have gained increasing interest, especially in the face of rapid environmental changes. However, research on functional traits of island floras has been underrepresented so far. This is despite the fact that islands harbour an exceptionally high diversity of endemic plant species that often are assumed to have extreme and unique morphologies. Hence, we used the functional diversity (FD) of endemic and non-endemic plant species of an entire archipelago's flora to better understand general processes involved in species distribution.

Location: Canary Islands, Spain.

Methods: We measured functional differences between endemic and non-endemic plant species to identify how abiotic drivers influence their distribution. Therefore, we collected data on species occurrences and functional morphological traits, associated with resource allocation and colonization capacity of the flora of the Canary Islands ($n > 1000$). Subsequently, we calculated different FD measures and their association with climatic and topographic variables.

Results: We found that endemic plant species were functionally less diverse and had less extreme trait values than non-endemic plant species. We further observed that endemic and non-endemic FD was influenced by different abiotic drivers. Interestingly, endemic FD increased with slope and climatic rarity whereas non-endemic FD increased with temperature and decreased with precipitation.

Main conclusions: Our results indicate that endemic plant species radiated into 'micro'-habitats and are therefore less influenced by large-scale climatic patterns. On the other hand, non-endemic plant species were mainly distributed in warm and dry habitats, indicating that their distribution is limited by environmental filtering. Our results show that the dissimilar distribution of FD is likely a synchronous result of colonization processes and climatic filtering. This underlines the importance to employ different conservation strategies for the two plant groups to preserve the total breadth of FD on islands.

Tuesday, 12th March 2019: Session 3 (14:00-15:45)

Using airborne laser scanning to quantify fine-scale habitat structures at macroscales

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Aim: Local habitats are of key importance for the distribution and abundance of animal species, but quantifying high-resolution 3D vegetation structure at macroscales remains challenging. Here, we aim to present the eEcoLiDAR project which currently builds an eScience infrastructure for ecological applications of point clouds derived from Light Detection and Ranging (LiDAR).

Location: Netherlands and other European countries

Methods: We use available multi-terabyte point cloud datasets (derived from airborne laser scanning), high performance computing as well as existing and newly developed open source software tools to derive country-wide LiDAR metrics at high resolution (10-100 m grid cells). These LiDAR metrics are applied as predictor variables in species distribution models (SDMs) to understand and predict animal-habitat relationships at fine resolution and across broad spatial extents.

Results: The obtained LiDAR metrics allow to quantify 3D habitat and vegetation structure at unprecedented detail (meter resolution). This includes multiple metrics related to vegetation height, vegetation coverage, and horizontal and vertical vegetation distribution as well as terrain properties. First applications of SDMs with LiDAR metrics and nationwide bird atlas data show the potential to reveal fine-scale habitat niches of wetland and reedbed birds for which currently available land cover maps are insufficient to describe their habitats.

Main conclusions: Our project demonstrates how advancements in ecoinformatics and macroecology can improve our understanding of the relationship between organisms and their environment, especially via providing fine-scale (high resolution) habitat data across broad spatial extents.

Linking assembly processes and community patterns - Dynamic models and approximate Bayesian Computation (ABC)

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Aim: Statistical techniques exist for inferring community-assembly processes from community patterns. Habitat filtering, competition, and biogeographical effects have, for example, been inferred from signals in phenotypic and phylogenetic data. We aim to contrast such methods against mechanistic models as an inference tool. We revisit current knowledge on community assembly and we argue that trait-based dynamic eco-evolutionary models in combination with recently developed model-fitting, and model-evaluation techniques can provide avenues for inference. To exemplify, we implement a trait-based, spatially explicit eco-evolutionary model and discuss steps of model modification, fitting, and evaluation as an iterative approach enabling inference from diverse data sources.

Location: Theoretical study generalizing over local, regional and global scales.

Methods: Dynamics eco-evolutionary modelling and Approximate Bayesian computation (ABC)

Results: Through a case study on inference of prey and predator niche width in an eco-evolutionary context, we demonstrate how inclusive and mechanistic approaches – eco-evolutionary modelling and ABC – can enable inference of assembly processes that have been largely neglected by traditional techniques.

Main conclusions: Much literature points to the limitations of current inference techniques. Many of the challenges associated with novel inference techniques are, however, already to some extent resolved in other fields and thus ready to be put into action in a more formal way for inferring processes of community assembly from signals in various data sources.

Temporal environmental variation interacts with genetic and ecological traits to shape community composition

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Aim: Studies investigating the drivers of community composition often focus on environmental variation as determining factor --- both temporally and spatially. A large body of evidence indicates that intermediate levels of spatiotemporal variation affects community composition by facilitating coexistence and thus leading to higher species richness. Furthermore, recent studies reporting negative impacts of intraspecific variation on species coexistence sparked an increased interest in the role of biotic factors in community composition. Yet, so far there are few indications as to the underlying eco-evolutionary processes and factors shaping community composition and how they feed back to one another. One promising candidate to understand such interactions is genetic architecture -- the way ecological traits (including those responsible for survival under environmental heterogeneity) are arranged in the genome. Here we use a process-based modeling approach to address the question of how temporal environmental variation interacts with genetic and ecological traits to shape community composition.

Location: *In silico.* Artificial landscapes with two perpendicular environmental gradients (i.e. niche axes).

Methods: We present an individual-based, niche and genetically explicit model considering three aspects of genetic architecture: gene linkage, number of loci and intra-genomic variation. While gene linkage affects how independently genes are recombined during reproduction, number of loci control the variability of realized quantitative ecological traits. We analyse community composition between scenarios with and without temporal environmental variation.

Results: Realized communities reveal complex relationships among the genetic architecture traits and community trait composition. Furthermore, we identify eco-evolutionary trait syndromes that differ between the different scenarios of temporal variation.

Main conclusions: Our results provide clues to how real-world communities might react to variable environmental regimes and highlights that functional evaluation of species should also encompass genetic traits.

bRacatus: an R platform to estimate the accuracy and biogeographical status of point-occurrence records

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Aim: Understanding species distributions is critical for addressing manifold ecological questions, but available data are typically highly heterogeneous and rife with various information gaps and uncertainties. Crucially, the accuracy and biogeographical status (native vs. alien) of individual data points is often unclear, thus challenging their confident use in distribution modelling or other downstream analyses. We developed a framework, currently being implemented as an R package, for estimating the accuracy and biogeographical status of a given occurrence record.

Location: Our methods have been developed and tested based on terrestrial species data from all continents.

Methods: The estimation is based on the spatial/environmental context provided by coarser-grain reference regions of native and/or alien distributions as well as by other records. By estimating records' likelihoods along two axes, i) "certainly false to certainly true", and ii) "certainly native to certainly alien", the framework avoids the artificial thresholds of simplistic data filtering and instead allows propagating uncertainties in subsequent analyses. We trained and tested different models with independent datasets, adopting the one that showed the best predictive power.

Results: The first implementations of the models have showed high performance for most test datasets.

Main conclusions: This package provides support for researches working with SDMs, biogeographical patterns and other analyses that rely on point-record data. I will present first implementations of this tool and discuss its performance for different data sources.

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Bridging landscape ecology and macroecology: a data aggregation method for environmental heterogeneity

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Aim: A key aim of ecology is to understand what drives global ecological patterns. However, the datasets available at sufficiently broad extents to study key global drivers, such as climate, are available at coarser spatial resolutions than are relevant for understanding the ecological effects of finer-scale environmental heterogeneity. We develop a method for data aggregation that results in minimal loss of information on environmental heterogeneity.

Location: Great Britain

Methods: We present a data-aggregation method that, unlike current approaches, reduces the loss of information on fine-scale spatial structure in environmental heterogeneity for use with coarse-scale ecological datasets. Our method contains three steps: 1) define the scales of analysis (predictor grain, response grain, scale-of-effect); 2) use a moving window to calculate a measure of variability in environment (predictor grain) at the process-relevant scale (scale-of-effect) 3) aggregate the moving window calculations to the coarsest resolution (response grain). We illustrate our method with an empirical case study: the effect of forest heterogeneity on Eurasian Jay (*Garrulus glandarius*) abundance.

Results: Our method enables us to find the appropriate scale-of-effect of land-cover diversity on *G. glandarius* abundance in the UK. We then model the interactive effect of land-cover heterogeneity and temperature on *G. glandarius* abundance. Our method enables us quantify this interaction despite the different scales at which these factors influence *G. glandarius* abundance.

Main conclusions: Our data aggregation method allows us to integrate variables that act at varying scales into one model with limited loss of information, which has wide applicability for spatial analyses across all disciplines. Key ecological applications include being able to estimate the interactive effect of drivers that vary at different scales (such as climate and land cover), and to systematically examine the scale-dependence of the effects of environmental heterogeneity in combination with the effects of climate change on biodiversity.

LiDAR-based species distribution modelling reveals fine-scale habitat associations of wetland birds

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Aim: Light Detection and Ranging (LiDAR) provides high precision point clouds for characterizing the 3D structure of ecosystems and habitats. Previous LiDAR studies have mainly focused on forests whereas other habitats remain underexplored. Here, we derived country-wide LiDAR metrics at high resolution (10-100 m grid cells) to quantify 3D vegetation structure of wetlands and use this information in species distribution models (SDMs) to test ecological hypotheses about fine-scale bird-habitat relationships.

Location: The Netherlands

Methods: We derived various LiDAR metrics to quantify 3D habitat structure within wetlands, incl. (1) vegetation height, (2) vegetation coverage, (3) horizontal and vertical vegetation distribution, and (4) terrain properties. We implemented several SDM algorithms (GLM, GAM, MAXENT, RF, SVM etc.) of selected wetland bird species (Great Bittern, Reed Warbler, Bearded Reedling, Great Reed Warbler, Savi's Warbler) using nationwide bird atlas data at 1 km (presence-only) and 5 km (presence-absence) resolution. We then assessed the relative importance of LiDAR metrics in SDMs and their ecological meaning for bird-habitat relationships.

Results: Vegetation height (90th percentile of height) and vertical variability (e.g. standard deviation of points) were key predictors for the habitat suitability of most wetland birds. However, the calculation of several LiDAR metrics (e.g. kurtosis and skewness of height) is sensitive to micro-scale terrain heterogeneity and can potentially bias the prediction of fine-scale habitat suitability (e.g. reed patches along ditches). Our LiDAR analysis further shows that the habitat niche of some rare wetland birds (e.g. the Great Bittern) can be better predicted than the niche of more wide-spread species (Reed Warbler).

Main conclusions: The high-performance processing of newly available country-wide, high-resolution LiDAR datasets has great potential to improve our understanding of the 3D habitat structure of animals. This will allow to predict species distributions with unprecedented detail, not only in forests but also in other habitat types.

Environmental heterogeneity as a driver of plant diversity on oceanic islands

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Aim: Oceanic islands have complex geological histories and high environmental heterogeneity (EH). The General Dynamic Model (GDM) by Whittaker et al. (2008) links geological dynamics, key biogeographical rates and diversity patterns on oceanic islands. A central assumption of the GDM is that island area and EH peak at intermediate island age. However, in the frame of the GDM, the temporal trajectory of EH has never been empirically tested. Here, we quantify EH on oceanic islands worldwide, inspect the temporal trajectory of EH and evaluate the importance of EH as a predictor for native plant species richness and endemism on oceanic islands.

Location: 138 oceanic islands belonging to 44 archipelagos worldwide.

Methods: We calculated a set of 26 EH metrics capturing the heterogeneity of elevation, precipitation, temperature and of two geomorphometric indices. First, we tested the GDM proposition of a hump-shaped EH trajectory over island age. Second, we evaluated the predictive power of different EH metrics for the number of native and endemic plant on islands. We used generalized linear mix effect models and Akaike Information Criterion (AIC) for model selection.

Results: We found that several EH metrics were strongly correlated (e.g. heterogeneity of elevation and temperature). Most EH metrics followed the expected hump-shaped trajectory, particularly measures based on standard deviation, range and roughness. In contrast, metrics capturing the dissection or fractal dimension on islands showed flat or even u-shaped trends. EH was a significant predictor for plant species richness and endemism on oceanic islands. The lowest AIC values were found for models that included metrics calculating heterogeneity of temperature and elevation, e.g. roughness and range.

Conclusions: The EH metrics calculated here showed different trends, hump-shaped and u-shaped trend over time, reflecting a different facet of EH. Our results provide empirical support for the effect of EH on plant species richness on oceanic islands.

Tuesday, 12th March 2019: Session 4 (16:15-18:00)

Improving the reliability of geographic records from biological collections for macroecological research and conservation assessment

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Aim: To test and improve the reliability of large-scale occurrence records from public databases for macroecological research using a novel pipeline for automated data processing. A special focus is on taxon-specific bioregionalization and automated conservation assessments.

Location: Global

Methods: Here we present a pipeline of the R-packages *CoordinateCleaner*, *speciesgeocodeR* and the java script program *Infomap Bioregions*, which based on geographic matching, signal recognition and Information theory I) identifies common errors in databases of biological and palaeontological databases, II) identifies taxon-specific bioregions and III) generates automated conservation assessment. We use approximately 15.000 species in the pineapple (Bromeliaceae) and orchid (Orchidaceae) families as case studies to benchmark the results on independent bioregionalizations and conservation assessments.

Results: The results confirm the presence of recurrent, common errors in public databases and suggest that on average up to 19% of records might be erroneous or overly imprecise. Automated flagging can identify the majority of these problematic records and the resulting filtered datasets can identify species threat status with an accuracy of >80%.

Main conclusions: Species occurrence records from online databases are an indispensable resource in ecological, biogeographic and palaeontological research. Automated flagging can significantly speed up the curation of such data, and help to improve the reliability of downstream analyses. Automated conservation assessments, based exclusively on geographic occurrence records can identify threaten species with a convincing accuracy and are a valuable tool to prioritize conservation strategies.

Cryptic diversity along the onshore-offshore gradient: marginal marine environments were a cradle of early vertebrates

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Aim: In evaluating the evolution of marine diversity across Earth history, marginal-marine environments are rarely sampled. This is due to their apparent lack of organisms, commonly associated with their ephemeric character: rapidly changing salinity, periodic emergence, high amplitude temperature oscillation and exposure to wind and wave energy. The shallow end of the onshore-offshore gradient is therefore commonly assumed to be characterized by low-diversity or even monospecific communities formed by taxa highly specialized to thrive is these extreme settings. Recent research, however, indicates that such environments were an evolutionary cradle for early vertebrates. We evaluate the taxonomic diversity and the niche breadth of an early vertebrate group across the onshore-offshore gradient and estimate, what proportion of total taxonomic diversity is constrained to the extreme marginal settings.

Location: We used field data from middle Silurian outcrops in the island of Saaremaa, Estonia, as well as a global literature compilation of coeval observations.

Methods: The model group in this study were conodonts, a now extinct group of jawless vertebrates which were the first in this clade to have developed a mineralized skeleton. Their mouthparts show an extreme morphological diversity suggestive of highly diverse trophic habits. The literature compilation was based on 376 samples reported in the literature, spanning a total of 45 species. Their occurrences were assigned to one of seven environments along the onshore-offshore gradient and based on that we calculated the average alpha and beta diversities in each environment along the gradient, as well as the environmental niche breadth for each species and the average thereof for each environment. Additionally, we documented occurrences of specialized species of conodonts and other groups of early vertebrates in outcrops with sedimentological evidence for elevated salinity.

Results: Against the expectations, the total (gamma) diversity in extreme marginal settings was higher than in more open-marine settings. This was due to very high beta diversity and a high proportion of taxa found only in these environments. The average niche breadth in these environments was very low, reflecting the high degree of specialization. The omission of these environments would result in an underestimation of global taxonomic diversity of conodonts during that time by 15%.

Main conclusions: The low alpha diversity of conodonts in marginal marine environments is deceptive: early vertebrates showed a high degree of specialization and a wide range of tolerated salinity, as supported by recent molecular data. These environments require adapting sampling strategies to capture their patchiness and the high degree of specialization of organisms therein.

Brain expansion in early hominins explains carnivore extinctions in East Africa

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Aim: While the anthropogenic impact on ecosystems today is evident, it remains unclear if detrimental effects on co-occurring biodiversity is a recent phenomenon or has also been the pattern for earlier hominin species. We test this using the East African carnivore fossil record to analyse the relationship between diversity decline in carnivores and increase in hominin cognitive capacity and compare it against alternative hypotheses of environment-driven extinctions.

Location: Plio- and Pleistocene fossil sites from East Africa

Methods: We analysed the temporal patterns in extinction rates in African carnivores based on expert curated records of fossils in order to infer if the pattern is best explained by climatic fluctuations, vegetation changes, or by the effects of the increasingly intelligent hominins on the ecosystem. In order to tease apart effects of temporally correlated factors we investigated the contemporary spatial importance of vegetation cover versus anthropogenic activity for the carnivore fauna within Africa.

Results: We find that extinction rates in large carnivores significantly correlate with increase in hominin brain size and with vegetation changes, but find no correlation with precipitation and temperature changes. While temporal analyses cannot distinguish between the effects of vegetation cover and human brain size, we show through spatial analyses of contemporary distributions of carnivores in Africa that only the hominin causation is mechanistically plausible.

Main conclusions: Our results suggest that substantial anthropogenic influence on biodiversity started millions of years earlier than currently assumed, and call into question the existence of pristine African environments and a harmonious co-existence of hominins with other mammals.

Contrasting patterns of biomass allocation of woody species to abiotic stress tolerance

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Aim: Functional Equilibrium Theory (FET) predicts that plants should allocate greater proportion of biomass to the organs acquiring the most limiting resource. Thus, a trade-off between biomass allocation to above- and below-ground organs seems to be inevitable. We tested the generality of such trade-off and to what extent it is affected by species-specific trait syndromes to cope with stress factors.

Location: Global

Methods: We built a dataset including estimates of leaf, shoot and root mass fraction, total plant dry mass (DM, g) and species-specific shade, drought and cold tolerance scores (expressed on a 5-point scale) for 140 woody species of the Northern Hemisphere. Species-specific estimates of leaf life span (LLS, months) and xylem pressure at which 50% of conductivity is loss (Ψ_{50}, Mpa) were added as traits reflecting trait syndromes. Relationships between the considered variables were explored via both simple and multiple regression analysis. A complementary 3-point scale dataset including observations for 570 woody species world-wide was used to further test the consistency of the patterns.

Results: In contrast with FET prediction we found that: shade tolerant species allocate less biomass to leaves, when compared at common DM and LLS, and more to roots; drought and cold tolerant species consistently allocate less biomass to leaves, independently of LLS, and to roots in order to achieve a water-saving strategy as reflected by more negative values of Ψ_{50}.

Main conclusions: Only the simultaneous analysis of the effect of LLS and Ψ_{50} allowed us to isolate the effect of stress tolerance scores. Therefore, species-specific strategies to cope with stress as modulation of leaf turnover rates (i.e. differences in LLS) or safety water transport can define how biomass is “optimally” allocated to different plant compartments, undermining the strict trade-off predicted by the FET.

Community weighted means of resource economics traits predict vegetation index in global compilation of grassland plots

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Aim: Theoretical, experimental and observational studies show that biodiversity ecosystem functioning (BEF) relationships are influenced by functional community structure (i.e. trait distributions in a community) through two mutually non-exclusive mechanisms, described by *dominance* and (2) the *niche partitioning.* While both mechanisms have been extensively studied in plant communities at small spatial scales, a global analysis across continents has not been yet attempted. The objective of this study was to simultaneously evaluate dominance and diversity effects in grassland systems worldwide.

Location: 2941 grassland plots globally

Methods: Plot based data on functional community structure (CWM and FD) were obtained from the global vegetation plot database sPlot in combination with the plant trait database TRY using 18 ecologically relevant plant traits. We measured NDVI at the sPlot grassland sites (n = 2941) at a spatial resolution of 250m using the MODIS product MOD13Q (annual peak NDVI being a proxy of productivity). Multiple regression commonality analysis and structural equation models were used estimate the contributions of dominance and niche partitioning effects to the variation in NDVI, while controlling for climate variables.

Results: The so-called plant community economics spectrum referring to the "fast-slow traits" of the dominant species in the community was the strongest predictor of the peak NDVI values in the grassland systems (dominance effect), while there was weak support for an effect of functional diversity. There was a strong positive relationship between annual precipitation and peak NDVI.

Main conclusions: Plant functional community structure influences global patterns in greenness through the resource economics traits of the dominant species.

General patterns of species-area relationships emerging from nearly 5,000 grassland plots

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Aim: Species-area relationships (SARs) are probably the most fundamental and most studied scaling law in ecology. Still there is on-going dispute on their shape. At coarse grain sizes, several analyses of island SARs have demonstrated that the power law overall performs best. Yet, at fine spatial grains in continuous vegetation, it was unresolved whether SARs follow a power-law, logarithmic or other function. We thus asked which function type is most suitable in such situations and whether the prevalence of functions or their parameters are related to ecological or methodological settings.

Location: Grasslands of the Palaearctic biogeographic realm.

Methods: We used the new GrassPlot database, containing standardised vegetation-plot data from a wide range of grassland types throughout the Palaearctic, including nearly 5,000 nested-plot series with at least four grain sizes. Besides vascular plants, often also terricolous bryophytes and lichens were sampled, allowing to evaluate differences in scaling laws between these ecologically contrasting taxa. Using non-linear regression modelling, we assessed the appropriateness of a set of proposed SAR-function types and evaluated their parameters. We then tested whether the relative ranking (based on AICc) of function types or their parameters differed between taxonomic groups, geographic regions or grassland types.

Results: Our results demonstrate that for the studied fine grains the power law was on average the most suitable function. Its slope parameter (*z*) was significantly larger for lichens than for other taxa, with little difference between regions and grassland types.

Main conclusions: We conclude that SARs at any spatial scale are best approximated with power laws. Together with the established range of typical *z*-values this allows making richness data sampled on differently sized plots comparable by interpolation, thus providing an important tool for the analysis of the heterogeneous data stored in big continental to global vegetation-plot databases such as EVA and sPlot.

Amphibian diversity in the Amazonian floating meadows

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Aim: To investigate large-scale amphibian diversity patterns of floating meadows.

Location: Floodplains of the Amazon river system.

Methods: We studied 62 floating meadow localities, covering >7,500 km along the Amazon and its tributaries, and examined their Zeta (ζ) diversity, i.e. the number of species shared by multiple assemblages. This new concept and metric unifies incidence-based diversity measures, patterns and relationships, turning into a propitious method for measuring biological diversity. We also performed cluster and Multi-Site Generalised Dissimilarity Modelling analyses.

Results: A total of 55 anuran amphibian species were identified. The number of species inhabiting by any floating meadow in any location is ten (ζ_1, alpha diversity), by any two localities is six (ζ_2, beta diversity), by any three localities is five (ζ_3), and so on. No shared species are expected from any 14 localities on. Temperature seasonality (Bio4), geographic distance and precipitation of the wettest quarter (Bio16) were the most important environmental (abiotic) variables explaining species distributions. Cluster analyses showed a structured pattern only at the broad scale, with well-defined regional clusters formed in the Upper Amazon and Purus sub-basins.

Main conclusions: Stochastic processes are the main forces driving anuran diversity in Amazonian floating meadows. Although there is a small set of widespread species shared by several localities, the global composition of species assemblages differs widely. Pairwise turnover (ζ_2) is driven by the gain or loss of rare species. Recent studies suggested that major rivers might work as barriers for amphibians in the Amazon region. Although we do agree, this might apply especially for terrestrial (*terra-firme*) forest species, while floodplain (*varzéa*) species might benefit from the passive dispersal provided by floating vegetation islands. In this sense, floating meadows could act towards homogenization of the local biota in the Amazon river system.

Wednesday, 13th March 2019: Session 5 (9:30-10:30)

Coupled species' responses to global change in ecological networks

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Aim: Ecological networks of plant-animal interactions are ubiquitous in nature and are critically important for ecosystem functioning. Nevertheless, interaction-mediated responses to global change have been little studied, due to the lack of data and integrative concepts.

Location: Global

Methods: I explore how the increasing availability of trait data provides new avenues for quantifying linkages between plants and animals in ecological networks. Such analyses can be used to understand the structure of current ecological communities and to project community changes into the future.

Results: I show which species traits determine the matching of plant and animal species in ecological networks and how the functional trait diversity of plants and animals reciprocally impacts their interaction partners. Despite their coupling in ecological networks, plant and animal functional diversity are associated with different abiotic factors on large scales. These findings suggest a high risk of decoupled responses of plants and animals to global change.

Main conclusions: I propose a trait-based framework that could help to assess the (de)coupled responses of plants and animals to global change. A refocused collection of plant and animal trait data and their incorporation into an integrative, trait-based framework would allow to model how plant-animal interactions can modulate biodiversity responses to global change.

Future changes in drivers of avian diversity in Pakistan

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Aim: We aim to determine the drivers of avian diversity and their future changes, as this is of utmost importance for avian conservation. Different environmental drivers, such as climate, land-use and water availability can directly or indirectly affect biodiversity and are likely to act synergistically. Land-use and water availability strongly depend upon human population density, which makes the biodiversity in densely populated countries, such as Pakistan, particularly vulnerable to these changes.

Location: Pakistan

Methods: We extracted species ranges for birds occurring in Pakistan and identified environmental and land-use factors, which drive species richness of breeding and wintering birds using regression models. We then quantified the future change in these drivers and compared them among regions of low, medium, moderate and high species richness.

Results: Mean annual precipitation, urbanization and minimum river discharge explained more than 50% of variation in breeding bird richness and together with mean annual temperature explained around 40% of variation in wintering bird richness. Most bird species, both in the breeding and wintering season, were aggregated along the five main rivers, which are situated in the central and northern part of Pakistan. These areas will experience the largest reduction in precipitation in the future, while the change in temperature will be relatively small. In these regions, human population is also the highest and land-use is projected to undergo the highest increase in the future.

Main conclusions: Climate may affect distributions and thus avian richness in the future. On top of that, an increase in human population and land-use change will continue to cause changes in landscapes and habitats as well as the depletion of water resources. In Pakistan, both birds and humans aggregate in areas where water is available through rivers, which will lead to enormous pressure on bird richness in these areas in the future.

Increased intraspecific temporal aggregation in egg hatching of Finnish birds

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Aim: Numerous studies over the past few decades have shown that species phenologies are shifting. Behind the large-scale patterns of shifting phenologies lies, however, large variability across species and space in terms of both the sign of the shifts (advance or delay) and their magnitude (rate of change). Shifts in the timing of seasonal events are usually studied by measuring change in one part of the phenological distribution over the season, such as the mean or first appearance of the event. This, however, gives us a mere glimpse of how (part of) the population under study is changing, thus limiting our ability to understand underlying mechanisms. Here, we take a holistic approach to describing phenological change by considering shifts in the complete phenological distribution and interrelationships within it.

Location: Finland

Methods: Here, we take a holistic approach to describing phenological change by considering shifts in the complete phenological distribution and interrelationships within it. By simultaneously modeling change in the different parts of the within-season temporal distribution for egg-hatching of 117 bird species across 43 years and 4 bioclimatic zones distributed across Finland, we specify and test hypotheses regarding the possible mechanisms which allow (or prevent) populations to shift their phenology under climate change.

Results: Preliminary results indicate that egg-hatching in bird species is stacking up towards earlier and more compressed peak periods. The majority of change can be attributed to an advance of the tail of the distribution, with an only minor advancement of the beginning of the season.

Main conclusions: We conclude that the observed shifts potentially intensify intraspecific competition by increasing the temporal co-occurrence of broods across large geographical areas.

Long-distance migratory birds face multiple risks from global change

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Aim: Long-distance migratory birds travel thousands of kilometres annually between summer and winter ranges. Although global change can affect both ranges and also the migration route, impact assessments primarily focus on breeding ranges. Here, we examine how potential climate and land cover change may affect migratory birds in terms of (1) summer (breeding) range loss, (2) winter range loss and (3) migration distance increase.

Location: Global.

Methods: We concentrate on long-distance migratory birds of the Holarctic (n=715). We estimate species distribution models at 0.5° resolution with occurrence information stemming from IUCN range maps on summer and winter distribution. We project the models to the period 2041-2060 for different scenarios of climate change and land cover change and estimate the relative magnitudes of risks. Last, we assess how species risks relate to geographic and ecological traits and to IUCN red list status.

Results: Our results indicate that the different risks are largely independent from each other and their magnitudes also vary geographically. In consequence, impact assessments focussing on summer ranges alone could underestimate the number of potentially threatened species by 18-49% and underestimate the potential impact from multiple risks for 17-50%. Many species that could suffer from multiple global change risks are not currently listed by IUCN as threatened or near threatened.

Main conclusions: This study provides a first indication how neglecting seasonal ranges in impact assessments could misguide conservation targets, both spatially and at the species level. We hope that our global assessment will inspire more detailed work taking into account the full annual cycle and complex behaviour of migratory species.

Wednesday, 13th March 2019: Session 6 (11:00-12:45)

Towards a better understanding of global change impacts on biodiversity by integrating data and approaches across disciplines and scales

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Aim: We will present two examples on how to integrate data from biogeography and physiology to improve our understanding of species responses to global change.

Location: Bavaria, Pakistan.

Methods: We combine species occurrence data with data on temperature preferences based on biogeographical analyses as well as on physiological experiments in order to analyse (1) temporal trends in distributions of selected bird, butterfly, dragonfly, and grasshopper species in Bavaria over the last decades and (2) intra- and interspecific patterns of thermal tolerances of different arthropod taxa along elevational gradients in Pakistan.

Results: Our results (which are still preliminary upon abstract submission) suggest (1) that warm-adapted species show range expansions in Bavaria and (2) that microclimatic conditions influence the elevational patterns of thermal tolerances of insects and spiders in different mountain ranges of Pakistan.

Main conclusions: With both study examples we demonstrate how the inter-disciplinary integration of data and methods from biogeography, physiology and ecology as well as across taxonomic and spatial scales may both confirm and challenge current assumptions on species responses to climate change. Thereby, we outline pathways for the development of more realistic projections of global change impacts on biodiversity.

Impacts of climate change on the community compositions and diversity of the world's terrestrial birds under different warming scenarios

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Aim: Climate change is a major threat to biodiversity. Typically species have been found to shift their ranges towards higher latitudes and altitudes, but species' abiotic tolerances and dispersal abilities can lead to individualistic responses to climate change. These heterogeneous responses are likely to reshuffle species communities. Potential consequences include changes to the competitive balance and trait composition as well as the phylogenetic diversity (PD) of species communities. Under the assumption that the loss of PD implicates a reduction in the evolutionary potential of a community and thus decreases the likelihood of its future persistence, this could be an additional threat making communities increasingly vulnerable to climate change. Here we investigate the impacts of different scenarios of climate change on terrestrial bird distributions and, subsequently, species diversity.

Location: Global

Methods: We use species distribution models (SDMs) for the worlds' terrestrial birds, incorporating species specific traits (dispersal capability and generation length) to improve the realism of the projections. We project range changes and derive current and future community compositions. We then compare impacts on species richness (SR) as well as changes in community compositions and PD of species communities across the globe under a low and a high warming scenario.

Results: We found that areas where diversity patterns are changed markedly by the mid-century are significantly reduced under the low compared to the high warming scenario. Furthermore, we show that individualistic responses to climate change are wide spread across the globe, but less frequent at higher northern latitudes.

Main conclusions: Our results show that climate change has a significant impact not only on SR but also on PD as well as on species community compositions. The area affected by these changes is significantly larger under the high warming scenario, highlighting the importance of keeping global warming to a minimum level.

Linking local and continental success of alien woody ornamental plants

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Aim: To understand how large-scale patterns of alien plant naturalization may be linked to their local post-introduction success and failure, and spatial variation thereof.

Location: Europe.

Methods: We used a dataset about outdoor cultivation and reproductive success of alien woody ornamental plant species in ~200 gardens and parks across Europe. We further compiled data about the origin, traits and residence time of the species, as well as two measures of their naturalization success in Europe, namely naturalization incidence (whether or not a species had naturalized in Europe), and naturalization extent (how widely it had done so). We analysed the drivers of local reproductive success, and those of naturalization incidence and extent in Europe, and specifically tested (1) if local reproductive success contributed to naturalization incidence and extent in Europe, and (2) if the geographic distribution of the gardens where a species was planted better explained naturalization success than their mere number.

Results: On a local scale, we found that the reproductive success of a species in a garden depended both on the species' traits and on the geographic location of the garden where it was planted. On a continental scale, both naturalization incidence and extent in Europe were positively associated with a higher frequency of local reproductive success. Furthermore, models that accounted for the geographic range over which gardens were scattered had the best fit.

Main conclusions: Our findings are twofold. First, we highlight how patterns of plant species performance can be connected across scales. Second, we show that the observed distribution of alien plant species depends to some extent on where they were originally introduced, which has implications for the prediction of future widespread invaders.

Spatiotemporal changes in the intensity of global land cover fragmentation

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Aim: Degradation of natural ecosystems might drive species and populations to extinction and can modify the functioning and composition of ecological communities. Ecosystem degradation typically leads to habitat fragmentation which creates detrimental edge effects and worldwide declines in biodiversity and ecosystem functions. Here, we aim to quantify the intensity, magnitude and spatiotemporal dynamics of changes in land cover fragmentation over nearly a quarter century at the global scale.

Location: Global.

Methods: We used the first long-term time series of global land cover (ESA CCI-LC) which provides consistent maps at 300 m spatial resolution on an annual basis over 24 years (1992-2015). We then used a new metric, the entropy-based local indicator of spatial association (ELSA), to quantify the magnitude of fragmentation at the pixel level for each year. We quantified the contrast (dissimilarity) among multiple land cover classes and thereby assessed the magnitude of fragmentation. A simple linear regression between fragmentation estimates and years was fitted at each pixel to characterise the fragmentation trend over time. The slope of the trend line was used to quantify the strength and intensity of fragmentation change for each pixel over 24 years. We summarize these results at the biome and country level.

Results: At the global scale, our results show that the largest increase in land cover fragmentation occurred in biomes such as “Temperate savannas” and “Mediterranean forests”. In contrast, biomes such as “Montane grasslands” and “Temperate coniferous forests” showed the lowest land cover fragmentation increase. Countries with the highest increase in land cover fragmentation included French Guiana, Suriname and Guyana.

Main conclusions: Our new global map of land cover fragmentation provides novel insights into the status and change of ecosystems worldwide and can help informing decision makers about sustainable use of habitats and resources.

Evaluation of agri-envrionment schemes on biodiversity: Analysing local scale data in order to contribute to national strategies

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Aim: In order to conserve and promote biodiversity in agricultural landscapes, the establishment and financial support of agri-environment schemes (AES) is one recommended instrument. We aim to evaluate the effect of AES on floral and faunal biodiversity.

Location: In Switzerland, agricultural production spreads out over five zones from the lowlands to mountainous regions and summer pastures.

Methods: Data was collected in the agricultural landscape within 1 km^2 squares (n=134) distributed across Switzerland. Within these squares, plant species were identified in 10 m^2-samples inside and outside of farmland under AES according to a stratified design. Butterfly and bird species were recorded on transect walks. We analysed the biodiversity related to types and classifications of farmland under AES, environmental parameters and land use intensity. In terms of biodiversity measures, we focused on the diversity of all species occurring in the agricultural landscape, and on species that have their main distribution range in the agricultural landscape and are dependent on agricultural use (i.e. species from the Agriculture-Related Environmental Objectives, AEO).

Results: Our results showed a general pattern of higher diversity of AEO species in farmland under AES than in other farmland for plants and butterflies. For birds, a similar pattern was detected in zones with preferable conditions for intensive agricultural production. However, in disadvantaged zones, biodiversity of birds was poorly related to amount and characteristics of farmland under AES.

Main conclusions: Our results confirm the general positive effect of AES on biodiversity in agricultural landscapes. Nevertheless, detailed analyses for specific types of farmland under AES show high potential for further improvements based on appropriate management strategies for the respective location. Evaluating effects of AES using floral and faunal aspects allows for a more comprehensive assessment of biodiversity regarding scale and various aspects.

Temperature driven biodiversity redistribution on Earth

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Aim: The redistribution of species in response to global warming is reshaping biodiversity on Earth, leading to shifts in ecosystem composition, functions and services. As the pace of climate change is predicted to increase, quantifying its effects on biodiversity is essential, in order to predict and adapt to changes in the biosphere. However, the net effect of species reorganization on local-scale biodiversity remains a critical knowledge gap, and the extent to which recent temperature change may have resulted in local assemblage change is unknown.

Location: Global.

Methods: We coupled the largest compilation of assemblage time-series to date with high-resolution temperature records, and used a meta-analytical Bayesian framework to quantify if local biodiversity has responded to changes in temperature over the past century, across both the marine and terrestrial realms, and for different taxa including plants, invertebrates, birds, mammals and fishes.

Results: Overall, both species richness and total abundance increased on average in locations undergoing warming. However, responses were three times stronger in the ocean than on land, and contingent on local climate conditions. Species richness increase with warming was particularly evident in the warmest marine locations in our data, while abundance declined in such locations. In contrast, the terrestrial locations with the strongest warming signals experienced species richness declines.

Main conclusions: Our results indicate that recent temperature change is reshaping marine and terrestrial systems along different trajectories, with marine assemblages experiencing stronger biodiversity change. Additionally, we show the effects of warming (and cooling) depend on the local climate, where initial increases in richness and abundance may be followed by losses if warming continues. Reducing greenhouse gases emissions is essential to prevent the further disruption of ecosystems and avoid potentially severe biodiversity loss in the future.

Implications of three diverging shared socio-economic pathways for terrestrial biodiversity worldwide

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Aim: Scenario-based biodiversity modelling is a powerful tool to evaluate how possible future socioeconomic developments may affect biodiversity. Here we aimed to evaluate the implications for terrestrial biodiversity of three of the recently developed shared socio-economic pathways (SSPs) linked to three distinct representative concentration pathways (RCPs).

Location: Global

Methods: We first revised and updated the GLOBIO model, which is a global model to assess anthropogenic impacts on biodiversity intactness, expressed by the mean species abundance (MSA) metric. The new model runs at a higher spatial resolution (10 arc-seconds; ~300 m), contains new modules for downscaling land use and quantifying impacts of hunting, and updated modules to quantify impacts of climate change, land use, habitat fragmentation and nitrogen pollution. We then used the updated model to project terrestrial biodiversity intactness from 2015 to 2050 based on pressure data according to three SSPxRCP scenarios.

Results: For SSP1xRCP2.6 (‘sustainability scenario’), the global mean MSA showed a slight increase relative to 2015 (0.3%). In contrast, 2.8% and 4.4% loss in global mean MSA were projected for SSP5xRCP8.5 (‘fossil-fuelled development scenario’) and SSP3xRCP6.0 (‘regional rivalry scenario’), respectively. Projected changes differed considerably among world regions. Irrespective of scenario, losses in MSA were projected for regions in sub-Saharan Africa, whereas the sustainability scenario showed slight gains in MSA for various regions in Asia, Europe and the Americas. Overall, changes in MSA were primarily caused by land use change, yet hunting contributed substantially in (sub-)tropical regions.

Main conclusions: Reducing land demands by increasing agricultural productivity and change of consumption patterns is urgently needed in order to halt or revert the ongoing decline of terrestrial biodiversity worldwide, whereby regions in sub-Saharan Africa require extra conservation efforts.

Wednesday, 13th March 2019: Session 7 (14:00-15:45)

The paleontological legacy in climate-related extinction risk

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Aim: Climate change related extinction risk depends on the evolutionary history of the focal species. Throughout earth history, the reaction of species to climate changes likely depended on their adaptations to the previous long-term climate situation. Understanding the interactions between the effect of short-term temperature changes with previous long-term temperature trend is thus crucial when evaluating intrinsic extinction risk of species facing current warming.

Location: Global calcareous nannofossil occurrence as available from deep-sea ocean drilling programs throughout the Cenozoic.

Methods: Survival and extinction of genera was estimated from fossil occurrence information. In a temporally continuous analysis, generalized linear mixed effects models with binomial family error were implemented to explain survival and extinction by temperature changes interacting with long-term temperature trends. The approach has the advantage that it neither depends on a perfect fossil record nor on continuously reconstructed phylogenies and is thus highly suitable for the imperfect nature of deep-time biotic data.

Results: Survival and extinction probabilities of calcareous nannofossils seem to be influenced by the magnitude of temperature change interacting with past temperature trends. The effect strongly differs between groups and is influenced by data quality.

Main conclusions: Tracking species occurrence though time using the fossil record provides the unique opportunity to study the interaction between climate change, past climate trends and the phylogenetic history of species on extinction risk, while approaching this crucial question only with extant data is impossible.

Testing for differences in evolutionary dynamics between marine and freshwater environments

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Aim: Classic and contemporary theories predict differences in evolutionary rate between marine and freshwater organisms. Actinopterygian fishes, which possess 32,000 species and have repeatedly explored both environments, represent a model system to test for differences in evolutionary rate between these habitats at a broad scale.

Location: Extant fishes globally.

Methods: Using a dataset of body size for 10,987 fishes and a new phylogeny of ray finned fishes, we quantified rates of evolution using BAMM. We then compare rates of phenotypic evolution between marine and freshwater environments using both traditional and phylogenetic comparative approaches at a variety of taxonomic scales to reveal the sensitivity and generality of our findings.

Results: We recover considerable rate heterogeneity between environments across actinopterygian fishes. A majority of tests for differences in rates between marine and freshwater environments within orders were not statistically significant. However, when significant differences did emerge, they were heavily biased in favour of higher rates in freshwater taxa. Further comparison of evolutionary rates using alternative phylogenetic groupings (which contained greater numbers of taxa in each habitat type) revealed numerous significant differences with traditional statistical approaches, with freshwater taxa three times more likely to show higher rates than marine taxa. While use of phylogenetic comparative approaches substantially reduce the number of significant comparisons, almost all of the comparisons that remain significant represent instances where freshwater taxa display higher rates.

Main conclusions: Our findings provide some evidence that freshwater environments can encourage higher rates of phenotypic evolution. However, there are notable exceptions to the general pattern. These findings lay the groundwork for a deeper understanding of these emergent patterns, such as why the magnitude of habitat rate differences varies markedly across actinopterygian phylogeny, and the ultimate significance of these rate differences on other aspects of the evolutionary process.

A novel approach to define evolutionary units in Phanerozoic reefs

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Aim: Several researchers have attempted to subdivide the Phanerozoic record of reefs into discrete units. Modern analytical tools now enable an advanced categorization of Phanerozoic reefs and facilitate determination of underlying causes of large-scale reef evolution. The aim of this study is to subdivide the evolutionary history of reefs into discrete units to quantify evolutionary and ecologic change at the ecosystem level.

Location: Worldwide

Methods: Our analysis is based on the PaleoReefs Database (PARED). PARED currently holds data on more than 4200 Phanerozoic reef sites with geological, geographical, and paleontological information on every sampled reef. Using these data, regression tree analysis was applied to determine which parameters are most relevant for the ecologic change in reefs through time. Non-metric multidimensional scaling then classifies major Phanerozoic reef units.

Results: The four main parameter determining evolutionary and ecologic change of reefs are: Biotic composition, paleolatitude, nutrient availability, and bathymetry. The Neogene can be interpreted as an outstanding evolutionary reef unit based on the distinct composition of its coral-algal buildups. Cambrian and Ordovician reefs tend to be closer to the tropics and show a common trend in nutrient preference of their reef-builders. Slightly higher latitudinal distribution and high diversity of reef types account for the Jurassic as an own distinct reef unit. Reefs of the remaining stratigraphic are not clearly separated in terms of their attributes.

Main conclusions: Categorization of evolutionary reef units is mainly uncorrelated to stratigraphic systems, indicating a minor role of mass extinctions in reef evolution. Especially the Neogene can be identified as distinct unit based on the distinct composition of reef-communities.

Diversity dynamics of bivalves and brachiopods across the marine mesozoic revolution

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Aim: The aim of this study is to explore whether bivalves outcompeted brachiopods because of higher origination rates, lower extinction rates, or a combination of the two factors. The correlation of bivalve and brachiopod diversity dynamics will be through deep time to investigate if the modern bivalve dominance results from a competitive dominance of bivalves over brachiopods or whether bivalve diversity surpassed brachiopod diversity without directly harming brachiopod diversity.

Location: Data from the Paleobiology Database. This database contains global paleontological data from across the Phanerozoic.

Methods: Species occurrence information from the Paleobiology Database was binned into stages using the DivDyn package. Generalized first differences were run in order to remove autocorrelation and show the change in the three main diversity dynamics: diversity, extinction rates, and origination rate. Correlations between brachiopod and bivalve diversity were assessed for the whole Phanerozoic, the Paleozoic through the Early-Jurassic, and the Late Jurassic through the Pleistocene.

Results: Brachiopods and bivalves responded similarly to most biological events in the Paleozoic and early Mesozoic; extinction and origination rate as well as overall diversity were tightly correlated. However, all metrics of bivalve diversity decoupled from brachiopod diversity starting in the middle Jurassic. Antagonistic relationships between bivalve and brachiopod diversity were not observed at any time period.

Main conclusions: The current dominance of bivalve over brachiopods is not the result of competitive replacement but likely reflects differences in the adaptation to environmental conditions.

Facilitation of coral reef growth by coralline red algae – patterns during the last 150 million years

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Aim: Modern crustose coralline red algae (CCA) play a key role in the construction of coral reefs. It is unclear, however, if their function as consolidators of coral reefs was similar pronounced in the geological past. Accordingly, we tested (1) when the presence of CCA was crucial for the formation of coral reefs throughout the last 150 Ma. We further investigated if (2) the capacity of CCA to reinforce coral reefs suffered two transient crises as a result of the diversification of major herbivore groups.

Location: The study involves reef structures from tropical and subtropical environments on a global scale, ranging from the Cretaceous (145.5 Ma) to the Pleistocene (0.01 Ma).

Methods: For 736 reef sites, we tested if the fractions of coral reefs are positively correlated with the fractions of those reefs with CCA as secondary reef builders. Implementing generalized linear models (GLM), we tested if fluctuations in the functioning of CCA as secondary reef builders can be explained by the diversification of herbivores or other potential explanatory variables – sea level, $\delta^{18}O$, CO_2 and CCA species diversity.

Results: The presence of CCA was found to positively correlate with the abundance of coral reefs throughout the analysed period. Model results show that the probability that reefs contain CCA as major reef builders increases with CCA diversity and $\delta^{18}O$ while the presence of newly evolved herbivores has a negative effect. High correlations between explanatory variables limit the interpretation of model results.

Main conclusions: The presence of CCA is crucial for the formation of coral reefs. This facilitation suffered two crises probably linked to diversification of major herbivore groups. As CCA have evolved adaptations to grazing pressure they now facilitate the formation of modern coral reefs.

Macroecological patterns in the extinct cephalopod subclass Ammonoidea

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Aim: Ammonoids are important index fossils and model organisms for different paleobiologic approaches like the determination of evolutionary rates or paleobiogeographic reconstructions. Still, macroecological patterns are mostly unknown for this clade, albeit robust datasets to analyse such patterns have been gathered at least for the Paleozoic record. The aim of this study was to analyse occurrence and trait data for expected spatiotemporally patterns in the macroecology of Paleozoic ammonoids.

Location: Global.

Methods: Spatiotemporal occurrence data of Paleozoic ammonoids inherited from the database AMMON was combined with trait data on body size, shell morphotype, and embryonal conch diameter from new datasets and the literature. The patterns were analysed as multivariate linear models of each trait in relation to chronostratigraphic stage and paleolatitude. The model with the lowest Akaike information criterion (AIC) was chosen by stepwise model selection. Analyses were performed for all Paleozoic ammonoids as well as for each order separately. All analyses were performed with R.

Results: For most models a significant relationship between trait and paleolatitude and stage was found. Some orders significantly increased in body size over time. Shell morphotype changed systematically with latitude, probably reflecting differing environmental adaptations. Depending on order and temporal interval evidence for a “polar dwarfism” was found. In some cases, a trend to produce more and smaller eggs was also observed in the highest latitudes. Previously proposed trends to more nektonic morphotypes and smaller eggs in the earliest ammonoids could be supported by this study. Temporal morphotype patterns further indicate the presence of two major adaptive trends in Paleozoic ammonoids.

Main conclusions: Paleozoic ammonoids exhibited a variety of macroecological patterns, possibly due to different ecological strategies and temporal changes. In some cases, they clearly differ from most recent cephalopods, highlighting our current lack of knowledge on the paleoecology of these organisms and the importance of this pioneer study.

Recent developments in dental ecometric modelling

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Aim: Given communities of living or fossilized large mammals the aim is by analysing distribution of their dental traits to reason quantitatively about their climatic and environmental contexts, as well as evolutionary processes.

Location: The world now and in the past.

Methods: Dental ecometrics is a computational approach for modelling relationships between communities of large plant eating mammals and their edible environments. The methodologies have been developed in the Helsinki evolutionary palaeontology community over the last twenty years.

Results: The talk will highlight how and when this methodology works best, as well as recent developments of tailored solutions for estimating palaeoclimate and climatic extremes, vegetation cover and productivity. An outline of recent efforts to take into account metabolic scaling and energy tradeoffs within and across faunal communities will be presented.

Thursday, 14th March 2019: Session 8 (9:30-10:30)

The complex history behind biodiversity in mountain ranges: new insights from a synthesis of the two old fields of geology and biogeography

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Aim: To understand the history behind mountain biodiversity, and in particular, how regional biota responded to environmental changes associated with surface uplift.

Location: Anatolia (Turkey), a region characterized by a dynamical template of topography (and related environmental factors) for the evolution of biodiversity.

Methods: We reconstructed the Anatolian paleogeography (approximately 13-5 Ma) using multiple lines of evidence, including oxygen isotope-based paleoelevations and a series of geological observations, particularly to establish the time line of surface uplift in different parts of the Anatolian plateau. We then compared this time line to the history of vegetation system transition and mammalian faunal turnover, both of which were reconstructed from the fossil record of paleofloras and paleofaunas.

Results: Paleogeographic reconstructions show that the plateau interior and the margins did not rise simultaneously, the impacts of which can be detected in the compositional turnover of regional floras and faunas. In particular, the plateau interior and margin areas show different patterns of faunal composition turnover, following the beginning of the uplift in the reciprocal regions. In addition, the distribution of species body size in the Anatolian fauna (as a whole) also shows complex temporal patterns that appear to reflect the surface uplift as well as the rise and fall of the Pikermian paleobiome at a larger scale (central Europe).

Main conclusions: Our results suggest a significant role of the spatial dynamics of lineages in shaping the regional faunas. Further, the environmental changes associated with surface uplift probably worked in concert with the larger-scale changes (e.g. paleobiome transitions across Eurasia and the global climate cooling since late Miocene) to drive various biodiversity dynamics. Overall, this case study demonstrates the value of an interdisciplinary approach: integrating geology and biogeography to understand how biodiversity changed in relation to the spatial and temporal variation in different, but interactive environmental factors.

Climate-mediated changes in the functional composition of dung beetle communities determine rates of dung decomposition along extensive environmental gradients on Mt. Kilimanjaro, Tanzania

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Aim: Mountain biodiversity is increasingly threatened by anthropogenic climate and land use changes, with little understood consequences for ecosystem functions. Here, we investigate direct and indirect effects of climate and dung beetle functional composition on rates of dung decomposition along a 3600 m elevational gradient.

Location: Mt. Kilimanjaro, Tanzania.

Methods: Dung beetles were collected with baited pitfall traps on 66 study plots along the elevational gradient. Simultaneously, we conducted an exclosure experiment on all plots to explore the impact of different extinction scenarios on dung decomposition, consisting of three treatments: the first comprised cow dung piles accessible to the whole dung beetle community, the second excluded large dung beetles, while the third did not allow decomposition by any dung beetles. We applied path analysis to unravel the effects of climate, dung production and dung beetle richness, body size and biomass on decomposition.

Results: Dung decomposition rates declined with increasing elevation and was, on average, highest for open pads, intermediate for treatments excluding large dung beetles and lowest for treatments barring all dung beetles. Path analysis revealed that climate-mediated changes in dung beetle abundance and body size were the major drivers of dung decomposition by whole dung beetle communities, while species richness became increasingly important when large dung beetles were excluded from the dung. Temperature was the major driver of dung decomposition in the absence of dung beetles.

Main conclusions: This study shows that the functional composition of species assemblages, which is mediated by climate, strongly influences ecosystem functions. Our results emphasises the importance of large dung beetles for maintaining high rates of dung decomposition. Their loss from ecosystem will probably be connected with a strong decline in decomposition rates. Therefore, the conservation of intact dung beetle communities in mountain ecosystems is pivotal to ensure ecosystem service provision in the future.

Nutrient utilization by tropical ant communities along three extensive elevational gradients: a cross-continental comparison

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Aim: We studied the elevational trends in feeding preferences in ground ant communities in three different tropical mountain regions. We focused on the changes in nutrients utilized relative to elevation and seasonality (dry and wet seasons) using three diversity parameters i.e., species richness, species occurrences and relative nutrient use.

Location: Ecuador (Eastern Cordillera), Tanzania (Mt. Kilimanjaro) and Papua New Guinea (Mt. Wilhelm).

Methods: We exposed six types of experimental baits (treatments) in several sites along each of the three elevational gradients (5 replicates per site and per season; elevational min. 200 m to max. 4000 m): 1) CHO (20% sucrose), 2) NaCl (1% salt), 3) Amino acid (20% L-Glutamine), 4) CHO + amino acid (honeydew mimic), 5) lipid (pure olive oil) and 6) Pure H_2O (as a control).

Results: Both ant species richness and individual species occurrences at baits declined with increasing elevation indicating its strong effect on the communities in all three gradients. However, there were significant differences between the gradients due to interaction effects between region and season. The relative nutrient use by the ant communities were not consistent among the three regions as preferences for each of the nutrients varied with elevation and season differently, indicating variation in nutrient requirements between the regions.

Main conclusions: General trends in ant diversity and activity are similar across mountains i.e., decreasing along elevational gradients. However, the regions vary in the ant activity between dry and wet season, and there is also no consistency in the relative nutrient use by ants. These spatial and temporal variations in nutrient requirements by natural ant communities along elevational gradients are probably driven by differences in their nutrient limitations (i.e. forest net primary productivity) and in composition of their communities among the regions.

Climate and food resources shape species richness and trophic interactions of cavity-nesting Hymenoptera on Mt. Kilimanjaro

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Aim: Climatic conditions, the availability of resources and top-down regulation are major drivers of biodiversity patterns and biotic interactions. Host-antagonist systems are especially sensitive to environmental change because many antagonists depend obligatorily on the ecology and physiology of their hosts. However, little is understood at which conditions specific predictors of diversity become more important than others.

Location: Mt. Kilimanjaro

Methods: Using trap-nests colonized by bees and wasps, and their natural antagonists as a model system, we investigated the combined effects of climatic conditions, resource availability and top-down effects on the species richness and biotic interactions along a 3370 m elevational gradient at Mt. Kilimanjaro, Tanzania. Trap-nests were installed at ground and canopy level in a total of 41 study sites in natural and agricultural habitats. We controlled trap-nests monthly over 15 months and packed incubated reed stalks in metal nets to collect hatching bees, predatory wasps and parasitoids for later identification. Floral resources and climate were continuously monitored.

Results: In total, we recorded 14,937 broodcells of bee and wasp nests, with 81 morphospecies of hosts and 49 morphospecies of antagonists. We found, first, changing elevational species richness patterns between trophic levels, second, that temperature was the most important predictor for Hymenoptera at different trophic levels, but food resources gained increasing importance at higher trophic levels and, third, that higher parasitism rates occurred with higher temperature and higher trophic levels.

Main conclusions: Since the proportion of hosts and their antagonists strongly changed with climate, it is likely that host-antagonist interactions will shift with climate change, which would also affect the ecological function antagonist species play as regulators of host densities.

Thursday, 14th March 2019: Session 8 (11:00-12:30)

Global diversity and biogeography of vascular epiphytes

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Aim: Vascular epiphytes represent a unique plant growth form – being functionally dependent on a host tree for structural support and reliant on atmospheric humidity to meet their water requirements. However, global plant diversity studies generally focus on explaining species numbers, and rarely consider variation in plant growth form. Here, we focus solely on the epiphytic growth form and present the first global analysis of vascular epiphyte diversity and biogeography.

Location: Global

Methods: Using a combination of the Global Inventory of Floras and Traits (GIFT) database, and a comprehensive checklist for vascular epiphytes that includes 28,168 species, we explored global trends in epiphyte diversity.

Results: Epiphyte diversity was skewed towards the tropics, with outstanding diversity along the Ecuadorian and Colombian Andes, and significantly increased with increasing area, elevation, precipitation, and forest cover, but decreased with increasing precipitation seasonality. Additionally, we found strong asymmetries in epiphyte diversity with increasing latitude – with epiphyte diversity displaying a much stronger negative relationship with latitude in the northern hemisphere relative to the southern hemisphere.

Main conclusions: Given their aerial habit and thus intermittent water supply, epiphytes are likely more restricted to humid tropical forests relative to terrestrial growth forms. Similarly, asymmetries in the latitudinal diversity gradient between hemispheres can be linked to the steeper decline in temperature in the northern hemisphere, thus implicating an intolerance to frost. Our results highlight that while epiphytes account for 9% of the world's vascular flora, they can represent a huge proportion of the total vascular flora in tropical montane regions.

Species diversity and vegetation structure drive functional organization of avian communities along a continental-scale latitudinal gradient

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Aim: Disentangle direct and indirect effects of vegetation structure on functional diversity of avian communities

Location: Australia

Methods: In 2016 and 2017 we established 21 sites along a latitudinal gradient spanning 3000 km along the east coast of Australia from the tropics to temperate regions. All sites were situated in Eucalypt woodlands and open forests. At each site, we surveyed three transects, each 2 km long. We quantified foraging behavior of all songbirds (Passeriformes) in terms of foraging method (n = 8; e.g. gleaning, flycatching, snatching) and substrate used (n = 8; e.g. leaf, bark, ground). We thus obtained individual- and abundance-based functional (behavioral) diversity for each site. We also surveyed vegetation at the transects (n = 630 sampling plots) in terms of the height and cover of vegetation layers (ground, shrub, subcanopy, canopy).

Results: Altogether, we recorded 5894 prey attacks by 2624 bird individuals (2.25 prey attacks per individual) belonging to 112 species of songbirds. Canopy height varied from 10.3 m in dry areas to 31.5 m in moist areas. Moister areas with higher canopy and richer vegetation structure had more bird species and higher functional diversity. Using path analyses, we disentangled independent effects of vegetation structure and species richness on functional diversity. Functional diversity increased with species richness (which increased with the number of individuals recorded), but also independently with vegetation structure. Thus, we showed that structurally rich vegetation not only supported more individuals of more species, but also communities with higher functional diversity.

Main conclusions: We obtained uniquely detailed data on foraging behavior of birds along a continental-scale latitudinal gradient. We showed that vegetation structure was a critical aspect of Eucalypt woodlands and forests in eastern Australia that shaped bird abundance, species richness, and functional diversity.

Trends in German Plant Distribution – a synthesis study across six decades

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Aim: Synthesize plant occurrence data across Germany

Location: Whole Germany

Methods: We built on the Frescalo Algorithm developed by Hill (2012) to elucidate changes in species distribution from pure occurrence records. Synthesizing plant occurrence data from federal organizations as well as from vegetation plots distributed across Germany, we aimed at analysing trends in species occurrences. We extended toe Frescalo Anylsis to a framework that allows for spatial as well as temporally explicit analysis of trends in plant species distribution in Germany.

Results: We compiled a dataset of a total of 28 Mio plant species records from 1960 to 2017. Species showed positive as well as negative trends in their distributions. There were more species declining in occupied area than those increasing. Potential drivers can be analysed in future research.

Main conclusions: Our method allows combining data on plant occurrence from different sources and is able to evaluate changes across space and time. At the same time our method is flexible enough to allow the incorporation of possible drivers, extending the possibilities of the original method.

Using sPlot - the global vegetation plot database - to explore global patterns of plot-specific plant species pools

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Aim: Focusing on species pools, i.e. all species present in a region that can both disperse to and potentially persist in a focal locality, is a promising approach for exploring global patterns of biodiversity. It allows controlling for stochastic variation due to site-specific idiosyncrasies and sampling artefacts, and for the effect of sampling grain. We use the data contained in the 'sPlot' database, a vegetation-plot database incorporating more than 1.1 million plots worldwide, to produce the first standardized global maps of species richness density and site-specific species pool size.

Location: Global

Methods: For each plot, we first defined a probabilistic set of species that may co-occur with the species of the target community based on Beals' index of sociological favourability. We then extracted all plot records that fulfil a minimum similarity criterion within a given geographical distance to build empirical species area relationships and estimate the size of the target plot's species pool, as well as species richness density at different spatial grains. Finally we modelled how species richness density and pool size varied along the main macroecological (climatic, soil) gradients using boosted regression trees.

Results: The global pattern in species richness density differs markedly from the pattern in species pool size. Macroecological gradients were important predictors of both metrics, but the relative importance of different variables changed across scales.

Main conclusions: The relative role of macroecological factors at influencing biodiversity varies across scales, and determine different patterns of biodiversity at fine and coarse geographical scales. By comparing biodiversity patterns at multiple scales, we can infer the relative importance of macroecological vs. local environmental conditions in shaping local plant communities and biodiversity patterns across regions.

Trends in the conservation status of the global centres of plant diversity during the last 25 years

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Aim: I analyse trends in the conservation status of the global centres of plant diversity during the last 25 years using data on human population density, protected area coverage, and deforestation.

Location: global

Methods: Using the 'World Database of Protected Areas', the 'Gridded Population of the World', and global forest change data, I analyse the trends of (1) human impact and (2) protected area coverage in the 20 global centres of plant diversity identified by Barthlott et al. 2005. The results of these analyses are used to classify the plant diversity centres according to conservation risks and conflicts.

Results: More than 1 billion people live in the 20 global centres of plant diversity. Between 1990 and 2015, overall human population in these centres increased by 289 million people or 37 percent. Fourteen percent of the global human population growth thus took place on just 5.2 percent of the continental surface area. Mean population density is almost twice as high as the global average. In most centres, it also exceeds the respective regional averages. Protected area coverage increased by at least 5 percent of their total area size during the last 25 years in 18 of the 20 centres. The CBD Aichi target 11 (conservation of at least 17 percent of the land surface) is already met in 11 centres. Eight centres have both below average protected area coverage and above average (and still increasing) human population density. Very high rates of forest loss during the last 15 years are documented especially for many of the SE Asian centres.

Main conclusions: High human population densities and large scale logging within the global centres of plant diversity severely limit the potential for the further extension of the protected area coverage.

Poster presentations: Tuesday, 12th March 2019 (18:00-20:00)

Global diversity patterns and drivers of plants

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Aim: I will examine the relationships between historical and contemporary environmental factors and observed vascular plant species richness from small/local grain size (e.g. small islands and protected areas) to large/regional grain size (e.g. countries and biogeographic regions) and from the continental to global extent, based on a unique global data set of plant species distribution information (GIFT; http://gift.uni-goettingen.de).

Extending previous attempts and using modern methods, the resulting global combined multi-predictor geostatistical model will be able to predict plant diversity at various spatial grain sizes from local to regional scales. Specifically, I will quantify the relative importance of different sets of environmental variables (area and connectivity, local site conditions, past and present climate, and biogeographic history) for plant diversity at the different spatial scales.

Location: Global

Methods: The analyses planned will be carried out based on checklist data from GIFT, which is a global collection of regional plant checklists that integrates ecological, paleogeographic and phylogenetic information for macroecological analyses.

Putative predictor variables describing the contemporary environment comprise the current climate, environmental heterogeneity and geographic connectivity. To understand the relationship between historical drivers of plant assembly and the present-day structure of plant diversity jointly at regional and local scales, I will include the past biome distribution, past climate and idiosyncratic historical events.

The ADAPT project: Adaptation of alpine pollinators in times of global change

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Aim: Alpine ecosystems are particularly affected by climate change: first, temperature rises much faster here than the global average. Secondly, alpine habitats harbor a unique diversity of animal and plant species, including many cold-adapted organisms that find the last suitable climatic conditions in the highlands. ADAPT aims to understand how the rapid shift of temperature affects alpine pollinators, plants and their mutualistic interactions. We are particularly interested in the mechanisms and limits of potential adaptation processes to warmer temperatures at different levels of biological organization, i.e. from a community level down to molecular processes within pollinator individuals.

Location: National Park Berchtesgaden (German Alps)

Methods: In 2019, we will record pollinator and plant species, and their interactions on 34 grassland sites along elevational gradients in the National Park Berchtesgaden and compare it with identically sampled data from 2009. We will measure physiological, morphological and behavioural traits and try to link them with species responses to climatic changes. *Bombus lucorum* colonies will be reared in semi-automated nesting boxes along the elevational gradients, in order to track bumblebee colony performance *in situ* under different climatic regimes. In 2020, those colonies will be transplanted to lower elevations, to investigate the adaptation potential of bumblebee colonies to warmer temperatures and shifting plant/ parasitoid communities. Parallel transcriptome and microbiome analyses are supposed to reveal potential mechanisms behind adaptation processes.

ADAPT is a junior research group within the Bavarian Network of climate change research (BayKliF).

Results & Main conclusions: This poster presents concepts and methods.

A framework for analysing cross-taxon biodiversity trends in central Europe

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Aim: We present a framework for the development of future projections for animal diversity based on an integration of occurrence and environmental data across scales and animal groups.

Location: Bavaria, Germany

Methods: We combine distribution data on four ecologically and physiologically different animal taxa (birds, butterflies, dragonflies and grasshoppers) based on survey data over the course of more than 30 years. We provide an assessment of the biases in the data used for our analyses, and, after accounting for these biases, we explore population declines and range shifts of selected taxa as well as changes in species communities in Bavaria using species distribution models.

Results: While our poster will focus on a conceptual outline of the different elements and steps of integration across scales, data, and taxa, we also aim to present an overview on the first, preliminary results.

Main conclusions: Our conceptual framework highlights both opportunities and challenges of integrative approaches that use occurrence data across taxa as well as environmental data across scales. Even if such multi-dimensional integration remains ambitious, it is the way forward to develop more realistic and policy-relevant projections of potential biodiversity change.

Foraging specialization and niche overlap in Australian songbirds

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Aim: Niche partitioning is presumed to play a prominent role in shaping species richness by facilitating species coexistence. The assumption is that narrow specialization enables finer partitioning of resources and thus enhances local coexistence of species and allows higher species richness. While niche partitioning is assumed to be most important on fine spatial scales shaping local coexistence of species, the role of abiotic conditions and historical effects should be more prominent on coarser regional scales shaping spatial variation in species richness.

Location: Australia and Tasmania.

Methods: We used comprehensive data on five sets of ecological traits in Australian songbirds (Passeriformes) to test the specialization-richness relationship across three spatial scales. We not only employed commonly used coarse habitat and diet categories to calculate specialization, but also used detailed data on foraging (stratum, substrate and method used by birds when foraging), which might play prominent role in fine niche partitioning.

Results: Richness-specialization relationships were steeper and stronger at regional scales than at the local scale. Positive richness-specialization relationships were equally common in assemblages both exceptionally species rich and exceptionally species poor for given environmental conditions. Finally, we found that species partition the ecological space in terms of what part of vegetation they forage on, but not in terms of the foraging method they use for obtaining food.

Main conclusions: We showed that species richness and specialization in Australian songbirds were often tightly related, but the relationship changed between individual ecological and behavioural traits and across spatial scales.

The extinction-abundance relationship through deep time

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Aim: Fatal virus infections or other biotic interactions are suggested to have caused sudden extinctions of well-stablished and globally widespread plankton microfossils. These species disappear rapidly after reaching peak abundances in the fossil record. The suggested pattern contrasts with the observation of a decreasing extinction risk with increasing species abundance. Investigating the extinction-abundance relationship with well resolved fossil occurrence data will allow resolving this mismatch of observations, thereby contributing to the ongoing debate whether extinction risk is independent from a clade's age (Red Queen hypothesis) or if extinction risk is clade-age-dependent. An age dependent extinction risk is indicated by occurrence trajectories following a slightly positively skewed hat-shape that shows a rise and fall of species (systematic waxing and waning of species).

Location: Global calcareous nannofossil occurrence as available from deep-sea ocean drilling programs throughout the Cenozoic.

Methods: The interaction between extinction-risk and abundance was studied by analysing the fate of calcareous nannofossil species throughout the Cenozoic. Targeting for population crashes we tested if the magnitude of abundance declines systematically exceeds abundance increases (linear regression). We further analysed if abundance trajectories of single species resemble the systematic waxing and waning proposed by mean occurrence trajectories and how that pattern is influenced by sampling biases and time binning. Furthermore, we address the question whether there is a phylogenetic signal that can be observed among the trajectories, and how species' occurrence trajectories relate to important Cenozoic climatic events.

Results: There is little evidence that severe abundance decreases occur more often than abundance increases of similar magnitude. Mean occurrence trajectory over multiple species mask very different trajectories of single species hiding underlying processes. The choice of time bins as well as the removal of zero abundance records highly affects observed patterns.

Main conclusions: Species abundance trajectories of different species do not follow systematic patterns through time. A detailed investigation is hindered by strong effects of sampling bias and data manipulation. Abundance estimates need to acknowledge that occurrence probabilities in the fossil record are influenced by two self-enforcing filters: a taphonomic filter with a higher chance for more abundant species to become fossils, and a detection filter with a higher chance of detection those more abundant fossils. Focussing on drilling cores with systematic presences and true absences information can improve the statistical power of analyses.

EpIG, the epiphyte inventory group database

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Aim: We present EpIG, a global initiative that brings together vascular epiphyte inventory data from across the world and makes it available to the research community.

Location: Latin-America (currently).

Methods: Data comprise complete samples of vascular epiphyte species composition and abundance recorded in a well-defined area (a tree or in most cases a plot), thus following the general procedure of community sampling, but here restricted to a single (hyper-diverse) plant community. Data are standardized using TurboVeg database manager and a protocol adapted to this particular life form. Nomenclature is revised through a comprehensive taxonomic list of vascular epiphytes defined by the EpIG consortia and then standarized to global checklists using the package Taxonstand.

Results: We have compiled 60 epiphyte datasets from nine countries and over 20 regions of Central and South America that span elevations from the sea level till over 3 000 m a.s.l. Most datasets provide abundance data as well as presence-absence data. The average number of sampling units is ca. 180, the average species richness 60 and the average abundance ca 900 individuals. We plan to further increase the number of datasets and expand the geographical distribution worldwide. We use this database to assess large-scale variation and drivers of alpha diversity of epiphytes in the Neotropics as well as continental scale patterns of epiphyte beta diversity. The database will be soon associated with the consortium sPlot.

Main conclusions: Vascular epiphytes are amongst the least studied components of diversity in the tropics despite their very high diversity, as reflected in a large number of datasets which have been collected throughout the Neotropics. With this initiative, we want to move from idiosyncratic local studies to “thinking big” in epiphyte ecology.

Domination and invasion of Spartina Alterniflora cordgrass in Yancheng Rare Birds Natural Reserve as sensed by Satellite Remote Sensing from 2003-2018.

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Aim: To ascertain the dominating cordgrass, Duration it takes for the invasion from the shoreline towards inland of the natural reserve restricted area as there are many local and introduced cordgrass habituating the zone and its coastal wetlands, using Remote sensing technology.

Location: Yancheng Rare Bird Natural Reserve.

Taxon: Salt marshes.

Methods: Retrieving 15 years Landsat Tm satellite data of two seasons of the year, showing exclusively the spatial, spectral and temporal location of the restricted zone. Envi software used for the classifications, radiometric and atmospheric corrections of the data to show a true data and performing NDVI in the restricted area.

Results: Spartina Alterniflora marshes appears to be the only invasive plant in the region, having a thick forest or bush within the shoreline/tidal flats and spreading rapidly and invading other local or introduced salt marshes within the restricted zone.

Main conclusion: Spartina Alterniflora shows to be most visible and healthy cordgrass as sensed by the satellite data and will dominate and invade other cordgrasses within a period in the restricted zone without any human factor or interference.

Will arctic reefs disappear with ongoing global change?

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Aim: The coralline red algal species *Lithothamnion glaciale* forms rigid frameworks of magnesium calcite. In the high Arctic, these so-called rhodoliths cover large areas of the Svalbard shelf. Thereby, the calcified structures act as ecosystem engineers, comparable to corals in tropical regions, providing habitat for a large variety of organisms. Furthermore, drilled by boring mussels, many rhodoliths become hollow ecospheres and their interior is intensely colonized by benthic macro- and megafauna. Within this study, we investigate whether the distribution pattern of these arctic reefs will be affected by ongoing global change. Rhodolith beds occur worldwide and have similar ecological impact. Because the effects of global change are projected to be most severe and fast within the Arctic, this ecosystem represents a very appropriate model also for the global impact on rhodolith communities.

Location: This study involves rhodolith beds around the Svalbard shelf in the high Arctic.

Methods: The distribution of *L. glaciale* is linked to local ranges of physical parameters like temperature, pH, light regime, and salinity. Following the RCP scenarios provided by the IPCC, we estimate the influence of anticipated large-scale shifts on the rhodoliths. Based on these results, we analyse the future functioning of rhodoliths as niche-providing ecosystem engineers.

Results: The first results of this ongoing study indicate that increasing temperatures enhance the respiration of the algae. However, this effect will be outcompeted by reduced water transparency – and therefore reduced photosynthesis – induced by deglaciation.

Main conclusions: The geographical distribution of Arctic rhodolith beds is threatened by global change. Due to their key role as ecosystem engineers, this might also result in a decrease of Arctic biodiversity.

Range size predicts the risk of local extinction from habitat loss

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Aim: The abundance and spatial distribution of a species are not independent. Species with small geographic ranges tend also to have smaller local populations. The range size of species therefore may be a predictor of the risk of local extinction from anthropogenic change. We assess the relationship between probability of local persistence and amount of habitat loss for species with small and large ranges.

Approach: We collate 70 million occurrence records of 180,000 species of vascular plants from three biodiversity data-sharing networks. We combine these with global land use change data to find grid cells (quarter degree) with biodiversity data before and after habitat loss. We examine changes in the frequency distribution of the range sizes of species before and after habitat loss. We expect a net loss of small ranges. Next we find for each species and grid cell it has occupied the amount of habitat that remained at its last record. We hypothesize that species with small ranges withstand less habitat loss.

Results: The median of the species-range-size frequency distribution was higher after habitat loss. In addition, the persistence curve of species with small ranges descended more steeply with the amount of habitat loss compared to species with large ranges.

Main conclusions: Range size can predict local extinction risk from habitat loss. This has two important consequences. First, species with small ranges are disproportionately more vulnerable to global extinction. Second, habitat loss creates a linkage between temporal and spatial species turnover, in that the former decreases the latter. Our findings therefore also provide empirical evidence of biotic homogenization.

Trophic network comparison of the Paratethys, Mediterranean Sea and Barents Sea based on ichthyofauna

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Aim: Determining environmental differences using trophic network properties.

Location: Paratethys, Mediterranean Sea, Barents Sea

Methods: Based on the ichthyofauna of the Paratethys in the Oligocene, the Mediterranean Sea and the Barents Sea, trophic networks have been modelled on family level. Data of the fish families included in the networks were provided by publications of Bienkowska (2010) for the Paratethys and of Goren et.al. (2016) for the Mediterranean Sea, and for the Barents Sea a bachelor's work of Friedsam (2017, unpublished) was used. Food habits, maximum, minimum and common sizes of all families were identified by further literature research. With this, trophic links have been interpreted and entered in matrices in Microsoft Excel. Based on these matrices the networks have been created with RStudio and the packages "Igraph" and "NetIndices". The "NetIndices" calculated the values of total taxa richness S, number of all trophic links L, the links density and the Connectance C and the trophic levels of all taxa.

Results: The results show lower values of links, link density, connectance and almost all trophic levels of taxa for the Barents Sea as an open system in comparison with the other oceans. The trophic levels of the Barents Sea taxa are never reaching a trophic level of four. The comparison of the two isolated oceans showed that the Paratethys has lower trophic levels for all fishes, whereas the Mediterranean Sea is characterized by higher levels.

Main conclusions: Trophic network analysis showed that the Barents Sea has continuously lower values of links, link density, and connectance indicating an intrinsic difference compared to the other two oceans. This lowering of trophic level probably derives from the influence of adjacent oceans to the Barents Sea.

Megachilid bees in pollination networks

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Aim: Solitary bees provide invaluable services as pollinators in every landscape with flowering plants. Our aim was to investigate their foraging preferences and gain essential information on their association with specific plant species.

Location: Northern Bavaria, surface=886 km^2

Methods: Solitary bee nests were collected with the use of trapnests, established at 15 localities throughout the study region. While conventional pollen identification with the use of microscopy is limited in terms of accuracy and throughput, the use of genetic markers allowed us to identify plant species from samples of mixed pollen. We used DNA metabarcoding of the ITS2 gene in order to examine the composition of pollen provisions from 150 bee solitary nests belonging to seven megachilid bee species.

Results: We found pollen from over 400 plant taxa in the pollen provisions of the collected bee nests. In the nests of three oligolectic bee species, pollen consisted mainly of one plant family, while the pollen provisions of the rest four bee species consisted of more; the overall plant diversity discovered in the nests of the latter, however, was not higher. Moreover, we constructed a plant-pollinator interaction network, associating each bee species with specific plant species. Finally, we highlighted several specialized relationships between plant and bee taxa and distinct ecological niches for each bee species included in the study.

Main conclusions: Specialized bee-plant relationships indicate the importance of bee diversity for the efficient pollination of a wide variety of plants. On the bee-side, these interactions highlight the significance of plant availability for their nutrition, as well as for the acquisition of floral chemical compounds or bacteria, which may be necessary for a suitable nest environment ensuring successful offspring recruitment.

Distribution of functional types of freshwater macrophytes across Bavarian lakes

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Aim: Freshwater ecosystems are highly vulnerable to environmental change. For instance, increasing water temperatures due to Global warming or enhanced turbidity in consequence of more intense land use can cause severe alterations like algae blooms. Macrophyte communities may respond to those changes as their physiological processes, and thus also geographical distribution, are highly dependent on environmental factors such as light, temperature and nutrient availability. However, most studies on macrophytes focus on physiological equilibrium shifts, feedback with plankton, or on single (invasive) species, with little quantification of diversity distributions and underlying processes. Therefore, our aim is to assess how freshwater macrophyte diversity is distributed along environmental gradients.

Location: Lakes across Bavaria. Bavaria has a wide range of lake types from low mountain lakes up to layered alpine lakes.

Methods: We classify occurring macrophyte species into functional types. Open source occurrence data from the Water Framework Directive for 53 lakes are used to describe the spatial distribution of macrophyte types and analyse their distribution in different abiotic conditions within and across lakes.

Results: Bavaria has a variety of more than 100 different macrophyte species and 16 different growth forms. The most diverse lakes are “Chiemsee” and “Starnberger See” with 38 different species. Preliminary results show that 1) species richness and composition vary across and within lake types; 2) species richness and composition vary along the depth gradient within lakes and across macrophyte functional types.

Main conclusions: The distribution of macrophyte composition has the potential to refine lake type classification, which may assist conservation efforts. The quantification of the lake depth diversity gradient may also assist in our understanding about factors driving richness gradients. Statistical models will address the drivers of diversity and distribution of macrophytes. Significant drivers will inform eco-physiological models assessing macrophyte diversity response to environmental change.

Modelling Species Invasions on oceanic islands

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Aim: Across the world, species invasions threaten ecosystem stability and have led to numerous extinctions. To better understand the factors affecting invasion success, we investigated the relative importance of ecosystem productivity and disturbance, as well as propagule pressure.

Location: *in silico*

Methods: We used an individual-based model for plants on a hypothetical island ecosystem to assess the dynamics of plant invasions. We predicted that high productivity, combined with high disturbance, would maximise invasion probability, as would high propagule pressure. The model is spatially and genetically explicit and includes a range of physiological and ecological processes. The island community was initialised with random species and allowed to stabilise before non-native species were introduced. Propagule pressure, productivity (proxied by temperature) and disturbance varied across scenarios. To address our hypothesis, we measured biodiversity variables throughout the run and counted the number of successful invasive species at the end of a simulation.

Results: Propagule pressure had a strong effect on invasion success. There was no significant effect for productivity and disturbance. Preliminary analyses assessing functional traits linked to invasion success reveal that environmental preferences followed by a mean dispersal distance were the most consistently important species-specific traits across simulated scenarios.

Main conclusions: Our findings agree with previous studies indicating the prominent role of propagule pressure on invasions, strongly indicating the importance of management practices that restrict propagule pressure. However, the importance of productivity and disturbance should be investigated further, as our findings do not align with general theoretical expectations. We expect that further contrasting the trait composition between native community vs. invasive species will provide additional insights.

Impact of oil palm cultivation on deforestation rate over the last three decades in the southwest of Colombia

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Aim: To identify the impacts of oil palm cultivation on the deforestation rate in southwest Colombia over 30 years.

Location: Southwest Colombia.

Methods: I classified, identified and assessed land use changes, fluctuations in carbon stock and deforestation in the southwest of Colombia, in three time periods (1985-2000-2015). I utilized classifications of Landsat images with an object-based and hierarchical approach and through multi-temporal and fragmentation analysis.

Results: The data showed that the area of oil palm cultivation increased over 30 years, with a growth rate of 260 ha/year (from zero to 8,557 ha). Moreover, deforestation resulted in the loss of 74.514 ha of forest and the transformation of 37.3% of the landscape. Additionally, the loss of this forest area generated carbon emissions of 11,177,115 tons of Carbon per year.

However, 67% (11,860 ha) of the tropical forests still retain the conditions of size, shape, and proximity among patches to maintain the biodiversity of the area.

Main conclusions: This study constitutes the first evidence of the impact of palm cultivation on deforestation in southwestern Colombia. The results show oil palm cultivation poses a threat to the conservation and maintenance of biodiversity in the rainforest.

The increase of oil palm crops is associated with the economic situation of the country and new policies supporting the investments in oil palm cultivation.

Finally, palm oil plantations are not the only driver of deforestation. Unfortunately, there is a lack of studies on land use changes and its consequences for deforestation.

Increasing numbers of rare species in local assemblages are related to more new species entering assemblages.

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Aim: Rarity is one component of biodiversity change yet to be explored at the global metaanalysis scale. Rare taxa, that is those represented by small numbers of individuals, are often make up the largest fraction of species in local assemblages, particularly at lower latitudes. The small population sizes of rare taxa however make them vulnerable to anthropogenic impacts. We aim to address this knowledge gap by asking whether there has been a shift in assemblage structure as a consequence of the change in the pattern of rarity, and relate these findings to shifts in species richness.

Location: Global

Methods: We used a subset of 120 studies with ≥10 years of data from the BioTIME (biotime.st-andrews.ac.uk) global database of assemblage time series. We quantified rarity as the fraction (and number) of singleton and doubleton species, and additionally used Fisher's alpha as a measure of assemblage structure sensitive to rarity. We evaluated patterns against a null model based on a cyclic shift permutation and used a mixed model to assess overall trends.

Results: Our analyses indicate a systematic change in the rarity component of assemblages, with rare species (as defined in our analysis) becoming more numerous. This shift can be partly explained by increasing immigration of species into assemblages.

Main conclusions: Our results suggest that new species entering assemblages in low numbers are maintaining or increasing local species richness. The causes of this increasing immigration are unclear, but may relate to climate migrants and invasive species. Regardless, these results point to widespread restructuring of the world's ecological assemblages with far-reaching consequences for ecosystem functioning and conservation initiatives.

Static landscape, uplift availability and energetics of soaring birds across Europe

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Aim: Investigate the relationship between static landscape features, uplift availability and energetics of soaring birds in order to produce a static map of uplift suitability across Europe.

Location: Europe

Methods: Soaring birds rely on atmospheric uplifts to move across the landscape. Uplifts result from the interaction of local weather conditions with the underlying landscape structure. So far, the energy available in the landscape and the cost of transport of soaring birds have been mainly studied in relation to the weather information. Here we compared the accuracy of static landscape features and commonly used uplift estimators (based on weather information) in predicting the flight behaviour of an obligate soaring species, the white stork *Ciconia ciconia*. We used soaring and flapping flight locations of 60 storks as proxies for the presence and absence of uplifts. We then tested if static landscape features alone could predict and map the availability of uplifts across Europe.

Results: We found that storks encountering fewer uplifts along their routes, as predicted by static landscape features, suffered higher energy expenditures, approximated by their overall body dynamic acceleration. This result validates the use of static features as uplift predictors and suggests the existence of a direct link between energy expenditure and static landscape structure.

Main conclusions: Our uplift availability map provides a base to explore the effects of changes in the landscape structure on the energy expenditure of soaring birds, identify low-cost movement corridors and ultimately inform the planning of anthropogenic developments.

Emergence of two solitary spring bees advances less strongly with warming temperatures than flowering of an early spring plant

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Aim: Species-specific phenological shifts as a response to climate warming have the potential to alter plant-pollinator interactions. However, the effect of temperature on the emergence phenology of solitary bees and on the flowering phenology of their food plants is barely known.

Location: Our study was located on eleven calcareous grasslands in an area of about 840 km^2 around Würzburg, Germany.

Methods: To study the effect of temperature on the emergence phenology of the two spring bee species *Osmia cornuta,* which is one of the first solitary bee species to emerge on the study sites, and *Osmia bicornis,* we placed bee cocoons on eleven grasslands, which differed in mean site temperature. We furthermore studied on seven grasslands the effect of temperature on the flowering phenology of the plant *Pulsatilla vulgaris*, which was the first plant species to start flowering and is visited by both *Osmia* bee species.

Results: A temperature increase of 0.1 °C advanced the first emergence of *O. cornuta* males by 1.2 days and of *O. bicornis* males by 1.3 days. Mean emergence of *O. cornuta* males advanced by 0.4 days and of *O. bicornis* males marginally by 0.2 days per 0.1 °C temperature increase. Females of both species did not shift their emergence. Flowering onset of *P. vulgaris* advanced by 1.9 days per 0.1 °C temperature increase, mean flowering by 1.3 days and flowering end by 6.7 days.

Main conclusions: Our results show that temperature advances bee emergence less strongly than flowering of one of its food plant, which may result in an increased risk of pollinator limitation for the first flowers of *P. vulgaris.*

Population change across Europe’s land abandonment hotspots

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Aim and methods: Land-use change is thought to be the greatest driver of change in terrestrial ecosystems across the Anthropocene. While much research has focused on land-use intensification, we know far less about the effects of land abandonment. Here, we asked 1) how rates of land abandonment in Europe vary over space and time, 2) what are the dominant land cover trajectories following abandonment, and 3) what are the temporal trends in vertebrate population abundance in areas with land abandonment.

Location: Europe.

Results and main conclusions: We found that land abandonment is accelerating across Europe, leading to pronounced land cover and ecosystem structure changes. We uncovered distinct land cover trajectories after abandonment, with grassland and shrublands concentrated in the mid-latitudes and woodlands occurring across the continent. In areas with abandonment, herbivorous mammal and carnivorous bird species showed population increases. As urbanisation and rural depopulation continue across Europe, land abandonment is increasingly growing in importance as a driver of large-scale alterations to habitats and biodiversity, with potential impacts for ecosystem function and services.

Defaunation affects carbon stock in tropical forests

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Aim: Animal loss is a silent threat of forest ecosystem. Tropical forests are becoming defaunated ecosystems, especially defaunated of large animals. The loss of animals goes beyond than the loss of charismatic animals, what we are losing are key interactions that modulate the functionality and therefore of the associated ecosystem services.

Location: Tropical Forest. Atlantic Forest. Brazil

Methods: We explore the potential effects of defaunation of large animals in carbon stock ecosystem services of tropical forest by analyzing 33 forest plot composition and a large dataset of 2014 tree species traits and more than 8000 frugivore interaction records. We test relations of dispersal and carbon traits. In each plot, we simulated extinction of large seeded trees (with reposition of trees) and observed the carbon stock potential behavior. We explore the effects of defaunation in disperser and predator communities in a field experiment with *Cryptocaria mandiocana,* a large seeded tree with high carbon stock. Finally, we explore the carbon potential of 961 restoration projects.

Results: We found that the carbon stock ecosystem service is supported by large animals due to large frugivores are the main dispersers of large-seeded trees and, large-seeded trees tend to be tall trees with dense wood, therefore, store high quantities of carbon. Moreover, strong defaunation effects in the seed predator communities can also affect the carbon stock potential of the forest. In addition, we explore the impact of defaunation and carbon stock relation in conservation programs. We show that reforestation projects are promoting defaunated ecosystems because they are dominated by abiotic trees or small-seeded trees, which will not provide enough food to large animals.

Main conclusions: We argue the urgent necessity of integrating the animal role in reforestation and climate mitigation strategies such as REED+ markets to protect forests from ‘defaunation fronts’.

Minicourses and discussion panels

Minicourse: Animal Movement Analysis

Anne Scharf[1], Jakob Schwalb-Willmann[1]

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Background: Animal movement is critical for maintenance of ecosystem services and biodiversity. The study of complex movement patterns and of the factors that control such patterns is essential to inform conservation research and environmental management. Technological advances have greatly increased our ability to track, study, and manage animal movements. But analyzing and contextualizing vast amounts of tracking data can present scientific, computational, and technical challenges that require scientists and practitioners to master new skills from a wide range of computational disciplines.

Our offer: In this workshop we will visualize, explore and perform basic analysis of animal movement data. We will give an insight into Movebank (database of animal tracking data) and how to get these tracking data into R. Additionally to visualizing, manipulating and analyzing the movement data in R, we will relate these to remote sensing data. Finally we will animate the movement of animals over time on a static or dynamic background of remote sensing data.

We will provide course materials in form of R scripts. Participants should bring a laptop with R and RStudio installed. Please also install the packages *raster*, *move* and *moveVis* and their dependencies.

Maximal number of participants: 10

Requirements: Every participant should bring a laptop with R installed.

Minicourse: Towards more mechanistic distribution models

Malin Fischer[1], Tobias Gutzmann[1], Jakob Rieser[1], Giovanni Joy[1]

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Background: How can and why should Open Source tools like R and QGIS be used for spatial data analysis, especially in the field of remote sensing?

Recent developments allow the use of vast amounts of free-to-use satellite data for numerous ecological applications. Open Source software provides free and convenient tools to process and analyse such data. The methods and results can then easily be reproduced and shared within the scientific community.

Our offer: This workshop will introduce participants to the basic tools of Open Source spatial data analysis in R and QGIS with a little theoretical input and much hands-on practice following an ecology-related example. Depending on the participants' previous knowledge, we will cover topics like how to get spatial data into our software, mapping, land cover classification and time-series analysis. Basic knowledge of R, GIS and remote sensing is desired and please bring your own laptops with the latest versions of R (**https://www.r-project.org/**), RStudio (https://www.rstudio.com/) and QGIS (https://qgis.org/en/site/).

Maximal number of participants: 15-20

Requirements: Every participant should bring a laptop with R installed.

Minicourse: Towards more mechanistic distribution models

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Background: Correlative species distribution models (SDMs) constitute the most widely used modelling approach in global change research. At the same time, we are well aware that they have several shortcomings when making predictions into the future. For example, they assume that species are (and will be) in equilibrium with the environment ignoring transient dynamics, they do not explicitly take into account interspecific interactions and adaptation, among others. Many scientists have called for more mechanistic models for more than a decade now. However, although several modelling platforms have been introduced, these models are still rarely applied. Why is that so?

Our offer: We will discuss the pros and cons of SDMs versus more mechanistic approaches, for example in terms of expected knowledge gain versus data limitation. A major advantage of SDMs is that software packages are readily available, many guides are available how to use SDMs, and they are really fast - at least these seem to be common perceptions. Here, we will try to correct some of these perceptions by introducing simple to complex approaches for taking into account mechanisms in dynamic distribution models. As we are quite time-limited, we can merely provide a brief overview about available software, mostly for coupling SDMs with dispersal and population dynamics models. Specifically, we will introduce a couple of R packages such as *MigClim* and *demoniche* but also highlight more sophisticated approaches like RangeShifter. Also, we will discuss aspects of calibration, sensitivity and robustness analyses, and model transferability. If time allows, we would be happy to discuss how these approaches could be further extended in the future, to improve on data integration and solve circularity issues.

We will provide course materials in form of R scripts. Participants should bring a laptop with R installed. Please also install the packages *raster*, *MigClim* and *demoniche* and their dependencies.

Maximal number of participants: 15-20

Requirements: Every participant should bring a laptop with R installed.

Discussion panel: Meet the editors discussing hot topics

Organization team Macro 2019 and editors present

Description: Participants of Macroecology 2019 that are editors will participate in a discussion panel about what are the research topics the editorial boards are mostly excited about, what are the journal policies about reviews, peer-review and preprints, open science, gender/ethnic diversity, special issues, this year's meeting logo: 'from local patterns to global challenges', and further topics. The panel will interact with questions from the audience and anybody interested and other editors present in the audience can join the panel (no limit in participants). Confirmed panel: Holger Kreft (Journal of Biogeography); Susanne Fritz (Proc B, Frontiers in Biogeography, Ecography); Christian Hof (PeerJ); Maria Dornelas (PeerJ, GEB); Jürgen Dengler (Phytocoenologia, Applied Vegetation Science); Matthias Schleuning (Functional Ecology).

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