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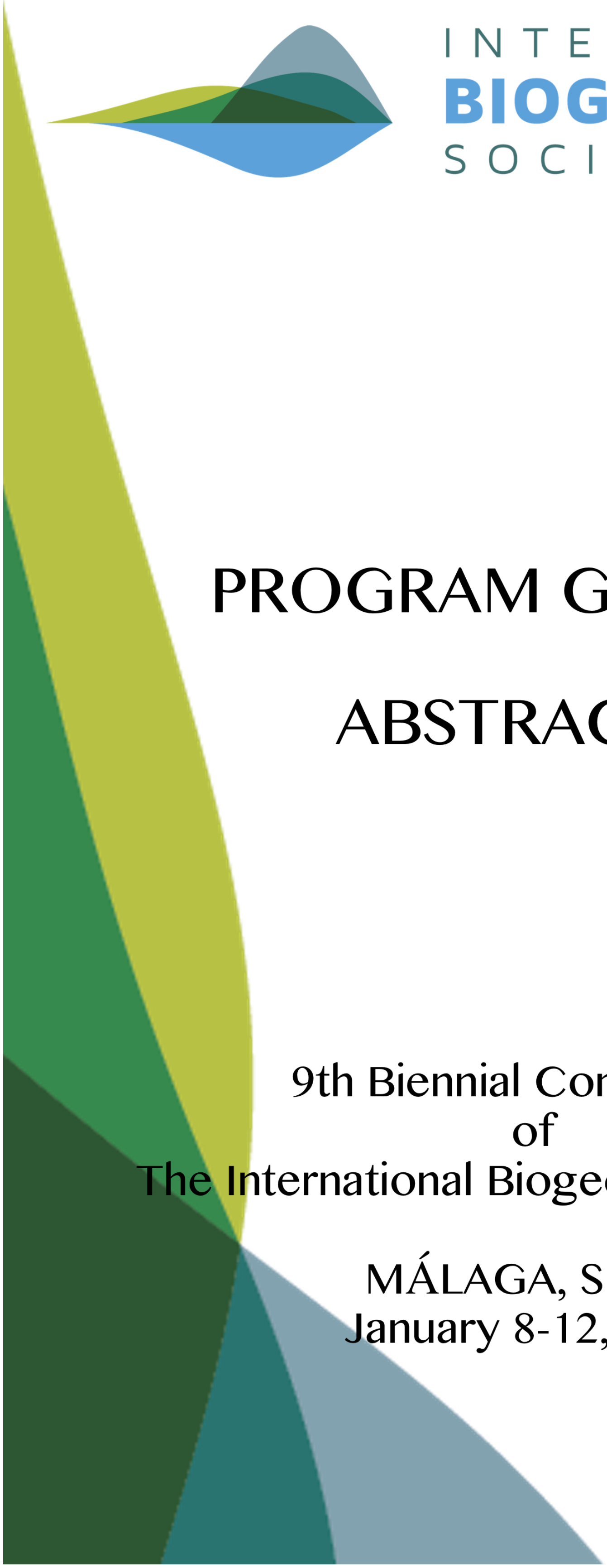

PROGRAM GUIDE &
ABSTRACTS

9th Biennial Conference
of
The International Biogeography Society

MÁLAGA, SPAIN
January 8-12, 2019

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SCHEDULE OVERVIEW - IBS Málaga 2019

	8-Jan	9-Jan	10-Jan	11-Jan	12-Jan
8:30	workshops	**opening** Wallace Award, Symposium 1	MacArthur & Wilson Award, Symposium 2	Dissertation Award, Symposium 3	**field trips**
	coffee break	coffee break	coffee break	coffee break	
	workshops	Symposium 1	Symposium 2	Symposium 3	
12:40	**LUNCH BREAK**	**LUNCH & Discussion**	**LUNCH BREAK**	**LUNCH BREAK**	
14:00	workshops	15 min presentation sessions: CS1, CS2, CS3, CS4	15 min presentation sessions: CS9, CS10, CS11, CS12	15 min presentation sessions: CS17, CS18, CS19, CS20	
	coffee break	coffee break	coffee break	coffee break	
16:30	workshops	5 minute presentation Sessions CS5, CS6, CS7, CS8	5 minute presentation Sessions: CS13, CS14, CS15, CS16	Business Meeting, Closing and Awards Ceremony	
18:00 to 20:00	Registration, Welcome reception, Publishing panel discussion (16:30 - 20:00)	Poster Session A	Poster Session B		
20:30 to 22:30			**Banquet**		

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General Information

Symposia

Concurrent Session Presentations

PLENARY SPEAKERS – 2019 AWARD WINNERS

2019 Wallace Award

Origins of diversity on islands: The nexus of ecology and evolution in community assembly

Rosemary Gillespie
University of California Berkeley, California, United States

Research on the dynamics of biodiversity has progressed tremendously over recent years, though in two separate directions – in ecology, to determine current relationships between organisms and their environment, and in evolution, to understand how organisms change and diversify over time. Integration of these approaches has remained elusive. Archipelagoes with a known geological chronology (a chronosequence) provide an opportunity to study ecological interactions over evolutionary time. Here, I will use this framework, and focus on arthropods, to highlight insights into biodiversity dynamics from such island chronosequences in the Pacific, emphasizing the Hawaiian archipelago. Surprisingly, although there are multiple patterns of adaptive diversification, the different patterns can be both predictable and repeated across different archipelagoes, and across different lineages within an archipelago. A key question is whether the communities themselves evolve in a predictable manner. I consider how attributes of entire communities across the chronosequences can reveal not only how diversity has been shaped in the past, but also how it might be expected to respond, through accommodation or transformation, to the massive changes in biotic and abiotic environments, as we move into the future.

2019 MacArthur & Wilson Award

The race for new space: how dispersal and disturbance influence biogeographic patterns

Ceridwen Fraser
Australian National University, Acton, Australia

Dispersal is a fundamental process that shapes the distributions of many plants and animals. Dispersal does not always result in ongoing gene flow among populations, but is critical for initial colonisation events, particularly following large-scale disturbances such as those resulting from climate change, earthquakes and volcanic eruptions. I will give an overview of how dispersal and disturbance interact to structure spatial patterns of biodiversity, particularly in the context of density-dependent processes. I will focus on examples from my molecular research on diverse Southern Hemisphere systems including marine communities in Australasia and the Antarctic, intertidal ecosystems affected by earthquakes in New Zealand and Chile, and terrestrial plants and animals on volcanoes (and in volcanic caves) in Antarctica.

2019 International Biogeography Society Dissertation Award

How to resist the heat? Modelling plant population dynamics under a warming climate

Johannes Wessely
University of Vienna, Vienna, Austria

The possible consequences of climate change for the future of biodiversity have become an active field of research. Individual species may respond to the altered climatic conditions by phenotypic or evolutionary adaptation and/or by shifting their geographical distributions, which is furthermore confronted by a human modified fragmented landscape. Changes in geographical distributions for past periods of climatic change and growing empirical evidence suggests that plants and animals have already started to shift their ranges in response to the last decades' warming trends. The pronounced climatic change predicted until the end of the 21st century will further increase pressure on species to adapt their geographical distributions and hence likely accelerate these range dynamics. Therefore, it is more important than ever to develop more realistic models in order to predict the changes to come and be able to react appropriately. I take this step by extending a so called hybrid model that combines predictions of climatic suitabilities with a stage structured demographic model and a dispersal model, and applying it to a wide range of questions. After briefly discussing uncertainties of the used model, I will focus on possible future predictions including evolutionary adaptation as well as possible changes of populations standing genetic variation. Finally, I will present modelling results evaluating the effectiveness of different habitat based conservation measures in Central Europe under future climate changes.

Symposium 1: Geography and Genes - insights and advances for biogeography

Organizers: Brent Emerson (IPNA-CSIC, Tenerife, Spain), Jairo Patiño (University of California, Berkeley, USA)

S1-1

Species Divergence Shaped by the Intersects of Ecology and Climatic Change

Lacey Knowles
University of Michigan, University of Michigan, Ann Arbor, Michigan, United States

From the patterns of genomic variation in individuals living today, phylogeographic analyses provide a window into a species' past. When viewed in a comparative context, examples of concordant genetic structure across assemblages of species, despite their biological difference, have reinforced a conceptual and methodological focus on abiotic factors in shaping species' histories. This emphasis has also promoted an adherence to generic expectations of phylogeographic concordance irrespective of the composition of communities and a tendency to attribute discord to the idiosyncracies of history. However, from the increased sampling densities and unprecedented amounts of genomic data, what is emerging in comparative phylogeography is a complex of concordant and discordant genetic structure across community members. In my talk, and with reference to computational advances and recent developments at the molecular level, I will highlight how discordant patterns of genetic variation may arise from difference in the traits and ecologies of taxa. That is, discord across species may reflect deterministic processes linked to species-specific traits. In addition to reviewing the methodologies that are propelling this promising area of research, and based on examples of comparative phylogeographic studies, I will show how considering the contribution of taxon-specific traits, rather than adhering to the concordance-discordance dichotomy, can provide more meaningful insights about the evolutionary history of organisms. These studies emphasize that to understand how the divergence process may differ among geographic regions, or why genetic structure may differ among members of communities, the biotic and abiotic effects need to be considered jointly.

S1-2

Metagenetics for Community Biogeography

Alfried Vogler[1], Thomas Creedy[2]

[1]Imperial College London, London, United Kingdom
[2]Natural History Museum, London, United Kingdom

Biodiversity research is being revolutionised by powerful sequencing technology that allows the study of taxonomically intractable groups and entire 'specimen soup' community samples. This talk lays out a framework for the application of metagenomics and metabarcoding in community biogeography. To a large extent, biogeographic distribution patterns are determined by historical divergence and physical distance of organismal lineages, at global, regional and local scales. DNA sequencing of bulk samples can now assess these patterns for entire local communities. Whole mitochondrial genomes are readily obtained by shotgun DNA from bulk samples. Sets of specimens, each collected from disparate locations over the globe, mitogenomes are used to build the high level phylogenetic tree, and place each local community in a phylogenetic framework of continental samples. When sampling multiple sites within a region, PCR-based barcode and metabarcode sequencing is a more efficient way for data gathering, enabling us to fit those sites and specimens into the global tree, and to assess geographic turnover among communities. We will show how DNA sequences can be obtained from bulk-sample sequencing at various spatial scales, to produce an image of the distribution of biodiversity in a seamless way from continental levels to the scale of individual trees in a single patch of rainforest.

S1-3

Whole-community assembly from metabarcoding data reveals the structure of the soil mesofauna at multiple genetic levels and spatial scales

Paula Arribas[1], Carmelo Andújar[1]

[1]IPNA-CSIC, Spain

Soils are among the most diverse habitats on Earth, but at the same time they are the most poorly studied terrestrial ecosystems. Our understanding is extremely limited for the arthropod mesofauna (0,1–2 mm body size), because conventional morphological and molecular approaches are in many cases insufficient for the characterisation of their complex communities. This paucity of knowledge translates to great uncertainty about total species richness, geographical structure and the main drivers of soil community assembly, even in relatively well-known regions such as Europe. The implementation of high-throughput sequencing for metabarcoding now offers unprecedented opportunity to overcome past constraints to characterise and understand soil biodiversity. However, its application is still very limited. Here we take advantage of newly developed protocols for sample-processing and bioinformatics to metabarcode soil mesofauna, to explore whole-community assembly of belowground biodiversity, both at and below the species level. We have generated a matrix of approximately 34,000 mtDNA haplotypes of mites, springtails and beetles across a latitudinal gradient from southern Spain to Belgium. Our results reveal strong geographical structuring of soil communities at multiple hierarchical levels, where the impact of dispersal constraints scales up from landscape to continental scales. Our results cast light on the open question of whether the distribution of above- and belowground biodiversity is governed by the same laws, and raise questions regarding current estimations of biodiversity on Earth.

S1-4

An integrated model of population genetics and community ecology

Isaac Overcast
The Graduate Center City University of New York, The Graduate Center City University of New York, Brooklyn, NY, United States

Biodiversity in ecological communities can accumulate via colonization from a regional source pool, in situ speciation, or some combination of these. Reconciling the relative importance of these processes is hindered partially because the two extremes are currently the domain of different fields of study. In situ speciation is commonly studied through the lens of phylogenetics and trait evolution, whereas communities assembled via colonization are the focus of neutral and non-neutral models of community ecology. However, population genetic variation at the community scale has been rarely studied, and could provide a complementary axis of information to aid in disentangling processes shaping ecological communities. To this end I introduce a mechanistic model of community assembly that roots itself in classic island biogeography theory (MacArthur & Wilson 1967; Hubbell 2006) to make historically dynamic joint predictions of observed data along three axes that unify macro-ecology, phylogeography, and macro-evolution: species richness and abundances; genetic diversities and divergences; and trait evolution within the context of phylogenetic diversification. Using simulations and empirical data I demonstrate that each data axis captures information at different timescales of assembly, and that combining all these axes results in much finer resolution inference. Finally, I demonstrate our simulation-based inferential framework (massive eco-evolutionary synthesis simulation; MESS), which combines ABC and supervised machine learning to test competing models of community assembly and evolution (niche vs neutral and evolved vs assembled) and to estimate an array of model parameters relevant to a complex history of island assembly and evolution.

S1-5

Comparative phylogeography: the origin of variation in dispersal patterns

Josselin Cornuault[1], Isabel Sanmartin[2]

[1]Real Jardín Botánico de Madrid - CSIC, Spain
[2]Real Jardin Botanico, CSIC, Madrid, Spain

A major goal of phylogeography is to understand the link between geography and species evolution. In particular, inferring past dispersal patterns, including determining the main dispersal routes or quantifying dispersal rates, helps us understand patterns of species distribution and diversification.
Many phylogeographic studies have been conducted in various species and various geographical regions. Probably a small proportion of these studies have investigated the movements and diversification of several species at the same time, across the same geographical template. Yet, such comparative phylogeographical approaches are important as they enable testing for the existence of general phylogeographical patterns.
We studied phylogeographical patterns of hundreds of Coleopteran OTUs across four islands of the Canarian archipelago. For each OTU, we used phylogenetic methods to estimate the genealogies of sampled sequences, along with a geographically-structured coalescent model to estimate dispersal rates between (and possibly within) islands. Our goal is then to use such estimates to try and determine general patterns of dispersal in Canarian Coleopteran, and in particular to understand the determinants of the variation in dispersal rates across dispersal routes and OTUs.

S1-6

Next generation island biogeography: applying genomics to understand speciation

Jairo Patiño[1], Victor García-Olivares[2], Antonia Salces-Castellano[3], Brent Emerson[4]

[1]Universidad de La Laguna, La Laguna, Spain
[2]Instituto de Productos Naturales y Agrobiología (IPNA-CSIC)
[3]Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), Spain
[4]University of East Anglia, Norwich, United Kingdom

Understanding the mode, tempo and drivers of speciation is a critical element of ecological and evolutionary study, particularly so for island biogeography. Until recently, however, research on the drivers and dynamics of differentiation and speciation within islands has received relatively little attention. Within this context, it has been increasingly highlighted how climate change over glacial cycles could have been consequential in shaping insular diversity. Much of the focus to date has been on how transitions between glacial and interglacial climate conditions have affected speciation and demographic trajectories between islands, with less focus on potential speciation consequences within islands. In this presentation I will discuss the potential roles of climate and topography for intra-island speciation, using sub-genomic sequence data (RADseq) for species of beetle in the Canary Islands, with a majority of them being presumably characterized by limited dispersal capabilities. First, I will present a case-study focusing on individual-level genomic relationships within a clade of four taxonomically described species on the topographically complex island of Gran Canaria, revealing the otherwise hidden complexity of a speciation history involving multiple episodes of isolation and secondary contact. Then, using a number of beetle species with limited environmental tolerances on Tenerife island, I will show how community-level assemblages can respond in concert to climate oscillations occurred during the Quaternary, ultimately pointing to community-wide signatures of incipient speciation.

S1-7

Tropical Tree Genomics: the African rainforest during the Ice Ages

Rosalía Piñeiro[1], Olivier Hardy[2], Carolina Tovar[3], Shyam Gopalakrishnan[4], Filipe G. Vieira[4], M. Thomas Gilbert[5]
[1]University of Exeter, London, United Kingdom
[2]Evolutionary Biology and Ecology Unit, Faculté des Sciences, Université Libre de Bruxelles , Belgium
[3]Royal Botanic Gardens, Kew, London, United Kingdom
[4]Evolutionary Genomics, University of Copenhagen
[5]Natural History Museum of Denmark, University of Copenhagen

Today tropical rainforests are continuously distributed in Central Africa but genetic evidence indicates strong differentiation of the tree populations that cannot be explained by geographic barriers such as rivers or mountain chains. Available studies suggest that this is the result of past fragmentation of the forest due to arid conditions during the Ice Ages. Alternatively to forest fragmentation, climatic barriers might be contributing to the remarkable structuring of the genetic variation.
In order to investigate the genetic signal of rainforest fluctuations, we sequenced reduced representation libraries in five Legume tree species. Overall 475 GBS libraries from 792 DNA extractions from 150 individuals were run on four Illumina lanes. RAxML phylogenies identified at least three main lineages in each species: an early divergent lineage in West Africa (Upper Guinea) and two reciprocally monophyletic clades in Central Africa (Lower Guinea): Lower Guinea-North and Lower Guinea-South. The time of divergence between the North and South clades was estimated with demographic model testing in ∂a∂i. In all species divergence occurred within the Pleistocene, suggesting forest fragmentation in Ice-Age refugia. We then traced the spatial signal of recolonisation by identifying declines in genetic diversity with distance from hypothesised forest refugia. The correlation between genetics and climate in Central Africa was examined accounting for spatial autocorrelation with Toroidal and Rotation tests. While variables showing gradients along a West-East axis did not seem to be relevant, we found significant associations between genetic distances and summer rainfall, which exhibits a sharp North-South gradient.

S1-8

How Communities Evolve: A high throughout metabarcoding analysis to infer biodiversity dynamics of arthropods across the Hawaiian Island chronosequence

Henrik Krehenwinkel[1], Rosemary Gillespie[2]

[1]University of Trier, Germany
[2]University of California Berkeley, Berkeley, United States

Biodiversity is shaped by interactions between members of a community that change over space and time. While models have been developed to infer the dynamic processes shaping the evolution of these communities, empirical data are almost entirely lacking. We have developed an approach to understand how entire communities change over extended evolutionary time using next generation sequencing based metabarcoding. Metabarcoding enables the study of biological communities at unprecedented taxonomic breadth and resolution. We present a metabarcoding analysis of arthropod community assembly in native rainforest ecosystems of the Hawaiian Archipelago ranging in age from 40 to $6*10^6$ years of age. We measured total abundance and diversity of all arthropods across the different snapshots in time, controlling for elevation, precipitation, and type of rainforest (all dominated by *Metrosideros polymorpha* trees). This sampling effort led to a collection of $> 10^6$ arthropod specimens. We developed a semi-automatized multilocus metabarcoding protocol to process such large community samples. Size sorting prior to sequencing allowed us to perform abundance-informed analyses of biodiversity. Using the resulting dataset, we show some emerging patterns of community evolution across the island chronosequence, including changes in diversity, specialization, and resilience to biological invasion. Using several abundant, invasive groups of Collembola as a model, we find a strong association of island age and invasion success, with islands of intermediate age being particularly resilient against invasion. Given the current massive impacts affecting biodiversity in the world today, developing metrics of change in biological communities has never been more important.

Symposium 2: Do we need to reclassify the tropical and sub-tropical biomes and if so, into what?

Organizers: Katherine J. Willis (University of Oxford, UK), Dov Sax (Brown University, RI, USA)

S2-1

Phylogenetic classification of the world’s tropical forests

Ferry Slik[1], Janet Franklin[2], Victor Arroyo-Rodríguez[3], Richard Field[4], et al. [4]

[1]Universiti Brunei Darussalam, Brunei Darussalam
[2]Arizona State University, Tempe, AZ, United States
[3] Universidad Nacional Autónoma de México, Mexico City, Mexico
[4]University of Nottingham, UK, Nottingham, United Kingdom

We present a global classification, based on phylogenetic similarity, of forests located between 35°S and 35°N, using plot-based inventory data for angiosperm trees >10cm diameter at breast height, pooled into 1° grid cells. The full dataset includes 925,009 angiosperm trees in 15,012 taxa, in 439 grid cells. Our classification identifies five principal floristic regions and their floristic relationships: (i) Indo-Pacific, (ii) Subtropical, (iii) African, (iv) American and (v) Dry forests. Our results do not support the traditional neo- versus palaeotropical forest division, but instead separate American and African forests from their Indo-Pacific counterparts. We also find indications for the existence of (1) a (sub)tropical dry forest class with representatives in America, Africa, Madagascar and India, and (2) a northern-hemisphere subtropical forest region across eastern Asia and the neotropics, consistent with a historical link between Asian and American northern-hemisphere forests.

S2-2

Tropical forest biomes and biogeography: views from a model clade

Wolf Eiserhardt[1], Sidonie Bellot[2], Thaise Emilio[3], Robert Muscarella[4], Bill Baker[5]

[1,4]Aarhus University, Aarhus C, Denmark
[2,3]Royal Botanic Gardens, Kew, United Kingdom
[5]Royal Botanic Gardens, Kew, Twickenham, Surrey, United Kingdom

Biogeographers commonly divide the world's terrestrial surface into biomes, defined by vegetation physiognomy, and biogeographic regions, defined by the evolutionary history of lineages. Both biome and biogeographic boundaries remain fluid and are regularly shifted in the light of new evidence and methods. In terms of evolutionary processes, areas where biome and biogeographic boundaries coincide are of particular interest. The causes of such phylogenetic biome conservatism remain underexplored. A recent study (Slik et al. 2018 PNAS 115, 1837-1842) provided a new biogeographic classification of the world's tropical forests, highlighting unexpected geographic relationships (such as an Indo-Pacific region) and incidences of biome conservatism (such as a biogeographic region reflecting the global dry forest biome). These important insights were derived from broad-scale analysis across angiosperm trees. In this talk, we will view the findings of Slik et al. through the lens of one of the most important model clades of tropical forest ecology and evolution, the palms (Arecaceae), which were not part of the analysis of Slik et al. With their pantropical distribution, large ecological diversity and abundance of data, the palms can provide an important complementary perspective on tropical forest biomes and biogeography. Using published and unpublished evidence we will discuss, among other things, biogeographic relationships among continental and island systems and the extent to which phylogenetic biome conservatism occurs.

S2-3

A bird's eye view on tropical and sub-tropical biomes

Carsten Rahbek[1], Ben Holt[2]

[1]CMEC Univ. of Copenhagen, Copenhagen, Denmark, Denmark
[2]Center for Macroecology Evolution and Climate, Truro, United Kingdom

Recent global-scale analysis of the phylogenetic composition of tropical tree communities has suggested a fundamental biogeographical division, splitting tropical flora into two major regions: an Indo-Pacific region and a combined American-African region. Such biogeographical patterns in floral communities can be expected to impact taxa at higher trophic levels, and therefore have important implications for traditional classifications of ecosystems or 'biome types'. Here we present the results of our phylogenetic, regionalisation of the global avifauna (over 10,000 bird species in total). We ask i) are bird biogeographic patterns consistent with those recently shown by tropical angiosperm trees, ii) what are the implications of our bird regionalisation results for traditional tropical biome classifications and iii) what are the ideal data and methods for classifying biomes using global scale bird data. Our results show a contrast to those produced for trees, with tropical regions not closely linked across continental landmasses and a clear split between South American regions and the rest of the world. Within continents, regions show evidence of associations with climatic factors and previously recognised floristic biomes, suggesting that birds can represent an important taxonomic group for global biome classification.

S2-4

A deep-time perspective on the tropical and subtropical biomes

Jennifer McElwain[1], Michelle Murray[2], Wuu Kuang Soh[3], Charilaos Yiotis[2], Robert Spicer[4]

[1,2,]3 Trinity College Dublin, Dublin, Ireland
[4]The Open University UK, Milton Keynes, United Kingdom

Paleo-biomes have been broadly mapped for the past 400 million years based on a combination of fossil plant diversity, taxonomic, and physiognomic data together with the geographical distribution of climate indicator sediments. Throughout geological history the relative biogeographical extents of the tropical and subtropical moist biomes (termed everwet) and tropical and subtropical dry biomes (termed summerwet) have shifted in concert with the global climate state and greenhouse gas composition of the atmosphere. Global scale mapping approaches of paleo-biome evolution are however hampered by very low spatial and taxonomic resolution. More detailed local and regional palaeobotanical studies provide insights into the likely timing of biome evolution for the sites studied as they incorporate taxonomic as well as functional attributes of fossil floras. This talk will provide an overview of current knowledge on the deep time record of the tropical and subtropical biomes from the palaeobotanical record. Biome-level responses to long-term (millions of years) and short-term (last 40 years) CO_2 induced global warming will be assessed using fossil palynofloras and macrofloras and a new contemporary dataset of field-based ecophysiology and ecology trait measurements from Puerto Rico and Fiji. Predictions on the likely functional and ecological responses of tropical and subtropical forests to future increases in atmospheric CO_2 will be considered. The biogeographic classification of extant tropical forests will be pondered in the context of differences that have been observed in the strength of relationships between leaf physiognomic traits and climate variables in different floristic regions.

S2-5

Integrating ecology and evolution to delimit savanna

Caroline Lehmann
University of Edinburgh, University of Edinburgh, Edinburgh, United Kingdom

Biomes are complex ecological machines comprising the biosphere, linking the atmosphere, hydrosphere and lithosphere. But what is a biome? These global vegetation units are responsible for the Earth's terrestrial primary production, carbon sequestration and biodiversity, as well as regulating climate. In an era of global ecology facilitated by Earth observation from space and big data, the application of “biomes” is central to assessing the consequences of global anthropogenic change. Traditionally, biomes have been considered physiognomic units based on vegetation structure. However, the biome concept is poorly comprehended, lacks transparency and is often not transferable across ecology, evolution and biogeosciences, largely, as biome delimitation is not exact and biomes and their boundaries are not static. Here, I argue that the biome concept must be "functional" to meaningfully link from evolution through to biogeosciences. I examination data on the biogeography and functional ecology of tree and grass species from tropical savannas and grasslands to elucidate how a biome concept can be meaningfully applied across scales, space and disciplines.

S2-6

Beyond climate control: The importance of soils in predicting the future of plant habitat suitability in a tropical forest.

Gabriela Zuquim[1], Flávia Costa[2], Hanna Tuomisto[3], Gabriel Moulatlet[4], Fernando Figueiredo[2]

[1]University of Turku, Finland
[2]National Institute of Amazonian Research
[3]University of Turku, Turku, Finland
[4]IKIAM, Ecuador

Even though species occurrences are known to be strongly affected by edaphic properties, assessments of the future of biodiversity under climate change are mainly focused on climate-only models or including coarse surrogates of soil conditions. Future climatically suitable areas can be inadequate for species establishment if soils are a constraint. We therefore investigated the effects of including soil information when predicting future suitable areas for selected plant species in Amazonia. Due to the lack of proper soil representation in Amazonia, we first developed and validated a map of soil nutrient concentration based on plant occurrence records with modeled species-soil affinities. Then, we modelled current and future suitable habitats for 35 plant species. We compared results of climate-only models with those obtained when climatic and edaphic variables were included for six scenarios of the climate in 2050. For most of the species, the areas predicted by climate-only and climate+soil models were clearly different in size and/or spatial configuration. Climate-only models predicted larger suitable area for more than half of the species in future scenarios. Future suitable areas were often predicted to be reduced in relation to the present, especially when soils were included in the model. Our results highlight the importance of moving beyond climatic scenarios when modelling biodiversity responses to climate change. Failure to include soils in species distribution models can overestimate future habitat suitability for many plants in Amazonia.

S2-7

Rethinking tropical Asia's woody biomes: History, climate and woody plant traits distinguish savannas from forests

Jayashree Ratnam
Tata Institute of Fundamental Research, NCBS, India

An unresolved problem in the vegetation nomenclature of the Indian subcontinent is that many of its mixed tree-grass systems, characterised by open formations of deciduous C_3 trees in a predominantly C_4 grass understorey are classified as ‘dry deciduous forests’ when they are functionally savannas. More problematically, these formations are widely regarded as degraded descendents of moist forests, both because they occur in areas with a long history of human presence and habitat modification, and because the mesic regions where many of these savannas occur can also climatically support closed forests. Here I examine multiple lines of evidence to try to untangle this issue. First, paleobotanical evidence establishes that C4 vegetation, most likely grassland, was established in the subcontinent by the Late Miocene. Marine isotopes further suggest that C_4 prevalence has continued to increase since the Last Glacial, both pointing to non-human agency in the establishment and spread of C_4 ecosystems in this region. Second, recent analyses establish that the ‘dry deciduous forests’ in the subcontinent fall within established bioclimatic

envelopes of extant natural savannas in the African continent. Third, functional trait data of tree species from multiple moist forest and ‘dry deciduous forest’ sites across peninsular India clearly distinguish between these habitats. Specifically, ‘dry deciduous forest’ trees have significantly thicker barks, lower height-diameter ratios, lower specific leaf areas and higher wood densities, all of which are consistent with expected differences between trees growing in open and dessicating savanna environments versus those growing in closed and moist forest environments. Critically, the significantly thicker barks of ‘dry deciduous forests’ protect them from fires, which occur much more frequently in these habitats than in moist forests, something that is characteristic of mesic savanna systems. Combined with the fact that it is C 4 grasses that form the fuels for these fires and these habitats support an ancient and diverse mammalian grazer assemblage, these data confirm that the ‘dry deciduous forests’ of the Indian subcontinent are indeed ‘dry deciduous savannas’.

S2-8

Anthrobiogeography: Mapping Biomes in an Anthropogenic Biosphere

Erle Ellis
University of Maryland, Baltimore County, University of Maryland, Baltimore County, Baltimore, MD, United States

Human societies have been transforming habitats, ecosystems, and species distributions across all continents except Antarctica since late Pleistocene. These transformations include unprecedented pressures from intensive social hunting and foraging and the engineering of ecosystems both intentionally and unintentionally through altered fire regimes, the propagation of favored species, land clearing using fire, soil tillage, the cultivation of domesticates, and the transport and introduction of species locally, regionally, and globally. Here I present a conceptual framework based on anthroecology theory aimed at understanding and mapping the terrestrial biogeographic patterns produced by human transformation of ecosystems over the long-term. From the first hunter-gatherer societies, to the first farmers, to the expansive colonial enterprises of past centuries, to the increasingly globalized industrial societies of today, more than three quarters of the terrestrial biosphere has already been transformed by long-term processes of human sociocultural niche construction. The resulting anthropobiogeographic patterns range from the global patterning of the anthromes to the local patterns of used lands, remnants, recovering novel ecosystems, and introduced and propagated species. These continue to evolve together with human societies through long-term processes of sociocultural change and anthroecological succession. To better understand and map Earth’s present and future biomes and ecoregions, both inside and outside the tropics, the human sociocultural processes that now shape biogeographic pattern and process must become as much a part of biogeographic theory and practice as biological and geophysical processes are now. Strategies for achieving this goal and for conserving biodiversity in an increasingly anthropogenic biosphere are presented.

Symposium 3: Towards a more applied biogeography: combining process-based and niche approaches to address practical questions

Organizers: Ignacio Morales-Castilla (Universidad de Alcalá, Spain), Raúl García-Valdés (Universidad Autónoma de Barcelona, Spain)

S3-1

A pathogeographical approach to the Ebola-virus disease

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Pathogeography is the theory and application of biogeography to the research and management of infectious diseases. Concepts and tools from biogeography have helped to map individual disease distributions, and to understand the processes shaping them in time and space; but biogeography offers much more than this. Distribution modeling; patterns of co-occurrence, turn-over and diversity; disease-based regionalization; and the combination of these approaches contribute to integrate knowledge on temporal and spatial relationships between pathogens, reservoirs, vectors, the environment and the socio-economy. Ultimately, this translates into disentangling the distribution of risks for human health. Recent Ebola outbreaks illustrate the urgent need for defining hotspots for Ebola virus disease. Recent and ongoing pathogeographic studies are setting the bases for the ability to forecast when and where future outbreaks could occur. Distribution modeling has been used recurrently to map the area potentially suitable for Ebola virus. The latest contributions, however, incorporate information on likely virus reservoirs, on a combination of co-occurrence and diversity patterns regarding mammal species potentially involved in the virus' transmission, or on disease co-occurrence patterns more broadly. Such models provide the geographical context for seeking natural and anthropogenic factors favoring transmission from the wild to human populations. With this aim, pathogeograpic analyses have demonstrated that deforestation can increase the chances for short-term Ebola-virus outbreaks. Efforts are now being made to unveil links between outbreak probability and weather events with high potential to make spatially- and temporally-explicit forecasts, which could form the foundation of early warning systems for Ebola.

S3-2

Using forest succession models to predict species ranges and range changes: potentials and limitations

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Dynamic Vegetation Models (DVMs), i.e. models that consider mixed-species, uneven-aged vegetation and its development over time as a function of abiotic and biotic processes, have long and successful history of use at the local scale, with the JABOWA model being presented the first time almost 50 years ago (Siccama et al. 1969, *Bull Ecol Soc Amer* **50**: 93); and at the global scale, with LPJ-GUESS being used since nearly 20 years (Smith et al. 2001, *Glob Ecol Biogeogr* **10**: 621-637).

Although some DVMs have focused on low-stature vegetation, the bulk of the effort was spent on providing realistic and increasingly accurate representations of the complex canopies that characterize forests, with most models either ignoring non-tree species entirely, or modelling them in a very coarse manner only. Moreover, species range dynamics, which clearly fall between local-scale and global-scale applications, were not the focus of much research until a few years ago. In the meantime, several lines of research have evaluated the utility of local-scale models for predicting species ranges and range dynamics. In this presentation, I review the state of affairs for the case of forest succession (forest "gap") models, which have the potential to project not only the distribution, but very importantly also the abundance of tree species in time and space.

A case study from the Pacific Northwest of North America shows the potential and pitfalls of local vs. continental-scale model parameterization, suggesting that structural improvements of the models are

needed if they are not to provide the right answer for the wrong reason. Continental-scale sensitivity analyses of DVMs built for local application can help to identify processes that are modelled with insufficient accuracy, but improvements may bring their own pitfalls. Lastly, combined models of overstory and understory dynamics underline the potential of simulating at least the dynamics of functional groups of understory (and thus also non-forest) plants, if not species distributions of the understory. Overall, I conclude that an enhanced conversation and exchange of experience between "Species Distribution" and "Process-based" approaches can push the frontier of science, but has not been fully exploited to date.

S3-3

Spatio-temporal links between phenology and herbivory of blueberries across the eastern US

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Predicting how ecological interactions will respond to global change is a major challenge. Plants and their associated insect herbivores compose much of macroscopic diversity; yet, how their interactions have been altered by recent environmental change remains underexplored. We quantified herbivory from herbarium specimens of two blueberry species *Vaccinium angustifolium* and *Vaccinium corymbosum* with records extending back more than a century. We found that insect damage to blueberries has increased over time, with links to climate warming. We discuss the role of phenological sensitivity in mediating species interactions, and whether patterns in temperature over space might predict future effects of climate change on plant-insect interactions.

S3-4

Understanding global variation in treeline spatial patterns: a community database and spatial process model

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Alpine treelines are distributed globally and their position can be predicted well at that scale based on temperature. However, at more local scales treeline positions are more variable and less predictable, because other factors play an increasingly important role. Similarly, treeline responses to global climate change appear highly variable, and responses remain unpredictable due to a lack of synthetic studies on treelines globally. To facilitate such global studies, we propose a classification system for treelines, based on their spatial pattern, that incorporates tree cover, spatial clustering, tree height, tree deformation, woody species diversity and species turnover. Additionally, to better understand treeline-forming processes and to predict treeline shifts in response to climatic changes, we are studying the links between spatial patterns and ecological processes at alpine treelines using a spatially-explicit individual-based model. This model will be used to test hypotheses of pattern-process relationships using spatiotemporal treeline datasets from different parts of the world. These data are shared in a joint database which is open to further collaborations. Recently initiated and still in development, this model and database should become important tools for treeline researchers to study processes specific to their field sites and to explore global patterns in treeline functioning.

S3-5

Connecting mechanistic macroecological models with global biodiversity data – state-of-the-art and perspectives

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Strengthening the mechanistic underpinning of macroecology has been a long-held aspiration of the field. The idea has recently gained new momentum, with several reviews and perspective papers calling for a systems view on classical macroecological questions. Inspiration for this movement comes from advances in computing power, rendering dynamic system models of continental or macroecological processes feasible at last. An open question, however, is how these models should connect to global biodiversity datasets, and if they will be able to replace classical statistical approaches for synthesis and inference with large datasets. Here, I provide a critical review about the challenges of the model-data interface, drawing also on examples from other fields, such as weather, climate or dynamic vegetation models. I highlight that mechanistic macroecological models are not build from “first principles”, and thus at least some of their parameters need to be calibrated. Building up the statistical and computational infrastructure for this task will be critical for reducing parametric and structural uncertainties. Once these methods are established, mechanistic models could also be used for inference and synthesis, for example by examining how fitted model parameters vary in space or with environmental variables. Generally, however, model-data integration is still a critical bottleneck for this new research direction, calling for new ideas in model design, data collection and computational methods.

S3-6

Combining niche and process-based models to project climate change impacts on forest functioning

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Climate change will affect forest functioning via two main mechanisms. First, climate change will alter tree physiology (e.g. growth), directly affecting forest functioning (e.g. wood production). Second, climate change will trigger local colonization and extinction of tree species, indirectly affecting the functioning of the whole community. Yet, the long-term impact of these two mechanisms combined has been rarely addressed. In this study we developed a novel approach to project changes in forest tree wood productivity, by integrating several models working at different spatial and temporal scales. We first used Species Distribution Models (SDMs) to forecast future pools of species in 11 temperate forests across central Europe. These pools were then used as inputs for a Forest Succession Model (FSM). The FSM is a process-based model that simulates tree level growth and competition to estimate plot level wood productivity in the long-term. Our simulations show that with a moderate rise of temperature (< +1.7ºC), changes in productivity in all the studied forests will be caused by the direct effect of climate change on tree growth. However, if the temperature rises more (> +3.7 ºC), the indirect effect of climate change, through local colonization and extinction, will become the main driver of productivity change at both ends of the altitudinal gradient (coldest and warmest-driest forests). Most importantly, climate change is forecasted to dramatically impact the warmest (and second driest) forest, reaching the point of complete destruction if the radiative forcing increases above 8.5 W/m2 relative to pre-industrial values (RCP 8.5). Our findings call for more studies about climate change impacts on ecosystems functioning that allow for a better understanding of the two processes put into motion, direct impact on individual physiology and indirect impact through species composition. The integration of models that operate at complementary spatial scales is a promising tool to achieve such a task.

S3-7

Do advantages of process-based species distribution models offset their weaknesses?

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The most commonly used approaches to describe distributions of species are known as correlative species distribution models (SDMs). These models aim to describe the patterns in the association between species occurrences and a set of variables that describe the environment very often limited to climatic conditions. This association is supposed to be driven by causal relationships between biological processes involved in survival as well as reproductive success and the environmental conditions. Another approach emerged more recently that aims to describe the mechanisms that relate a species presence or absence to environmental conditions. This approach is known as process-based SDMs, and their application still lags behind correlative SDMs. In my presentation, I will try to address the three questions raised by this symposium, i.e. the feasibility of developing process-based SDM models, the utility of developing process-based SDMs, and the identification of data gaps. I will also present the future challenges process-based SDMs need to take in the next decade to provide valuable projections of species distribution change and inform decisions of natural resource managers and policy makers.

S3-8

Applied biogeography under global change: lessons from process-based applications in agronomy and forestry

Ignacio Morales-Castilla
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Macroecology and biogeography are genuinely concerned with ecosystem services and their continuity given the ongoing threats they face. These disciplines operate at spatial scales allowing to assessing and forecasting global change impacts on biodiversity and thus, would seem suited to tackling related applied questions. However, the scope of applied research in biogeography has typically focused on wildlife conservation and much less on humanized ecosystems and domesticated species. This is surprising because agricultural and forestry species provide services of major concern to humankind – e.g. food and raw material provision. In addition, there is far more data at high spatial and temporal resolutions for domesticated species than for wild species, which makes them ideal study cases to expand our knowledge about some of the processes – e.g. physiological, phenological, demographic– underlying biological responses to global change. Process-based modelling methodologies usually applied in agronomy and forestry can complement common macroecological approaches – e.g. niche models – to generate more accurate forecasts of ecosystem services provision under global change scenarios and thus, to responding so far neglected applied questions. Here, I first review major contributions of applied biogeography to forecasting the effects of climate change on domesticated biodiversity. Following, I provide an illustrative example, where combining niche and process-based modelling allows addressing the question of whether agrobiodiversity could be used to adapting agriculture to climate change. Finally, I identify and discuss potential research avenues where upscaling agronomic and forestry models at biogeographical scales would yield outcomes relevant to inform decisions of farmers, forest managers and policy makers.

Concurrent Session 01: Gradients, range-limits, and beta-diversity

CS1-01

Biogeographic patterns for breeding passerines in the Himalayas

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Himalayas are one of the most species-rich regions on the planet, with a clear east-to-west decline in bird species richness. By comparing eastern and western Himalayas, latitude, climate and resource-availability have been implicated as important determinants of this gradient. It is not yet clear though where exactly the major transition occurs from the species-rich eastern to species-depauperate northwestern Himalayas. We measured changes in various topo-climatic and habitat variables at fine-scale to elucidate region of transition as potential drivers influencing species distributions. We also investigated the impact of putative barriers and conducted phylogeographic analyses on birds varying in their dispersal abilities (using the Hand-Wind Index as a proxy). Northwestern Himalayas (NWH) showed highest total turnover for breeding passerines. This region in NWH correlated with sharp topo-climatic transition and highest habitat turnover (elevation-wise). Weak fliers (bush and mid-canopy foragers) faced more barriers, showed higher number of sub-species and more genetic differentiation than strong fliers (top-canopy foragers).
Understanding mechanisms driving species distributions may help predict species' response to future climate, habitat modification and anthropogenic impact in general, owing to our ever-increasing footprint on nature and natural resources. Our work would be crucial in prioritizing conservation areas, especially in northwestern Himalayas, keeping weak fliers in mind as they are poor dispersers and may fail to cope up with change. We are currently extending this investigation to global biogeographic scale for migratory birds.

CS1-02

Why and when do introduced species colonise available climate?

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Recent research has highlighted the very variable success of introduced species both before and after establishment. Introduced species have very variable range sizes and rates of spread, and many species fail to spread extensively and remain in small, isolated populations years after establishment. The availability of suitable climate, the spatial distribution of available climate, species characteristics and introduction history all affect a species range in its naturalised region. In order to spread successfully over a wide area, species must overcome some or all of these barriers. The relative importance of these factors on species ranges, however, remains unknown.
Here we undertake a global assessment of the potential for introduced species to spread beyond their current ranges, and ask what characteristics of species or geographic regions hasten or slow this spread. We consider a wide cross-section of 649 plants, 70 mammals, and 114 birds that have been introduced around the world, with a wide variety of life history traits, and measure their success at filling the potential range in their naturalised region. We find very variable range filling across different regions and taxa: in plants residence time was the best predictor of range filling, however in birds and mammals we find that instead dispersal ability and region are the best predictors of range filling. We conclude that information on species' potential range in a landscape will help identify not only those areas with a high potential risk of invasion, but also the factors that aid or hinder species' successful spread.

CS1-03
Determinants of zoogeographical boundaries differ across vertebrate clades

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The distribution of living organisms on Earth is spatially structured in multiple zoogeographical regions, characterized by faunas with homogeneous composition that are separated by biogeographical boundaries. Previous analyses have shown that tectonic movements, sharp changes in climatic conditions, and orographic barriers determine extant boundaries between biogeographical regions. Taxa could show different responses to these factors, for instance because of variation in life-history traits. Yet, no global-scale study has assessed whether biogeographical boundaries are related to different drivers across taxa. Here, using spatial regression analyses, we assess the factors determining zoogeographical boundaries of vertebrates, comparing the response of mammals, birds and amphibians. For mammals, tectonic movements, climatic conditions, and orographic barriers jointly determined extant biogeographical boundaries; mountain chains and tectonic history were the most important driving factors. For birds, abrupt climatic transitions played a strongest role, while the effect of mountain chains and orographic barriers was weaker. For amphibians, biogeographical boundaries mostly corresponded to areas with abrupt climatic transitions. The strongest transitions of amphibian faunas corresponded to areas with abrupt shifts of precipitation regimes. Our analysis confirms that multiple drivers jointly have shaped the biogeographical regions of the world, and highlights that taxa with different features show heterogeneous responses across the globe. Eco-physiological constraints can increase the importance of spatial heterogeneity of climate, while dispersal limitations magnify the relevance of physical barriers (mountain chains and tectonics). Integrating among-taxa heterogeneity into analyses can thus provide a more complete view of how different processes determine biodiversity variation across the globe.

CS1-04
Stability predicts diversity, but what kind of stability?

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Past stability is often used to explain patterns of diversity in biogeography and macroecology, but are we clear enough about what kind of stability we mean, and how to measure it? There are various ways of measuring stability, and the biological interpretation of any correlations with diversity depends on the measure of stability used. This is made more complex when we model stability for multiple taxa at once. We compared two methods of identifying regions of stability – a community level approach using generalised dissimilarity models and a species level approach using stacked species distribution models. The models were fitted across the Australian monsoonal tropics using squamate distribution data and paleoclimate reconstructions for the last 80,000 years. We looked at whether our measures of past stability explain current day patterns of richness and endemism. We found that different diversity metrics are best explained by different measures of stability. Testing stability hypotheses like this can help us understand the processes behind diversity as well as the patterns themselves. Future studies looking at past stability should consider multiple measures of stability for hypothesis testing, or at least be clear about the biological meaning of the measure used.

CS1-05

The frequency of environmental conditions mediates the coexistence of generalist and specialist species - a theoretical model and test on terrestrial vertebrates

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Understanding which types of species are assembled into local communities from a regional pool of potential colonizing species is a key goal in ecology and has clear implications to global change research. Although environmental heterogeneity is known to be associated with more generalist species, the role of environmental frequency (i.e., the commonness or rareness of a given set of environmental conditions) has been largely ignored. Here we set out to assess how environmental frequency affects the distribution of specialists and generalists. We hypothesize that environments that are low in frequency should select against specialists given that specializing on a rare combination of environmental conditions in contrast to common ones should restrict species to smaller amounts of suitable habitat, thereby increasing extinction risk. We first investigated the impact of environmental frequency on ecological specialisation using a metacommunity simulation model to generate theoretical predictions. We then contrasted those predictions against empirical data on terrestrial vertebrate distributions and climatic data. Model predictions and empirical evidence were consistent with our hypothesis as common environments were found to harbour mostly specialist species, while rare environments harboured both specialist and generalist species. Our results suggest that common environments strongly select against generalists as they are outcompeted by specialists, while rare environments restrict specialization, thus leaving opened niche spaces for generalists to occupy. Our conclusions show that beyond environmental conditions per se and environmental heterogeneity, the frequency of a given set of environmental conditions also affects how specialist and generalist species are selected to inhabit local communities.

CS1-06

Revisiting plant biodiversity-productivity relationships using a multifaceted approach

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Environmental stress and competition are expected to allow fewer species to coexist at the extremes of the productivity gradient than in its center. Yet, how these stressors shape other facets of biodiversity remains unexplored. Using a survey of >11'000 plant communities in the French Alps, a phylogeny and trait data for >1200 plant species, and high-resolution productivity estimates from remote sensing, we demonstrate that the unimodal diversity-productivity relationship dominates for taxonomic diversity, but not for functional and phylogenetic diversity. These two facets generally increase with productivity, potentially as a consequence of an increasing diversity of available niches. Relationships within grasslands deviated from the general pattern: productive grasslands harbored more species than random assemblages but they were disproportionately similar, highlighting the impact of land use activities on the relationships. Biodiversity measures accounting for similarity can capture structural changes in communities that are not well reflected in species numbers and provide a deeper understanding of how competition and other processes act along a productivity gradient.

CS1-07

Were mountain passes higher during the middle Miocene?

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In “Why mountain passes are higher in the tropics,” Janzen hypothesized that low temperature seasonality in the tropics leads to narrow thermal tolerances of organisms, limiting species’ elevational ranges more than in temperate montane regions. Mountain passes in the tropics are thereby highly effective barriers to dispersal, influencing community turnover and resulting in high allopatric speciation. We expand on Janzen’s hypothesis to test drivers of mammal species richness patterns in western North America in relation to Neogene tectonic activity and climate. We 1) quantify faunal similarity among fossil-rich regions from 17 to 6 Ma, 2) assess whether elevated spatial turnover in species composition contributed to peak regional diversity during the warm Miocene Climatic Optimum (17-14 Ma), and 3) test which landscape variables best explain the dynamics of mammalian assemblages. Using quantitative integration of crustal kinematic and deformation models in the Basin and Range Province through the Neogene, we estimated regional paleotopography, produced elevational profiles between fossil regions for 1-myr intervals, and calculated paleo-distance, maximum elevation, and two relief indices. We found a strong decay-by-distance signal in faunal similarity between regions today and during the warm middle Miocene, but not from 13 to 6 Ma. The best-fit model for explaining similarity from 17-14 Ma included paleo-distance and paleotopography variables. We conclude that mountain passes were more effective barriers during the Miocene Climatic Optimum, shaping the regional species pool and faunal turnover. Future paired topography and climate models will help distinguish the influence of relief versus thermal gradients on faunal diversity patterns.

CS1-08

Predicting species turnover from space - does it work in Amazonia?

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Satellite imagery offers great potential for identifying spatial and temporal patterns in vegetation, especially in large and inaccessible areas such as Amazonia. Earlier studies have found that plant species turnover can be predicted from reflectance differences at the landscape scale, but the use of satellite imagery across the entire Amazon basin is more complicated. Two issues are especially problematic. Firstly, most images over the rainforest area are cloudy. Secondly, ecological interpretation of reflectance values is blurred by haphazard effects of weather conditions as well as by an artifactual east-west brightness gradient. We have now successfully solved both of these problems for Landsat images, and have built a cloud-free Landsat TM/ETM+ mosaic that covers all of Amazonia at full resolution (30 m). The mosaic provides an amazing visual overview of forest heterogeneity in Amazonia. We are now evaluating to what degree the spectral variability can be interpreted in terms of plant species turnover and composition.

Concurrent Session 02: Paleoecology and Paleobiogeography

CS2-01

Brain expansion in early hominins explains carnivore extinctions in East Africa

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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. 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. 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.

CS2-02

Welcome to migrants in a borderless Europe: bryophytes show the way to go

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Climatic fluctuations during the Pleistocene exerted a profound influence on current biodiversity patterns in the northern hemisphere. In Europe, which has long served as a model in post-glacial biogeographic history, plant and animal species colonized formerly ice-covered regions from southern, micro northern or mountain refugia. Here, we used coalescent simulations utilizing information from ecological niche models and population genetics to show that the post-glacial recolonization patterns in European bryophytes involves a complex history from multiple sources, which contrasts with the commonly admitted southern and northern refugium models. Our best-fit scenario indicates that the post-glacial recolonization of Europe by bryophytes rapidly proceeded with migrants from extra-European origin. The prevalence of an allochtonous origin of post-glacial migrants reinforces the view of bryophytes as extremely efficient long-distance dispersers and supports recent paleontological evidence according to which the full-glacial landscape of Eurasia was largely treeless, with a dominance of steppe and other tundra types of vegetation. European refugia may therefore have been too small and scattered to actually contribute to the post-glacial recolonization of the continent. The rejection of a dominant southern refugium pattern, which informed concerns about the genetic implications of current climate changes, has important implications for understanding present species ranges and making predictions about their future distributions. In particular, our results suggest that, in the ongoing context of rapid environmental change, bryophyte species may not be constrained by dispersal limitations to track areas of suitable climate, and hence, are ideal indicators of climate change.

CS2-03

The botanical consequences of the dinosaur extinctions

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Mega-herbivores (>1000 kg) have shaped terrestrial vegetation since the Jurassic. With the KT extinction of the dinosaurs, terrestrial ecosystems faced a 25 Myr 'mega-herbivore gap' before the rise of large-bodied mammals from c. 40 Ma onwards. The botanical consequences of this mega-herbivore gap remain puzzling. Here, we hypothesize that plant functional groups that were adapted/exapted to mega-herbivores, such as open-habitat grasses due to grazing, plants with megafaunal fruits for seed dispersal, and spines for defence, show diversification slow-downs during the mega-herbivore gap (65-40 Ma). Additionally, we expect these functional groups to show increased trait transition rates during this time, evolving, shade-tolerance, small fruits and spineless growth forms, respectively. We use a comparative framework to fit time-dependent diversification models to fossil-calibrated phylogenies of grasses (Poales) and palms (Arecaceae)– clades with spectacular species and functional diversity that currently dominate grassland and rainforest biomes globally. We find a general tendency for diversification rates to slow-down during the mega-herbivore gap, regardless of functional traits. Furthermore, palms show elevated transition rates from megafaunal to small fruits and vice versa, indicating rapid functional turnover during this period. In line with our expectation, we find increased transition rates from open to closed habitats in grasses between 65-40 Ma, and the transition rate towards evolving spines in palms shows a moderate increase during the rise of large-bodied mammals from 40 Ma onwards. Our results suggest that the KT extinction event influenced plants globally, but that functional responses are less predictable and possibly obscured by simultaneously rising global temperatures.

CS2-04

Out of the Mediterranean: worldwide biogeography of snapdragons and relatives (tribe Antirrhineae, Plantaginaceae)

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The tribe Antirrhineae (Plantaginaceae) has an amphiatlantic disjunct distribution pattern and is particularly abundant around Mediterranean climate areas in the northern hemisphere. This configuration makes the tribe an excellent study subject from a biogeographic perspective and numerous suggestions about the ancestral area of origin for the tribe have been made. The lack of an explicit and detailed reconstruction of ancestral ranges for the complete group has kept most proposals untested thus far. A phylogenetic biogeographic approach was taken, accounting for area connection shifts through time. An ancestral origin for the tribe in the ancient Mediterranean Basin was tested, dispersal events between biogeographic regions and speciation within them were explored with different methods: Dispersal-Vicariance Analysis (DIVA) and Dispersal-Extinction-Cladogenesis (DEC). A circum-Mediterranean origin during the Late Eocene is proposed and the significant role played by the Mediterranean region in dispersal and speciation was confirmed. The establishment of current Mediterranean climates in the northern hemisphere appears to have contributed to the recent diversification within the group. Congruent patterns of long-distance dispersal across a northern Atlantic route from the Mediterranean Basin to southwestern North America were recovered for at least three of four clades displaying an amphiatlantic distribution. Southwestern Asia stood out as another relevant area in the evolutionary history of Antirrhineae and a significant floristic exchange between Europe and Southwestern Asia was detected. The possibility of developing deeper biogeographic studies incorporating ecological components could contribute to a deeper understanding of the evolutionary history of the tribe.

CS2-05

Modeling potential Pleistocene dispersal corridors between Afromontane forest regions

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Since the 1960's biogeographers have noted an unusually high floral and faunal similarity between the three disparate sub-Saharan Afromontane forest regions (East African Rift, Cameroon Volcanic Line, and Drakensburg Range), suggesting that they were connected in the recent geological past. Pollen core data indicates that montane vegetation extended further into the lowlands during Pleistocene glacial periods than at present, and habitat corridors may have formed that allowed dispersal between these isolated mountain ranges. However, the location and extent of these corridors has been widely debated due to a lack of data from Central Africa. In this study, we used paleo-species distribution modeling to estimate the possible location and extent of these Pleistocene dispersal corridors. We focus on montane tree, shrub and avifaunal species or super-species complexes with distributions spanning multiple isolated montane regions. Our models identified widespread areas of potential environmental connectivity between the three mountain ranges during the last glacial maximum, but with differing patterns between avifaunal and floral species. Avifaunal models suggested a well-defined dispersal corridor south of the Congo Basin connecting the Cameroon Volcanic Line and the East African Rift, with limited connectivity between the East African Rift and the Drakensburg Range, while floral models suggested a much broader connectivity across sub-Saharan Africa. This study is congruent with previous phylogeographic patterns in montane avifaunal and floral species and highlights the utility of paleo-distribution modeling in situations where in-situ data collection is difficult.

CS2-06

Winners and losers in ancient Ecuador with the introduction of cultivation

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Humans have altered Neotropical landscapes for more than 10,000 years, causing extinction, altering diversity, reducing ecological resilience and increasing the probability of climate inducing ecological shifts. Evidence of domestication of Camelids and crop cultivation is seen in paleorecords, and by 4000 calibrated years before present (cal yr BP) agriculture had spread in many Andean regions resulting in manufactured landscapes. Yet, the history of human occupation in the region before 5000 cal yr BP is poorly known. We used fossil pollen to track vegetation changes and crop presence, sedimentary Ti to provide an index of erosion, and *Sporormiella* spores as a proxy for Camelid presence. We provide c. 15-30 year-resolution for pollen and charcoal, and biennial resolution for sedimentary XRF data, to form a record of mid-Holocene landuse. Low-intensity pastoralism was supplemented by maize agriculture at 6200 cal BP, making this one of the earliest known sites for maize cultivation in the Andes. Changes in fire frequency, and increased erosion accompany the shift in landuse. In the natural community, after the shift in landuse, there were clear winners and losers among the Andean forest species.

CS2-07

Homo Sapiens migrations and the peopling of the Americas

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During the Late Pleistocene (*c*. 126–10 ka), modern humans (*Homo sapiens sapiens*) expanded their geographical range across Eurasia and eventually colonized the Americas. The routes by which they migrated, the shifts in their climatic niches and the mechanisms triggering those migration are still largely debated. I will showcase how macroecological approaches are unveiling our own colonization of the planet. Using them we found that the climatic niche of modern humans changed across the Late Pleistocene, as the result of both climatic and cultural changes. Moreover, I will reveal complex migration patterns across north Eurasia, likely driven by climate change as suggested by Species Distribution Models and ancient genomics. Lastly, I will present preliminary evidence of our species reaching the Americas as earlier as 30,000 years, pushing back the peopling of the Americas almost 15,000 years.

CS2-08

Regional patterns of Pleistocene extinctions in South America: interacting impacts of climate, humans, taxonomy, and biogeography

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The late-Quaternary megafaunal extinction event (LQE) represented the greatest faunal change that terrestrial ecosystems experienced during the Cenozoic, but the exact dynamics of this event remain poorly understood. Problematically, most LQE studies emphasize a single extinction driver, and consider only either very broad or very local geographic scales. Here we present the first study to investigate the LQE from a regional perspective, integrating regional analyses across a continent. We focus the study on South America, where the LQE coincided closely with both human migrations and end-Pleistocene climate changes. We assembled and analyzed chronological datasets of megafauna presence, human occupation, and climate and vegetation change across the South American continent to determine whether human activities and/or environmental change correlated with regional megafauna disappearances, and whether these two factors interacted synergistically to hasten extinctions. Taken together, our results indicate that: (a) Megafauna taxa responded individualistically to environmental changes and human impacts, with different species disappearing from regions at different times; (b) High-altitude and high-latitude regions more sensitive to climate warming may have lost megafauna earlier, and in concert with late-Quaternary climate changes, while other regions with more stable environments may have served as temporary refugia; and (c) Human impacts, where they existed, were often drawn-out, potentially driving megafauna populations to tipping points following thousands of years of cohabitance. These patterns are relevant for understanding and mitigating biodiversity loss today, as human pressures and a warming climate once again are intersecting to drive extinctions on regional, continental, and global scales.

Concurrent Session 03: Biodiversity Patterns and Maintenance

CS3-01

Is there a large-scale carrying capacity for species richness? Species-based equilibrium theory of regional diversity dynamics

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There is discussion on whether species richness is bounded or continuously expanding. The finding that macroecological diversity patterns are related to climate and largely independent of particular diversification histories supports the idea that diversity is limited by energy availability. However, there is little consensus as to the exact processes driving this species-energy relationship. Several theories assume that the limits of species richness are related to the total number of individuals. However, they are either vaguely formulated or based on quite restrictive assumptions (e.g. interchangeability of all individuals across species). We propose a new theory that explicitly considers complex relationships between energy availability E, total number of individuals J, and species richness S. It does not assume that species necessarily have the same access to resources, and thus covers a wide range of processes and species interaction. We assume that although J constrains the dynamic of S, S may in turn positively affect J as new species utilize niches not used when the community is less species-rich. The stable equilibrium of S (i.e. carrying capacity) is driven by diversity-dependence due to the negative relationship between S and population sizes, and is modulated by resources, population fluctuations, and species origination rates. The theory provides unique predictions concerning diversity patterns related to productivity, environmental stability and speciation rate. We test these predictions using multiple datasets, showing that the theory is able to predict a wide spectrum of non-trivial patterns, and thus it represents a useful general framework for understanding diversity dynamics.

CS3-02

Co-occurrence patterns in a mega-diverse tropical tree community

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Tropical tree diversity is hypothesized to derive from dynamics of ecological interactions. Pairwise interactions depend on species' spatiotemporal co-occurrences, evolutionary history and ancestrally inherited traits. Co-occurrences can arise at random, or via species responses to their abiotic environment or to each other. Here, we tested the effects of limiting similarity and environmental filtering on species co-occurrence patterns and inferred scale-dependencies of these effects. To evaluate their relative importance, we modelled jointly occurrences of >1000 tropical tree species at multiple spatial scales in five South American biomes. We found strong signals of scale-dependency in species co-occurrences. At local scale, positive associations were more abundant compared to negative associations, whereas at ecoregion and biome scales frequencies of associations were equal, albeit overall lower than at local scale. Contrary to the limiting similarity hypothesis, we did not find phylogenetic or functional similarity to limit tree species co-occurrences independent of the spatial scale. However, positive and negative associations were structured according to trait-based clusters, similar groups sharing more associations. In line with environmental filtering hypothesis, abiotic environment explained >60% of the variation in species occurrences across the studied biomes. Therefore, abiotic environment is overarchingly important across spatial scales, but mechanisms driving co-occurrence patterns and maintaining tropical biodiversity appear to differ scaledependently. At large scale, biogeographical and evolutionary history play important roles, while at small scale, species have direct and indirect interactions that shape the local community composition. With detailed understanding of these mechanisms, conservation science can counteract biodiversity loss in the most efficient way.

CS3-03

Ecological drivers of variation in global language diversity

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Global patterns of human language diversity and biodiversity are broadly similar, suggesting that both kinds of diversity may be shaped by similar ecological mechanisms. Increasingly, analyses of language diversity are applying tools from macroevolution and macroecology to deal with analytical challenges that are common to both, such as phylogenetic non-independence. Here we use an approach that will be familiar to biodiversity scientists to explore global patterns of language diversity. We focus on the relative influence of two ecological mechanisms, isolation and ecological risk. Our results provide stronger support for the ecological risk hypothesis, that high year-round productivity promotes language diversity by permitting language groups with smaller distributions to be viable. The existence of a number of hotspots with higher language diversity than expected from their environmental features suggests that historical processes such as the age of language groups could also be important.

CS3-04

The signal from our past: historical human land use as a predictor of mammalian bioregions

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A key step towards understanding the organization of biodiversity is the characterization of the assemblage of regions based on their shared species. Biogeographers have long documented that the world's terrestrial fauna is organized hierarchically in large regions - or realms - and subregions at the continental scale. Recent work documenting the factors shaping the world's zoogeographical boundaries have found that tectonics, climate and mountains have acted in concert - but with variable importance - to determine these assemblages. However, little is known about how global biodiversity patterns are assembled below the continental level and the factors triggering faunistic differences as the biogeographical scale becomes smaller. Using global terrestrial mammals, here we show that the hierarchical organization of the zoogeographical regions does extend coherently below the region level to reach a local scale. Our results show that determinants operating in a nested way from millions of years ago to nowadays have driven the extant biogeographical patterns. The Quaternary climate changes are key in understanding the taxonomic differences among bioregions at smaller scales. Unexpectedly, anthropogenic land uses during the Late Holocene have also left their footprint across biogeographical scales, predicting on their own 22% of the taxonomic differences among the larger bioregions. This historical period coincided with the development of large cities and a substantial transformation of ecosystems into agricultural land. These results suggest that present-day biogeographical patterns were partly driven by past human activity, showcasing a long-lasting and broad signal of anthropogenic impacts.

CS3-05

Mountains: the biogeographer's Petri dish

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Mountains are key features of the Earth's surface and host a substantial proportion of the world's species. However, the links between the evolution and distribution of biodiversity and the formation of mountains remain poorly understood. To tackle this problem, we show results from two lines of investigation focused on i) current biodiversity and ii) diversification analyses. In the first case, we integrate multiple datasets to assess the relationships between species richness in mountains, geology and climate at global and regional scales. Specifically, we analyse how erosion, relief, soil and climate relate to the geographical distribution of terrestrial amphibians, birds and mammals. We find that centres of species richness correlate with areas of high temperatures, annual rainfall and topographic relief, supporting previous studies. We unveil additional links between mountain-building processes and biodiversity: species richness correlates with erosion rates and heterogeneity of soil types, with a varying response across continents. In the second case, we use dated molecular phylogenies, models of geographic range evolution, surface uplift estimates and biotic interactions to infer the interplay between abiotic and biotic variables on speciation, extinction and migration rates. We find that different clades often responded differently to similar factors. For instance, the Andean uplift led to an increase in speciation among bellflowers and orchids, but to a decrease in speciation among hummingbirds. Taken together, these findings showcase mountains as exemplary models for studying the evolution and distribution of the world's biodiversity – 'Petri dishes' for natural experiments.

CS3-06

Historical contingencies, scale-dependence and contemporary- and past-environmental variation determine the phylogenetic structure of bat assemblages across the globe

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Patterns of phylogenetic relatedness among co-occurring species are traditionally assumed to be caused by three mechanisms: environmental filtering, competitive exclusion, and neutrality. Nevertheless, these mechanisms are built into assumptions that have been continuously contended by evidence related – but not limited – to evolutionary changes in niche requirements and competitive abilities, fitness, diversification rates, dispersal barriers, and species pool extent and isolation. Here, we use the geographical distribution and phylogenetic history of bats (Chiroptera), and the current- and paleo-climates to assess how historical, environmental, and spatial and temporal scale-dependent factors jointly determine the phylogenetic structure of bat communities across the world. We found strong effects of geographical isolation and species pool extent on the phylogenetic structure of bat communities, especially between the New World and the Old World. Phylogenetically overdispersed communities are more frequent in the Afrotropical, Indomalay and Australasian regions, which may result from a combination between trait divergence, flight possession, and frequent biota interchange among these regions. Furthermore, both past and contemporary colder, drier and more seasonal environments exert increased influence in bat community structure, suggesting a stronger role of environmental filtering and phylogenetically conserved traits in stressful conditions. Finally, distinctions between deep-time and contemporary patterns of phylogenetic clustering between and within regions, especially in the Afrotropics, indicate that recent glacial-interglacial climatic oscillations may have structured bat communities. Our study shows that different temporal and spatial scales, dispersal barriers, past climatic oscillations, and contemporary environmental gradients shape the phylogenetic structure of bat assemblages across the globe.

CS3-07

Species-by-species associations: On their measures, spatial scale, links to macroecological patterns, and our ability to detect them

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Macroecology deals with patterns of biodiversity, their spatial scaling, and their temporal change – these are useful for assessments of past, current, and future states of living nature. Particular quantities of interest are species richness, species turnover (beta diversity), relative abundances, intra-specific aggregation, and their spatial scaling reflected in rarefaction curves or species-area relationships. We argue that one fundamental facet of biodiversity, inter-specific spatial association, is not reflected by the classical macroecological patterns. Although there is a voluminous literature on species associations and segregations, particularly in community ecology, they are largely absent in the theory of biodiversity patterns and measures. The reasons are: (1) the classical biodiversity patterns are often insensitive to species associations, (2) there is a confusing variety of approaches to measure species associations, (3) and they are critically scale-dependent.

Here, we offer a concise synthesis of different approaches to measure species associations; specifically, we focus on approaches based on site-by-species matrices (e.g. the C-score), approaches using additional spatial information such as community variograms, network-based approaches, and techniques for point pattern data. We show both complementarity and redundancy among the approaches, we demonstrate their different ability to detect species associations, and we briefly explore their spatial scaling. With this we hope to stimulate development of macroecology of speices-by-species associations, and its use in applied biodiversity assessments.

CS3-08

Species interactions shape vertebrate diversity across Europe

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Recent evidence is casting doubt on the assumption that competition has a limited role in influencing

diversity at large spatial scales. Here, we test how species interactions (competition and predator-prey) influence the ranges of individual species and how that, in turn, scales up to diversity within areas (e.g. species richness). To do this, we couple a newly assembled food web for all European vertebrates with species distribution information, and use statistical models to quantify the effect of species interactions (derived from the food web) and climate on the distributions of species. In general, we find that a species is more likely to occur if their prey species are present, but less likely to occur if their competitors are present (while considering the effect of other interactions and climate). This suggests that competition in particular is acting to limit the distributions of species from otherwise suitable climate space. By statistically 'releasing' competition in the models, most species are predicted to expand beyond their current range. This effect scales up, such that the models suggest species richness is limited by competition, especially in already diverse, climatically moderate areas—linking theory on species niches and species richness gradients.

Concurrent Session 04: Conservation and Invasion Biogeography

CS4-01

Measuring the robustness of bioregions against changes in species composition

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Bioregions are hierarchical classifications of the Earth's surface defined by characteristic assemblages of species. Changes in the composition of those assemblages over time are important since they may influence ecological and (co)evolutionary processes at multiple spatial scales. Human activity is altering the distribution of species by means of human-mediated introductions and extinctions, potentially altering those assemblages. Previous studies have suggested that bioregions may be susceptible to change. However, species are not homogeneously distributed within bioregions, and some areas may be expected to hold assemblages more prone to change due to introduction and/or extinction. Here, we present an index that measures the robustness of the geographical areas within a zooregion, based on the species that are present in a zooregion but distinguishing between the species that do and do not characterize it. Our metric can be used to measure the robustness to change of species assemblages at any spatial scale. Here we measure the robustness of the largest bioregions of amphibians, mammals, and birds. Our results show that the robustness of bioregions largely varied across vertebrate groups and within bioregions. For instance, we detected that bioregions of birds are more robust than those of mammals and these ones are more robust than those of amphibians. Our results also show that bioregions representing Amazonia or Indo-China are among the most robust, and bioregions located in Central America or the Arabian Peninsula are among the least robust. Indeed, our index may identify those geographical areas more susceptible to suffer biogeographical changes.

CS4-02

The loss of megafauna: implication for freshwater biodiversity conservation

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Freshwater megafauna, i.e. all freshwater animals that can reach 30 kg, play essential ecological roles. At the same time, they are highly susceptible to extinction due to their large body size and habitat requirement, late maturity and low fecundity. Freshwater megafauna species are facing multiple threats including overexploitation, habitat degradation, dam construction and pollution, and, according to the IUCN Red List, more than 50% of the assessed species are listed as threatened. To get a comprehensive understanding of global diversity patterns of freshwater megafauna and threats to them, we mapped their global distributions and analysed human threats throughout their distribution ranges. Amazon, Congo, Orinoco, Mekong and Ganges River basins are among the biodiversity hotspots of freshwater megafauna. Concurrently, species in the Mekong and Ganges River basins are facing high human pressures. In addition, we tracked change in freshwater megafauna populations from 1970 to 2012. Our results show that global population of freshwater megafauna has declined by 85% while the decline rate in Asia is over 95%. However, there remain large gaps in freshwater megafauna monitoring and assessment. Information is insufficient to assess conservation status of a quarter of all freshwater megafauna species. Populations of many freshwater megafauna species, especially reptiles and fishes, remain unmonitored. Since freshwater megafauna species can be seen as surrogates for the overall freshwater biodiversity, the global status of freshwater megafauna reflects the highly threatened but largely overlooked status of freshwater biodiversity. We discuss the potential of these charismatic animals in promoting conservation for overall freshwater biodiversity.

CS4-03

Inclusion of geodiversity indices improves models of aquatic plant richness in boreal lakes and rivers

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Conserving freshwater biodiversity in a rapidly changing world requires updated planning schemes and efforts. Geodiversity and biodiversity are interlinked at a fundamental level and considered in growing number of studies; however, the existing research does not cover freshwater environments yet. We used three geodiversity variables (rock-type and soil-type richness, geomorphological diversity) and four local and climatic variables to find out whether geodiversity can be used as a surrogate for aquatic plant richness in Finland. We compared novel geodiversity variables to well-studied local (e.g., area, alkalinity) and climate (e.g., growing degree-days) variables, and examined the detected patterns between habitat types (lakes and rivers) and among all taxa and major functional groups. We modeled lake (n=150) and river (n=148) plant richness with GLMs, and further partitioned variation to measure the contributions of the geodiversity, climate and local environmental variable groups. As a complementary analysis we utilized boosted regression tree analysis. As a result, we found a positive relationship between species richness and catchment geodiversity that was constant across two freshwater habitats and two functional groups. Although some local water quality and physical habitat variables (alkalinity, lake surface area, and river channel width) were the most important single variables in influencing variation in aquatic plant richness, inclusion of geodiversity indices invariably improved models. This outcome indicates that geodiversity brings added value to biodiversity modeling and should be included in conservation schemes and efforts. Our results also support the Conserving Nature's Stage strategy, as higher geodiversity in a catchment area supported higher freshwater biodiversity.

CS4-04

Evaluating Niche Models with Presence-Only Data is Uninformative for Many Applications

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Species distribution models and environmental niche models are used across evolution, ecology, conservation, and epidemiology to make critical decisions and study biological phenomena, often in cases where experimental approaches are intractable. Choices regarding optimal models, methods, and data are typically made based on discrimination accuracy: a model's ability to predict subsets of species occurrence data that were withheld during model construction. However, empirical applications of these models often involve making biological inferences based on continuous estimates of relative habitat suitability. Using a simulation approach, we demonstrate that discrimination accuracy is a poor indicator of a model's ability to estimate habitat suitability or species responses to environmental gradients. These results suggest that many empirical studies and decisions are based on model selection criteria that are unrelated to models' usefulness for their intended purpose. We argue that empirical modeling studies need to place significantly more emphasis on biological insight, and that the current approach of maximizing discrimination accuracy at the expense of other considerations is detrimental to both the empirical and methodological literature in this active field. Finally, we argue that future development of the field must include an increased emphasis on simulation, as methodological studies based on ability to predict withheld occurrence data may be largely uninformative about best practices for many modeling applications and will unduly penalize more biologically informative modeling approaches.

CS4-05

A global picture of biological invasion threat on islands

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Biological invasions are among the main drivers of biodiversity losses. As threats from biological invasions increase, one of the most urgent tasks is to identify areas of high vulnerability. However, the lack of comprehensive information on the impacts of invasive alien species (IAS) is a problem especially on islands, where most of the recorded extinctions associated with IAS have occurred. Here we provide a global, network-oriented analysis of IAS on islands. Using network analysis, we structured 27,081 islands and 437 threatened vertebrates into 21 clusters, based on their profiles in term of invasiveness and shared vulnerabilities. These islands are mainly located in the Southern Hemisphere and many are in biodiversity hotspots. Some of the islands share similar characteristics regarding their connectivity that could be useful for understanding their response to invasive species. The major invaders found in these clusters of islands are feral cats, feral dogs, pigs and rats. Our analyses reveal those IAS that systematically act alone or in combination, and the pattern of shared IAS among threatened species, providing new information to implement effective eradication strategies. Combined with further local, contextual information this can contribute to global strategies to deal with IAS.

CS4-06

A biogeographic perspective on trophic rewilding

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Most current real-world ventures named as rewilding fall under the concept of trophic rewilding, as do most discussion of rewilding. Trophic rewilding is an ecological restoration strategy that uses species introductions to restore top-down trophic interactions and associated trophic cascades to promote self-regulating biodiverse ecosystems (http://bit.ly/rewildingPNAS). Trophic rewilding is often focused on large-bodied animals (herbivores and carnivores) due to their ecological and societal importance and the widespread, strong historical losses of megafauna in most regions around the world. In this presentation, I will first discuss the concept of trophic rewilding as well as outline the scientific background, integrating paleobiology, biogeography, and ecology. Key themes here will the fact that megafauna-rich ecosystems have been the norm world-wide on evolutionary timescales, with the widespread modern-day megafauna-poor ecosystems being a novel situation, and the emerging evidence for the strong ecological importance of large-bodied animals. I will then outline the current role of trophic rewilding in nature conservation as well as its potential, hereunder as seen in relation to widespread Anthropocene land use dynamics, e.g., land abandonment and forest transitions. As part of these discussions, I will present the results of relevant new biogeographic and macroecological analyses. Finally, I will provide an overview of the key priorities and possibilities for rewilding research.

CS4-07

Global distribution of Lyme disease: reservoirs and vectors´ favourability

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Lyme Borreliosis is an infectious disease caused by spirochetes of the genus *Borrelia*, which is mainly transmitted to humans by ticks of genera *Ixodes* and *Haemaphysalis*. It is one of the most prevalent diseases in the northern hemisphere. Mammals are main reservoirs of this pathogen, especially small-size species such as those in the orders *Rodentia*, *Lagomorpha* and *Eulipotyphla*. Our biogeographic analysis aims to explain the spatial distribution of this infectious disease throughout the world. Using the favourability function, we develop a distribution model of Lyme disease based on global records of endemic disease areas. The model is built on a combination of several factors that could condition the incidence of the disease: 1) environment (climate, topography and human variables); 2) spatial structure (probably linked to the history of the disease); 3) favourable areas for the presence of vectors (ticks); and 4) the distribution of all small mammals that could be potential reservoirs of the bacterium (represented by their types of distribution or chorotypes). The favourability map predicts a widespread distribution of Lyme borreliosis throughout the Holarctic region, principally excluding Greenland and Siberia. The model shows the emergence of new foci and points to a number of factors that could influence the global distribution of Lyme cases. We discuss the possible risk hotspots, and reveal the usefulness of this pathogeographic approach as a tool for the prevention of zoonoses with high relevance to human health.

CS4-08

Maximizing the conservation of biodiversity in the design of a regional reserve network

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The conservation of biodiversity is becoming ever more urgent, especially because of the link between biodiversity and ecosystem services. To better address conservation goals, policy and management decisions need to maximize more than just the number of species preserved, by also considering phylogenetic and functional diversity. By measuring biodiversity based on the variation among species in trait characteristics and evolutionary relatedness, we can simultaneously address these manifold goals. While we strive to preserve all species, the design of a regional reserve network may face cost and spatial constraints resulting in the preservation of areas that contain less than the full set of species in that region. Unknown is whether the goals of maximizing species richness, phylogenetic diversity, and functional diversity will be congruent (i.e., maximizing one maximizes the others) or will be in conflict. We demonstrate that for two data sets – birds in the state of Connecticut, USA, and bats in the country of Paraguay – a reserve network designed to maximize species richness also maximizes other aspects of biodiversity.

Concurrent Session 05: Global Change Biology

CS5-01

SoilTemp: towards a global database of soil temperature

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Many questions in current ecological research deal with large-scale patterns, as global databases of species distributions and traits become increasingly accessible. Current analyses of these patterns and their predictions under anthropogenic climate change are however often based on free-air temperature conditions with a coarse resolution, and thus fail to capture apparent temperatures (cf. microclimate) experienced by living organisms within their habitats. This microclimate however starts operating as soon as a habitat includes a vertical dimension with significant variation along it, originating from either biotic, abiotic or human-made features (e.g. in mountains, forests, or cities).
Recent research also suggests a crucial role for the location of temperature measurements. Countless species groups (e.g. soil micro-organisms, insects or herbs) will indeed relate more strongly to temperatures close to the soil surface than those at 2 meter above the soil. However, while the quality and resolution of free-air and surface temperature data at the global scale is rapidly improving thanks to elaborated networks of weather stations and satellite data, soil temperature datasets are still largely restricted to the regional scale, or to coarse resolutions.
We brought together a global database of soil temperature data and use it to explore the drivers of soil temperature in space and time and to calibrate globally-valid hybrid models of soil temperatures. Ultimately, we will provide a set of global maps of relevant summary statistics (i.e. bioclimatic variables) based on interpolated soil temperatures. We demonstrate the applicability of this database with several regional and large-scale species distribution models.

CS5-02

Woody plant encroachment intensifies under climate change in biomes at the extremes

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Woody encroachment has been increasingly reported at locations worldwide, including in the tundra and the savannah – two structurally similar biomes that are particularly vulnerable to climate change due to their presence at temperature and precipitation extremes. This process can lead to consequences in ecosystem function and structure, altering species distributions and richness, ecosystem services and the persistence of these biomes at local scales. While woody expansion has taken place similarly in both biomes, their drivers and magnitude of change have not been quantified yet.

Through an analysis of climatic data and the available literature and databases reporting cover vegetation change, I provide a synthesis of the global status of woody encroachment. This includes a quantification of woody expansion in both tundra and savannah biomes, a comparison of their vegetation change rates, and the identification of different mechanistic drivers to encroachment.

Results indicate that encroachment is widespread in these two biomes across geographical scales, time, and the climatic space. Woody cover is increasing annually by 0.35% in the tundra and 0.6% in the savannah. Additionally, larger encroachment rates coincide with high temperatures and precipitation for the savannah, and average to warmer conditions for the tundra. Drivers of change differ between them – warming air temperatures are the most reported cause in the tundra, and herbivory and wildfires the chief causes in the savannah. These results enable cross-biome comparisons of climate change response and provide a basis to identify whether species' responses are generalizable or highly linked to the biomes they inhabit.

CS5-03

The physiological responses behind F. serratus biogeographic distribution: phenotypic differentiation and niche underfilling.

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The change occurring in the oceans in the last decades is influencing physiological and ecological processes of diverse taxonomic groups, which eventually may affect their ranges of geographical distribution. Species could adjust their physiological responses to local conditions, via acclimatization or local adaptation, which could facilitate the persistence of species of southernmost populations. This study aims to determine the effect of different environmental factors on the vital rates of different life-stages of the brown macroalgae *Fucus serratus*, and the inter-population variability in the response. Overall, in adults, no variability in growth and survival was found among populations in response to increases in seawater temperature, except for one of the southernmost populations, which presented higher survival physiological threshold than the other populations. The large decoupling between thermal tolerance and environmental temperature experimented in the field suggest a niche underfilling in *F. serratus*. In early stages, the temperature during emersion reduced survival and growth, but this effect was dependent on the origin population, with more pronounced effect in benign conditions of marginal populations. The phenotypic inter-population differentiation observed in early stages, support the detected differential survival of adult thalli, suggesting that both seawater and air temperature are relevant for the understanding the current distribution of species and forecasting *F. serratus* distributional shift and could explain the niche underfilling detected in adults. Although we found differences in the response of populations to environmental factors, this physiological divergence is not enough to cope with the rapid climate change along its southern limit of distribution.

CS5-04

The consequences of the European motorway network on mammals populations

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Roads affect wildlife through mortality and isolation of populations by barrier effects. Motorways present greater barrier effects than other roads because of speed, traffic, width, and fences, likely applying significant constrains on populations at continental scale. While reducing movement opportunity, barrier effects reduce mortality, a trade-off with consequences on populations' persistence not well studied yet. Similarly, we still lack clear estimations of how habitat amount interacts with motorway density to impact populations in European landscapes. This study aims to investigate the combined impacts of motorway density and habitat amount on the persistence of mammal populations in Western Europe, and their potential mitigation by barrier effect strength.

We tested impacts of fenced and unfenced motorways on populations of virtual species representative of European mammals, characterized by different traits linked to road sensitivity. Across Western Europe, we selected 27 landscapes (100 x 100km) based on habitat proportion and motorway density. Using a population dynamics model, we first generated species' distribution in landscapes where motorways were removed. We then added either fenced or unfenced motorways, to test impacts of both scenarios on populations' size.

Taken independently, increasing motorway density and decreasing habitat amount decreased population sizes. The impact of motorway density was stronger when the habitat amount was low, leading to population extinctions at gradients' end. This impact was limited by unfenced motorways, which had a positive impact only in that situation.

Our results highlight on a continental scale the strong barrier effect of motorway network in Western Germany and the Benelux countries.

CS5-05

Extinction can be also a creation phase: the conceptual framework of perfugia and the 'trailing-edge' relicts

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During the species range restriction, populations are typified inter alia by a reduced gene flow and smaller size. However, they can also be driven by the creation of new relationships with changing abiotic and biotic factors. The extinction phase can then be paradoxically a dynamic period when the ecological foundation can be laid for the future long-time species persistence in the region in microrefugia. The concept of 'trailing-edge relicts' (young relict populations) and 'stabilized relicts' (old relict populations) clearly corresponds to the above processes. Younger 'trailing edge' populations often occur near the core range of the species and have recently become isolated. In contrast, the oldest 'stable' climate relicts have persisted for a long time over changing climate conditions.

To distinguish between the sites with young and old relict populations, we propose the Latinised term 'perfugium'. During unfavorable changes in the region, species extinction occurs and increasing numbers of isolated localities are established. These can be termed perfugia. Over time, unsuitable abiotic conditions, degenerative genetic processes or the lack of adequate (new) ecological configurations can result in extinctions. The occurrence of the species in the region becomes possible only in microrefugia – perfugia with the highest refugial capacity.

The conceptual schemes given in our presentation summarise and develop the patterns which occur during species range shift. We highlight the importance of sites harbouring 'trailing-edge' young relicts in the future long-term persistence of the species, as old relicts.

CS5-06

Extreme climatic events reduce climatic disequilibrium on semiarid shrubland communities, but lithology matters.

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Species distribution models can provide a useful tool to assess climatic disequilibrium dynamics of communities in a climate change context in which extreme events are more likely to occur.
Since communities' velocity to adjust to climate is lower than recent climate changes, local community composition is frequently out of equilibrium with the observed climatic conditions. However, this climatic mismatch could be reduced through extensive decay of less suitable species if critical weather thresholds are exceeded. Here we assessed the effect of an extreme drought episode which led to important compositional changes on rich shrubland communities growing on three contrasted bedrocks, portraying different water balances, in SE Iberian Peninsula. We calculated Community Inferred Climate (CIC) before and after the drought episode using species' climatic niches and species' observed changes in abundance, and then we estimated community climatic disequilibrium by comparing this CIC with the observed community environmental position. We found that these extreme events could act as environmental filters reducing the mismatch between CIC and the observed climate. Nevertheless, soils over different bedrock types could buffer or exacerbate this effect depending on their water retention capacity. Indeed, we found that under similar historical climatic conditions, less favorable bedrocks showed the lowest climatic disequilibrium, suggesting stronger filtering.
The study highlights the role of soil-climate interactions as drivers of disequilibrium dynamics in a rapid changing climate.

CS5-07

African vegetation change since the last glacial maximum: climate versus pastoralism

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Prehistoric vegetation change on the African continent is not well understood, especially surrounding the controversial termination of the African Humid Period, circa 5500-3500 years before present (BP), when important changes in land use for animal production were simultaneously underway. In order to improve our understanding of continental-scale vegetation trends, we reconstruct changes in the climatic envelope of selected vegetation biomes from the last glacial termination (~20,000 BP) to the modern day, using fossil and modern pollen datasets. We map and compare vegetation reconstructions with broad climatic trends, as well as the development of animal production and hunting land uses. Our results show that the extent and establishment of vegetation classes in climatic space responded closely to changes in northern hemisphere summer insolation prior to the Holocene climatic optimum (~9,000-10,000 BP), but responded non-linearly during the past 9,000 years, as pressure from land use increased. We overview possible climatic and anthropogenic drivers of these changes, and discuss the role that animal production could have played. Furthermore, our mapped analyses highlight geographic areas where more data coverage is necessary in order to improve reconstructions of vegetation change.

CS5-08

Native climatic niche explains establishment success in exotic mammals

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Biological invasions represent increasing threats to biodiversity, ecosystems, but also to human economies and health. Major effort was accordingly put in recent years to better understand why some exotic species fail to establish, but others are successful. Successful exotics have passed several filters: geographic, abiotic and biotic. One key hypothesis in this regard is that, when introduced in a new range, an exotic species initially develops in environmental conditions similar to those in its native range, i.e. within its native niche. Yet, this hypothesis has so far remained largely untested. Here, using a large dataset of 989 introductions of 177 mammal species worldwide, we show with SDM suitability and niche innerness - two indices of the relative position of the introduction sites within the species' native niche - that climate matching to the native niche is a strong predictor of establishment success. The integration of such indices in pre-border risk assessments could improve chances to prevent invasions before introduction, and possibly avoid costly eradications.

CS5-09

Individual-Based Models Predict Loss Of Range And Genetic Diversity In Cold-Adapted Amphibians With Climate Change Due To Dispersal Constraints

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Two prominent questions in ecology regarding climate change are how biodiversity will be redistributed over the landscape and whether potentially adaptive genetic diversity will be lost. Forecasting models that only include climate data are limited because they predict potential species distributions that may not be realized due to dispersal limitations, and they are unable to evaluate if genetic diversity in the southern range will be lost. Projecting how species respond to change is particularly important for amphibians because range shifts are likely limited by their dispersal abilities. We used MigClim to forecast range shifts and loss of genetic diversity for six North American cold-adapted amphibians. Predicted range sizes were reduced compared to climate-only models. Dispersal distance or dispersal rate was the most important parameter, as opposed to age at dispersal or number of years of dispersal, depending on species. Because the evaluated parameter space for each species was identical, this indicates that geographic position or initial range size influence range shift dynamics. Second, we ran simulations for only the southern populations of each species to evaluate whether adaptive variation may be retained for the species by northward-dispersing individuals as ranges shift. Southern ranges experienced > 50% net range reduction within the models across all species, indicating that the range was reduced at a rate that was faster than individuals could migrate northward to within their current range. This generation of more sophisticated models enabled us to determine that range reductions and loss of genetic diversity are expected for cold-adapted amphibians.

CS5-10

The importance of considering adaptive genetic variation in climate change projections

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Although intraspecific variation in local adaptations leads to differences in population responses to climate change, adaptive genetic variation is commonly ignored in models forecasting species vulnerability and biogeographical changes under future climate change. We integrated genomic and ecological modelling approaches with biogeographical data to first identify genomic variation associated with climate, and then incorporate this information directly into forecasts of range changes under future climate change and into assessments of the potential for evolutionary rescue. We focus on wild populations of two cryptic forest bat species, *Myotis escalerai* and *Myotis spA*, that are sympatric in the Iberian Peninsula, but whose distributions appear to be limited by interspecific competition. We found that considering adaptive climatic genetic variation reduces range loss projections, suggesting that climate change vulnerability projections that do not account for intraspecific variability are overestimating future species range losses. On the other hand, incorporating adaptive genetic variation increased projected range overlap between species, indicating that interspecific competition is likely to play an important role in limiting species future ranges. We found that evolutionary rescue in response to climate change is possible, but it depended on both population adaptive capacity and population connectivity. Our study highlights the importance of combining genomic and biogeographic approaches to understand biodiversity responses to climate change.

CS5-11

Climate adaptation lag across the range of European forest trees

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Local adaptation to climate is an ubiquitous process in plants that is still unexplored at a wide-range scale. The centre-periphery theory stems from the idea that gene flow asymmetry across a species range promotes adaptation lags to climate at range margins, i.e. prevents peripheral populations to reach their local optima. We used extensive networks of common garden experiments across Europe to test adaptation lags to both temperature and precipitation gradients across the range of major broadleaved (*Fagus sylvativa* L., *Quercus petraea* (Matt.) Liebl.) and conifer trees species (*Abies alba* Mill., *Pinus nigra* Arnold, *Pinus pinaster* Aiton, *Pinus pinea* L.). We used mixed-effects models that account for both the climate of the common garden and the climate of population origin to understand the main climatic drivers of natural selection and to compute adaptation lags among populations of the climatic core of the species range and at climatic margins. Results show weak to strong geographical patterns in differences of climatic optimums among populations, suggesting contrasting importance of selection and history among species. However, we found consistent patterns of adaptation lags. Populations inhabiting the climatic core of the species range were mostly locally adapted whereas range margin populations exhibited high adaptation lags. Furthermore, our results show that recent climate change brought cold margin (leading-edge) populations closer to their local optima but have exacerbated adaptation lags in warm margin populations (rear-edge) making them the most vulnerable to rapid climate change.

CS5-12

Quantifying decadal change in carbon storage potential in high altitude tropical forests.

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Rapid changes in global climate are driving shifts in forest distribution across the globe with significant implications for global carbon cycling. There is particularly high uncertainty surrounding the response of tropical mountain forests to climatic change with little understanding of how changes in forest distribution impacts carbon sequestration in high altitude systems. The distribution of Taiwan fir (*Abies kawakamii*) has changed rapidly across Taiwan’s Central Mountain Range with increases in treeline elevation and forest density reported. Altitudinal treeline advance can be slow and periodic, such that changes in forest demography must be identified on decadal time scales and at fine spatial scales. Here we combine a network of field observations with aerial photography and satellite imagery to quantify change in above-ground forest carbon storage potential over a three-decade period. To identify areas indicative of forest expansion we classify trends in spectral indices from a time-series of satellite imagery with a classification accuracy of 85%. We find that 8% (14823 ha) of the area above 2400 m a.s.l. in the Central Mountain Range is currently undergoing afforestation, leading to a gain of 172177.2 tonnes of carbon in above-ground forest carbon stocks. During the past three decades 126033.8 tonnes of above-ground forest carbon have been lost due to disturbance events resulting in a net gain of 46143.4 tonnes of carbon in above-ground forest carbon stocks in the Central Mountain Range. Our work facilitates robust estimation of changes in the carbon sequestration potential of high altitude forest in data-poor tropical mountain regions.

CS5-13

Local climatic changes influence biodiversity responses to land-use change.

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Rapid human population growth has resulted in increasing exploitation of the environment and conversion of land for human use. These changes in land use can alter land cover, which mediates local climatic conditions and in turn may modify ecological assemblages. In human-altered landscapes, sites are generally hotter and drier than in natural habitats. By using the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project database, we have been analysing, globally, whether human land uses and land-use intensification systematically favour species with certain climatic tolerances. We found that local climatic changes ensuing land-use change are favouring species with particular climatic niches and, consequently, impacting community composition. On average, communities within human-altered landscapes are composed of species affiliated with warmer and drier climates compared to natural habitats. Thermal niche breadths are also wider within human-dominated land uses. In addition, the size of these effects differed across a tropical to temperate gradient, between land used at different intensities and between taxonomic groups. This work enhances our understanding of how biodiversity responds to the interaction between climate and land-use change, which can help identify species at risk, predict future biodiversity changes and create suitable conservation and management plans in an ever-changing environment.

CS5-14

Deep-sea biotic response to oxygen variability and Pleistocene global changes: paleoecological and macroevolutionary dynamics in a marginal sea

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The Sea of Japan is a marginal sea, connecting to adjacent seas by four shallow straits (water depths <130 m). Marginal seas are ideal for studying biotic responses to large-scale environmental changes as they often are sensitive to glacial-interglacial and stadial-interstadial climatic cycles as well as longer scale changes. However, only a limited number of studies cover time periods beyond the last two glacial-interglacial cycles. Here we present a two million year record of benthic biotic response to paleoceanographic changes in the southern Sea of Japan, based on ostracode assemblages at the Integrated Ocean Drilling Program (IODP) Site U1426 and U1427. Results show that (1) orbital-scale faunal variability have been influenced by eustatic sea level fluctuations and oxygen variability, and (2) faunal composition showed distinct difference between the post-MBE and pre-MBE (Mid-Brunhes Event) periods. Long-term oxygen variability in the bottom water has been the major control impacting the marginal-sea biota. The MBE was a major disturbance event in deep-sea ecosystems, as several studies have recently reported major faunal events during the Mid-Pleistocene in various oceans and seas. Benthic ecosystems in marginal seas are sensitive and vulnerable to both short-term and long-term climatic changes.

CS5-15

Interaction of land use and climate change impacts on breeding birds in North America

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Climate change has driven large-scale population decline of many species and habitat fragmentation threatens decline in species abundance beyond those expected from total amount of habitat lost. While many studies have focused on studying the impacts of individual global change drivers on species, species are experiencing multiple changes to their environment simultaneously. As a result, empirical evidence of how the dimensions of anthropogenic change act in concert to impact biodiversity is needed. Recent studies have examined the combined effects of climate change and changes in habitat on breeding bird communities by using species presence and absence records at limited geographical scales. Examining the interaction of these drivers at large geographic extents provides essential insight in developing a general framework to predict how interactions between global change drivers will affect biodiversity. To address this question, we use land bird abundance data from the Breeding Bird Survey along with land cover and climate data between 1992 and 2011 to model how habitat fragmentation and climate change predict changes in population trends of breeding bird species throughout the continental United States. Secondly, we determine whether ecological traits such as habitat specialization and thermal niche width can predict the susceptibility of species to the impacts of habitat fragmentation and climate change. The results of this study will contribute to developing a general understanding of how biodiversity is impacted by the simultaneous effects of global change drivers.

Concurrent Session 06: Gradients, range-limits, and beta-diversity

CS6-01

Big data suggest migration and bioregion connectivity as crucial for Neotropical biodiversity

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Tropical America (the Neotropics) harbours three times as many flowering plant species as tropical Africa, despite comparable environments and area. The evolutionary history generating this pattern remains poorly understood, partly because data on the geographic distribution of species is scarce. Collections from museums and herbaria can overcome this gap, but uncertain data quality hampers their use, especially in historical biogeography invoking phylogenetic trees. Here we present novel software to process large amounts of species occurrence data for biogeographic research ensuring data quality. We then apply these tools to identify processes underlying the evolution of Neotropical biodiversity across taxonomic groups. The results point towards Amazonia as major source for Neotropical biodiversity on the evolutionary scale, and suggest that shifts among different bioregions and biomes were common. This was particularly the case for shifts into open and seasonally dry biomes, which increased during the last 20 million years, especially in the Bombacoideae (Malvaceae), a pantropical group with highest diversity in the Neotropics. The presented results shed further light on the evolutionary history of the differences in biodiversity across Earth's tropical regions, and provide a methodological route forward to integrate large-scale species occurrence data with information on species' evolutionary relationships.

CS6-02

A meta-analysis of niche breadth – species richness associations

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Although narrow niche breadth has long been assumed as either an explanation or an outcome of high species richness, it gained only equivocal empirical support. This may be the result of scale and methodology differences between studies, which in turn reflects different possible mechanisms that drive this association. We suggest two such mechanisms: (1) climatic - where low seasonality at lower latitudes enables species to specialize in specific environmental conditions, which results in high species richness, and (2) community assembly - where species rich sites forces species to specialize, in order to allow co-existence. For each of these mechanisms we expect to find different patterns of richness-niche breadth correlations.

Under the climatic mechanism we expect associations between species richness and niche breadth over large scales, specifically across climatic gradients, and only when using environmental measures (e.g. habitat breadth). While the community assembly mechanism would yield such associations mostly over small scales, across many types of richness gradients, and when using both environmental and functional measures (e.g. diet breadth). Thus, distinguishing the scale dependence, and the niche breadth type may shed light on the underlying processes.

We conducted a meta-analysis on studies that report the correlation between niche breadth and species richness. We found (1) negative correlation between species richness and niche breadth; (2) species richness has a stronger effect on niche breadth compared to latitude; (3) lack of any effect of scale or type of niche breadth. These results suggests that community assembly processes drive niche breadth patterns.

CS6-03

Avian blood parasite prevalence is governed by bird community assemblies and colonization histories

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The prevalence of parasites can be influenced by the communities of their hosts. Cosmopolitan host-parasite interactions, such as vector-transmitted haemosporidians (blood parasites) of birds, provide opportunities to investigate how host communities drive parasite prevalence. Over space, haemosporidian prevalence may be higher in warmer lowlands compared to colder highlands with more limited vector abundance. Similarly, bird species in geologically younger regions may experience lower parasite prevalence and pressure due to the lag time of parasite/vector colonization. We tested these hypotheses for haemosporidians in bird communities along an elevational gradient (200-3700m.a.s.l) on the tropical island New Guinea, and between two comparable bird communities in mountains of different geological ages. We found a mid-elevational peak of haemosporidian prevalence, primarily driven by differences in bird communities between elevations. Mid-elevation communities were occupied by multiple bird species with higher haemosporidian prevalence than low- and highland communities. However, parasitism in individual bird species did not show a mid-elevational peak, confirming that haemosporidian prevalence across space is not driven by individual species but by the composition of the community. As predicted, we found significantly lower parasitism levels in comparable bird species communities in the geologically younger than older mountain areas, in support of a lag time in vector colonization. Our findings suggest that haemosporidian prevalence across space is shaped by the communities of bird species, and that birds moving into geologically younger regions may temporarily escape blood parasites.

CS6-04

Analysis of community phylogeny along elevation gradient in subtropical island Taiwan supports "Out of Tropical Lowland" hypothesis

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Understanding the mechanism of species assembly in response to temperature is challenging; however, information about phylogenetic relatedness among species in the community may provide some important insights. Two opposing hypotheses are tested here: “Tropical Niche Conservatism” (TNC) predicts that as temperature decreases, the mean clade age of species in a community tend to be younger as niches are temperature-constrained, causing certain lineages to continuously adapt to temperate climate. A contrasting “Out of Tropical Lowland” (OTL) hypothesis signifies a rapid migration of randomly distributed tropical lineages to mountains where they diversified slowly, therefore lacking younger lineages. Taiwan offers a strong case for the observation of community assembly due to its young geological age, diverse climatic range and steep elevation gradient. In this study, we focus on determining underlying assembly mechanisms in the woody flora of Northeast Taiwan, a region characterized by heavy rainfall and frequent cloud coverage with elevation-influenced climate ranges from tropical to warm temperate. By analyzing nearly 300 vegetation community plots, we found that with decreasing temperature toward higher elevation, phylogenetic relatedness of species within the community decreases and the mean family age (MFA) increases. This pattern is coherent with the OTL hypothesis and is further supported by findings that show MFA correlates to factors such as lowest minimum temperature of the coldest month. By applying phylogenetic methods to community distribution, our results tell us more about Taiwan's community assembly mechanisms, providing new information about the biogeographical and evolutionary source of species in plant communities at different elevations.

CS6-05

Early-branched fern lineages are confined to northern latitudes in Europe; insights from a phylo-regionalization analysis

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Phylogenetic regionalization can provide insight on the evolutionary and ecological mechanisms shaping species assemblages at broad scales, and particularly for taxonomic groups with long and complex evolutionary histories, such as ferns. Here, we used an exhaustive distributional dataset including all fern species in Europe (110 × 110 km grid) along with a molecular phylogeny to (i) define fern phyloregions based on phylogenetic beta diversity (i.e. turnover, pß$_{\text{sim}}$), and (ii) elucidate the contribution of historical and ecological drivers in shaping phyloregional membership. We also quantified the degree of affiliation of phylogenetic clades to the phyloregions using an index of confinement based on phylogenetic diversity (i.e. PD). We identified six distinct phyloregions, with a primarily division between northern and southern latitudes. Phylogenetic beta diversity between phyloregions was overall low, thus mirroring the widespread distribution of most fern lineages in Europe. Yet, northern phyloregions hosted a higher evolutionary distinctiveness (i.e. mean phylogenetic turnover) than those in southern latitudes. As such, the phylogenetic affiliation analysis revealed a major confinement of early-branched fern lineages to northern latitudes. Overall, phylogenetic turnover across phyloregions was higher than nestedness. Contrary to previous evidence, the high evolutionary distinctiveness hosted by northern Europe phyloregions together with low phylogenetic nestedness do not support the hypothesis of recolonization from southern refugia after ice retreated. We speculate that the confinement of early-branched lineages towards northern latitudes may be explained by retention of ancestral niche requirements of past fern floras that once originated under cold climatic conditions, and subsequent adaptation to warmer climates.

CS6-06

New approaches to assess the role of competition in shaping species ranges

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Despite increasing awareness of the importance of including biotic interactions in Species Distribution Models (SDMs), a robust methodological framework to measure their effect at broad spatial scales has yet to be developed. This study presents simple and applicable measures that identify patterns of geographic avoidance across species ranges based on SDM outputs to infer broad-scale competitive effects. We used ensemble SDMs to model the continental range of four sets of Palearctic cryptic bat species in which

competition is thought to occur, and applied to them our measures of geographic avoidance. We compared this approach with other available methods to measure competitive effects, the direct inclusion of competitor's range in the models and recently developed Joint SDMs. The two proposed measures identified geographic avoidance among some of the cryptic species pairs, and alongside information on species ecology gave support to the role of biotic interactions in shaping these species' ranges. We show that our measures have important advantages, including low data requirements and ability to detect individual effects in asymmetric interactions, making them particularly suitable for broad-scales applications and for species that have not been sampled intensively. The high community-type data requirements of Joint SDMs limit their ability to infer broad-scale interactions in most taxonomic groups and across many regions of the world. . Understanding the effects of competition is essential for modelling species responses to global climate change. Therefore simple measures like the ones we propose are particularly relevant for enabling better integration of biotic interactions into SDMs.

CS6-07

The future keepers: assessing the effects of thermal stress and resource limitation on ants

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Across Australia, different regions have experienced climatic changes to varying degrees, both seasonally and annually. One of the most fundamental issues is how our biota will respond to rapid changes in climate. Changes in population abundances, modified via changing behaviour, physiology or competition for food resources, could cause major population restructuring of currently common species, leading to the collapse of trophic interactions and depletion of ecosystem function. AIMS: To predict how key species (ants) that provide core ecosystem functions may change under thermal stress and resource limitation. QUESTION 1: What influence does differential resource limitation have on ant food preference and biological traits along biogeographical gradients? QUESTION 2: Does differential resource limitation change ant foraging along the gradients under increased temperatures? QUESTION 3: How do physiological traits of ants collected from more arid zones of Australia compared with more coastal populations. PREDICTIONS: More ants found on salt diet up to 100km from coastal areas, but not further inland. Ant foraging strategies may change along gradients and with seasonal changes. In chambers – more ants attracted to salt food sources. In extreme temperature sites – summer thermophilic taxa will be more active in the chambers. Sites with greater seasonal variation, will see a bigger change in nutritional preferences. CTmax and thermolimit responses will not change along transects. CONCLUSION: Understanding how ants respond to temperature and moisture changes will help determine the impact of climate change on ecosystem engineers: answers to the questions posed here will address this.

CS6-08

Saturniid and sphingid moths as novel models for the study of insect diversity and macroecology

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Insects are the most speciose group of terrestrial organisms and are strongly affected by global environmental and climatic changes. They exhibit a remarkable variety of forms and life history trait combinations not represented among vertebrates and are responsible for many ecosystem services and disservices. Yet, our knowledge of their diversity and distributions, as well as our understanding of their evolution and diversification dynamics through space and time, remains fragmentary. We have identified a group of herbivorous insects – the Saturniidae and Sphingidae, two sister families of moths – that represent

an unparalleled insect model. This group comprises about 5000 species and has been thoroughly documented worldwide, through comprehensive DNA barcode libraries, hundreds of thousands of occurrence records in databases, and a broad documentation of their life histories. Thus, they offer for the first time an opportunity to study patterns of diversity and distribution at a global scale in insects, together with their underlying macroevolutionary processes. Here we present the comprehensive database built by our research group and the different approaches – such as integrative taxonomy, biogeographical analyses, phylogenomics, analysis of traits and community ecology – that we combine to address key questions about the macroecological patterns and their evolutionary history. We expect that it will shed light on the processes governing the extant diversity of insects and help us understand how global changes will affect them, how they may or may not adapt to these changes, and how best we can act to conserve their species and preserve their roles

CS6-09

Conditional love? Investigating interactions shifts along continental-scale water availability gradients

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Joint Species Distribution Models (JSDMs) can help disentangle the role of environment and biotic interactions in species co-occurrence patterns. These models have gained quite some popularity in the past years and can, for example, be used to generate hypothesis on the specific species interactions. However, most joint models assume that interactions between species are static. In reality, species interactions may be mediated by the environment. Recently, environmentally dependent JSDMs have been developed that allow species associations to change with the environment.

Here, we tested whether shifts in species interactions along a water deficit gradient influence the European scale distributions of species and whether the resulting pattern complies with the Stress Gradient Hypothesis. We used the recently developed context dependent JSDMs to infer the interactions of 287 grassland species in mesic and dry grasslands across a water deficit gradient in Europe. We expect that a low water deficit (i.e. low stress), negative associations (competition) will dominate while at a high water deficit, positive associations (facilitation) will become more prevalent.

Our results show that associations between the species in our models vary along a gradient of water availability at large scale as expected. This may indicate that biotic interactions between grassland species are modulated by the environment (i.e.: water availability), and that this in turn of influences their large scale distribution. Furthermore, we show how these models might be used generate and investige large-scale hypotheses on species interactions such as the Stress Gradient Hypothesis.

CS6-10

Topographical barriers and LGM refugia affect phylogenetic turnover in European vascular plants

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Phylogenetic turnover quantifies the lineage distance among species assemblages and is used to understand the main drivers shaping biodiversity. Turnover of clades in geographic space results from geographic and environmental barriers to certain lineages or single species. Compared to species turnover, phylogenetic turnover can reveal evolutionary mechanisms rather than only ecological aspects. During the last glacial maximum species were exposed to environmental and geographical barriers and had to track suitable habitats available in refugia. The pattern of these refugia can be expected to having left an imprint on contemporary phylogenetic turnover, which has not been tested yet. Here, we apply a moving window approach to represent phylogenetic turnover of European vascular plants in geographic space. We remove environmental distance effects within moving windows to directly assess spatial distance effects. We demonstrate that phylogenetic turnover strongly varies along spatial gradients in European vascular plants. The found patterns can be explained by topographic barriers and distances to refugia during the last glacial maximum. Our results provide new insight into the effects of evolutionary history on observed biodiversity patterns.

CS6-11

How environment modulates primary succession dynamics

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Assessing the modulating effect of the environment on diversity and endemism as well as the speed and trajectory of primary succession allows for a more general understanding of this fundamental ecological process shaping species communities through time. Here we present the successional divergence hypothesis that focuses on environment-driven changes of plant species diversity, changes in successional speed and changes of successional trajectories during primary succession. We recorded vascular plants and bryophytes in 210 plots along a chronosequence of nine lava flows (max. ~6000 years and elevational range of 1100 m) on the subtropical island of La Palma, Canary Islands. We quantified successional speed and temporal trajectories using compositional dissimilarity metrics along elevation in relation to time and deconstructed betadiversity into its turnover and nestedness components. Species richness and endemism increased with time. Successional speed peaked at early to mid-successional stages. While turnover (as a component of betadiversity) mainly contributed to the successional dynamics, nestedness only had a minor contribution. Successional trajectories along the gradient of energy and water availability clearly diverged through time, from initially similar composition at all elevations of early succession to increasing dissimilarity between different elevations with time. Our study suggests that primary succession on lava flows is a directional process with abiotic environmental conditions acting as a major modulator of plant diversity, successional speed and trajectories. The successional divergence hypothesis that conceptually links important processes shaping primary succession dynamics contributes to understanding the biotic and abiotic processes shaping long-term dynamics of species assembly in plant communities.

CS6-12

What are the determinants of temporal occupancy for birds in North America?

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Understanding how biotic and abiotic factors shape species distributions is a fundamental question in ecology. We examined the relative importance of competitor abundance and the environment in determining the species distributions of 104 bird species across North America. Unlike previous studies, which tend to model distributions in terms of presence and absence, we take advantage of a geographically extensive dataset of community time series to calculate the temporal occupancy of species at sites throughout their expected range. We calculated the variation in temporal occupancy across geographic range and then used variance partitioning and Bayesian hierarchical models to evaluate the relative importance of 1) the abundance of potential competitors and 2) the environment (elevation, temperature,

precipitation, vegetation index) for determining avian temporal occupancy. We found that on average, the environment explained more variance in occupancy than competitor abundance, but competitor abundance could explain a far higher proportion of variance for certain species than the environment. We also found that certain migratory and trophic groups had a higher proportion of variance explained by the environment than competitor abundance, especially granivores and resident species. Finally, we used a null model to determine that the species we identified as main competitors had a stronger impact than expected on focal species occupancy compared to a random non-competitor. The results of this study can be used to gain a better understanding of what factors influence species distributions and persistence at sites and compile a more comprehensive picture of how species are distributed throughout their range.

CS6-13

Battling the global antimicrobial crisis: Phylogenetic and spatial distribution of anti-infective metabolites in the flora of Java

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The continued high rates of use of antibiotics in healthcare and agriculture has led to a dramatic increase in antimicrobial resistance, with multidrug-resistant bacteria emerging as a major public health problem worldwide. However, despite the urgent need for new antibiotics, many pharmaceutical companies have largely suspended their antibiotic drug discovery efforts, mainly due to very high investment but low returns. To help battle the global antimicrobial crisis, we here evaluate the phylogenetic patterns of anti-infective compounds across taxonomic and biogeographic scales in one of the most species-rich regions on Earth and assess the predictive power of phylogenies to identify clades with naturally occurring substances potentially suitable for the development of new active pharmaceutical compounds. Specifically, we (1) estimate the degree of phylogenetic signal of anti-infective compounds using a genus-level phylogeny of the flora of Java, and (2) identify 'hot nodes' in the phylogeny, indicating overrepresentation of anti-infective compounds in a given clade. Finally, we (3) assess the spatial patterns of plants with anti-infective compounds relative to total plant diversity across the region. By identifying clades of overrepresentation, drug discovery can be guided into promising clades with high possibilities of finding more plant species useable for drug production. Clades underrepresented with activity might constitute lineages with low numbers of activities or poorly-studied lineages, these clades are therefore high risk - high reward clades. This is the first full approach combining bioactivity of all angiosperm plant genera on Java with spatial and phylogenetic data.

CS6-14

Biogeography, not temperature,controls species richness in Australia

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The majority of studies indicate that temperature is the key environmental control on species diversity across a wide range of temporal and spatial scales. The most important is the species-energy hypothesis, wherein lower extinction rates and higher primary productivity support a higher richness at the equator. We used a large dataset of marine mollusc occurrences in coastal Australia to test for the effects of various controls. We defined biogeographic regions using a variety of objective means. When all variables are considered, biogeographic structure is the only significant factor, regardless of biogeographic scheme or the number of taxa included. These results suggest that species richness is primarily controlled by historic and geographic factors, and not solely by temperature as suggested by other taxa.

CS6-15

Compiling plant diversity data in Southeast Asia: a symbiotic partnership between research projects and local herbaria

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Biodiversity estimation of tropical biomes is critical to understand the mechanisms of ecological diversification among biogeographic regions. Large-scale data of species occurrences over taxonomic clades is a fundamental asset for a comprehensive description of distribution patterns of tropical plant diversity, and essential to designate important areas for biodiversity conservation. However, occurrence data of plant species is strongly biased in countries and regions having larger researcher communities, while regions, in particular Southeast Asia, have been poorly explored by scientists. Plant diversity information has been compiled conventionally by two different communities of researchers, botanists and macroecologists, which correspond to the separation between data providers and users. Macroecologists mostly benefit asymmetrically from efforts and investments by botanists on processing and maintaining specimens, while research funding allocations may not appreciate properly their importance. To overcome the imbalance in supply and demand, we have to build a symbiotic partnership between the two communities. In this view, we are launching a project networking macroecologists and local herbaria across Southeast Asia, and targeting for a large-scale occurrence data of woody species. Based on this dataset, we evaluated the clade/region-specific sampling coverages and estimated potential diversity patterns along environmental gradients. We specified undersampling areas in the data which in turn coordinates the compilation process. This project proposes a novel approach of proactively informed data compilation of plant diversity, which not only contributes to future projects of botanists and macroecologists but also reorganizes specimen data at local herbaria into accessible formats.

Concurrent Session 07: Functional Biogeography & Island Biogeography

CS7-01

Linking biogeography and evolution: environmental variation and evolutionary dynamics of phenotypes in wild bird populations

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Natural selection is the main mechanism and most powerful explanation for adaptive evolution, and environmental variation is the main fuel that feeds the engine of natural selection. From a microevolutionary perspective, evolution can be detected within populations where natural selection acts on the expression of phenotypes. We are starting to unravel how and what agents of selection can cause evolutionary adaptation within a temporal perspective. However, our knowledge is rather limited towards very few species that are experiencing particular environmental conditions. In addition, and unsurprisingly, biogeographically dispersed populations of the same species can respond differently to the same agent of selection, i.e. climate change is expected to have different evolutionary responses depending on the environmental conditions that every population experiences. Here we illustrate how evolutionary dynamics of phenotypes and biogeography can be married using species distribution models built with the favourabilityfunction. We use own and bibliographic-based data gathering more than 1400 estimates of evolutionary traits in wild European populations of birds. We found that selection gradients increase as environmental favourability increases for secondary sexual traits in pied flycatchers (*Ficedula hypoleuca*). At multispecies level, we also found that both evolvability and selection gradients of multiple phenotypes are linked to environmental favourability in a non-linear way: selection and evolvability decreases at both ends of environmental favourability. We suggest how intra- and inter-specific interactions within populations might explain these patterns. More importantly, we present a new methodological approach to link both fields of research and discuss its limitations and benefits.

CS7-02

Global patterns of intraspecific leaf traits responses to elevation

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Elevational gradients are often used to quantify how leaf traits of plant species respond to abiotic and biotic variation along single slopes or mountain ranges. Since we know little on the response of intraspecific leaf traits to elevation across species, we here quantitatively summarized multi-taxa results for 104 species from 71 studies published between 1983 and 2017. Specifically, we hypothesize that intraspecific trait adjustment appears in the same direction showing a common trait-elevation relationship across species worldwide. We measured the change of seven morpho-ecophysiological leaf traits along the elevational gradients selected: specific leaf area (SLA); leaf mass per area (LMA); leaf area (LA); nitrogen concentration per unit of area (N*area*); nitrogen concentration per unit mass (N*mass*); phosphorous concentration per unit mass (P*mass*) and carbon isotope composition (δ^{13}C). We found LMA, N*area*, N*mass* and δ^{13}C to increase with increasing elevation, while SLA decreased with increasing elevation. Conversely, LA and P*mass* showed no significant pattern with elevation. In addition, we found N*area*, N*mass* and P*mass* to be higher with increasing elevation in gradients with overall higher mean summer temperature. Furthermore, the δ^{13}C increased more largely in gradients with lower soil aridity. Finally, trait changes of herbaceous species showed overall higher variation in response to elevation compared to woody species. Our study demonstrates that there are common cross-species patterns of intraspecific leaf traits change across elevation worldwide. To account for environmental changes along elevational gradients it is key to further our understanding of such patterns in future ecological research.

CS7-03

Big brains for big cities: Relative brain size and tolerance to urban environments in birds

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The current trend towards a more urbanized world represents a major threat for wildlife, leading to important declines in local biodiversity. For some organisms, however, cities provide novel ecological opportunities, allowing increases in abundance beyond that found in natural habitats, but the mechanisms allowing some species to exploit urban environments have only recently been studied. A particularly attractive idea is the “cognitive buffer hypothesis”, suggesting that a big brain should facilitate the persistence in urban environments by facilitating the construction of behavioural solutions to the new challenges. However, assembling evidence for this hypothesis has proven challenging, most likely because differences in life history may lead to alternative pathways to be an urban dweller. Here, we revisit the role of brain size on urbanization tolerance by means of a global comparative analysis in birds. To this purpose, we combine information of avian assemblages along urbanization gradients with a brain dataset of over 600 species. Urbanisation tolerance was measured as the change in species abundance between the urbanised environment and the surrounding wild environment. Our results confirm the association between brain size and urban tolerance, but they also suggest that the relationship is more complex than previously thought. While relatively larger brains increase urbanization tolerance in species that have a future returns life history, some small-brained species can attain high success in the urban environment by having a multi-brood life history strategy. Our results thus suggest that a larger brain size or a bed-hedging life history, are alternative strategies to successfully exploit urban environments.

CS7-04

Trophic conservatism predicts alpine plants responses to herbivore ecosystem incursion

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Climate change promotes asynchronous range shifts of species across trophic compartments potentially reshaping ecosystem structures and functions. While, herbivore abundance and plant defences show a coupled decline along elevation gradient, the current equilibrium of ecological systems could be disrupted with animals upwardly tracking climate change faster than plants. Here, we experimentally simulated climate-driven ecosystem incursion of herbivores from lower elevation on alpine plant communities. We report that herbivore trophic conservatism predicts the response of alpine plant communities to novel herbivore incursion. By feeding preferentially on alpine plants with functional traits and metabolomics profiles matching those explaining their original trophic interactions, herbivore colonizers reduced light competition and plant biomass, but increased small stature plant species and community diversity. Contrasted with a direct warming treatment using greenhouses, we showed a stronger effect of increased herbivory than temperature on plant communities. Indirect biotic responses to climate change through climate-driven herbivore incursion might represent a stronger driver of ecosystem modification than temperature.

CS7-05

Alternative strategies drive strong brain size bimodality in variable habitats

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Habitats that undergo large environmental fluctuations present a unique ecological challenge by exposing organisms to a breadth of biotic and climactic conditions. Enhanced encephalization (i.e. large brain size relative to body size) has been suggested as a potential solution because it equips species with an increased ability to mount flexible and varied behavioral responses in the face of frequent or unexpected change. However, our global analysis of over 1500 non-migratory birds shows that the Earth's most variable habitats, those at high latitudes that are characterized by high seasonality and low predictability, are preferentially occupied by not only the largest, but also the smallest relative brain sizes. Here, we explore how diet, body size, and reproductive output interact with brain size and environmental conditions in order to understand how small brains can facilitate persistence in these challenging habitats. We find that small-brained species in variable environments tend to be large bodied but also specialize on difficult to digest, consistently available resources and produce many offspring per year – characteristics that are not obtainable for larger-brained species. While large bodies and access to consistent resources may increase survival across environmental fluctuations, high reproductive output would allow recovery from high mortality suffered during particularly difficult conditions. Our results reveal that the link between brain size and environmental variability is more complex than previously thought and demonstrate that these opposite strategies are equally equipped to cope with some of Earth's most challenging habitats.

CS7-06

Are organisms with dispersal traits better colonizers within oceanic archipelagoes?

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When studying species dispersal, it is often assumed that species with specific traits -such as winged animals or plant diaspores with hooks, pappus or nutritious tissues- are better dispersed than unspecialized species and thus tend to have wider distribution ranges. However, recent studies have challenged this assumption. It has been described that plants with structures associated with specific long-distance dispersal vectors show only a small or negligible advantage. This finding raises two interesting questions: Do winged animals display a significant advantage for colonisation? And secondly, are mobile animals better colonisers than plants? To answer these questions, we analysed animal (Coleptera, Sauropsids and Mammals) and plant (Angiosperms) traits and distributions across the Canary Islands. We found that dispersal traits have played a more important role in animal dispersal than in plant dispersal. More surprisingly, we found that despite lacking voluntary movements, plants have been at least as effective inter-island colonizers as animals.

CS7-07

A phylogenomic and population genomic test of the taxon cycle hypothesis of island biogeography

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The taxon cycle is an integrative model of the ecological and evolutionary dynamics of community assembly, but many aspects of the hypothesis have historically been difficult to test empirically. Phylogenomic and population genomic analyses allow the investigation of two critical but independent aspects of the taxon cycle: the arrival sequence of colonizing lineages and their eco-evolutionary trajectories after colonization. The taxon cycle predicts that lineages arrive by colonizing low-elevation, high-disturbance habitats, followed by niche shifts into interior, high-elevation habitats. These shifts are associated with declines in dominance and dispersal ability, and increases in ecological and morphological specialization. Using the ants of the Fijian archipelago as a model system, we examine these predictions using phylogenetic and population genomic analyses of two hyperdiverse ant genera, *Pheidole* and *Strumigenys*. We find that, consistent with the taxon cycle, niche shifts occurred after colonization as species adapted to interior and high-elevation habitats, 3D geometric morphometrics showed that extreme morphological diversification has occurred in both groups after colonization. However, contrary to the taxon cycle, we found demographic evidence that some lineages either retained or re-evolved a highly dispersive generalist syndrome and at least one species is undergoing a secondary range expansion out of Fiji. Moreover, there is no evidence that more recent colonizing lineages are displacing earlier arrivals; all cladogenic endemic species are derived from the first arriving lineage, suggesting a strong role for priority effects. In summary, combined genomic, morphological, and ecological analyses show mixed support for different taxon cycle predictions in Melanesian ants.

CS7-08

Intraisland assembly of soil biodiversity: habitat filtering and microendemicity across space and habitats

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The spatial scale of speciation depends on the dispersal capabilities of organisms. In this sense, oceanic islands offer an interesting arena where taxa need to arrive over long distances and then colonize and adapt through the limited available space. The soil is inhabited by a small fauna of arthropods, most of them with strong dispersal limitations i.e. apterous species adapted to special soil conditions, which in the continent results in pronounced microgeographical structure of endogean diversity. Here we use community DNA metabarcoding to study mesofauna of Acari, Collembola and Coleoptera in samples from the four main habitats across the island of Tenerife (Canary Islands). Our results point to a massive diversity of soil mesofauna within the island, with communities associated to habitat type and with many soil lineages showing a strong geographic structure and microendemicity. These results shed light on the magnitude of long distance dispersal by soil mesofauna and while highlight the existence of extremely high levels of soil biodiversity and endemicity on oceanic islands potentially linked to important intraisland dispersal limitations.

CS7-09

The island syndrome in plants

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Continental animals undergo rapid and predictable evolutionary changes on isolated islands that are collectively known as the *'island syndrome'*. Though the island syndrome has gained considerable empirical support, to date, no large-scale study has demonstrated whether it applies to the evolution of island plants. Here, we provide the first large-scale empirical test of the island syndrome in plants. We made phylogenetically informed morphometric comparisons of island plants and their closest living mainland relatives using a dataset comprised of field measurements, flora descriptions, and herbarium specimens. Results are remarkably consistent with those seen in insular faunas. Large-statured plants tend to become dwarfed on islands, while smaller-statured plants become gigantic. Contrastingly, leaf size was overwhelmingly larger in island taxa, irrespective of changes in stature. Overall results demonstrate that the theoretical predictions applied to insular animals are equally applicable to insular plants. Future work will attempt to disentangle differences in the evolution of island taxa that result from cladogenisis versus those that result from anagenisis.

CS7-10

Time to abandon the loss of dispersal ability hypothesis in island plants?

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The loss of dispersal ability hypothesis predicts that selection favours the evolution of reduced dispersal potential in isolated populations. Here I review previous tests of the loss of dispersal ability hypothesis in island plant populations. Despite its widespread appeal for over 150 years, relatively few studies have tested the hypothesis' predictions. Results from this small body of work indicate that many island plant species don't actually exhibit a loss of dispersal ability. When a loss of dispersal ability is observed, it is usually associated with increased seed sizes, rather than the loss of functionality in dispersal aides. This raises the possibility that the loss of dispersal ability, when it is observed, may evolve as a passive by-product of selection for large seeds, for reasons that may be wholly unrelated to their dispersal. These issues advocate a fresh approach to the study of how selection shapes the evolution of dispersal potential in island plant populations.

CS7-11

Revealing controls on distribution and microhabitat use of Anolis lizards in a changing island landscape

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In these times of rapid environmental change and species extinction, understanding the drivers governing species' abundance and distribution is more important than ever. The goal of this work is to further our understanding of what drives variation in species' abundance and microhabitat use through space, particularly in the context of rapid land cover change. Using the little explored anole fauna of the Honduran island of Utila as a natural ecological laboratory. By pioneering emerging technologies in airborne remote sensing for predicting animal abundance and distribution, the project is designed to improve our ability to predict species' ecological responses to habitat conversion and identify key ecological interactions between habitat structure, microclimate, and species' distribution. Pilot work has revealed a distinct habitat preference in the endemic *Anolis bicaorum* and has noted an increased range and habitat usage of the invasive *Anolis sagrei*. Data collected on operative temperature from morphologically accurate 3D models (fitted with ibutton data loggers) and at a plot scale (20 x 20m) is being coupled with leaf area index from hemispherical photography and UAV imagery. This may be the key in determining whether habitat usage and distribution is primarily due to habitats being more thermally favourable for these ectotherms. Alternatively, whether factors such as habitat structure, derived from UAV imagery and standard plot vegetation metrics are a driving factor. This work is allowing us to improve our understanding of Utila's *Anolis* fauna, promote its conservation and demonstrate how emerging technologies can help us understand and preserve the natural world.

CS7-12

A population genomics approach to island biogeography: shedding light on the colonisation of Santorini following the Minoan eruption.

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"Sterilised" islands, which have been destroyed by catastrophic volcanic eruptions provide biogeographers with natural experiments to study the process of island colonisation. When such events occurred too long ago to be monitored, a population genomic approach can provide insights into the colonisation history of island taxa, while allowing to distinguish between scenarios of single vs. multiple founding lineages. We here focus on the colonisation of the volcanic island of Santorini (Thera) in the Eastern Mediterranean, which was allegedly sterilised in 1620BC by one of the most catastrophic volcanic eruptions in human history. Santorini is surrounded by continental islands that have been separated from each other for thousands or millions of years and harbour largely distinct beetle faunas at the species/subspecies level. The mixed faunal composition of Santorini suggests colonisation from different source islands, while a striking lack of congeneric beetle species could be an indication of competitive exclusion or merging of closely related lineages. We sampled 5 flightless beetle taxa from Santorini and the surrounding islands and generated genome-wide SNP data. Demographic inference based on the site frequency spectrum was used to reconstruct the origin (single or multiple founding lineages), direction and timing of colonisation for each focal taxon. We identify differences among taxa and discuss them in the light of taxon-specific traits. Our results highlight the utility of population genomics for disentangling alternative processes involved in community assembly and shed light on the colonisation of Santorini, which has been subject of speculation for many decades.

CS7-13

Elucidating speciation mode between Canary-Mediterranean sister species by combining ancestral niche overlap and Genotyping-By-Sequencing

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Canary Islands endemic species that have Mediterranean sister groups constitute suitable systems for addressing classical questions of island biogeography and speciation. This is the case of two polyploid (2n=44) species of plants: *Lavatera acerifolia*, endemic to the Canary Islands and its sister species *Lavatera maritima*, distributed along the Western Mediterranean basin, including NW Africa, for which phylogeographic studies are available.
To assess whether divergence between these two species occurred in North Africa or, subsequently, *L. acerifolia* diverged within the Canary archipelago, we used environmental niche overlap approaches and genomic data (SNPs) obtained through Genotyping-by-Sequencing (GBS).
Specifically, we reconstructed niche evolution over time up to the split of both species by (1) inferring phylogenetic relationships among genetic groups identified based on SNPs, (2) studying niche overlap at each node between lineages descending from such node, i.e., within species and (3) analyzing the niche overlap between both species.
Our results suggest that *L. maritima* exhibits a broader environmental niche, which is partly overlapped with that of *L. acerifolia*, and it might have the capacity for adapting to substantially different climatic environments. We also propose that both geographic and ecological factors played a role in speciation and favor the hypothesis that *L. acerifolia* shifted its niche from *L. maritima* along with or after the colonization of the Canary Islands following a peripatric speciation model.

CS7-14

Host-parasite interactions and their role in speciation in crate lake cichlid fish

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A thrilling topic in evolutionary biology is understanding the mechanisms generating biodiversity. Adaptive radiations are particularly good models for the study of speciation, since phenotypic divergence leading to speciation happens rapidly and repeatedly, often after colonization of empty novel habitats like islands or isolated lakes. The Neotropical Midas cichlid adaptive radiation in Nicaragua has evolved while colonizing several isolated crater lakes. Local adaptation has shaped species distribution, and has contributed to the development of reproductive barriers. Here we evaluate the role of parasite distribution and their interactions with their fish host in promoting diversification and ultimately speciation. We have investigated parasite communities in each lake detecting a large number of endemic lineages, and any associations with the fish immune response measured and variation at the Major Histocompatibility Complex (MHC) genes, detecting lake-specific signatures. We suggest that this mechanism might play a relevant role in cichlid diversification.

CS7-15

Can plant traits surveys complement phytodiversity studies? a comparative study on dry juniper woodlands in Doñana National Park and El Hierro Biosphere Reserve Island.

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The hypothesis that the study of plant functional traits can complement phytodiversity studies, and in what way the information can be obtained in a short time with few funding scenarios, for plant community management and other purposes, is tested. This study is based on the nominal soft plant traits from our own botanical surveys drawn up from Doñana and el Hierro. Plants traits influence the survival of the taxa present in different plant communities. These dry woodlands are high micro hot-spots of biodiversity (97 taxa have been located as a result of our own studies in Doñana, and 131 taxa of vascular plants in el Hierro). The presence of a higher number of phanerophytes in Doñana than in El Hierro, and a comparable number of chamaephytes in both places, are at variance with the theory of “empty niche”. The higher presence of hemicriptofphytes in Doñana than in El Hierro could be the result of a greater herbivory pressure in the National Park. The greatest abundance of annuals in el Hierro is explained by the episodes of severe drought in this oceanic island. It is essential to combine phytodiversity studies in order to reach conservation targets and to get a more detailed understanding of how plant biodiversity works in dry juniper woodland.

Concurrent Session 08: Neotropical Biogeography & Models and drivers of biogeographic patterns

CS8-01

Isolation and Introgression in a Replicate Radiation of Neotropical Viburnum

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Replicate radiations -- where multiple lineages diversify along similar morphological axes among distinct regions -- provide strong evidence for the role of selection and constraints in directing patterns of evolution. Although evidence for replicate radiations generally relies upon phylogenetic evidence, few studies of replicate radiations have used genome-wide data, or investigated alternative network-based approaches to describing relationships among lineages and regions. Here we present evidence for a replicate radiation of Viburnum species among distinct isolated neotropical cloud forests regions from Mexico to Bolivia. In each region we find at least two distinct eco-morphs repeatedly: a shrub with small glabrous and entire leaves, and a small tree with large pubescent and toothy leaves. Using genomic RAD-seq data we show that species within each region are each other's closest relatives, suggesting in situ divergence has occurred repeatedly into the two eco-morphs. Genome wide data allow us to investigate additional hypotheses such as introgression between species within regions, or between regions. We describe a framework and methodology for distinguishing these alternative hypotheses and show that the radiation of Viburnum in neotropical cloud forests does appear to have been facilitated by gene flow between isolated mountainous regions.

CS8-02

Patchy pre-Columbian human impacts in western Amazonia

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Human populations in Amazonia are thought to have increased rapidly after c. 3000 years ago and peaked at the time of European Conquest. Here we ask whether that trajectory of increased human population and impacts are manifested in western Amazonian paleoecological records. We present high-resolution, paleoecological reconstructions from Lakes Ayauch[i] and Kumpak[a] (Ecuador) that span the last 2400 years. Pollen, phytoliths, charcoal, and sediment chemistry were used to investigate the impacts of climate and land use on the tropical forest. We found evidence of maize agriculture that caused declines in old-growth forest elements and replacement by secondary forest and disturbance taxa or an independent increase of palms. Further, high Ca values, most likely related to increased drought conditions, were associated with reduced values of old-growth forest and increased values of disturbance taxa. Maize cultivation was documented in the records c. 400 BC–AD 400, AD 900–1400, and after AD 1900, while times between cultivation were characterized by high values of palms at Kumpak[a]. No such peaks of palm were documented from Ayauch[i]. Charcoal was rare and sporadically distributed along the Kumpak[a] core, but always related to pre-Columbian maize cultivation or modern land use. At Ayauch[i], however, charcoal was abundant throughout the core. The records suggest that humans were moving in and out of this landscape rather than occupying it continuously for the last 2400 years. There is little evidence of a sustained population increase and, notably, neither site was heavily used at the time of contact.

CS8-03

Margay (Leopardus wiedii) occupancy in relation with habitat suitability

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Recently there have been attempts to combine occupancy (OM) and ecological niche models (ENM) for building hybrid models with the aim to get a better understanding of species distributions. From this arises as a fundamental question how OM and ENM are related. Here, we analyze the relationship between margay (*Leopardus wiedii*) occupancy and the habitat suitability derived from ENM. We used the WorldClim2 bioclimatic variables and an arboreal cover variable because of magay arboreal habits. We selected the best MaxEnt model from different settings and features. For the occupancy estimation, we used single-species, single-season model with site covariates for camera trap data of six different sites throughout the Neotropical realm. We used as covariates the vegetation percentage (PV), the Normalized Difference Vegetation Index (NDVI), the Normalized Difference Water Index (NDWI) and the land surface temperature (LST), by means of remote sensing techniques. For every site, all possible models were built and with the best (AIC <2) we built an average model to obtain occupancy. Finally, with the habitat suitability and occupancy values for each sample point, we applied a Pearson correlation. We got a positive correlation ($r = 0.5343$, $p < 0.05$), this means that a higher habitat suitability corresponds a higher occupancy. We observed there is a clear correspondence between occupancy and habitat suitability in low ($S \leq 0.25$) and high ($S \geq 0.50$) habitat suitability values, while in medium values there is not a clear pattern, which can be explained by different factors such as biological interactions.

CS8-04

Leaf morphometric variation and biogeographic inferences of a Neotropical species

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Blepharocalyx salicifolius relationship over Neotropical Myrtaceae is complex and is supposed to be sister group of Myrtaceae from the new world or considered to be of highly interest in the resolution of evolutionary relations in this important taxonomic group. This species is widely distributed in the main Neotropical biomes, it is highly plastic, and combines two ecological characteristics that are dominant in the Neotropics: bee-pollination and bird dispersal. We hypothesized that this species would present biomes-structured leaf plasticity, which would correspond to a biogeographic structure observed in an independent phylogenetic analysis resulting from a broad genetic sampling of this species. To do so, we analyzed eight foliar morphometric variables of this species using data collected from different biomes to explore possible ecological structuring within morphological polymorphism. We performed correlation analyses between variables, tests of variance between means, outline (shape) analysis and principal component analysis (PCA). We also performed the leaf outline reconstruction forms of this species inferred from Elliptic Fourier analysis. The modeling leaf shapes correspond virtually to the major phylogenetic lineages observed for *B. salicifolius*. There was no evident structural difference among biomes, however the combination of some leaf characters appears to be selected under certain environmental conditions. Based on morphometric analysis, we give analytical support to the high foliar plasticity of *B salicifolius* and indicate a model of leaf shape. Our work is a step forward to clarify the taxonomic and biogeographic aspects of this species.

CS8-05

Analogous responses of tropical and temperate pond metacommunities to environmental, spatial and temporal factors

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Metacommunities are structured by a complex set of processes involving historical, environmental and spatial components. Here we contrasted patterns of species sorting across a large diversity of taxonomic groups (from phytoplankton to vertebrates) in temporary ponds of Costa Rica and the eastern Iberian Peninsula. Given the low temperature gradient in the tropical area, we expected species sorting to be less important in this system. However, variation partitioning of the thirty ponds sampled twice during a hydroperiod in each area revealed similar relative percentage of variation explained for most groups within both geographical zones: Bird and phytoplankton assemblages showed a greater influence of the environment compared to space, probably related to higher dispersal abilities (either active or passive, respectively). Despite large differences in diversity of amphibians and reptiles between the two areas, their distributions were highly spatially structured as expected from their reduced dispersal capacities. Aquatic macroinvertebrates, with a wide variety of ecological strategies, showed higher differences between both metacommunities in terms of relative spatial and environmental effects, the latest being stronger in the temperate area. Temporal effects, i.e. differences between sampling periods were significant but weak, and

higher in the temperate system where we found also the highest environmental effects (except for the herpetofauna). Finally, the percentage of explained metacommunity variation was higher in the temperate compared to the tropical system, probably because of the stronger environmental filters and the lower diversity.

CS8-06

Progressive habitat degradation caused by the urban sprawl documented through remote sensing monitoring in central Veracruz, México

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An extensive tropical mountain cloud forest (TMCF) originally existed in central Veracruz. This tropical forest is one of the most threatened ecosystems in the world and the most biodiverse in Mexico, in relation to the surface it occupies. Most of this habitat has been lost to human encroachment. The remaining areas are at risk of disappearing, if urban sprawl and the expansion of agriculture continues. The human population of this area has increased by 26% in period 2000-2015, with a total population close to 1.5 million inhabitants. We detect this situation also in the shade coffee agroecosystem, where traditional management preserves the tree canopy of the TMCF. The analysis of vegetation index time series can addressed the early detection of habitat degradation. We mapped the progressive habitat degradation using Moderate Resolution Imaging Spectroradiometer vegetation index products (MOD13Q1) at a spatial resolution of 250 m and Breaks For Additive Season and Trend (BFAST) change detection algorithm. Our finding revealed those areas that have decreased gradually their greenness indicated by a negative trend in the time series of vegetation index. The results showed that 41% of the surface has changed in the last 17 years and 75% of the unchanged areas with a negative trend are located in urban environments or zones less than 1.5 km from them. Xalapa and Coatepec were the most affected municipalities.

CS8-07

Statistical approach reveals additional impact of invasive species on Moorea, French Polynesia, at both high and low elevations

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New genetic diagnostic approaches have aided efforts to document global biodiversity and improve biosecurity. This is especially true for organismal groups in which species diversity has historically been underestimated due to difficulties associated with sampling, the lack of clear morphological characteristics, and/or limited availability of taxonomic expertise. DNA sequence barcoding, and now metabarcoding, has emerged as one of the most frequently utilized methods for DNA-based species identifications. Unfortunately, the use of DNA barcoding is limited by the availability of complete reference libraries (i.e., a collection of DNA sequences from morphologically identified species), and by the fact that the vast

majority of species have yet to be described and/or do not yet have sequences present in reference databases. This is particularly true in remote locations such as islands that suffer from a lack of exploration and DNA characterization by trained taxonomic specialists.
We developed a novel machine learning/statistical method that categorizes unidentified species as being either likely introduced or indigenous based solely on measures of nucleotide diversity. We demonstrate the utility of this approach by categorizing a large sample of specimens of terrestrial insects and spiders (as part of Moorea BioCode http://www.mooreabiocode.org/ and the Hawaiian Dimensions in Biodiversity, https://nature.berkeley.edu/hawaiidimensions/).
We document unexpected counts of invasive species in two areas (1) high elevations otherwise dominated by indigenous species, but also (2) beach/strand areas comprising primarily introduced species. We outline several practical applications for this approach in regards to biosecurity purposes and/or monitoring biodiversity and highlight additional steps that could improve this technique.

CS8-08

Predictive biogeography of soil bacteria in mountain environment

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Soil bacteria forms a large proportion of biodiversity, yet little is known of their biogeography. Further, very few forecasts of influence of changing environment on soil bacteria exist.
Here, we aim to fill these gaps by applying spatial modelling techniques on a bacterial metagenomics dataset representing soil samples from 265 sites in mountain environment and covering wide environmental gradients (e.g. elevation 425-3119 m.a.s.l.).
Targeting V5 region of the 16S rRNA gene, bacterial DNA of the soil samples were sequenced in Illumina HiSeq 2500 platform. The resulting paired-end sequences were clustered to operational taxonomic units (OTUs) both using close-reference (QIIME with gg_13_8 database from Greengenes as a reference) and De Novo approaches (custom scripts with SILVA rRNA database as reference for taxonomic annotation). Close-reference approach identified 15’769 OTUs, while De Novo clustering resulted in 75’009 OTUs. Taxonomic annotations for the OTUs were found at least until family level for most identified OTUs. Based on a subset of the data, edaphic factors (e.g. soil pH and moisture) were found as most influential in driving distribution and abundance of bacteria. Number of OTUs decreased with elevation.
Bacteria also responds to climatic factors, and changes therein, according to our preliminary habitat suitability models: with warming temperature, most bacterial genus and orders benefit from warming with increased habitat suitability within our study area. Increases in suitable habitat occurs especially in higher elevations, resulting in positive change in richness of bacterial genus, and strong change in community composition of both genus and orders in higher altitudes.

CS8-09

Mechanistic niche approaches allows to explain, rather than to predict, invasive species range distributions.

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Understanding which species traits underlie the invasion success of alien species in order to predict invaders’ potential distributions remains a key challenge of invasion biology. Criticisms have been levelled at forecasts of invasion risk derived from correlative distribution models, as they do not explicitly account for the mechanistic links between organism's functional traits and their (climate) environment. Here, we test whether incorporating biophysical, morphological and behavioural processes allows for accurate predictions of invasive species potential range dynamics. For about 20 bird species successfully introduced to Europe, we applied an animal energetics model (NicheMapper) that relies on a set of functional species' traits to solve heat-energy-balance equations, allowing identification of areas within the invader's niche. Invasive range occurrences were then used as an independent validation of our mechanistic model range forecasts. We found that overall, model predictive accuracy was moderate to low, as our invasion risk forecasts were prone to both omission and commission errors. Sensitivity analyses revealed a set of key functional traits strongly influencing model accuracy. For comparatively larger avian invaders, estimates of basal metabolic rates, body temperate and body mass are crucial while for smaller birds, feather characteristics such as feather length and plumage depth are important as well. Our results indicate that complex and parameter hungry mechanistic modelling approaches such as the one applied here may be better suited to uncover processes driving species invasions, rather than for obtaining highly accurate spatial predictions of where invaders are likely to establish.

CS8-10

Testing methods in species distribution modelling using virtual species: what have we learnt and what are we missing?

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Species distribution models (SDMs) have become one of the major predictive tools in ecology. However, multiple methodological choices are required during the modelling process, some of which may have a large impact on forecasting results. In this context, virtual species, i.e., the use of simulations involving a fictitious species for which we have perfect knowledge of its occurrence-environment relationships and other relevant characteristics, have become increasingly popular to test SDMs. This approach provides for a simple virtual ecologist framework under which to test model properties, as well as the effects of the different methodological choices. This simplification is therefore very useful in setting up modelling standards and best practice principles. As a result, numerous virtual species studies have been published over the last decade (> 700 citations of virtual species papers in 2016 alone). The topics covered include differences in performance between statistical models, effects of sample size, choice of threshold values, methods to generate pseudo-absences for presence-only data, among many others. However, the simulation procedure has not been homogeneous, which introduces some subtleties in the interpretation of results, as well as differences across simulation packages. Here we (1) review the main contributions of the virtual species approach in the SDM literature; (2) compare the major virtual species software packages; (3) identify the major areas of SDM methodology that remain to be explored; and (4) propose a set of minimal requirements for best simulation practices in future virtual species studies in the context of SDMs.

CS8-11

Hidden assumptions of spatial theories and models in biogeography and ecology

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Spatial theories and models play an increasingly important role in biogeography, macroecology, community ecology, and metapopulation ecology. When we argue for these theories or models, important assumptions are often left implicit. Such hidden assumptions may, if they are revealed, partly or completely overturn conclusions. A recent example is He & Hubbell's article in Nature, where they model expected extinction rates, under the heading; "Species-area relationships always overestimate extinction rates from habitat loss". This statement caused a wave of protests, though already early on, in a reply, Pereira and colleagues revealed why this conclusion is not general but depends on the pattern of habitat loss. He &

Hubbell had assumed that habitat loss grows from centre and outwards instead of, for example, by shrinking from the edges and inwards. They would also have had to assume no extinctions from fragmentation. Such hidden or implicit assumptions may either weaken the claim or (as in the case above) mislead us to draw the wrong conclusion. In addition, hidden assumptions may also inflict presumptions that affect other theories or models by constraining patterns and outcomes. We can illustrate this by looking at consequences of assumptions implicit in the mathematical descriptions of species-area relationships (SARs). Accepting SARs to be power law entails establishing a presumption that beta-diversity is scale invariant, whereas logarithmic SARs would mean that beta-diversity decreases monotonically with increasing scale. Also great theories as MacArthur and Wilson's equilibrium theory of island biogeography and Diamonds's reserve-design principles harbour a number of hidden assumptions.

CS8-12

Is the distance-decay of similarity isotropic?

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The decay of assemblage similarity with spatial distance is usually modelled as if distance-decay patterns were isotropic. In other words, it is assumed that the relationship between assemblage similarity and spatial distance is the same in all spatial directions. This implicit assumption is testable and the degree of anisotropy in distance-decay patterns can be used to infer the role of alternative major processes. Isotropic distance-decay patterns are predicted by neutral dynamics, while anisotropic patterns are predicted by non-neutral processes. In particular, because climate is structured in East-West bands, if climatic niches were the major constraints of species distributions, North-South distances should be more correlated with assemblage similarity than East-West distances. We tested these predictions for continental patterns of 21 beetle taxa in Europe and amphibians, mammals and birds in Europe, North America and South America. Our results show that the degree of anisotropy in distance-decay patterns varies across taxa and continents and how the deviations from isotropy could be related to the effect of climatic niches or historical processes as glaciations. In general, we show that the implicit assumption of isotropic distance-decays patterns does not hold in most systems, and that deviations from isotropy provide relevant clues about the relative importance of climatic niche and historical processes as glaciations.

CS8-13

Towards a mechanistic understanding of latitudinal body size gradients in terrestrial ectotherms

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Understanding the mechanisms underpinning broad-scale gradients in animal body size remains challenging. In contrast to endotherms, the extent to which temperature and water regulation of ectotherms scale up into latitudinal body size gradients remains elusive. Our aim here is to investigate what body size gradients are expected to emerge from first biophysical principles regarding heat and water balances in terrestrial, vertebrate ectotherms. To achieve this, we develop a biophysical model to derive heat balances and rates of water loss of dry- and wet-skinned ectotherms from microclimatic variables. We projected geographically model predictions for different size classes to explore how body temperature (T_b) and cutaneous evaporative water loss (EWL) are influenced by body size in the Northern Hemisphere. The greater thermal inertia of large-bodied ectotherms (over 50g) increases their risk of overheating at warmer latitudes. By contrast, all organisms, irrespectively of body size, are constrained by low temperatures experienced at boreal latitudes. Regarding water balances, a larger size allows reducing water loss of small wet-skinned ectotherms, which is an advantage in more evaporative environments. To conclude, size differences in heat balance offer a mechanistic explanation for a pattern of increasing body size northwards.

Water conservation is also identified as a potential mechanism for larger body sizes in dryer areas in wet-skinned ectotherms. Moreover, our model reveals non-linear relationships involving size and optimum states of thermal and hydric functions, accounting for complexities that are unnoticeable by traditional, correlative investigations.

CS8-14

A multifaceted approach of tree diversity to fill a knowledge gap in the Mediterranean basin

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The Mediterranean Basin, the largest Mediterranean climate region of the world, is a critical biodiversity hotspot with 10% of vascular flora for only 1.6% of the Earth's surface. Before the first human impacts, forests were estimated to cover 82% of the region. Today, the current distribution of the Mediterranean tree biodiversity is still poorly known but constitutes a key issue for biogeography and conservation.
Our study aims to describe and understand the spatial distribution patterns of three facets of tree diversity in the European part of the Mediterranean basin: taxonomic, functional, and phylogenetic. Botanists have identified the status of 209 tree species and 244 subspecies in 13 Mediterranean countries. We gathered available data on current distribution of tree taxa from many sources and designed a long-lasting database of tree occurrences. We also collected functional traits and built a species-level phylogeny by completing available sequences from sequencing of new samples. This challenge of collecting data has been addressed by scientists and botanists from five Mediterranean countries. The Mediterranean-European biogeographic region includes an unsuspected number of trees, almost 200 trees more than the central European region. We identified 44 cryptic tree species, representing 21% of the total trees, a diversity often neglected in the existing datasets. From these data and a strong conceptual basis provided by a literature review, we aim now at analyzing the congruence and mismatches of these diversity components and discuss the implications for conservation of Mediterranean woody diversity.

CS8-15

Combining physiological threshold knowledge and species distribution models in predicting the future distribution of intertidal macroalgae along a latitudinal climatic gradient

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The species distributions are determined by climate change and the analysis of the factors involved in such distributions have always been considered as a key issue in ecology. Thereby, species distribution models (SDMs) are a useful tool for predicting species range shifts in response to global warming. For making robust predictions in this area, we can combine the SDMs and the physiological threshold knowledge of the studied species. Through growth and survival manipulative experiments simulating thermal gradients, we obtained the thermal thresholds of some foundational macroalgae, which are proxies of the fundamental thermal niche. To predict the distribution of these macroalgae we used the distributional records of species and environmental layers with ecological influence over the species in the Maxent software. Finally, both approaches, correlative and mechanistic, were combined in order to obtain more robust predictions of the intertidal macroalgae distributions along the European Atlantic coast. In this way, the predictions in a climate change scenario are improving to meliorate the accuracy of conclusions in terms of marine biodiversity conservation.

Concurrent Session 09: Global Change Biogeography

CS9-01

Likelihood of future regime shift in the temperature regime: implications for biodiversity at the global scale

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Forecasting the long-term impacts of future climate changes on biodiversity is challenging not only because the responses of organisms are contingent on several mechanisms (e.g. demography, physiology), but also because there is a lack of data for the majority of species on Earth, precluding the use of available bioclimatic modelling methods. As an alternative approach, researchers have developed climate change metrics whose aim is to quantify the exposure of geographic areas to different facets of change and relate these facets to different threats and opportunities for biodiversity at a global scale. In this study, we used the regime shift theory to explore whether particular geographic areas over the world display evidence for upcoming critical transitions in the temperature regime. Specifically, we used five Early Warning Indicators (EWIs) to investigate the probability for upcoming critical transitions in nearly 100,000 temperature time series encompassing marine and terrestrial systems. Overall, while all EWIs revealed strong spatial variations regarding the likelihood of approaching critical transitions we found differences regarding the strength and the distribution of trends across the world. Nonetheless, a composite EWI, constructed from individual ones, showed congruent trends in several areas and highlighted variations across latitudes, between marine and terrestrial systems and among ecoregions within systems. Although the underlying mechanisms are unclear, our results suggest that some areas over the world, especially the ones that have undergone major changes in land-cover and land-use, might change toward an alternative temperature regime in the future with potentially large implications for biodiversity and ecosystem functioning.

CS9-02

What can Essential Biodiversity Variables offer to biogeography?

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The Group on Earth Observations Biodiversity Observation Network (GEO BON) has the aim to improve the acquisition, coordination and delivery of biodiversity observations and to develop a global biodiversity observation network that contributes to effective management policies for the world's biodiversity. In 2013, GEO BON introduced the framework of Essential Biodiversity Variables (EBVs) to derive coordinated measurements that are critical for detecting and reporting biodiversity change. In this talk, I will briefly introduce the EBV concept with its key components (genetic composition, species populations, species traits, community composition, ecosystem structure and ecosystem function) and provide an overview of recent advancements over the last few years. I will argue that EBVs have much to offer to biogeography and that biogeographers can make important contributions to EBV development. For instance, major progress is feasible through the repeated and periodic collection of in situ and remote sensing measurements across space and time, the standardization of data and metadata, development of reproducible workflows, support for semantic data integration, and through publishing of open data in a machine-readable form. The development of EBVs would greatly benefit biogeography in studying species distributions, macroecology, (phylo)genetic diversity, functional biogeography, species interactions and the structure and functioning of ecosystems. I encourage biogeographers to engage in GEO BON efforts and to contribute to building global EBV data products.

CS9-03

The changing importance of functional traits in mammalian co-occurrence across the Pleistocene-Holocene transition

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The study of communities over time allows us to evaluate the degree to which ecological processes are affected by climate change and human activity. Such knowledge is critical to predicting how species will assemble into communities in response to future climate change. Recent work documenting the co-occurrence structure of communities over the past 300,000,000 years attributed a shift from aggregated (species that occur together more frequently than expected by chance) to segregated (species that occur together less frequently than expected by chance) species pairs in the mid-Holocene to human impacts. Here, we investigate the complex role of climate and species traits in the co-occurrence structure of mammals across the late Pleistocene to the modern. We find that the climate change and biodiversity loss at the terminal Pleistocene fundamentally changed species associations: extinct species were more likely to form significant, positive associations than surviving species. Moreover, the interaction strength of pairs that contained an extinct species was stronger for aggregations, but not segregations suggesting that the loss of the megafauna had differential effects on the co-occurrence of surviving species. Specific species traits, such as body mass or trophic interaction, declined in their importance or switched from promoting aggregations to promoting segregations amongst surviving species. We conclude that future climate change and extinction are likely to exacerbate these trends.

CS9-04

Spatiotemporal changes in the intensity of global land cover fragmentation

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Degradation of natural ecosystems drives species and populations to extinction and modifies the functioning and composition of communities worldwide. Ecosystems degradation typically leads to habitat fragmentation which creates detrimental edge effects and worldwide declines in biodiversity and ecosystem functions. Despite many efforts, global patterns and dynamics of habitat fragmentation have not been consistently quantified. Here, we quantified the spatiotemporal dynamics of changes in the intensity of land cover fragmentation over 24 years (1992-2015), using the first long-term time series of global land cover (ESA CCI-LC) which provides 24 consistent maps at 300 m spatial resolution on the annual basis. 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, using dissimilarities among land cover classes. The strength of trend, obtained from time series of changes in fragmentation, was used to characterise the intensity of changes at each pixel. Our results, summarised at the biome level, showed that the highest intensity of land cover fragmentation occurred in the "Temperate savannas", as well as in "Mediterranean forests", while "Montane grasslands" and "Temperate coniferous forests" showed the lowest fragmentation intensity. The resulting new global map of land cover fragmentation intensity provides novel insights into the status of ecosystems and can help to inform decision-makers about sustainable use of resources.

CS9-05
Biotic interactions may buffer climate change effects on species distributions

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Projecting future distributions of species under climate change remains a particular challenge for species that are trophically interacting. Interaction partners are often assumed to react differently to climate change, causing spatial mismatches in future distributions and increased extinction risks. We compared potential direct effects of climate change on occurrences of European nutcrackers (*Nucifraga caryocatactes*) with potential combined direct and indirect effects via projected occurrence changes of its main food sources, Swiss and Siberian stone pine (*Pinus cembra*, *Pinus sibirica*), and common hazel (*Corylus avellana*). We used climate-based species distribution models to project probabilities of occurrence. We combined direct and indirect climate change effects by calculating the probabilities of plants and nutcrackers occurring together. We find considerable projected northward shifts in future occurrences of nutcrackers under climate change and similar effects on hazel; whereas both pine species' projections indicate minor altitudinal upwards shifts. Combined projections of direct and indirect effects of climate change indicate less pronounced shifts of nutcrackers' occurrences, due to relatively small changes in pine species' occurrences and to suitable hazel occurrence shifts. Our study suggests that potential effects of climate change on the future distribution of the nutcracker are largely offset when integrating trophically interacting plants into projections. Direct effects of climate change on nutcrackers' occurrence probabilities may be greater than combined direct and indirect effects via resource plants. Therefore, considering biotic interactions does not necessarily increase the risks that climate change may impose on species distributions, but interactions may support species survival in rapidly changing environments.

CS9-06
Long-distance migratory birds face multiple independent risks from global change

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Long-distance migratory birds travel thousands of kilometres annually between summer and winter ranges. They are thus affected by environmental conditions in different parts of the world. Unfavourable conditions in the wintering grounds or en route can have detrimental effects on breeding populations through carry-over effects. Although these facts have been widely acknowledged, impact assessments primarily focus on breeding ranges. Here, we examine potential climate and land use change impacts on migratory birds using range maps and species distribution models. We concentrate on long-distance migratory birds of the Holarctic (n=715) and estimate potential global change risks resulting from summer range loss, winter range loss, and from increased migratory distance between seasonal ranges. 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. Our results are based on large-scale range data and simplified measures of migratory connectivity and dispersal. Nevertheless, they provide 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.

CS9-07

A quantitative assessment of climate and human-mediated invasion threat across Antarctica's biogeographic regions

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Non-native species are driving current global biodiversity loss. Antarctica, internationally governed by the Antarctic Treaty System, is no exception. Indeed, efforts continue to be necessary to control priority species and prevent the introduction and establishment of others. We assessed establishment suitability between Antarctic Conservation Biogeographic Regions (ACBRs) using Extrapolation Detection analyses which describe climatic similarity. At a continental scale, we found that 95% of ice-free areas have climate analogues in another ACBR. Thus, an efficient prevention mechanism would include robust biosecurity controls for intra-continental human movements. Broadly, our analyses clustered ACBRs into Western and Eastern groups. In the Western element, existing human transport routes connect climatically similar regions, particularly in the Antarctic Peninsula. Noting recent calls by the Antarctic Treaty Consultative Meeting for more information on the risk of intra-continental movement of Antarctic species, our findings reinforce the importance of prioritizing biosecurity measures in this area to reduce the invasion threat.

CS9-08

Better capturing global land-use dynamics as central system drivers for Biogeography, Macroecology, and Global Change Biology

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Current patterns and historical changes in land-use extent and intensity are increasingly vital for manifold applications in Biogeography, Macroecology, and Global Change Biology. By directly affecting the quantity, quality, and spatiotemporal configuration of habitats, land-use dynamics constitute the dominant proximate drivers of change in most terrestrial ecosystems, e.g., by driving shifts in species populations, altering ecosystem functioning, and constraining conservation interventions. Despite this central role, available data products on different land-use dimensions are extremely limited in quality, scope, and interoperability, rendering them largely inappropriate for most biodiversity applications. On the other hand, recent remote-sensing advances in developing longer and higher-quality covariate time-series, ongoing progress in mobilizing subnational land-use statistics, and an emerging cultural shift towards more *Open-Science* offer new opportunities for more accurate depictions of global land-use dynamics and more robust attributions of biodiversity drivers. I will provide an overview of major caveats when using existing global land-use information in typical downstream biodiversity applications. I will also report on a recently launched initiative to develop global, multi-annual, high-resolution, and mutually consistent data products on selected *"Essential Land-Use Variables"* that together capture status and trends in the three globally dominant land use classes (cropping, grazing, and forestry). Capitalizing on modularized workflows and a highly collaborative, *Open-Science* setup, the project is designed to enable the quality of developed data products to successively evolve via continuous updates and independent improvements of the workflows' different sub-components. I will highlight selected IT-infrastructural and sociological considerations that may inspire similar collaborative data initiatives in Biogeography and related fields.

Concurrent Session 10: Historical and Paleo-biogeography

CS10-01

Trait-dependent biogeography: model-based inference of dispersal and distribution patterns of Indo-Pacific trap-jaw ants (Hymenoptera: Formicidae: Odontomachus)

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Dispersal is influenced by ecology, but many popular biogeographical methods do not consider ecological variation among lineages. Here we use a novel trait-dependent dispersal model to infer the historical biogeography of Indo-Pacific trap-jaw ants (Formicidae: *Odontomachus*). Our working hypothesis is that macroevolutionary dispersal across archipelagos is influenced by habitat preferences, categorized here simply as undisturbed forests or open/disturbed habitats. Based on a multi-locus, fossil-calibrated phylogeny and the new trait-dependent dispersal model implemented in the R package *BioGeoBEARS*, we found strong evidence that habitat preference shifts from undisturbed forest to open/disturbed habitats increase dispersal rate. This approach allowed us to expand on E.O. Wilson's seminal work, "The Nature of the Taxon Cycle in the Melanesian Ant Fauna". The Taxon cycle is a non-equilibrium island biogeography model that narrates the tight links among ecology, adaptation, dispersal, and speciation. In line with predictions of the taxon cycle model, transition rates to the forest interior state were significantly higher than to open/disturbed habitat in trap-jaw ants. The phylogenetic predictions outlined in this study can be used in future work to evaluate the relative weights of neutral (e.g., geographical distance and area) and non-neutral processes (trait-dependent, macroevolutionary dispersal) in historical biogeography and community ecology at phylogenetic scale.

CS10-02

End-Pleistocene mass extinction caused a fundamental shift in survivor mammal community structure

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Large mammals are at disproportionately high risk of extinction globally, and the ecological impacts of their loss will last beyond our lifetimes. Research shows that the end-Pleistocene mass extinction of large mammals left a significant ecological legacy, from shifting vegetation and fire regimes to changes in nutrient cycling and biogeochemistry. To better understand the consequences of their demise on the community structure of survivors, we tracked species co-occurrence patterns through the end-Pleistocene large mammal extinction in North America. We examined associations between pairs of species and measured the climatic and geographic niches of each species. Because the megafaunal extinction was accompanied by shifting climate, we investigated the relative influence of abiotic and biotic factors on the strength and direction (aggregation vs. segregation) of associations by comparing co-occurrence within shared niche space to total co-occurrence. Aggregations, which may signal mutual habitat preferences or biotic interactions such as predator-prey relationships, decreased in strength and frequency after the end-Pleistocene. Segregations increased in strength and frequency despite increasing niche sizes. We also saw a decrease in aggregations and an increase in segregations when we isolated biotic factors in shared niche space. Abiotic factors exhibited an opposing pattern. Thus, biotic factors likely played a key role in continental-scale community assembly before the extinctions, suggesting that megafauna fostered aggregations in the Pleistocene, and their loss contributes significantly to modern segregation-dominated assembly patterns.

CS10-03

Evaluating competing diversification processes in biodiversity hotspots

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Rapid developments in high-throughput sequencing technologies have increased the documentation of biodiversity in far greater detail than previously possible. The widespread generation of genome-wide SNP (single nucleotide polymorphism) datasets and adoption of High Performance Computing and bioinformatics enable a wide variety of ecological and evolutionary questions to be addressed for both model and non-model organisms. Leveraging these unprecedented data and resources, researchers focusing on the Afrotropics are beginning to characterise the historical and contemporary diversification processes that have shaped extant biodiversity. For many Afrotropical vertebrates, isolated forest refugia are thought to have played an important role in the diversification of intraspecific populations throughout Quaternary climate oscillations. However, this hypothesis has not been tested against alternatives due to a lack of appropriate high-resolution data. Here I demonstrate that using genome-wide SNP data and explicit demographic model-testing (∂a∂i) can quantitatively evaluate diversification hypotheses, applying this to novel datasets of amphibians (East Africa) and primates (West/Central Africa). I show how to incorporate different historical processes such as isolation, migration, secondary contact and population size changes in demographic models to discern between competing hypotheses (e.g. forest refugia, vs. rivers and mountains, or ecological gradients). Finally, I show that by integrating demographic model results with additional lines of evidence such as divergence dating, ecological niche models and connectivity modelling through time, we can improve our understanding of the processes that shape biodiversity patterns in tropical biodiversity hotspots.

CS10-04

Contrasting roles of competition and the environment in the ecological diversification of a large Australian plant radiation

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What role does competition play in driving trait diversity and co-occurrence patterns of species at a continental scale? Using a diverse Australian plant genus, *Hakea*, we developed a protocol to integrate

phenotypic, biogeographic, environmental, and community-survey data, to identify phenotypic traits involved in environmental filtering and those that are involved in mediating negative species interactions, to explore the contemporary distribution of phenotypic diversity. We then asked whether the evolution of these different classes of traits was shaped by either convergence in similar environments, or by divergence in response to competition with sympatric relatives, using recently developed phenotypic evolution models. Traits that we identified as being strongly environmentally filtered fit an evolutionary model of convergence in sympatry, while traits that seem to mediate negative interactions fit a phenotypic model of competition. These results suggest that the distribution of co-occurring species in the present is strongly shaped by both strong environmental constraints of key functional traits as well as by negative ecological interactions mediated by different reproductive strategies in co-occurring species over deep evolutionary history.

CS10-05

Patterns and processes leading to a geographically structured assemblage of montane birds in Nuclear Central America

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Examination of community assemblage involves studying patterns across a wide range of spatial and temporal scales, encompassing regional-historic and local-ecological processes. Recent studies highlight that species from the Neotropical region can differentially respond to geologic or climatic events. Intriguingly, congruent phylogeographic patterns still exist among species with overlapping geographic ranges, as in addition to geographic barriers, similarity in physiological constraints are expected from species that live in the same environment. Understanding the interplay of dissimilarities and commonalities in responses of sympatric species to a shared history and ecology is essential for the study of community composition. We show that species from an assemblage of montane birds inhabiting the cloud forests of Nuclear Central America differ in origin and colonization pathways. Geographic barriers isolate populations of distinct species in a similar way, promoting *in situ* diversification in isolated mountain ranges. The geographic barriers in the area are mainly associated with tectonic plate fault lines. Among these, the Motagua-Polochic system of faults and the Honduras Depression have been previously reported for other taxa, while the barriers located in northwestern and northeastern Guatemala are new to this study. The genetic breaks are located in interior valleys where precipitation is low and dry forests are present, adding environmental resistance to movement even when mountains are interconnected. Our results demonstrate how the genetic study of multiple overlapping taxa at a fine geographic scale can reveal details of community composition in a historical-ecological framework.

CS10-06

Climate drives dynamic shifts in vegetation communities over the past 20,000 years in North America

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Changing climates, human arrivals, and megafauna extinctions in North America all had the potential to culminate in major shifts in vegetation communities and their distributions on the landscape. We seek to determine the relative importance of these potential drivers of plant community change following the last glaciation (20,000 BP to present). Quantifying dynamic responses of plant communities to these drivers has important implications for understanding biome resilience and management strategies under projected climate change. This work used 22,612 fossil pollen assemblages from 504 sites in the Neotoma database to reconstruct vegetation community residence times across North America. We reconstruct 12 vegetation biomes using an established modern analog method and the biomization method for no-analog

communities. We find that the median residence time of any given biome is 390 years. Forest biomes have a longer residence time of 460 years while shrub/herb biomes have a shorter residence time of 320 years. Average residence times do not demonstrate a latitude gradient across North America, though biomes track glacial retreat during deglaciation. When glaciers are retreating and climates are fluctuating, from 18,000 BP to 13,000 BP, average residence times are relatively short. Residence times began a generally increasing trend starting 13,000 BP, approximately when Native Americans arrive in North America. Our work indicates that biome residence times are primarily influenced by climate, while top-down biotic influences had little impact on vegetation community shifts. Further work will test the hypothesis that high landform diversity leads to longer biome residence times.

CS10-07

Current, past and future potential and realised biogeographical distribution of an iconic terrestrial protist for microbial biogeography, Apodera vas s.l. (Amoebozoa; Arcellinida), inferred from bioclimatic niche-based distribution modelling

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After decades of heated but often sterile debate, microbial biogeography is maturing to become a dynamic field of research, yet the data remain patchy and global assessment of distribution patterns of individual taxa very rare. A notable exception is the testate amoeba *Apodera vas* (Amoebozoa; Arcellinida), an iconic and highly conspicuous flagship taxon in the debate over microbial biogeography. The distribution of *A. vas* stands out as being mostly restricted to former Gondwana, suggesting an origin in this landmass, with only limited subsequent dispersal. This taxon should theoretically find appropriate environments in

northern continental regions where protistologists have so far failed to find it, but its potential distribution has not yet been rigorously assessed. We compiled an extensive database of ca. 300 known records of *A. vas*. Based on the geographical coordinates, we built a bioclimatic niche-based distribution model and determined its potential distribution according to current climate, IPCC warming scenarios and last glacial maximum (LGM) climatic conditions. The modelled potential distribution of *A. vas* clearly shows that this taxon could potentially occur across the Holarctic; its absence can thus be interpreted as evidence for limited dispersal. Furthermore, LGM distribution identified refugia, where allopatric speciation may have occurred. To our knowledge, this is the first climatic niche-based distribution modelling study of a microbial taxon. Due to the presence of a morphologically distinct shell, testate amoebae are useful models for microbial terrestrial biogeography. The modelling results are valuable to develop hypotheses on phylogeographical patterns to be tested using molecular methods.

CS10-08

Changes in North American mammal niche preferences from the late Pleistocene to the present

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Human population has exponentially grown since the last glaciation, especially across temperate areas with easy access to water sources, excluding mammal species from their former habitats. Thus, we anticipate a change in environmental niche preferences for temperature and precipitation as increased human population forces mammal species into more extreme climates within their environmental tolerances. For our study, we collected species occurrences from 20,000 ybp to the present for 59 North American mammal species. We inferred temperature and precipitation for each location using paleoclimate simulations (CCSM3). Overall, we found that mammals now live in areas that are warmer and dryer on average, as mean annual temperatures rise and precipitation decreases. Their niches have significantly changed in the last 20,000 years for most climate variables except for maximum average monthly temperature and minimum average monthly precipitation, which still maintain a hard limit on geographic boundaries. Our results suggest that although they avoid some climate extremes, including hot temperatures and dry climates, most mammals in our dataset adapt to new climate conditions instead of moving to new geographic areas. This could be related to a high niche plasticity for climate or to geographic and anthropogenic dispersal limitations that prevent animals from migrating to new localities as human population increases and climate changes. Geographic models that integrate fossil and modern niche preferences and dispersal limitations will help elucidate the reasons behind the observed patterns. Moreover, understanding these patterns will help us formulate better conservation plans for the species we wish to protect.

Concurrent Session 11: Biodiversity Patterns and Maintenance

CS11-01
The first comprehensive study of insect body size for a complete elevational gradient in the tropics reveals a striking pattern

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The body size of an animal may well be its most important functional trait. For arthropods, geographical patterns and environmental drivers of body size variation are still poorly documented and poorly understood, especially in the tropics. Along a complete tropical elevational gradient in Costa Rica, we studied two species-rich, phylogenetically independent moth taxa (794 species of Geometridae, 308 species of Arctiinae; 19,214 individuals, total) to assess the following hypotheses: 1) body size increases with decreasing ambient temperature (a Bergmann pattern), as predicted by the temperature–size rule (temperature-dependent discordance between growth and reproductive maturation rates); 2) body size increases with increasing rainfall and primary productivity, as predicted from considerations of starvation resistance; and 3) body size scales allometrically with wing area, as elevation increases, such that wing loading (the ratio of body size to wing area) decreases with increasing elevation to compensate for decreasing air density. We analyzed mean forewing length (a proven proxy for body mass) along the elevational gradient within species, among species means, and for assemblage means. Body size consistently increased with elevation in both taxa—for individuals within species, species means, and assemblage means. Temperature was the best predictor for these patterns, whereas body size was poorly correlated with rainfall and enhanced vegetation index. Wing loading increased with elevation, counter to hypothesis. Our results support the temperature–size rule as an important mechanism for body size variation in arthropods along largely aseasonal tropical elevational gradients, whereas starvation resistance and optimization of flight mechanics seem to be of minor importance.

CS11-02
Are mountain uplift and temporal diversity dynamics really linked? An interdisciplinary case study of mammals in Turkey

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The link between topographic complexity and biodiversity has long been established, with many studies inferring the influence of topography on biodiversity through time from their present-day association across space. However, temporal biodiversity dynamics might not be synchronous with environmental fluctuations. Here, we investigate the effect of palaeotopographic and palaeoenvironmental change on the diversity of large terrestrial mammals in Turkey since the Miocene, i.e. approximately 23 million years ago (Ma). The present-day Anatolian plateau is bordered by steep northern and southern mountain belts, having emerged from the Mediterranean Sea since the middle Miocene through surface uplift of the central plateau (since ~11 Ma) and then its mountainous margins (since ~8 Ma). We would therefore expect signatures of surface uplift on mammalian diversity to differ in timing between plateau and margins. To test this, we investigated a fossil dataset containing 143 sites with 868 stratigraphic occurrences of 247 species from five orders of large terrestrial mammals (Artiodactyla, Carnivora, Perissodactyla, Primates, Proboscidea). Temporal patterns of alpha and beta diversity showed clear differences in the timing of diversity changes and compositional turnover between plateau and mountain margins that partially matched expectations generated from the uplift history, but surface uplift could not fully explain mammalian dynamics. In particular, pinpointing "uplift events" and matching the stratigraphic time scales proved difficult. Much work remains to be done to disentangle potential direct effects of increasing topographic complexity on

mammalian diversity from indirect paleoenvironmental effects of uplift, such as aridification of the central plateau.

CS11-03

Local abundance, range size, and phylogeny in Hawaiian woody angiosperms

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Previous studies hypothesize a negative relationship between the number of species in a lineage and both the range size and local abundance. Here, I examined woody species in the Hawaiian angiosperm flora to explore the relationships among these variables. A preponderance of phylogenetic studies permits species to be placed into colonist lineages, which vary in size from 1 to 140 species. Focusing on terrestrial, non-coastal habitats, I assessed the local abundance (as measured by percent ground cover) of each species found in over 1500 vegetation plots from across a wide range of habitats in the Hawaiian Islands. Analyses at the scale of individual species and whole lineages provided a hierarchical approach representing different spatial and phylogenetic scales. First, species detected in plots were disproportionately contained within smaller lineages. Second, among those species detected in vegetation plots, the average local abundance negatively correlated with lineages size. This underscores the ability of local abundance to mediate gene flow such that species occurring less frequently are more prone to speciation and subsequent subdivision of geographic ranges. The result is species-rich lineages containing species exhibiting lower local abundance and smaller geographic ranges. Lineages with fewer species exhibit a wide range of tendencies, however the most abundant species with the largest range sizes are concentrated in these small lineages. This also helps explain why large adaptive radiations tend to contain disproportionate numbers of rare and endangered species.

CS11-04

Regional and local determinants of island community assembly

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Local communities are assembled through biogeographic species pools shaped by geologic history, along with local-scale ecological dynamics such as competition. Here we examine the assembly of ant biodiversity in the Andaman and Nicobar Islands (A&N). First, we investigate the biogeographical affinities of the island fauna by measuring overlap with the surrounding source regions from published literature. Next, we conduct field surveys to examine multidimensional patterns of community structure on a local scale among habitats. We found that immigration from surrounding areas plays a more important role in shaping A&N ant diversity than in-situ speciation on the islands, as suggested by the low number of endemic species and high overlap with surrounding regions. Moreover, taxonomic overlap appears to be unrelated to geographic affinity since surrounding regions at vastly different distances have similar affinities to A&N. At the local scale on our model island, we found that the harsh littoral forest habitat had significantly lower ant species richness than the adjacently distributed, inland evergreen forests. However, despite significant difference in species richness, the two habitats showed similar functional diversity. This relative similarity was reached because littoral ant communities were overdispersed in their functional space, possibly due to competition or differences in thermal tolerance among ants. In contrast, human-modified areas tend to have few species as well as low functional diversity. Thus, anthropogenic vs. natural disturbance may have very different impacts on the structure of ant communities. Together, our study provides insights into the regional and local factors shaping the A&N ant fauna.

CS11-05

The biogeographic context of Dengue in the range of Aedes vectors in South America from fuzzy logic tools

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In the current South American epidemiological framework, describing the biogeographic interactions between vectors and diseases is a priority. In order to prevent and fight against outbreaks, it is necessary to understand the factors affecting both the vectors and the dengue virus. The geographic range occupied by Aedes mosquitoes (A. aegypti and A. albopictus) is wider than known dengue cases. This suggests that the relationship between Aedes mosquitoes and Dengue is not crisp, and that a fuzzy-logic approach is worth considering. Our aims were to establish the biogeographic context in which dengue cases occur in South America, and to map the risk areas favourable for new cases. We analysed A. aegypti, A. albopictus and Dengue occurrences using the favourability function and a set of environmental variables. According to vector and dengue models, we applied the fuzzy intersection to identify the biogeographical relationship between Aedes vectors and dengue cases. We detected that the A. aegypti model explained to a higher extent the distribution of dengue outbreaks. Favourability models detected that the occurrence of Dengue is associated nearly always with territories simultaneously favourable for the presence of A. aegypti, and to a lesser extent for A. albopictus. In order to manage the epidemiological risk of new dengue cases in South America, the intersection between favourable conditions for A. aegypti and for dengue contributes, compared to a model simply based on the disease, to a most accurate description of the areas at risk of dengue outbreaks.

CS11-06

Ecological legacies of the Amazonian rubber boom

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Recent evidence suggests that pre-Columbian people living in Amazonia left a legacy on the vegetation that persists in today’s forests. The post-Columbian era, including the time of European colonization and the Amazonian rubber boom (c. A.D. 1850-1920), has largely been omitted from the discussion of legacy effects from past human disturbances. Here, we examine the spatial distribution of early European colonists and the subsequent rubber boom period in Amazonian forests using a novel method that combines early collection records with species distribution modeling techniques.

The distribution of people living in Amazonia after European colonization was similar to that of the pre-Columbian era. The locations of forest inventory and recensus plots, which are used to measure Amazonian biodiversity and carbon dynamics, were disproportionately located in areas that were likely disturbed during the post-Columbian era compared with random site selection. By the end of the rubber boom, 20% of the forest inventory plots had likely been through at least two major disturbance and recovery periods due to past human activities, and 13% had likely experienced three major disturbance and recovery periods. The recurrent occupation or use of forests through time was positively related to accessibility via rivers. Our results suggest that Amazonian ecology is seen through the lens of a shifted baseline. Uncritical acceptance of forests as being mature, when they are actually early- to mid-successional, exaggerates the potential for the overestimation of the Amazonian carbon sink and has ramifications for global carbon budgets.

CS11-07

Niche Consistency: Assessing confidence when estimating a species' ecological niche from occurrence data.

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Species vary in the amount of occurrence data necessary to fully describe their ecological niche, but to date there is no tool that explicitly quantifies what sample size is sufficient to fully describe a species niche and to what extent more data improves niche characterization. Here, we introduce the concept of 'niche consistency', a variable that measures the confidence in niche characterization based on occurrence data. We provide a method, using a rarefaction technique, that describes niche consistency based upon the sensitivity of niche size relative to incremental increases in subsample size of existing occurrence data. We used our method to show how niche consistency varied among 42 species of Poa (Family:Poaceae). We observed variation in niche consistency regardless of number of occurrences or total niche size. We investigated two potential applications of niche consistency: 1) variation in results among alternative modeling approaches, and 2) removing sampling bias from occurrence data. First, we found a linear relationship (R2=0.8, $p<0.001$) between amount of occurrence data and the level of similarity in spatial predictions; however, niche consistency did not strongly impact this result. Second, we found that niche consistency can inform when spatial bias corrections reduce confidence in niche characterization and that this varied among species. We believe there are other questions (e.g., studies of climatic disequilibrium) that would benefit from considering niche consistency. We provide the code needed to apply this method and advocate that niche consistency be examined to better account for limitations in our knowledge of the species niche.

CS11-08

Colonization and diversification of wind-dispersed Festuca grasses in Afroalpine sky-islands.

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The high degree of isolation and altitude of the Tropical African mountains has led to consider them as "within-continent" islands or sky islands – geographically isolated high-altitude habitats occurring alongside different mountain ranges. Furthermore, Afroalpine sky-islands present one of the most interesting systems to study discrete biogeographic patterns in a terrestrial island system. Although several studies have addressed the biogeographical affinities in Eastern African sky-islands, the relationships with Western African (sky-) islands (Cameroon, Bioko) are almost unknown. Here, we used Afroalpine *Festuca* grasses to explore the role of Eastern and Western African sky-islands in the evolution of biodiversity and its dispersal patterns. Phylogeographic analyses were undertaken using plastid and nuclear sequences and AFLP fragments. Population genetic and phylogeographic analyses were performed to infer genetic diversity, genealogical relationships, genetic structure, gene flow barriers, colonization routes and the spatio-temporal evolution of populations. We found that genetic variation was structured across the Great Rift System, with the East Africa Western Rift sky-island populations showing greater affinity with the West African than with the East Africa Eastern Rift populations, despite the greater distances. We also detected different colonization events of the West African mountains, originating either from the Western and from the Eastern Rift areas. Additionally, our study highlights the role of the African sky-islands as long-term refugia and cradles of genetic diversity for the Afroalpine grasses.

Concurrent Session 12: Functional Biogeography

CS12-01

Global elevational gradients in functional diversity and trait space of birds

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Mountain ranges are under increasing threat from human development and climate change, yet hold some of the planet's greatest biodiversity and are key to understanding its origination and maintenance. Functional and trait aspects of biodiversity offer a particularly interesting lens into the mechanisms underlying community assembly, ecosystem-level consequences of global change, and crucial conservation actions, but to date lack a comprehensive and global evaluation across elevational gradients. Here, we fill this gap with a global assessment of the elevational gradient in functional diversity and trait space of birds. By considering both multivariate (e.g., collective functional diversity, overlap in traits space) and univariate (e.g., individual traits) components of avian diversity, we provide insights that would not be possible with only a singular perspective. We find that globally avian assemblages are functionally overdispersed in the lowlands and increasingly clustered toward high elevations. This high-elevation transition in assemblage structure is paralleled by a distinct shift in the position of the avian trait space and loss of several trait characteristics such as canopy foragers, a likely result of rapid turnover in vegetation structure at the tree line. Intriguingly, assemblages at highest elevations again see functional overdispersion. Altogether, we suggest that competition-driven limiting similarity in the lowlands, environmental filtering in the mid to high elevations, and a combination of a strict environmental filter and competitive exclusion in extreme highlands are predominant factors underlying elevational biodiversity gradients.

CS12-02

Greater tree species richness in eastern North America compared to Europe is coupled to denser, more clustered functional trait space filling, not to trait space expansion

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Our aim in this study was to determine if differences in species richness between currently climatically similar regions correlate to dissimilarities in functional diversity. Using classic functional traits defining distinct ecological strategies, we described the trait spaces of European and eastern North American tree floras. The trait space of each region was described based on the occupied area, species accumulation pattern, and the trait-space size, dispersion, and clustering. We then evaluated if the species richness differences between these two climatically similar regions correlate to the dissimilarities in occupied areas and species accumulation pattern; as well as differences in the trait-space attributes. Differences in species richness between climatically similar regions do not necessarily result in functional dissimilarities. Regardless of eastern North American having a larger trait-space, occupied areas and species accumulation patterns converged. Although in both regions species clumped towards the trait-space centroid, we observed statistically significant differences between Europe and eastern North America in the dispersion and clustering but not in size the trait space. Positional convergence between European and eastern North American trait spaces suggests that this species richness anomaly does fully translate to the functional space. Our results suggested that species accumulation within a region occurs within a climatically restricted trait space, and not via trait space expansion. Moreover, the consistent aggregation of species towards the trait-space centre aligns with the idea of a directional section towards a generalised morphology, which might provide the best way to interact with a broad array of environmental conditions.

CS12-03
Challenges to link physiological processes into macroecological patterns

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Macroecology is being invigorated by adopting mechanistic models for addressing broad-scale ecological patterns, especially through building on lower-level processes such as physiology as causal bases, thus adding a bottom-up perspective to the dominating top-down one. While this endeavor should improve inferential and predictive capacities of macroecology, it comes not without novel challenges. Here, we aim to discuss some of these challenges and possible solutions. Critical to face this challenge is to acknowledge the limitations of the most relevant fields involved. On the one hand, macrophysiology focuses on broadscale patterns of physiological traits and their link with macroecological patterns, but the putative coarseness of data disregards relevant, local-scale factors (e.g., variability and acclimation). On the other hand, biophysical ecology can derive ecological outcomes from exhaustive biophysical and microclimatic modeling but is still impractical for making multi-species, geographic-scale extrapolations. Nonetheless, three critical issues have difficulted integration of these fields in a 'mechanistic macrophysiology'. First, existing physiological data are scant, taxonomically biased and often fail to describe relevant properties for mechanistic models, requiring a new generation of ecophysiological data. Second, the scaling up mechanisms from organisms into macroscale entails transitions between scales and levels of organization, with multiple interfering factors at intermediate levels and scales, requiring the accommodation of multiple sources of uncertainties. Third, traditional analytical tools in macroecology may be insufficient to tackle these questions. We demonstrate, with examples, how mathematical and statistical approaches borrowed from physics, particularly statistical mechanics, can help us to link microscopic properties into macroscopic ecological phenomena.

CS12-04
Global changes threaten functional and taxonomic diversity on islands

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Current biodiversity loss, attributed to numerous threats, may have strong consequences for species assemblages and ecosystem functioning. However, the understanding of biodiversity patterns under global changes is currently biased towards taxonomic diversity, missing ecological and functional aspects of species. Therefore, we characterized both taxonomic and functional diversity of insular biodiversity threatened by global changes. We focused our analyses on 11 threats (including biological invasions, habitat loss, pollution, overexploitation and climate change) and more than 2,700 bird and mammal species. Functional aspects of species were based on five ecological traits related to diet, habitat, and body mass. We computed several taxonomic and functional indices (richness, specialization, originality, and vulnerability) of species pools associated with each threatening process to investigate relationships between both diversity dimensions and also associations between threats and the set of ecological traits. We found that functional richness facing global changes is much more threatened (~20%) compared to taxonomic richness (~8%). A high functional specialization and a low functional originality were also observed independently of the threat involved. Nevertheless, threats threatening high proportion of functional richness (e.g. cultivation and wildlife exploitation) do not necessarily imply high functional vulnerability due to functional redundancy. Our study provides important insights into taxonomic and functional diversity threatened at island level in the context of global changes. These findings reinforce the importance to explore functional consequences of global changes as it may result in a loss of unique traits/functions within species assemblages.

CS12-05

Land surface phenology drives species distributions across spatial scales

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Plants are adapted to the seasonality of their environments. Therefore, observations of the timing of vegetation activity, namely land surface phenology (LSP), may provide tools to 1) understand in depth the mechanisms driving species distributions, and 2) model and map species distributions and community compositions more accurately. However, the use of LSP variables in species distribution models (SDM) has not been rigorously verified across spatial scales. To test the use of remotely sensed LSP information to boost SDMs, we utilized satellite imagery and species data at two distinct resolutions and extents. First, we fitted SDMs for 132 vascular plant species (presence-absence dataset consisting of 1325 study sites) from a mountainous landscape in northern Norway (195 km^2). We included four LSP variables (derived from time-series of Landsat satellite imagery at 30-m resolution) into the models along with the main topoclimatic and soil variables. Then, we modelled the distributions for the same set of species but using data covering whole Fennoscandia (1 million occurrence records) and fitted the models with MODIS derived LSP variables (500-m resolution) and topoclimate and geology variables. The inclusion of the LSP variables significantly improved the predictive performance of the species and community level predictions across scales. Models fitted with only LSP predictors resulted in comparable predictive power to models with the more conventional topoclimatic variables. This indicates that LSPs are useful and low-cost environmental variables for modelling species distributions, and that LSPs can be used as relevant proxies for climatic and edaphic conditions at multiple spatial scales.

CS12-06

Can we reliably predict plant traits globally? Improving data selection criteria and assessing model predictive uncertainty.

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Trait-based models allow to predict trait distributions over space using trait-environment relationships. Recent models paved the road for global plant trait predictions and global change assessments, but discrepancies among studies indicate the need for an in-depth evaluation whether traits can reliably be predicted at the global scale. We aim to predict and assess global plant trait distributions by focusing on data selection criteria, explained trait variation, the extent of extrapolation areas, the suitability of different modeling techniques, model uncertainty, and realism of trait combinations. We selectively collected data for specific leaf area, leaf nitrogen content, plant height, and wood density of 8,379 terrestrial plant species across 446 locations worldwide. We related community means with environmental variables, including climate, soil properties, and fire frequency, using two statistical and two machine learning models. Global distributions of traits were then predicted using an ensemble forecasting framework. Plant height was best predicted, followed by specific leaf area and wood density, while leaf nitrogen was not well explained by the selected variables. The different modelling techniques varied in predictive performance demonstrating that a single approach strategy is not optimal. In terms of extrapolations, trait predictions were mainly only extrapolated in the Arctic and deserts. While the ensemble approach provided realistic trait combinations over the globe, it also highlighted specific areas of strong disagreement between models and thus of high uncertainty. Overall, plant traits at the global scale can be predicted, but these are more accurate for some traits than others, and certainty varies over space.

CS12-07

From coast to coast – How environment drives functional diversity in an insular system

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Understanding the patterns and processes that shape ecosystems using functional diversity is essential, especially in the face of global change. However, results on how species functional diversity changes along environmental gradients are ambiguous. As a result of their relative simplicity, using islands that harbor strong environmental gradients as model systems offers the chance to uncover fundamental processes generating diversity. In this study, we used the entire coast of La Palma (Canary Islands) as a study region to analyse how the functional diversity of endemic and non-endemic plant species changes along environmental gradients. We collected data on species coverage and morphological traits capturing the essence of plant form and function. We assesed how plant functional diversity was associated with the underlying gradient in precipitation and soil pH around the coast. Along the studied environmental gradients, leaf area, leaf thickness and leaf brightness of endemic and non-endemic species increased with increasing precipitation and decreased with increasing soil pH. However, we found that neither precipitation nor soil pH were associated with plant height of endemic species. Our results suggest that in coastal systems leaf traits in plant species assemblages are the result of environmental filtering by precipitation and soil pH. On the other hand, plant height of endemic species is less sensitive to environmental filtering and might be governed by interactions with other species. This implicates that even in less favourable environmental conditions both environmental filtering and plant interactions play an important role in shaping plant species community patterns.

CS12-08

The future of biogeography with DiSSCo

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Many biogeographical, macroecological and biodiversity studies rely on digitized and georeferenced specimen data from natural history museums. Currently, the Global Biodiversity Information Facility (GBIF) is the largest and most important data portal for natural science data holding 149 million digitized records of preserved specimens. Within Europe, however, all collection institutes collectively hold an estimated 1.5 billion specimens, or 55% of the global collection. This means that only a small percentage of the European collection is digitally available for research and evidence based policy decisions. Furthermore, biodiversity data that is digitally available is still incomplete and inadequately connected. Recognition of the importance and shortcomings of these data, and the urgent need of digitized biodiversity data for scientific research, including studies on the impacts of climate and land use change on species distributions has resulted in the acceptance of DiSSCo <http://dissco.eu> , the 'Distributed System of Scientific Collections' on the 'European Strategy Forum on Research Infrastructures' (ESFRI) roadmap. DiSSCo is a pan-European research infrastructure (115 institutes from 21 countries, today) of scientific collections that will mobilise and harmonise natural science collection data and make them available as one big linked science cloud. DiSSCo links historical collection data with data emerging from new techniques such as DNA barcodes, whole genome sequences, proteomics, imaging data, chemical data and metabolomics using permanent and persistent identifiers. In this presentation I will showcase the DiSSCo framework and architecture, and illustrate the potential and added value of DiSSCo for future biogeographical studies on a number of worked examples.

Concurrent Session 13: Biodiversity Patterns and Maintenance

CS13-01

The road to evolutionary success: insights from an Amazonian palm

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Mauritia flexuosa has one of the widest distributions of all palms, covering millions of hectares across northern South America, where it forms extensive, high-density stands. How does a species reach this wide distribution and high abundance in the face of strong competition in hyperdiverse tropical forests, as well as persist through extreme landscape and climate changes throughout the Cenozoic (last ca. 65 mya)?Evolutionary success is related to historical contingency, genetic variation, and demography. Here I present a robust approach to understanding diversification in the tribe Lepidocaryeeae, showing how clade competition contributed to persistence through geological time. Within the *Mauritia* lineage, I show extinction patterns using the pollen fossil record, leading to low species diversity in the genus. I also review how climatic change during the Quaternary influenced the extant demography and distribution of *M. flexuosa*. *Mauritia flexuosa* presents significant genetic differentiation among different river basins and between the Amazonian and Cerrado biomes. Touching on environmental correlations across the genome, I conclude by contrasting adaptive selection with genomic plasticity. Our work provides new insights into the historical factors that affect geographical distribution and structured genetic diversity, contributing to long-term evolutionary success.

CS13-02

Reconciling large-scale landscape patterns and species occurrence of vascular plants in Europe

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The objective of macroecology – to examine ecological patterns and processes at large scales – can be complicated because ecological and environmental data at such scales typically originate from third parties collected at different scales and for purposes not directly related to a particular marcoecological issue. Macroecologists face the challenge of reconciling such data beforehand in order to address their questions. For instance, large-scale species distribution atlases are unlikely to provide suitably detailed environmental or local climatic conditions for each recorded species. Likewise, large-scale vegetation or land cover atlases are unlikely to provide information on species occurrences. Our objective was to estimate the completeness (the realised richness with respect to the size of the species pool) of vascular plants in 50x50km quadrants (as provided by the Altas Florea Europaeae) by assessing the probabilistic suitability of each species with respect to the land cover classification and heterogeneity of each quadrant (as gleaned from the Corine 2006 land-cover types), species frequency, and distance to species occurrences. This objective entailed calculating the respective probabilistic suitability in each quadrant of those species recorded as present with those deemed absent. Measures of completeness were expressed as the ratio of the sum of probabilities of present species and that of absent species, with greater values indicative of greater completeness. The decrease in species richness of vascular plants towards higher latitudes was accompanied by a corresponding increase in completeness. This gradient seems to reflect in part a relationship with landscape heterogeneity.

CS13-03

Time-dependent diversification under high species turnover shapes species richness disparities among tropical rainforest lineages of Bulbophyllum (Orchidaceae) on a global scale

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Tropical rainforests (TRFs) harbour almost half of the world's vascular plant species diversity while covering only about 6–7% of land. However, why species richness varies amongst the Earth's major TRF regions remains poorly understood. Here we investigate the evolutionary processes shaping continental species richness disparities of the pantropical, epiphytic and mostly TRF-dwelling orchid genus *Bulbophyllum* (*c*. 1,948 spp. in total; Asia-Pacific region: *c*. 1,564 spp.; Madagascar: 210; Africa: 80; Neotropics: 94) using diversification analyses based on a time-calibrated molecular phylogeny, coupled with ecological niche modelling (ENM) of geographic distributions under current and past (Last Glacial Maximum) conditions. Our results suggest a mid-to-late Miocene scenario of 'out-of-Asia-Pacific' origin and progressive, dispersal-mediated diversification in Madagascar, Africa and the Neotropics, respectively. Species richness disparities amongst these four TRF lineages are best explained by time-dependent diversification rather than differences in net diversification or diversity-dependent diversification due to current or past spatial-bioclimatic limits. Why the comprehensively sampled Madagascan, African and Neotropical lineages diversify under high turnover (speciation and extinction) rates deserves further study but might relate to various intrinsic features commonly invoked to foster rapid population turnover in tropical orchids (e.g., epiphytism, specialized pollination systems, dispersal by wind).

CS13-04

Niche evolution in the adaptive radiation of Hawaiian Tetragnatha spiders

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Adaptive radiation provides the ideal context for exploring the interaction of ecological and evolutionary processes in generating biodiversity. The Hawaiian *Tetragnatha* (long-jawed) spiders constitute a remarkable adaptive radiation, with approximately 50 known species across the archipelago, displaying a striking variety of morphologies and ecological affinities. The adaptive radiation consists of two clades: one which spins orb webs to capture prey, and another (the "Spiny Leg clade") which hunts actively. While the evolutionary history of the Spiny Leg clade has been well characterized, very little is known about the relationships within the web-builders, nor is it known whether the two clades originated from the same colonization event. We present the most taxonomically comprehensive phylogenetic hypothesis for Hawaiian *Tetragnatha* to date, based on four mitochondrial and six nuclear markers, and including representatives of every known Hawaiian species. We find some clades that are confined to a single island, with high rates of morphological and ecological diversification within the clades, while at the same time, convergent evolution of certain phenotypes appears to have occurred in multiple lineages. Conversely, one clade shows high levels of niche conservatism, with all of its species confined to dry forest habitats across the islands. We also find evidence that the web-builders and Spiny Leg clade do not form a clade together, and therefore likely arose from separate colonization events. Our results indicate a complex history of contrasting evolutionary processes leading up to the present-day diversity of Hawaiian *Tetragnatha*.

CS13-05

Niche conservatism goes back to ancient multicellular algae.

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The extent to which temperature-tolerance is conserved during evolutionary time has fundamental consequences for the current and future geographical distribution of the species. The evolution of physiological tolerance to cold and drought seems restricted in multicellular fungi, plants and metazoans that show phylogenetic niche conservatism (PNC), thus predicting widespread constraints on adaptation under a changing climate. Nevertheless, how far PNC dates back in geological time remains unknown. We tested the conservatism of Upper Survival Thresholds (UST) to temperatures across the phylogeny of green, red and brown macroalgae, which present three independently evolving lineages with green and red seaweeds dating back to the Neoproterozoic (at about 1200 Ma), while brown seaweeds originated in the Mesozoic and are therefore comparatively younger. We gathered the USTs for 280 species from physiological experiments and related them to a tree using phylogenetic signal analysis. Closely related species are more similar in their UPSs than expected by chance. The strongest support was for an OU-model of stabilizing selection towards an optimum thermal limit. Moreover, thermal tolerances remained relatively stable through time, with most variation accumulating recently. Tolerance to heat is conserved across the phylogeny of macroalgae, extending the discussion of the conservatism of ancestral niches to the earliest multicellular organisms.

CS13-06

How environmental spatial gradients and temporal variation interact with genetic and ecological traits to shape community composition

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Species coexistence has traditionally focused on environmental variation as determining factor - both temporally and spatially. A body of evidence indicates that intermediate levels of spatiotemporal variation facilitate coexistence and thus leads to higher species richness. Furthermore, recent studies of negative impact of intraspecific variation on species coexistence sparked an increased interest on the role of biotic factors to coexistence. Yet, so far there are few indications as to what are 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 an individual-based, niche and genetically explicit model to address the question "What are the effects of environmental spatial gradients and temporal variation on genetic and ecological trait composition?" Our model considers 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 traits. We find that surviving communities reveal complex relationships among the aspects of genetic architecture and community trait composition. Furthermore, we identify distinctive trait syndromes (combining genetic and ecological traits) that emerge between the different scenarios. Our results provide clues to how real world communities might react to changing environmental regimes and highlights that functional evaluation of species should also encompass genetic traits.

CS13-07

Ecology of diversification in mammals changes with phylogenetic scale

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Why some regions act as the engines of species diversity, while others act as diversity museums or sinks remains unresolved. Multiple mechanisms have been hypothesized to govern these dynamics, but their interactions and relative importance have yet to be uncovered. Here, we evaluate five classes of prominent mechanisms that govern the dynamics of species diversity in mammals (including the effects of climate, geography, topography, and regional competition). We find that the dynamics transition from an unbounded diversification toward slowdowns and equilibrium diversity. The unbounded expansion seems stochastic and dependent on multiple mechanisms. The slowdowns, however, depend primarily on regional competition between related species for resources, which seems to suppress the diversification process. Eventually, the dynamics converge toward equilibrium diversity, determined by regional climate, energy, and productivity. Highly productive regions (esp. the tropics) tend to be densely packed with species and clades, while the opposite holds for low-productive regions (esp. the temperate). These results held across multiple taxa within mammals (Carnivora, Artiodactyla, Chiroptera, Eulipotyphla, Primates, Rodentia) when controlling for different sources of possible errors. They demonstrate the intuitive, though rarely considered, possibility that multiple mechanisms together influence diversification. But their relative effects and their interactions vary systematically across scales, producing scale-dependent diversity dynamics.

CS13-08

Systematic variation in North American tree species abundance distributions along macroecological climatic gradients

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The species abundance distribution (SAD) is a fundamental pattern in macroecology. Understanding how SADs vary spatially, and identifying the variables that drive any change is important from a theoretical perspective as it enables greater understanding of what factors underpin the relative abundance of species. However, precise knowledge on how the form of SADs varies across large (continental) scales is limited. Here, we use the shape parameter of the gambin distribution to assess how meta-community scale SAD shape varies spatially as a function of various climatic variables and dataset characteristics. Using an extensive continental scale dataset of 863,930 individual trees in plots across Eastern North America (ENA) sampled using a standardised method, we use a spatial regression framework to examine the effect of temperature and precipitation on the form of the SAD. We found that temperature, precipitation and species richness can explain two thirds of the variation in tree SAD form across ENA. Temperature had the largest effect on SAD shape, and it was found that increasing temperature resulted in more log-series like SAD shapes (i.e. SADs with a relatively higher proportion of rarer species). Our results indicate that temperature is a key environmental driver governing the form of ENA tree meta-community scale SADs. This finding has implications for our understanding of local-scale variation in tree abundance, and also suggests that niche factors and environmental filtering are important in the structuring of ENA tree communities at larger-scales.

CS13-09

Universality in biodiversity patterns: causes of the variation of species-temperature and species-productivity relationships

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Biodiversity patterns, such as the relationship between species richness and temperature or productivity, are always defined for a particular taxon at a specific area (the entire range of the taxon or just an arbitrarily chosen region). The form of these patterns varies between taxa and regions. Weak relationship between richness and temperature or productivity is sometimes interpreted as a counterevidence against a hypothesis explaining diversity patterns by given variable. However, the strength and shape of biodiversity patterns may be affected by many effects including size of the taxon or exact delimitation of the study region. Although some of these effects (e.g. spatial scale) have been already investigated, most of them are usually ignored. Comparing (1) published data on different taxa and regions (46 datasets of species richness for a wide range of vertebrate, invertebrate and plant taxa) and (2) different (nested) clades within large vertebrate taxa globally (mammals, birds, amphibians), we evaluate the universality of biodiversity patterns and the factors affecting their strength. There is a strong effect of mean temperature and correlation between environmental variables (temperature and productivity) on the strength and slope of the richness-temperature and richness-productivity relationships. Richness-temperature relationships are stronger in colder areas, while richness-productivity relationships are stronger in warmer areas. These properties are additionally affected by taxon richness and range size in the nested taxa within vertebrate classes. Biodiversity patterns are thus not universal across all taxa or regions, and studies of diversity patterns should pay attention to the variation among observed diversity patterns.

CS13-10

The global biodiversity and climate sensitivity of seaweeds and marine plants

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Among taxonomic groups, marine plants and seaweeds are particularly understudied at a global biogeographic scale. Previous assessments of overall marine biodiversity have been based on occurrence of marine plants, ignoring the vast diversity of seaweeds. Further, the most recent analysis of seaweed biodiversity was built using range maps from taxonomic keys. The need for a comprehensive, quantitative assessment of marine macrophyte biodiversity is pressing. Seaweeds and marine plants contribute disproportionately to global marine net primary production, ameliorate climate change impacts, and are critical ecosystem engineers and foundation species. Importantly, seagrass meadows and kelp forests are being rapidly lost, due to a variety of anthropogenic factors, making an assessment of their extant coverage and diversity even more timely. Here, we assemble a novel database of > 4 million occurrence records from digital herbaria, museum and scientific records, and citizen science observations over the past 200 years. From this, we examine global patterns and predictors of biodiversity for ~400 families of seaweeds and marine plants.

CS13-11

Models of upland species' distributions are improved by accounting for geodiversity

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Recent research suggests that novel geodiversity data on landforms, hydrology and surface materials can improve biodiversity models at the landscape scale by quantifying abiotic variability more effectively than commonly used measures of spatial heterogeneity. However, few studies consider whether these variables can account for, and improve our understanding of, species' distributions. We assessed the role of geodiversity components as macro-scale controls of plant species' distributions in a montane landscape, creating an ecologically meaningful geodiversity dataset that accounted for hydrology, morphometry (landforms derived from geomorphometric techniques), and soil parent material (data from expert sources). We compared models with geodiversity to those just using topographic metrics (e.g. slope and elevation) and climate. Species distribution models (SDMs) were produced for 'rare' (N=76) and 'common' (N=505) plant species at 1 km^2 resolution for the Cairngorms National Park, Scotland. The addition of automatically produced landform geodiversity data and hydrological features to a basic SDM (climate, elevation, and slope) resulted in a significant improvement in model fit across all common species' distribution models. Adding further geodiversity data on surface materials resulted in a less consistent statistical improvement, but often added considerable conceptual value. The geodiversity data used here helped us capture the abiotic environment's heterogeneity and allowed for explicit links between the geophysical landscape and species' ecology. It is encouraging that relatively simple and easily produced geodiversity data have the potential to improve SDMs. Our findings have important implications for applied conservation and support the need to consider geodiversity in management.

CS13-12

Predicting climate-driven intraspecific lineage shifts in marine forests

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Distributions of marine species shift as a consequence of changing environmental conditions. Climate-driven changes in distributions shift species to higher latitudes, leading to retreating low latitude edges, with population extinctions and the formation of refugia. As populations across the distributional range generally show local adaptation and genetic sub-structuring it is questionable if each genetic lineage of a species will have the same potential to cope with climate change. For many sessile benthic marine organisms, it is predicted that their highly diverse and unique low latitude edge populations will go extinct in the near future. In this study, the Atlantic seaweed species *Cystoseira tamariscifolia*, that forms marine forests, is analyzed to understand how its population genetic structure might be affected in the future. This species is used here as a model to test future changes in intraspecific lineage distribution under different climate scenarios by niche modelling. Preliminary results show little spatial overlap among intraspecific lineages throughout the Atlantic temperature gradient. We will further explore the implications of these results for conservation of marine forests under climate change.

CS13-13

Influence of social-historical events and macroecological variables on the endemic plant description in the Iberian Peninsula

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1753 is established as the starting date of the scientific naming; since then, the description of vascular plants has been highly uneven. Given its high levels of plant endemism and long botanical history, the Iberian Peninsula is considered a suitable model to study the process of the species discovery. Two-way ANOVA was conducted to explore the differences on the description dates for categories of range size and life-form. Correlation and GLM analyses were carried out to examine the spatial relationship between the number of described species and the observed richness and the human influence variables. Two important peaks of description were identified: the first was associated to the extensive botanical exploration by Boissier of the Baetic Mountains Hotspot (mid-19th century), and the second to the taxonomic revisions for *Flora iberica* (late 20th). As found in other studies, a negative correlation existed between the range size and the description date. By contrast, no differences were found for the life-form categories, suggesting that this is not a constraining factor on the plant discovery in the Mediterranean region. Both the richness and the human influence had a positive effect on the number of described species, so caution is advised when using the type localities distribution as a tool for conservation planning. Changes in discovery effort have been governed by social-historical factors and consequently the discovery curves are not reliable to indicate the final approach to completeness. However, the high number of recently discovered species suggests that the inventory is still uncompleted.

CS13-14

Is titmice abundance an indicator of forest bird abundance and diversity over large spatial scales?

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Particular species are often used as surrogates in estimating diversity or abundance of target species group. However, using multiple species within a taxonomic group as surrogates is proposed to be a more effective ecological indicator for species diversity than merely one surrogate species. Furthermore, positive interactions, such as social information use, between species sharing resources has only recently been included in ecological research. Thus, community dynamics and diversity could be altered through social information use. Therefore, associations between forest birds and surrogate resident species (e.g. titmice) could provide novel perception in current abundance and diversity estimations. This study addresses the question: Does the abundance of titmice act as a predictor for forest bird abundance and diversity? Long-term datasets of breeding forest songbirds were used to analyze spatial and spatio-temporal variation in the total bird and titmice abundance and diversity patterns within France and Finland. The observed bird abundance/diversity were analyzed with Vector-autoregressive spatio-temporal (VAST) -models by using titmice abundance as a covariate. The density of forest birds was positively associated with titmice abundance. In addition, there was spatial and spatio-temporal variation in forest bird densities in France. The VAST –model was validated with data simulated by a Spatial Gompertz –model. VAST-model showed a better fit to data simulated with forest bird attraction to titmice than to a null-model including no attraction. The results suggest that titmice could act as a surrogate of forest songbird abundance/diversity. This supports the recent suggestions that positive species associations could affect community dynamics and biodiversity.

CS13-15

Exploring diversification drivers of scolopendrid centipedes of the peninsular Indian Plate (PIP) from tropical Asia

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We examined the role of historical contingency on speciation and diversification of the peninsular Indian Plate. Three genera belonging to the centipede family Scolopendridae (*Digitipes*, *Rhysida*, and *Ethmostigmus*) were sampled across the PIP. An integrative taxonomic approach was used to generate evolutionary species hypotheses based on DNA sequences, morphology, and geographic distribution data. Allopatric speciation was detected in seven species pairs, being the predominant modes of speciation, whereas sympatric speciation was observed in one species pair. Bayesian divergence time estimates using three fossil calibrations suggested that these taxa started diversifying on peninsular India in the Cretaceous Period and biogeographic analyses inferred their Gondwanan affinity. An endemic radiation of five species of *Ethmostigmus* in PIP was shaped by multiple dispersal events coinciding with geo-climatic events throughout the Cenozoic. The genus *Digitipes* diversified only in the Western Ghats of PIP, in which the southern Western Ghats were an ancestral area with more and older lineages. Both *Digitipes* and *Ethmostigmus* species are restricted to wet forests of PIP and have retained that niche throughout their diversification. In contrast, *Rhysida* has a widespread distribution, occupying varied habitats in PIP, and diversified in the Late Cretaceous and Cenozoic through dispersal, vicariance, and range expansion. Additionally, there were three independent dispersal events in *Digitipes* and *Rhysida* from PIP to mainland Asia that led to distinct species and range expansion in one species in Eocene-Oligocene, supporting the Out-of-India hypothesis.

Concurrent Session 14: Biogeography of the Anthropocene

CS14-01

Mammals may not be hugely important for the carbon cycle, but they used to be

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How important are herbivorous mammals for the function of the biosphere? We know that impacts of herbivory can be strong, but the overall general impact of mammal consumption has hitherto not been quantified. Many mammal ranges have decreased and numerous species have gone extinct after the world-wide colonization by modern humans. This means that herbivore impacts in many seemingly natural ecosystems must deviate from their pre-anthropogenic state, but how strong this shift is remains poorly understood.

To address these knowledge gaps, we generated a database of metabolic rate and population densities with missing values imputed based on phylogenetic information for all late-Quaternary terrestrial mammals. We mapped their consumption based on both current and present-natural (potential in absence of impacts of *Homo sapiens* through time) ranges. To understand their impact, we compared our results with plant primary production. We summarised our results for the wildest remaining natural areas around the world, to assess the impacts of mammal extinctions on the "Last of the Wild".

We found mammals to consume a large but quite variable portion of the plant productivity both within and between regions. Globally they consume a median of 23% of the productivity – lower than their potential present-natural impact of 36%. Areas with low human footprint also differed a lot between potential (52%) and current (32%) consumption.

Our results show that mammalian herbivores play an important part in the world's ecosystems. Our results further show that the late-Quaternary losses of herbivores still heavily affect even the wildest remaining ecosystems worldwide.

CS14-02

Biogeographical, multi-dimensional approach to analysis of relation between land use and surface water contamination: case study from the Baltic Sea basin to the Pilica River catchment

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The world is faced with problems related to quality and quantity of surface water resources due to extensive industrialization, increasing population density and a highly urbanized society. Export of nutrients to rivers and coastal zones driven by human-related activities is a major problem in river catchments and coastal marine ecosystems. The intensified anthropogenic input of nutrients, especially phosphorus (P) and nitrogen (N), to the environment and landscape from point and diffuse sources resulted in the spatial variation of the riverine nutrient export, which has been observed worldwide.
The aim of the study was biogeographical, multi-dimensional analysis of influence of land use on water quality – from the Baltic Sea basin scale – to the scale of the Pilica River catchment. The Baltic Sea drainage basin comprises 1,720,270 km^2 in which the southern and south-western parts of the Baltic Sea basin include areas with intensive agricultural activity and others with high population density. Whereas the Pilica River catchment, which is 9258 km^2 in area and is located in central Poland (the Baltic Sea basin) in which agricultural lands account for more than 60% of its total area, and forests cover about 31% of the catchment. The remaining area consists of urban areas and other forms of land use.

The research was conducted within the framework of the following projects:

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CS14-03

Fagus sylvatica L. Mediterranean peripheral population in Iberian Peninsula: climatic or anthropic relicts?

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Fagus sylvatica is a temperate shade tolerant broadleaved species with high requirements of moisture availability. In spite of this climatic requirement, it is present in Mediterranean mountains. Frequently, these Mediterranean beech forests have been considered climatic *relicts*. However, the use of this term does not always seem appropriate. On the one hand, beech post-glacial recent expansion makes difficult to disentangle climatic and anthropogenic effects on its distribution. On the other hand, the observed rapid recovery of Mediterranean beech forests after land use abandonment is not in accordance with what we could expect from a climatic relict.
Our objective is to shed light on this issue by studying one of the Mediterranean *relict* populations, located in the species Southwestern margin, the Spanish Central Range. Past and recent shifts in the species distribution were studied revising palaeobotanical records and historical and recent cartography. In addition, field data measuring structural and demographic parameters, as well as species interactions were

analysed. Finally, climate differences between these populations and the rest of European beech forests were also explored.
Results from both spatial and population dynamics did not show evidence of area reduction or confinement, neither the climatic analysis pointed to climatic marginality. Furthermore, the beech populations studied are thriving after the abandonment of past land uses, particularly since the mid-1900s. Our results do not support the climatic *relict* concept but rather highlight the importance of anthropogenic factors to explain the current Central Range beech populations' conservation status and area of distribution.

CS14-04

Teasing apart random, climate and land use change effects on species range dynamics

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Evidence is mounting that ongoing climate changes are leading to a globally consistent fingerprint of systematic shifts in species distributions. The *a priori* expectation is that species should shift poleward or upward as the climate changes. However, the evidence is surprisingly mixed about the causal links between species' distributions and climate. Here, we ask whether species' geographic distributions are more strongly related to climate (as hypothesized by much of the climate change literature) or to other spatially structured variables such as land use change and or population processes. We used the breeding-season of 82 British bird species in two different temporal scales, twenty years (1968-72 vs.1988-91), and forty years (1968-72 vs. 2007-11) of climate change. We compared observed range shifts in both time periods with distributional changes by climate, land use, and random occupancy (null expectations). Our analysis revealed that, on average, northward shifts of British breeding birds are more strongly and more directly related to both the random occupancy and land use change than climate. These results are against the hypothesis that the climate warming is the dominant factor causing range shifts of British birds during the twenty and forty years. We do not argue that climate plays no role in determining species 'distributions, rather our results reveal that accurate diagnosis of the effects of climate change on the distributional shifts requires a method that can distinguish changes driven by natural population dynamics from changes induced by external forcing (e.g. climate, land use).

CS14-05

Geographical patterns of forest fires in China: scale-dependency and determinants with thresholds

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Forest fire patterns and their determinants are fundamental for pyrogeography. However, the roles of natural and anthropogenic factors on the distribution of forest fires in China have remained a challenging issue. In this study, ground-based data of forest fires at the county level in China (1995–2015) were applied in studying forest fires and relevant factors including climate, fuel, topography, human activity at national and provincial scales. During the study period, the county-level forest fire frequency in China increased with decreasing latitude, whereas the burnt area was larger in Northeast China. Industry fires and recreation fires showed contrasting latitudinal patterns, and cultural fires dominated in North China. Lightning fires constituted less than 1% of forest fires, and dominated in only six counties. Results of a random forest model indicated that spring temperature and forest stock were respectively the most critical for the fire number and burnt area across China, and mean spring temperature of 15°C and forest stock of 5×10^8 m^3 were suggested respectively for abrupt changes in fire frequency and burnt area. Climatic conditions

generally dominated the variation in human-caused fires, but lightning fires were primarily influenced by fuel load. However, the dominant factor for fire features varied substantially across provinces, highlighting the complexity in the interaction among causal factors and their combinations for fire risk. Our results provided a first ground-based snapshot of forest fire patterns in China at a high spatial resolution, and highlighted the spatial variation and scale dependency of fire drivers.

CS14-06

Global rewilding potential

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Humans have triggered a wave of species extinctions and local population declines that may be comparable in rate to mass extinctions. A promising approach to restore functional and phylogenetic diversity lost by these extinctions and declines is trophic rewilding, the (re)introduction of species to promote self-regulating biodiverse ecosystems. However, there is little quantitative research into trophic rewilding and no study has examined the potential of rewilding on a global scale. Here, we use PHYLACINE, a recently assembled phylogeny of late Pleistocene mammals and extensive functional and occurrence data to investigate the potential of rewilding to restore lost Ice Age biodiversity. Using a counterfactual estimate of where mammals would live today had they not gone extinct, we select extant terrestrial mammals for rewilding based on how closely related and similar in function they are to missing species and whether target rewilding locations fall within their climatic tolerance. We found that *ca*. 66% of missing biodiversity can be restored just by reintroducing extant terrestrial mammals back into their native ranges, with a further *ca*. 13% being restored by introduction of closely related ecological replacements. Our quantitative model reveals regions of priority for trophic rewilding, when implemented in a phylogenetically constrained fashion, can restore most missing biodiversity in some regions (Asia and Africa) as well as highlights the limits of restoration that are achievable through trophic rewilding (lower recovery in the Americas and Australia).

CS14-07

Insect and disease threats to United States tree species and geographic patterns of their potential forest impacts

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Diseases and insects arguably pose the most destructive threat to North American forests. Recently, exotic and native insects and diseases have wreaked extensive ecological damage and caused billions of dollars of economic impacts. As part of an effort to identify United States tree species and forests most vulnerable to such epidemics, we compiled a list of up to the five most serious insect and disease threats for 419 United States tree species and assigned a severity rating for each of the 1378 host and insect/disease combinations. We then combined this list with data from a spatially unbiased and nationally consistent forest inventory to assess potential ecological impacts of insect and disease infestations. Specifically, potential host species mortality for each host/agent combination was used to weight species importance values on 133,000 Forest Inventory and Analysis plots across the conterminous 48 United States which, when summed on each plot, represent an estimate of the proportion of existing importance value that could be lost on the plot. Plot estimates were then used to identify statistically significant geographic hotspots and coldspots of potential forest impacts associated with insects and diseases in total, and for different agent types. We found potential impacts could be greatest in the northern Rocky Mountains, along the Pacific Coast, and in the Northeast. Markedly different patterns were evident for insects than for diseases, and for exotic versus

native insects. These results should be valuable for decision-makers determining where to target for monitoring efforts and pro-active management activities.

CS14-08

Predicting the global niche dynamics of human disease-vectors in non-analogue environments

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Vector-borne diseases kill ~1,000,000 people every year. As species, goods and people move around the globe, vector-borne disease risk is predicted to rise, facilitated by rapid climate and land use change. While multiple environmental, biological and socioeconomic factors can influence where and when disease outbreaks occur, mapping current and future distributions of disease vectors is fundamental to identifying regions at high risk of outbreaks now and in the future. Inaccurate forecasting of shifting disease vector distributions may lead to geographical mismatches between at-risk areas and target areas for prevention and eradication effort, wasting valuable economic resources and risking human life. Here, we evaluate the capacity of correlative environmental niche models to accurately predict the invaded ranges of vectors on multiple continents for six vector-borne diseases: malaria, Zika virus, West Nile virus, chikungunya virus, dengue fever, and yellow fever. Lastly, we evaluate the extent to which non-analogue environments, predicted to become increasing prevalent under future climate change, weaken the performance of predictive models of disease-vector distributions.

CS14-09

Worldwide biogeography of zoonotic and anthroponotic yellow fever

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Yellow fever is an acute viral haemorrhagic disease caused by an arbovirus of the genus Flavivirus. This disease is endemic in the tropical and subtropical areas of Africa and South America. The virus vectors in the “urban” transmission cycle, that occurs from human to human, are the mosquitoes Aedes aegypti and A. albopictus; in the zoonotic “jungle” cycle, primates can infect humans through mosquitoes of the genera Aedes, Haemagogus and Sabethes. The application of biogeographic tools and concepts allows us to understand the distribution of pathogens and the factors that condition risk of new disease outbreaks. Our objective was to map the worldwide risk areas for yellow fewer in the 21st century. This map reflects the distribution of favourable areas for the occurrence of the disease in humans, according to a combination of historical, ecological, zoogeographic and anthropogenic variables. The history was based on the spatial and ecological trend surface of the disease during the 20th century; and the zoogeographical information was represented by the types of distribution shown by primates in Africa and South America. Mosquitoes were included in the map-building procedure as limiting factors currently subject to distribution changes. This study provides methodological tools that could be applicable to different diseases, especially those that combine zoonotic and anthroponotic cycles. The ouput shows the existence of areas favourable for the occurrence of yellow fever in regions where it has not been reported.

CS14-10

Human-habitat associations in the native distributions of alien bird species

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The role of human tolerance is increasingly being proposed as a key driver of invasion success. Human habitat associations may first facilitate transport, making a species more available for introduction, and also facilitate establishment by creating environmental matching between human-altered habitats at the sites of origin and introduction. Nevertheless, the assumption that alien species exhibit associations with human habitats in their native ranges has been largely overlooked. We conduct the first global assessment of the relative importance of human habitat associations in shaping the native distributions of species introduced worldwide, in relation to other key important drivers, i.e., climate and land-use. For this, we applied deviance partitioning analysis and species distribution models (SDM) to 776 introduced alien bird species from five continents. While an independent effect of climate, and a joint effect of climate and non-urban land uses, appear as major factors governing alien species distribution in their native ranges, significant independent contributions of anthropogenic variables were found for most species. Notably, human-habitat associations in the native distributions of alien birds were significantly higher than expected relative to a pool of available species from the same bird families (N=3,565). Thus, introduced alien birds are a non-random sample with respect to their association with human-altered habitats. Our results support the hypothesis that association with humans may be an important driver of alien bird species distribution in their native ranges, and thus increase the likelihood that these species will end up being introduced.

CS14-11

Facing warmer winters: ‘Will I find a favorable place?’.

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Bird phenology is changing due to recent climate change. Typical Trans-Saharan migrants are increasingly using new wintering places in Europe on the face of warmer temperatures. Hence, several European regions are occupied by these migratory species when they are supposed to be further south, changing their distribution during winter. The Iberian Peninsula, as the shortest distance between Africa and Europe, is a frequent transit route of migrant birds. We aimed to reveal the patterns in the selection of the wintering areas, identifying and characterizing them. We have compiled ringing data from Spain and Portugal of those species considered as long-distance migrants, selecting those records reported during the winter season (December and January). We then classified the species into statistically significant groups of similar distribution – chorotypes – which we used to run distribution models with several environmental variables. Biogeographical patterns were detected on the occupancy of wintering places. A total of eight chorotypes were obtained, four of them monospecific and others grouping species with similar ecological characteristics. Resulting models showed that Mediterranean and southern coasts are the preferred areas where these species spend the winter, avoiding the crossing to Africa and subsequent hazards. They also use wetlands and great valleys, places with milder temperatures during winter. This proves the importance of the Iberian Peninsula for this fraction of the populations which change their phenology and migration status. These new “less-migrant” populations should be monitored with the wintering regions they occur, updating the information of the species during the wintering season.

CS14-12

Non-native palms as engineers of novel ecosystems in the Anthropocene: a global review

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Human activities generate novel ecosystems, ecosystems without historical precedent, by moving species around the world and introducing them into local plant communities. While the emergence of novel ecosystems is widely recognized, it is unclear whether species differ in their propensity to generate novel ecosystems. We provide the first global synthesis for non-native palms as agents of novel ecosystems, as many palms are keystone species in their native range and are likely to benefit from the ongoing human-driven global warming. They also have been introduced outside their native range by humans especially due to their ornamental value and economic importance: of the 2550 recognized palm species, 80 species have been recorded as naturalized outside their native range and 27 species are classified as invasive. The main recipient-areas for non-native palms are the tropics while the subtropics host a smaller number of species. Forests, wetlands and anthropogenically transformed habitats are the most frequently colonized habitats. The majority of studies in our literature analysis reported strong competitive effects from palms on native vegetation. Some of the documented effects in specific cases include impacts on native fauna, physical ecosystem structure, altered water and fire regimes, cascading effects on ecosystem functioning, and even biome shifts. In summary, there exist strong evidence that palms can be important drivers of the creation of novel ecosystems, suggesting that palms present a promising model group to study the generation of novel ecosystems under future global change.

CS14-13

It's the integration, stupid! Understanding and predicting global change impacts on biodiversity by combining data and approaches from different disciplines

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Climate and land-use change are by now well acknowledged to interact additively or synergistically in their effects on biodiversity. However, studies considering the interacting effects of both factors in an integrative way remain scarce. Furthermore, while experimental data e.g. on physiological capacities are important to understand species' responses to global change, they are still rarely integrated into studies trying to assess species' potential responses to environmental changes. Here, we present two examples on the opportunities but also the challenges of combining data on (1) future climate and land-use change as well as on (2) species' distributions and their physiological capacities. The first example demonstrates how the consideration of data on projected land-use changes alters assessments of climate change impacts on the global biodiversity of vertebrates under different scenarios of global warming. In the second example, we show how thermal tolerances of ectotherms (measured in physiological experiments) vary within and between species along elevational gradients in Pakistan and discuss how this variation may influence our understanding of species' responses to climate change, especially in mountain areas. Both examples call for more efforts to consider the joint effects of different anthropogenic threats and to integrate information from different disciplines in order to improve future projections of species distributions and biodiversity.

CS14-14

Extreme events and their influence on the contemporary distribution of genetic variation

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Extreme events, including environmental perturbations, disease outbreaks, and mass mortalities are increasing in frequency. The increase of these stressors on populations can have a number of consequences, including population declines, extinction, range shifts, and evolution. With an increase in genetic monitoring of wild populations and accessibility and affordability of genomic techniques, we are beginning to accumulate the data necessary to better understand the genetic responses of natural populations to such extreme events. Recent mass mortalities in marine species have gained notable attention for their severity. We explore in detail the ecological and genetic consequences of two extreme events — which differed in their magnitude, duration, and geographic extent — on a suite of marine invertebrate species to better understand the roles that life-history, demography, and microevolution play in restructuring (or not) genetic diversity across space and through time. We find species with high dispersal potential and large population size tended to recover more rapidly than species with low dispersal potential and small population size. A keystone species with approximately 80% mortality showed evidence of recolonization, evolutionary rescue, and nearly zero loss in genetic diversity. Brooding species are yet to recolonize large stretches of coast. In a time of unprecedented rapid climate change, it is important to identify the factors that contribute to the vulnerability and resilience of diverse species to stressors arising in the Anthropocene.

CS14-15

Direct and indirect impacts of climate change and land use change over biodiversity: a case of study with the brown bear in Europe

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Climate and land use changes are the main drivers of biodiversity loss and species distribution dynamic. When exploring global-change effects on biodiversity it is usually explored the direct effects, while ignoring the indirect effects, such as biotic interactions. This may drive to erroneous predictions on how global change impacts biodiversity. Here, we focus on the brown bear (Ursus arctos) to understand how direct and indirect effects of climate and land-use change would affect the future distribution of different populations across Europe. First, we compiled a list of ~100 species consumed by brown bears based on the literature and downloaded occurrence data from GBIF. Then, we built species distribution models for all these species, using biomod2 in R, based on current climate and land-use conditions. By combining the distribution model and the spatial variation of energy intake for each species, we obtained the potential energy for each species at each location. After that, using different scenarios of climate and land-use change, we projected the future distributions of the brown bear diet species. Finally, we calculated the potential current and future distribution of brown bear based on the potential energy of diet, climate and land use. Brown bear distribution changes were best explained when considering both direct and indirect factors. Accounting for energy availability (indirect effect) buffered the direct impact of climate and land-use change. Our results highlight the importance of taking a food-web ecosystem approach to evaluate the impact of global changes and predict modifications in the distribution of species.

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CS15-01

Drastic landscape change on Shola Sky Islands indicates rapid fragmentation and isolation of montane grassland habitats and its birds, more than forests

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Tropical montane habitats, including the shola sky islands in the Western Ghats, host several threatened taxa of which, the global distributions are restricted to these mountain-tops. The rapidly increasing human footprint and the spread of invasive alien plants have already resulted in the local extinction of several taxa. Here we examine the entire shola sky islands ecosystem to estimate the extent of habitat loss and to create a baseline of land use in this rapidly changing landscape. We further examine the occurrence of a montane-grassland specialist bird, Nilgiri Pipit across its global distributional range, to understand the impacts of habitat fragmentation. We used a combination of LANDSAT and Sentinel imageries from 1973, 1995 and 2017, with 840 ground truth points across the ecosystem. We find substantial landscape modification in the large high elevation plateaus (7-60%) over the last four decades while changes are muted in the other parts. The loss of grasslands to timber plantations (particularly Acacia) predominates (23.4%) the modification of this landscape, and, continues today at a rapid pace. Contrary to popular belief, shola forests have been relatively stable, implying that most timber plantations were established on grasslands—traditionally classified as “unproductive wastelands”. The existing grasslands are highly fragmented with only a few (<10) large remnant grassland patches that harbour Nilgiri Pipits today. The large-scale local extinction and the reduction of the global distribution of this threatened, sky-island endemic species (~400 sq.km) is an indicator of impacts of the continuing spread of invasive species.

CS15-02

A global synthesis of the small-island effect in habitat islands

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Habitat loss and fragmentation are generally considered as the leading drivers of biodiversity loss. The small-island effect (SIE) can be used to predict species extinctions resulting from habitat loss and has important implications for species conservation. However, to date, no study has explicitly evaluated the prevalence of SIEs in habitat islands. Here, we compiled 90 global datasets to systematically investigate the prevalence and underlying factors determining the prevalence of SIEs in habitat island systems. Among the 90 global datasets, SIEs were unambiguously detected in 36 cases. We found significant effects of habitat island types and taxon groups on the threshold area of SIEs. The number of islands, area range, species range, island type and taxon group were key variables that determined the prevalence of SIEs. Our study domonstrates that SIEs occur in 40% of cases and thus are quite prevalent in habitat island systems. We conclude that conservation biologists and applied ecologists should consider the prevalence of SIEs when making management strategies in fragmented landscapes.

CS15-03

Using favourability for detecting potential country participation in the international illegal wildlife trade through socio-economic approach

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The illegal and unsustainable trade of wild animals is severely affecting the survival of lots of species across the globe. In order to fight against this criminal business, it is important to identify the socio-economic drivers that motivate some countries to participate as wildlife suppliers and consumers. Using TRAFFIC data, we identified 39 exporter and 46 importer countries. By employing a hypothetic-deductive approach, we tested economic and cultural hypotheses that could explain the country participation in illegal wildlife trade (IWT). Proposed a-priori hypotheses are that lack of wildlife protection, poverty and corruption are main factors explaining high potentially for a country to become involved in export; whereas demand of luxury commodities from emerging economies, weak law enforcement, demography, and traditional medicine could contribute to high potential for import. Results suggest that exporter countries, concentrated in Africa and Asia, might be favoured mostly by economic needs and corruption. Consumer countries, located in Asia, America and Western Europe, could be motivated by a high demand of luxury products and a high population size. Our models also suggest that some countries not recorded by TRAFFIC could be potentially led by their socio-economies to become wildlife exporters or importers.

CS15-04

Is the invasive potential of Cortaderia jubata (Poaceae) dependent on native range environmental conditions?

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The purple pampas grass is an endemic species of the Andes with invasive stages in Australia, New Zealand, South Africa and western North America. Species Distribution Models are a common tool to predict the potential distribution of species. In the case of invasive species it is unclear if their potential distributions in new invaded areas depend on the same environmental drivers as in their native ranges. We used the favourability function to evaluate the potential distribution of *Cortaderia jubata* in an invaded area (Australia). We generated two favourability models for the invaded area: 1) a transferred model (logic results from a favourability model of the plant’s native area in South America), and 2) a direct model (a favourability model performed in the invaded area). The models in each area were built according to presence/absence data of *Cortaderia jubata* and a set of independent variables grouped in the factors: space, topography, climate, edaphology and land cover. We evaluated and compared both model results regarding to discrimination and classification capacities. Evaluation measures indicated poor results for the transferred model. However, these indices highlight highly explaining results of the direct model in the invaded area. Furthermore distribution determining variables of the direct model equally covered all factor groups whereas the transferred model was mainly driven by climatic factor variables. We conclude that the present invasive stage of *Cortaderia jubata* in Australia does not seem to depend on the same environmental conditions as in the plant’s native area.

CS15-05
Identifying the next invaders and the next invasions

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Invasive alien species greatly threaten biodiversity and human livelihoods worldwide. The most effective way to limit their impacts and costs is to prevent their introduction into new areas. For this reason, identifying invaders and invasions even before they occur has been for decades the Holy Grail of invasion biology. Here, we provide the first profiling method to predict which species will invade, with what ecological characteristics, and where they could invade. We illustrate our approach with ants, which are among the most detrimental invasive species; they are responsible for declines of numerous taxa, involved in local extinctions, disturb ecosystem functioning and impact multiple human activities. Based on the statistical profiling of from an extensive traits database of for more than 1,000 ant species, we pinpoint 13 native ant species which have an ecological profile that matches those of known invasive ants. Even though they are not described as such now, these species are likely to become the next global invaders. We couple these predictions with species distribution models to identify the world regions the most at risk from invasion of these species: sub-Saharan African coasts, Western Australia, South-East Asia and the Americas. This novel framework, applicable to any other taxa, represents a remarkable opportunity to implement timely and specifically shaped proactive management strategies against biological invasions.

CS15-06
Environmental and socio-economic drivers of insufficiency and uncertainty in biodiversity estimates: a comparison of wood plant diversity among biogeographical regions

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Species occurrence data is fundamental for macro-scale ecological research and conservation, while its spatial bias is a notorious issue. Many researchers have focused on how to overcome such biases computationally and/or analytically to observe reliable biodiversity patterns. However, mechanistic aspects of spatial bias remain relatively unexplored. Understanding the drivers of the insufficiency and uncertainty in biodiversity estimation helps us to recognize the limitation of current data and establish an effective strategy for the collection of additional information. In this study, we estimated the global distribution of woody plant diversity, and evaluated its insufficiency and uncertainty. Then, we conducted driver analysis to detect predominant explanatory factors for the geographical patterns in the insufficiency and uncertainty. We first created a list of woody plant species (94,960 species) based on botanical literature, and compiled 30,645,518 occurrence records from existing databases. As surrogates of insufficiency and uncertainty, we calculated four metrics based on the Hill's number approach: number of occurrence points, difference between observation and estimation, ratio of observation to estimation, and standard error of the estimation. Tropical regions were characterized by relatively fewer occurrence records, large discrepancies between observed and estimated diversity, and huge estimation error, compared with the temperate regions. The spatial patterns of the insufficiency and uncertainty were explained by both environmental and socio-economic conditions, while their relationships were not consistent among biogeographical regions. Our results suggest that a region-specific sampling strategy is necessary to effectively fill the information gap for drawing a reliable picture of global woody plant diversity.

CS15-07

Geodiversity and climate: buffering plant communities against rapid climatic change

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Significant increases in global temperatures are predicted, likely to exceed 2oC by the end of the century. In the Arctic, much greater warming is expected and, importantly, warming of the magnitude predicted globally by the end of the century has already been experienced in certain areas. In response to such rapid warming, individual organisms are forced to adapt, migrate or face extinction. Geodiversity has been shown to be related to biodiversity, such that conserving the abiotic may be important in conserving plant communities. The role of geodiversity in mitigating against climate change has not been assessed empirically, however. Using a large network of vegetation plots across the Arctic, each surveyed at least twice over a 27-year period, we test the role of geodiversity in buffering plant communities against recent, significant climatic change. Geodiversity metrics are derived using ArcticDEM and examined against distributions of individual species and plant communities within each plot, and crucially, their change through time. These results help us understand the nature of plant community responses to climate change, as well as providing valuable information for the designation of protected areas.

CS15-08

Global economic costs of invasive alien species

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As a pervasive component of global change, biological invasions are responsible for substantial economic, sanitary and ecological damages throughout the world. Some of the most important obstacles to mobilize against biological invasions are linked to the difficulty to quantitatively measure their impacts, and monetary value is considered as a good solution. However, a reliable global economic cost synthesis of invasive alien species is still lacking. Here, we provide the most comprehensive and robust global-scale data compilation of the monetary costs associated with invasive alien species. From a pool of 11,000 publications fully scrutinized, we found that the minimum economic costs associated directly and indirectly (including control and research costs) with IAS are in the order of thousands of billions of dollars annually worldwide. Moreover, these costs are grossly underestimated, emphasizing crucial gaps of different types, such as the relative scarcity of cost estimates compared to the large number of invasive alien populations, with in addition a biased research effort towards particular areas and/or taxa, and many unreliable estimates (i.e., not based on available and repeatable methodologies or traceable original references). We discuss (i) the reasons why these costs are likely to be grossly underestimated, and (ii) the mismatch between the colossal economic cost of IAS and the disproportionately lower concern of management authorities and the general public. By providing the first rigorous global summary of accessible monetized costs of invasive alien species, we provide an essential basis for national and international policies in the management of invasive species.

CS15-09

Dune-restricted plants on the Catalan developed shores (NW Mediterranean) as an ecological indicator of beach-dune system status

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Many of the plant species that colonize dune-systems have a range distribution beyond dune environments, but only a small group of species have their exclusive habitat in dunes. In Catalonia (NW Mediterranean coast), the data available on dune vegetation come from floristic studies corresponding to a broader territory than the strictly coastal area, and no detailed information on the range of distribution, structure and composition of dune vegetation is available.
The objective of this work is to update the floristic knowledge in dunes-systems of the Catalan coast, identifying the unique species with specific adaptations to the environmental conditions of dunes and find out if this typical dune species or dune-restricted plants could be used as an ecological indicator for beach-dune system analysis.
With this purpose, 26 of the 110 dune systems currently present in Catalonia were deeply assessed. 147 plant species were recorded and a group of 36 plant species were classified as exclusive dune plants. Most of this typical dune species (24) showed a general distribution on the Catalan shoreline, whereas the rest of them (12) have a restricted range of distribution.
Finally, the results show that the presence of dune-restricted plants is related to some beach-dune system environmental parameters as protected area, restricted area, non-eroded dunes or areas with well conserved beach-dune system profile. Thus, typical dune species can be helpful to quantify the current conservation status of the beach-dune systems of the Catalan coast.

CS15-10

Mediterraneity determines structure and endemicity of spider communities in Iberian oak forests

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The study of the patterns and drivers of species richness and endemicity is critical to understand how biodiversity is shaped, and provides basic indicators and criteria for conservation prioritisation and management. Although certain mechanisms may act in parallel to generate matching variations in both diversity and endemicity, this is often not the case. Here we aimed to determine what generates endemicity at different spatial scales and how it correlates with ecological traits, using a novel standardised dataset on the distribution and abundance of Iberian forests spider communities. Aligned with patterns in other taxa in the region, endemicity in communities from northern areas was lower than expected by chance. Species richness decreased and community endemicity increased with temperature, while both decreased with rainfall, contradicting claims that communities are more speciose in mesic regions due to greater resource availability but have greater endemicity in dry areas caused by selective pressure. Interestingly, specialists were more abundant in southern Iberia, which may indicate the presence of microhabitats that acted as micro-refugia through climatic fluctuations, limiting local extinctions, and promoting speciation and endemicity. Dispersal ability was a key player in characterising spider communities, with species having smaller ranges when their tendency to balloon was lower, and families of good dispersers (ballooners) showing low endemicity values. Our results support the idea that endemicity patterns are the result of

interactions between past migrations, selective pressures and speciation, all conditioned by ecological traits, and they highlight the role of refugia as sources of postglacial colonisers.

CS15-11

Predicting the spread of the Rose-ringed Parakeet in Spain using 15-year-old Data

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Species distribution models are widely used in ecology, biogeography, biodiversity conservation, and wildlife management. However, only in rare cases are the results temporarily validated in order to check the accuracy of the predictions. As a rule, it is relevant to develop accurate models, and it may be of particular interest to do this in the case of invasive species, even if this is done after the invasion process. Bird studies have considerably helped our understanding of biological invasions. Parrots are particularly successful invaders and a cause of increasing concern. In this study, we have modelled the distribution of the Rose-ringed Parakeet in 2002 to assess and validate the distribution of the species in 2017. The factors influencing its introduction and spread are related to human activity, climate and topography, with a clear tendency to occupy urban areas in lowlands, and exposed to weather seasonality. Although the new distribution data was not considered in the model, it retained good predictive capacity regarding the observed changes the species has undergone in its distribution during the last 15 years. These results bring to light the utility of predictive modelling and old distribution data to identify the factors determining species' distribution and to better predict the short-term expansion of an invasive species.

CS15-12

Remoteness promotes the biological invasions on islands worldwide

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Islands are hotspots of alien species invasions, and their distinct biodiversity is particularly vulnerable to invading species. While isolation has shaped natural colonization of islands for millions of years, globalization in trade and transport has led to a breakdown of biogeographical barriers and subsequent colonization of islands by alien species. We analyzed a large dataset for alien and native plants, ants, reptiles, mammals, and birds on 257 (sub) tropical islands, and showed that, except for birds, the number of naturalized alien species increases with isolation for all taxa, a pattern that is opposite to the negative SIR

of native species. We argue that the reversal of the SIR for alien species is driven by an increase in island invasibility due to reduced diversity and increased ecological naiveté of native biota on the more remote islands. Hence, geographical isolation does not protect islands from alien species, and island species richness may reach a new dynamic equilibrium at some point, likely at the expense of many endemic species.

CS15-13
Modeling distributions of Arctic mammals for effective conservation

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The Arctic marginal sea areas will be important as future transportation routes, however there is only a limited amount of information about the ecosystems and their vulnerability to marine traffic. This is due to the scarce survey data, especially along the Northeast Passage. Here we made an effort to reveal the habitat characteristics of polar bears, ringed seals and walruses and modeled their distributions in the Kara Sea along the Siberian shelf area. We tackled the data shortage by introducing a methodology for modeling different types of survey data jointly to increase the accuracy of the model predictions. The data consisted of *in situ* species sightings made by researchers but without information about the detection probability. Sightings were modeled as a point process, which was explained with known environmental conditions and unknown survey effort and spatiotemporal random effect. Polar bears and ringed seals were well explained with ice cover and distance to the coast, and additionally polar bears were explained with the predicted abundance of ringed seals highlighting their dependence on their main prey. Both species may be present, when sea ice covers over a half of the study cell, whereas polar bears stay further away from the coast than ringed seals do. Walruses were abundant in the coastal areas but their habitat characteristics came with high levels of uncertainty. Furthermore, we could predict the seasonally varying species distributions and give probabilistic assessments about species abundance along the main traffic lines and in areas of natural resource excavations.

CS15-14
Intersecting macroecological and landscape scales to assess species vulnerability to human disturbance

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Species vulnerability is determined by their exposition, sensitivity and adaptive capacity to a given impact. However, the sensitivity and adaptive capacity terms are usually neglected from the equation because it is largely unknown how most species would react or adapt to an environmental disturbance in their area of distribution. Moreover, these components have been traditionally conceptualized at local scale and individual levels but have rarely been conceived at upper levels, missing the opportunity to identify inter-specific differences in vulnerability. Here we rise the concept of sensitivity at landscape scale related to the persistence of populations to habitat loss and fragmentation, and propose a framework to incorporate this concept into a vulnerability analysis. We demonstrate that sensitivity at landscape scale is an emergent property of the system by running a simulation model that includes macro-scale physiological constrains on population growth rate, cellular automata logic for dispersal and habitat loss at landscape level, and difference-equations based on Allee effects for local population dynamics. Then, we illustrate the application of these concepts to assess the vulnerability of threatened mammal species of the Brazilian Cerrado, considering climate suitability and scenarios of species sensitivity to habitat loss and fragmentation caused by seven types of human impacts. Finally, we identify vulnerable landscapes close to habitat remaining thresholds in which further habitat loss could derive in species extinction. Our results highlight the relevance of considering species sensitivity at landscape scale and rise potential applications for conservation prioritization.

CS15-15

Impacts of agricultural land cover and land use change on biodiversity in southern Africa and implications for food systems and human health

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Land cover and land use change are expected to be the main drivers of biodiversity loss in the 21st century. With the loss of biodiversity, the provision of key ecosystem services could be compromised with severe consequences for human well-being, including the loss of stability and productivity of food systems. We use species distribution and demographic models to explore how the rapid expansion and intensification of industrial agricultural land and the recent pattern of urbanization in southern Africa has affected biodiversity and how further agricultural land cover and land use change will affect biodiversity under future climate change. Ultimately, we are interested in how changes in biodiversity will feedback on a broad range of ecosystem services related to food systems and human health. We propose research towards better decision support for efficient and practicable conservation strategies to safeguard key ecosystem services in the future.

Concurrent Session 16: Historical, Phylo- and Paleo-biogeography

CS16-01

Historical biogeography of the fern family Blechnaceae

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Blechnaceae is a primarily tropical fern family of 265 species in the eupolypods II. The family has two major centers of diversity, one each in the Neotropics and Australasia/Oceania, and most species occur in the southern hemisphere. Individual taxa occupy a wide range of habitats and growth forms, and family members are characterized morphologically by the presence of multiple vascular bundles in the stipe. Recent taxonomic and phylogenetic work on the family has clarified the relationships among major lineages in Blechnaceae and expanded the number of recognized genera to 24. Some of these genera are relatively large, including *Blechnum*s.s. (30 spp.), *Parablechnum*(65 spp.), and *Austroblechnum*(40 spp.), while most are fairly small, with 15 having ten or fewer species (seven genera are monotypic). We undertook the first family-wide historical biogeographic analysis of Blechnaceae, to explore how ancestral movements have led to the present distribution of the family. Our sampling included 153 members of Blechnaceae plus 35 outgroup taxa, to facilitate molecular dating and ancestral range reconstruction at the base of the genus. Our analyses suggest a circum-southern hemisphere distribution of Blechnaceae at the base of the family, around 100 million years ago, which corresponds geologically with the beginning of the breakup of Gondwana. A deep initial split in the family established lineages in the eastern and western hemispheres, but multiple long-distance dispersal events have criss-crossed the globe ever since, and many contemporary species in the Neotropics actually diversified there following a much later dispersal from the Old World.

CS16-02

Historical biogeography of Southeast Asia aquatic biotas

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In Southeast Asia (SEA), Sundaland is considered as one of the most important and threatened biodiversity hotspots. One of the major drivers for diversification in the area, “hypothetically”, is the cycle of sea levels fluctuation that repeatedly isolated and merged the major islands of Sundaland during the Pleistocene. This research aims to explore the diversification and biogeography of Sundaland, particularly regarding the impact of eustatic sea level fluctuations towards the distribution of molecular lineages of freshwater fishes within the palaeodrainages’ boundaries in the area. Pre-existing sequence data from several locally widespread species from genus *Dermogenys, Hemirhamphodon, Nomorhamphus* (Beloniformes, 266 individuals); *Clarias* (Siluriformes, 88 individuals); and Channa (Perciformes, 535 individuals) were mined from GenBank and BOLD system, and were analysed using different set of markers for each order. Maximum likelihood trees were reconstructed using RAxML followed by species delimitation using GMYC, ABGD, mPTP and RESL algorithms; divergence time estimates and phylogenetic relationships using the GMYC model as implemented in *BEAST2; and completed by ancestral state reconstruction (ASR). Our study evidences a high proportion of cryptic diversity and a diversification burst during the last 1.5 mya with 70% of the speciation events occurring during this period. Early result of ASR analysis shows more transitions between palaeodrainage-within Island than between island-within palaeodrainage. This result challenges the earlier hypothesis of eased dispersal among islands during sea level lowstands. Further ASR analysis is carried out to examine the most probable scenario for the diversification and biogeography of freshwater fishes in the region.

CS16-03

Landscape stability and the persistence of Pleistocene megafauna in the tropical Andes

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The last deglacial period (ca. 21ka - 11ka) was characterized by the loss of ca. 80% of South American megafauna. That extinction coincided with a period of climatic upheaval and the arrival of humans. The roles of climate change and humans in the demise of megafauna are still in debate. Tropical Andean sites currently located at timberline (3500 m of elevation) experienced a shift from glacial-aged grasslands to shrublands and forest. At this elevation, megafaunal populations showed a rapid decline coincident with the transition from grasslands to forest (ca. 20-16.8ka). The full megafaunal extinction occurred between 16.8-12.5ka. Intensification of fire events in sites close to the timberline suggest human incursion (between 15.8 and 14.8ka according to location). However, sites located in modern Puna grasslands (>3800m elevation) did not experience such a dramatic vegetation shift, having been grasslands throughout the glacial. We investigate the hypothesis that megafaunal population collapse occurred later in sites that always supported grassland compared with sites where forests were invading the landscape. We evaluate this hypothesis using long sequences of fossil pollen and *Sporormiella*, a proxy widely used for megafaunal presence, from two Andean lakes located at ca. 4000 m of elevation. The analysis of *Sporormiella* spores showed a later decline in megafaunal populations at Puna sites than at lower elevations.

CS16-04

Missing microrefugia and the last interglacial oaks of central Panama

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The last interglacial (LIG; c. 128,000 -115,000 yrs before present) is widely believed to have been somewhat warmer and more seasonal than present. As climates are warming and precipitation becoming more erratic the LIG may offer useful clues to the future resilience of lowland tropical ecosystems. The LIG was also the last warm period without human presence in the Americas and is therefore of considerable interest in determining the 'natural' state of ecosystems. Because there are so few paleoecological records that span this interval from the lowland tropics, basic ecological questions remain unanswered. What was the temperature change associated with the LIG? Was fire natural in lowland interglacial Panama prior to the arrival of humans? And what was the vegetation of the LIG?
We present fossil pollen, charcoal and diatom evidence from El Valle Crater in central Panama for the period from 137,000 -105,000 years ago. We show that lowlands tropical forest occupied the site, but there were some notable shifts in the flora: *Cecropia*, a common successional pioneer, was rare and the montane taxon *Quercus* was intermittently present, though absent at the peak of the LIG. The existence of *Quercus* microrefugia is hypothesized, but these were lost from the landscape in the Holocene. Human modification of landscapes creating a shifted baseline is inferred.

CS16-05

Distributional changes of the felid guild following the Pleistocene megafaunal extinction

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During the Pleistocene, meso-carnivores such as the cougar (*Puma concolor*), were potentially outcompeted by larger-bodied felids such as *Homotherium* and *Smilodon*. Extinction of these more massive hyper-carnivores at the terminal Pleistocene likely opened new habitat/niche space. Here, we examine if cougars began to exploit eco-space presumably vacated by the extinctions of the mega-felids. We employed a MaxEnt and Ecospat ecological niche modeling (ENM) approach using felid occurrences from the Neotoma Paleoecology Database and paleo-climactic records from the Community Climate System Model. We produced ENMs of New World felids for the late Pleistocene, mid-Holocene, and historical/modern time periods. ENM predictions were compared in environmental-space (as opposed to geography) for to test for niche stability in cougars across the Pleistocene-Holocene boundary. Comparisons were also made between cougars and extinct felids to test for cougar niche expansion into those previously occupied niches. Preliminary results suggest that niche stability was observed in cougars between the Pleistocene and mid-Holocene, but surprisingly niche contraction was the predominant observation into the Holocene. Further contrary to expectations, we find that cougars did not re-fill the niche space vacated by the mega-felids following their extinction. Our findings suggest that niche stability is not as common as presumed in many modern ecological analyses. Further, cougar ecological niches do not appear to have been constricted by interactions with other large felids during the Pleistocene.
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CS16-06

Drainage rearrangements in central Yunnan and its impact on freshwater crab phylogeny

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The Chinese province of Yunnan is situated at the eastern edge of the Qinghai–Tibetan–Plateau, resulting in a geographically extremely heterogeneous area. Steep valleys separated by high mountain ridges and high altitudinal gradients leading from alpine environments in the north to tropical conditions in the south are likely factors that induced frequent allopatric speciation and led to the species rich biodiversity hot spot of Yunnan. The continuous uplift of the Himalaya and Tibetan plateau since the Eocene—driven by the continental collision of the Indian and Asian plate—also influenced the fluviatile drainage systems in the area. Five big rivers have their origin deep in the mountains of the Himalaya: Irrawaddy, Brahmaputra, Salween, Mekong and the Yangtze. Geological studies suggested that the Upper Yangtze was initially connected to the Red River, and thus drained southwards into the South China Sea. Later, the Middle Yangtze captured the upper reaches of the paleo-Red River. We investigated (a) if this geological hypothesis is reflected by potamid freshwater crab systematics, and if yes, (b) if we can estimate a temporal window for this river capture event based on a time calibrated multi-gene phylogeny. Based on fresh collections and a morphological reappraisal we could identify several, yet undescribed, species. And in fact there was a high congruence with ancient, hypothesised river systems. The time of a likely capture event between upper Red River by the Middle Yangtze only a coarse time range between 23 to 2.6 Ma could be estimated using a fossil calibrated phylogeny of the Potamidae.

CS16-07

The colonization of novel habitats promotes niche evolution in Neotropical parrots

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The diversification of Neotropical parrots is associated with the advent of different climatic and geological events linked to the rise of the Andes, which have encompassed new selective pressures associated to the formation of new habitats (e.g., replacement of tropical forest for savannah). These new environments represent a source of ecological opportunity and thus, new niche space. Those lineages that exploited these new adaptive zones should show evolution in their niche influencing net diversification rates. Here, we determined whether the occurrence of the new habitats that appeared after Andean Uplift across evolution of Neotropical parrots affect their niche evolution and diversification We infer the biogeographic history of Neotropical parrots based on Maximum Likelihood using the R package BioGeoBEARS. We used Birdlife´s species distribution data and Morrone´s Ecoregions for South America. We compared six alternative models of geographical range evolution and selected the best model using Akaike Information Criteria (AIC). Our results supports the tropical niche conservatism hypothesis (TCH), where lineages that colonize new habitats, emerged mainly after the middle Miocene, and have higher niche evolution than lineages that remained in tropical habitats. These patterns of evolution, however, are not related to their net diversification.

CS16-08

Combining integrative systematics and comparative phylogeography to better understand patterns of nearctic sawfly diversity

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Sawflies, unlike most other taxa, are most diverse in northern regions, with species richness declining toward the tropics. The diverse subfamily Nematinae makes up much of the herbivorous insect fauna in boreal, subarctic, and arctic regions. Why? One hypothesis states that holarctic sawfly diversity may be explained by cyclical expansion and contraction of species distributions – a 'species pump' caused by climatic oscillations beginning in the early Oligocene (~35 Mya). There have also been oscillations on a shallower time scale: the glaciations of the Pleistocene (beginning ~2.58 Mya). Contemporaneous with these oscillations, episodes of historic connections between North America and Eurasia have facilitated numerous dispersals across the Bering Land Bridge, creating additional opportunity for biodiversity generation. The factors behind Oligocene-scale divergences can be evaluated with a phylogenetic analysis of the genus as a whole, while Pleistocene-scale divergences can be detected using phylogeographic analyses of intraspecific genetic diversity – but evaluation of these patterns is hampered by incomplete knowledge of sawfly biology, distributions, and taxonomy. I assess these issues with an approach combining taxonomic revision, molecular phylogenies, and biogeographic analyses of Nearctic *Pristiphora* – with special emphasis on biogeographic patterns of genetic diversity in three widespread species of *Pristiphora*, evaluated using a comparative phylogeography approach. My research will uncover routes of postglacial colonization, areas of high diversity, and likely refugia through glaciation events, all while improving base-level systematic knowledge of these cold-loving insects.

CS16-09

Biogeography and systematics of Cyrtandra: a mega diverse genus in the Malesian hotspot.

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Cyrtandra, a genus of rainforest understorey herbs and shrubs, is the largest in the family Gesneriaceae with over 800 species. It is distributed throughout South East Asia and across the Pacific to Hawaii, with centres of diversity in Borneo and New Guinea, each with over 150 species. Across its distribution, the vast majority of species are single-island endemics. This high species number and tendency to narrow endemism make it an ideal tool for examining biogeographic patterns in this geologically complex region. Recent fieldwork has provided a large set of samples from across Malesia and allowed us to produce a well sampled stable phylogeny of the genus across the region based on one nuclear (ITS) and four chloroplast regions (*trnL-F*, *rpl*32-*trn*L, matK and *psbA-trnH*). Preliminary biogeographic analyses have shown that this is a recent diversification, with most speciation taking place in the last five to eight million years; a west to east migration across Malesia corresponding with island emergence and mountain building and has also highlighted the importance of founder events in the evolution of this group.

CS16-10

The Atlantic connection: an unexpected finding in the radiation of the genus Dysdera (Araneae, Dysderidae) in the Madeira archipelago

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The spider genus *Dysdera* colonized and underwent major diversification on the Canary Islands, where approximately 50 endemics have been described. The genus, however, also managed to colonize other northeastern Atlantic archipelagoes. Pioneer studies on Madeira had already described 3 endemic *Dysdera* species, to which we have recently added 8 newly discovered species. Considering the much smaller size of Madeira, the diversity on these islands is even more remarkable that the one reported in the Canaries. To investigate their origin and evolution, we inferred a time-stamped phylogeny of Madeiran endemics using a target gene approach, under different methods and multiple calibration points. Our results revealed two independent colonizations of the Madeiran archipelago. The bulk of the diversity, all species but one, originated form a single ancestor that diverged from its Iberian relatives approximately 20 Ma, and subsequently diversified on the archipelago. Our data also supported that the single species found in the Ilhéu de Cima was the result of an independent colonization. More interestingly, this species closely resembles an undescribed *Dysdera* found in the Natural History Museum of London, apparently collected in Pico, in the archipelago of Azores, where the genus had not been described before. Following this connection, we conducted a field trip to the Azores and found relatives of the last species. Our results confirm the sister relationship of the Azorean and the Ilhéu de Cima specimens, which diverged approximately 7 Ma, in accordance with the younger age of the Azores.

CS16-11

Deep time perspective on the evolution of the Amazon River with implications for the biogeography of aquatic biota

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Understanding the geological origins of the Amazon drainage basin is central to the study of Neotropical biogeography and the formation of diverse Neotropical ecosystems. Estimates of the age of the river range from >10 to <2.5 million years ago (Ma). A consensus model is now arising that interprets the formation of the Amazon drainage basin as the result of multiple changes in the hydrological connections among several large sedimentary basins of northern South America. This model is based on multiple, sometimes independent data sources (geochronology, sedimentology, biostratigraphy) from studies in both terrestrial and marine settings. The first Andean-derived sediments are recorded near the Amazon mouth in the late Miocene (c. 9.4–8.1 Ma) indicating a megariver capture event in which sedimentary basins became connected across the Purús Arch. A substantial increase in Andean sediments reaching the Amazon mouth in the early Pliocene (c. 4.5 Ma) indicates either a separate megariver capture event across the Iquitos Arch, erosional response to early Pliocene uplift of the Central Andean Plateau, or most likely both. Transcontinentalization most likely was the result of multiple river-capture events over a period from 3.5 to 5.5 million years. In addition, Pleistocene glacial and interglacial fluctuations further reshaped and compartmentalized portions of the modern Amazonian drainage network. Recent studies show that modern Amazonian riverscapes change on millennial to century time scales, due to lateral river captures and channel displacements (avulsions), implying that the fluvial and interfluvial landforms of lowland Amazonia are continuously in a state of dynamic disequilibrium on evolutionary timescales.

CS16-12

Twenty thousand leagues of disjunctions: biogeographic patterns of the Schoenoxiphium clade (Carex, Cyperaceae)

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The so-called Schoenoxiphium clade of the genus *Carex* (Cyperaceae) is an assemblage of sedges belonging to different, non-monophyletic sections with unusual disparate morphological characteristics. Remarkably, the group is quite well-defined from a molecular point of view. It is formed by 60 species showing an interesting Gondwanan distribution pattern in the Southern Hemisphere (with disjunct taxa in South America, South Africa, and New Zealand). Additionally, it has also a few representatives in the Northern Hemisphere, depicting a Rand-Flora distribution around the Sahara desert (mountains of tropical E Africa, Macaronesia, and the Mediterranean Basin). Only *C. pulicaris* is widely distributed across Europe. The group is somehow ecologically diversified, with mostly temperate preferences, but with some species also occurring in subdesertic steppes and alpine environments. The clade has been dated as one of the earliest in divergence among *Carex* sedges (25-28 Mya; Upper Oligocene). Here we present a phylogenetic hypothesis using an almost complete sampling of the group (58 spp, 96% of the clade) and based on 2 nuclear (ETS, ITS) and 2 plastid markers (*matK*, *rps16*). We performed ancestral area reconstruction analyses to evaluate the relative contribution of vicariance vs. long-distance dispersal/geodispersal processes in order to get insights into the evolutionary history behind the striking biogeographic patterns found in this group of sedges.

CS16-13

Recovering the evolutionary footprint through bioregionalization analyses: in search for the best methods.

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Wallace proposed bioregions as broad territories defined by a common history that generates a distinctive biota. Despite the recent blossoming of research on bioregionalization, few studies focus on the evolutionary distinctiveness of the delineated regions. Here, we seek the best approach to pinpoint historically defined regions. We develop a simulation of diversification within a spatially explicit context and classify the resulting scenarios with different regionalization methods: a distance-based method and three network approaches (Map Equation and two versions of a method based in the inference of stochastic block models -SBM1 and SBM2-). In the first one a distance matrix of pairwise phylogenetic beta diversity between geographic cells is classified by UPGMA. Map equation and SBM1 classify a network with phylogenetic nodes directly as nodes of the network of distribution. SBM2 incorporate historical information as 'tags' in the network. Finally, we compare the classified regions with the ones expected based on the simulated, 'known' history. The distance-based method and SBM2 are the best methods in recover history, but the difficulty in obtaining an objective hierarchy of regions of the first one makes SBM2 a better option. SBM1 have similar results and is the only method able to detect the recent dynamics of the species. Finally, Map Equation recover only isolated parts of the history. These results provide a preliminary framework in the selection of regionalization methods, which depends on the final goal: the identification of units defined by a common deep history or by more recent processes.

CS16-14

Multi-lines of evidence deny fast post-glacial northward forest migration in China

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It was commonly regarded that no forests were distributed north of the Yangtze River and the current temperate forests in northern China were resulted from fast northward migration from southern China. We systematically compiled pollen data from 69 sites north of the Yangtze River, as well as available phygeographical data of dominant tree species, in order to figure out how three dominant forest types, pine, oak and birch, have been developed in northern China. Niche model and phylogeographical data suggested that mountains north of the Yangtze River could have served as refugia for dominant temperate tree taxa. Biomization model suggested that western China, with its east–west mountain chains, experienced a faster forest migration rate than that experienced in middle and eastern China, possibly due to mountain refugia. Even in eastern to middle China, the current distribution of the species originated primarily from the spread of local refugial populations, instead of long-distance migration, implying a quite slower migration rate than ever expected. This type of continental-scale biome migration could also balance fragmentation in species range-shifts. Different from pine and oak, climate changing ratio were the main driving factors for *Betula* migration, while the succession to *Quercus* and *Pinus* occurs during the mid-Holocene when climate maintains stable, implying that future fast climate warming will cause expansion of birch forest at the cost of pine and oak.

CS16-15

Are the pattern predicted by Tropical Conservatism hypothesis disrupted in the Himalayas due to plate tectonics ?

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Tropical Conservatism Hypothesis (TCH) states: phylogenetic ages of plant families in the species rich tropics are older than in the temperate zones. If solar energy causes this latitudinal pattern, it may be mimicked along the Himalayan temperature-gradient. However, the two-stage collision between the Indian and the Tibetan-Himalaya plates with the Eurasian plate may have altered the phylogenetic age structure during Eocene-Miocene (50-20Ma). We hypothesise that the phylogenetic oldest families are in the middle of the uplifted Himalayan elevation gradient (3000 masl) which may have been an evolutionary rescue zone. Elevation range-data of flowering plant families (>2 spp) and their phylogenetic age were compiled for Nepal. Peak family richness was in the warm temperate zone, and phylogenetic family age peaked in the temperate zone (2-3000 masl) that has a well-documented elevated species richness. The species-family-ratio increased towards the alpine zone, thus the maximum under dispersion was found around 4500 masl, and declined towards 6000 masl. TCH is rejected because the maximum species richness and the oldest families are on average in the temperate zone. An increase of phylogenetic relatedness with elevation towards 4500 masl is expect due to environmental filtering, but the decline from 4500 towards 6000 masl is unexpected and corresponds to the location of the Main Central Thrust (MCT) interpreted as the suture zone between the Tibetan-Himalayan platelet and the Eurasian plate. Several old families over 5000m corroborates with low relatedness, which probably reflects high elevations in the Tibetan-Himalaya since the 55-60Ma collision with Eurasia.

Concurrent Session 17: Island Biogeography

CS17-01

Assessing the generality of the island rule across vertebrate taxa using meta-analytical techniques

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The island rule, small animal gigantism and large animal dwarfism on islands, is a biogeographical rule that has been tested for a number of taxonomic groups in the past decades. However, its universality remains contentious, with mixed results found for different studies and taxa. Here we used meta-analytical techniques to assess the generality of the island rule across terrestrial vertebrates using body size data on 1039 island-mainland paired populations for mammals (N = 682, 156 species), birds (N = 109, 49 species), reptiles (N = 135, 31 species) and amphibians (N = 113, 10 species). We also test a number of hypotheses that have been posited to explain the island rule, such as the influence of island area and isolation (distance to mainland). After accounting for imbalanced sample sizes, precision in the estimates and phylogeny, we found that the island rule is universal across mammals and birds, and that the evidence is weak for amphibians and opposite for reptiles. For mammals, we found stronger support for the island rule in remote small islands compared to large islands close to the mainland. Shifts in body size of birds were induced by decreasing island area, but not isolation. We conclude that the island rule is valid for endotherms but not for ectotherms, particularly in small isolated islands where selective pressures (predator release, intraspecific competition and limited resource availability) are greater. Analytical methods able to deal with the heterogeneity of empirical data are useful to reassess the validity of long standing biogeographical rules.

CS17-02

Developing and testing a general model of island species–area relationships

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The species–area relationship has been described as one of ecology's few laws, although there are actually several distinct types of SAR, and the form can be rather variable. The island species–area relationship (ISAR) is a biogeographically important form of SAR, observable at local–global spatial scales, generated over ecological–evolutionary time scales, and typically describable by means of the log-log power model. The interpretation of the parameters of this model has long been debated. We test a causal model hypothesizing ISAR parameter variation as a function of taxon, isolation, and archipelago configuration, using a globally distributed database of ISARS including datasets for vertebrates, invertebrates and plants, from archipelagos ranging from inland islands to oceanic islands. Best fit models feature negative covariance between ISAR intercept and slope as a function of archipelagic species richness, in turn shaped by taxon effects and by the amount and disposition of archipelago area. Our findings support long-debated biological interpretations of ISAR form while demonstrating that local-scale (intra-archipelago) processes canalize/modulate the diversity patterns predicted by island biogeographic theory, hence questioning simplistic applications of ISAR theory in conservation science.

CS17-03

On being the right size – Body size patterns of introduced mammals on islands

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Introduced species often adapt their behaviour, morphology, and ecological niche in response to variables that differ from those of their native range. We analysed data on body mass and island characteristics for 385 introduced populations across 285 islands, comprising 56 species of extant, non-volant mammals to test whether body mass of these populations is correlated with the geographical and ecological characteristics of the islands. Introduced mammals follow the predicted island rule trend, with body size shifts more pronounced for populations with greater residence times on the islands. Individual populations varied substantially in their rate of body size evolution, with some populations of murids exhibiting significant body size change in less than 200 years. We propose that this likely coincides with increased levels of carnivory on nesting seabird colonies. Counter to earlier predictions, body size of most introduced mammals is negatively correlated with latitude and topographic relief, possibly correlated with higher primary productivity and a higher anthropogenic environmental impact on low-lying tropical islands. Body size of insular populations is negatively correlated with number of co-occurring mammalian species, especially other aliens, confirming an ecological hypothesis of the island rule. The island rule is a pervasive pattern in mammals, exhibited across a broad span of geographical regions, time periods and for introduced as well as native populations. We postulate that much of what we view as the natural character and ecological dynamics of recent insular communities may have been rendered artefacts of ancient colonisations by humans and commensals.

CS17-04

Disharmony of the world’s island floras

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Disharmony is a key concept in island biology that describes the biased representation of higher taxa on islands compared to their mainland source regions. Although differential colonization success of taxa is predicted by selective dispersal, environmental and biotic filtering, the empirical evidence for disharmony remains largely anecdotal. Here, we develop a novel method for delineating island source regions and present the first global quantitative assessment of island disharmony. We analyzed the overall compositional bias of 320 island floras compared to their most likely mainland source regions, and examined the global over- or under-representation of 450 plant families on islands. We found that the

compositional bias of island floras is strongly predicted by geographical and climatic island characteristics (isolation, area, geologic origin, temperature, precipitation), whereas the representation of individual families is only weakly related to family-specific characteristics (family size, family age, taxonomic group, functional traits), indicating that the taxonomic scope of the disharmony concept has historically limited its wider applicability. Our results provide a strong foundation for integrating disharmony with quantitative functional and phylogenetic approaches in order to gain a deeper understanding of assembly processes on islands.

CS17-05

Extinction-driven changes in frugivore communities on oceanic islands

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Global change and human expansion have resulted in many species extinctions worldwide, but the geographic variation and determinants of extinction risk in particular guilds still remain little explored. We quantified insular extinctions of frugivorous vertebrates (birds, mammals and reptiles) across 74 oceanic islands within 20 archipelagos worldwide and investigated extinction in relation to island characteristics (area, isolation, elevation, climate) and species' functional traits (body mass, diet, ability to fly). 33 islands have records of frugivore extinctions, with one third of the pre-extinction frugivore community being lost. Geographic areas with more than 50% loss of pre-extinction species richness include islands in the Pacific and the Indian Ocean. The proportion of species richness lost from original pre-extinction communities is highest on small and isolated islands and increases with elevation. Large and flightless species had higher extinction probability than small or volant species. Across islands with extinction events, a pronounced downsizing of the frugivore community is observed, with a strong extinction-driven reduction of mean body mass and maximum body mass. The results document a substantial trophic downgrading of frugivore communities on oceanic islands worldwide, with a non-random pattern in relation to geography, island characteristics and species' functional traits. This implies severe consequences for ecosystem processes that depend on mutualistic plant–animal interactions, including ecosystem dynamics that result from the dispersal of large-seeded plants by large-bodied frugivores. We suggest that targeted conservation and rewilding efforts on islands are needed to halt the defaunation of large and non-volant seed dispersers and to restore frugivore communities and key ecological interactions.

CS17-06

What if MacArthur & Wilson had used dated phylogenies?

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In the theory of island biogeography, MacArthur & Wilson hypothesised that island biodiversity depends on island features such as area and isolation, due to their effect on the critical underlying processes of colonization, extinction and speciation. Testing this hypothesis requires information on the timing of species arrival and diversification for entire communities on islands. These can be extracted from divergence-dated molecular phylogenies, which have only recently started to become widely available. We have put together the largest-ever global phylogenetic dataset of times of colonisation and speciation of birds on islands. Our dataset includes the complete terrestrial bird faunas of 42 oceanic archipelagos worldwide. We obtained DNA sequence data from the 612 taxa on these archipelagos, as well as their closest mainland relatives, combining published molecular data with newly generated sequences including 110 previously unsampled island bird taxa and 139 extinct species. We fitted a new version of the island biogeography model DAISIE to this global phylogenetic dataset, where instead of estimating individual colonization, speciation and extinction rates for each archipelago, we estimated the hyperparameters that control the relationship between these rates and island features (area, isolation) on a global scale. By bridging together the theoretical foundations of MacArthur & Wilson's model with the temporal information contained in molecular phylogenies, we are able to successfully reproduce global patterns of insular diversity, including number of colonisations and radiations on different islands, as well as infer the shape of several key macroevolutionary relationships, such as the cladogenesis-area, extinction-area, colonisation-isolation and anagenesis-isolation relationships.

CS17-07

Disentangling the mechanisms underlying the Island Species-Area Relationship (ISAR) of four taxa in the Andaman and Nicobar archipelagoes.

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The Island Species-Area relationship (ISAR) describes how the number of species increases with increasing size of an island (or island-like habitat), and is of fundamental importance in island ecology and conservation. Here, we specifically examine the influence of three hypothesized mechanisms that shape ISARs: 1) sampling effects, 2) area per se, and 3) habitat heterogeneity. However, rather than focusing merely on the number of species per island, we also consider other biodiversity metrics, such as the Probability of Interspecific Encounter (PIE), and use a rarefaction approach that can allow us to disentangle possible mechanisms underlying the ISAR using individual-based rarefaction curves. Specifically, we show how ISAR mechanisms can be inferred by comparing the relationship between island area and the number of species expected from a rarefaction to a common number of individuals (Sn). Using data on species abundances of four taxa (birds, butterflies, lizards and frogs) across the Andaman and Nicobar archipelagoes, we examine how these metrics of biodiversity (species richness, PIE and Sn) vary with island area. We found contrasting patterns of diversity between flying and non-flying taxa, whereby sampling effects appear to drive bird and butterfly ISARs, while frog and lizard ISARs are shaped by both area per se and heterogeneity mechanisms. Here, we show how the rarefaction framework used is critical in disentangling the ecological mechanisms that underpin biodiversity patterns across islands. Indeed, the approach that we advocate here is only one step towards creating a deeper understanding of patterns of diversity on islands and island-like habitats.

CS17-08

Why treelines are lower on islands – climatic and biogeographical effects hold the answer

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Despite their long history as ecological model systems, islands still hold answers to many fascinating questions in ecology and biogeography. One such question is why treelines are generally lower on islands than on the mainland. Two main hypotheses have been proposed to explain this phenomenon. First, high elevation areas on islands might be more exposed to the surrounding macroclimate, thus making growing conditions harsher compared areas of similar elevation within mainland mountain ranges. Second, treelines might be lower because specialized high-elevation species might not have colonized islands and the treeline is formed predominantly by rather widespread generalist species. Disentangling these hypotheses has been challenging, as we usually only know the actual elevation of an island's treeline but not the theoretical upper limit based on climatic conditions and an unfiltered species pool. Here we present results from a global comparative analysis of the observed treeline elevation with the potential climatically-determined treeline derived from new high-resolution climatological data (CHELSA). Using a climatic null model for the treeline, and investigating the global temperature niche of tree species, we demonstrate that oceanic islands show up to 2066 m lower treelines than mainlands. Roughly half of this deviation can be explained by climate, and the other half by island biogeographic effects. This difference also correlates with the degree of isolation and the number of tree species present on an island. It indicates that floras of oceanic islands are depauperate with respect to species with cold adaptation potential, especially on islands of warmer regions.

Concurrent Session 18: Phylogeography

CS18-01

Interdependent phenotypic and biogeographic evolution driven by biotic interactions

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Biotic interactions are hypothesized to be one of the main processes shaping trait and biogeographic evolution during lineage diversification. Theoretical and empirical evidence suggests that species with similar ecological requirements either spatially exclude each other, by preventing sympatry or driving coexisting populations to extinction, or show niche divergence in sympatry. However, the extent and generality of the effect of interspecific competition in trait and biogeographic evolution has been limited by a dearth of appropriate process-generating models to directly test the effect of biotic interactions. Here, we formulate a novel phylogenetic parametric model that allows interdependence between trait and biogeographic evolution, thus enabling a direct test of central hypotheses on how biotic interactions shape these evolutionary processes. We perform inference using a data augmentation approach within a Bayesian framework, allowing correct propagation of uncertainty in our posterior estimates. Our simulations show that our model has appropriate statistical properties to different scenarios of biotic interactions. We apply

our model to the radiation of Darwin's finches -a classic example of adaptive divergence- and find support for *in situ* trait divergence in beak size, convergence in traits such as beak shape and tarsus length, and strong competitive exclusion throughout their evolutionary history. Our modeling framework opens new possibilities for testing more complex hypotheses about the processes underlying lineage diversification. More generally, it provides a robust probabilistic methodology to model correlated evolution of continuous and discrete characters.

CS18-02

Species delimitation is key to asses phylogeographic patterns of terrestrial slugs and unveil the major role of interspecific differential dispersal abilities

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Dispersal processes are crucial for the interpretation of species' phylogeographic patterns. Dispersal ability can be inferred from patterns of population genetic structure within species, and therefore it necessary implies assessing which populations do or do not belong to actual biological species. We argue here that explicit species delimitation is crucial to discern phylogeographic patterns resulting from processes acting below the species level from other biogeographic patterns resulting from processes acting above the species level (i.e. inter-specific niche or dispersal ability differences). Species delimitation may be particularly challenging in taxonomic groups with deep evolutionary lineages and little morphological variability. This is the case of some terrestrial molluscs. We have followed an integrative organismal-centred phylogeographic approach for the assessment of phylogeographic patterns of *Geomalacus,* an endemic genus from the Iberian Peninsula. Prior to assessing species' dispersal abilities based on Isolation-By-Distance (IBD) patterns, we complemented molecular based delimitation of lineages with a morphology-based diagnosis indicative of reproductive isolation. This indicate three species with different phylogeographic patterns and evolutionary histories, probably linked to their variable levels of dispersal limitation, as inferred from the differences in the strength of the IBD patterns. Remarkably, the relevance of dispersal processes is unveiled only when species delimitation is based on a combination of phylogenetics and morphological information indicative of reproductive isolation. We also show that, although different phylogeographic patterns may be largely driven by the same major process (i.e. dispersal limitation), the strength at which they operate may vary among closely related species.

CS18-03

A phylogeographic process model to investigate landscape scale drivers of diversity

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Macro-ecological process models are showing great potential to increase understanding of the ways in which interacting processes of climate, geography and evolution have shaped the spatial distribution of biodiversity. When simulating expected biodiversity, a relatively simple set of parameters can shed light on the complex dynamics which generate and sustain biodiversity.
Here we extend macro-ecological modelling approaches, to focus on the phylogeographic scale, where new species arise through repeated processes of divergence and reintegration, isolation and secondary contact. By simulating spatially explicit gene flow, niche evolution, and range shifts on real and simulated landscapes, this approach aims to understand how different landforms generate and sustain diversity and produce areas of endemism.
Varying just three parameters: dispersal speed, rate of local niche evolution and the rate at which genomic divergence leads to reproductive isolation, this model elicits emergent properties observed in nature (but not coded into the model). These include range limitation due to gene flow along environmental gradients preventing local adaptation; and dominance of rare genomic variants on fronts of range expansion.

The new approach presented here will add to knowledge of the role of landscape dynamics in generating macro-scale patterns of phylo-diversity and endemism.

CS18-04

Biogeography of haemosporidian parasites infecting diverse bird communities inhabiting the Shola sky islands of the Western Ghats, India

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The Western Ghats are an ancient mountain range in southern India, characterized by three biogeographic barriers— the Chaliyar, Palaghat and Shencottah gaps. At high elevations, the Western Ghats host a unique system of sky islands: a natural mosaic of tropical evergreen forests (*Sholas*) and grasslands. The *Shola* sky islands harbor species-rich, diverse bird communities with disproportionately high endemism. Consequently, *Shola* sky islands present an ideal system to better understand the relative importance of geography, host phylogeny and host ecology in structuring parasite communities. *Plasmodium* and *Haemoproteus* spp. are a diverse group of vector-borne haemosporidian parasites that infect bird populations globally. Here, we elucidate the ecological and evolutionary dynamics associated with haemosporidian infections in bird communities inhabiting the *Shola* sky islands. We sampled 1177 birds across 28 species and characterized haemosporidian infections by sequencing parasite *cytochrome b* locus. We found 24 species infected with haemosporidians (41.6% prevalence) and many endemic lineages for *Haemoproteus* (24 of 29 lineages) and *Plasmodium* (10 of 18 lineages). The biogeographic barriers did not impact parasite phylogeographic structuring despite the effect of these barriers on phylogeography of some host species. *Haemoproteus* lineages were host specialists, infecting a lower diversity of hosts compared to *Plasmodium*. Parasite phylogenetic structure was primarily driven by host phylogenetic and/or ecological similarity in the case of *Haemoproteus*, but geographic proximity in the case of *Plasmodium*. Such labile host-parasite associations may facilitate frequent host shifts in *Plasmodium*, but not *Haemoproteus*, and contribute to higher disease emergence risk associated with *Plasmodium* in novel host communities.

CS18-05

Latitudinal and bathymetrical species richness patterns in the NW Pacific and adjacent Arctic Ocean

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Global scale analyses have recently revealed that the latitudinal gradient in marine species richness is bimodal, peaking at low-mid latitudes but with a dip at the equator; and that marine species richness decreases with depth. However, these patterns may conceal regional differences that help clarify the causes in these gradients. We analysed both latitudinal and depth gradients of species richness in the NW Pacific and its adjacent Arctic Ocean using distribution records of all marine species from the Ocean Biogeographic Information System (OBIS) and Global Biodiversity Information Facility (GBIF). We used 324,916 distribution records of 17,414 species to calculate alpha (average), gamma (total) and ES50 (estimated species for 50 records) per latitudinal band and depth zone.
We found that ES50, gamma, and alpha species richness decreased with latitude and depth. Most (73%) species occurred in shallow depths (0 to 500 m). The Visayas and Sulu seas had the highest alpha species richness (more than 13,000 species per 50,000 km^2). Both gamma and alpha diversity increased from the

equator towards the low-latitudes (5-10˚N), with a sharp increase at latitude 10˚N, then further decreased at higher latitudes. The latitudes 60-70˚N had the lowest gamma and alpha diversity where there is almost no ocean area available. Model selection on Generalized Additive Models showed that the combined effects of all environmental predictors including dissolved and saturated oxygen, temperature, primary productivity, chlorophyll a, current, salinity, and nitrate produced the best model driving alpha species richness in both shallow and deep sea.

CS18-06

Effects of geology, and climate on the biogeography, and phylogeography of freshwater snail family Viviparidae in the Indian subcontinent

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Distribution patterns of lineages are shaped by interactions of factors such as geology, climate, ecology and dispersal ability of the organism. The effects of these factors manifest at different time scales and different levels of biological organization. Indian subcontinent, owing to its geological and climatic history, provides an ideal setting to investigate such patterns and the underlying processes. Freshwater gastropod family Viviparidae is an excellent system to address questions regarding such processes considering their sensitivity to climatic changes and dispersal limitation. Hence, the biogeography of the Indian species of Viviparidae at both species and population level were investigated to understand the effects of geological and climatic events occurring in the subcontinent over time. First, we examined the effects of continental drift and climatic oscillations in the India-Southeast Asia interface on the dispersal of Viviparidae using molecular dating and ancestral area reconstruction analysis. The results suggested that the establishment of land connection between the two landmasses facilitated dispersal. However, out of the two Indian species, one dispersed during a warm-humid phase of Miocene, while, the other dispersal took place after the late-Miocene intense aridification commenced. We further investigated the effects of Quaternary climatic oscillations on the population level patterns in both the species using population genetic and statistical phylogeographic methods. Both exhibited signatures of geographic range shift in parts of the subcontinent in response to the Quaternary fluctuations. The study illustrates how the current distribution of species and the distribution of intraspecies genetic diversity, both were shaped by past climatic processes.

CS18-07

Comparative phylogeography and community turnover for North American amphibians reveal spatial congruency of divergence through time

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Comparative phylogeography investigates the recent history of populations, and can help link these histories -with population interactions at ecological time-scales. Thus, comparative phylogeography is a vital part of a unified and integrative approach to understanding current diversity patterns, especially while considering the spatial variability of mechanisms at the continental scale. For example, phylogeographic break zones, or regions where turnover among intraspecific genetic lineages occurs for multiple species, have been proposed as critical regions where eco-evolutionary processes (e.g. dispersal limitation, drift, niche sorting) may be continuously acting over time. If this is true, we would also expect to see turnover among species assemblages in these areas. To test whether North American amphibian communities have been structured by analogous processes over evolutionary and ecological time-scales, we estimated taxonomic and phylogenetic turnover among 1201 amphibian assemblages, and compared turnover among communities which span a phylogeographic break versus those that do not, based on published phylogeographic data for 66 amphibian species. We tested for correlations between phylogeographic

structure and taxonomic and phylogenetic turnover using ANOSIM on the raw data, and after removing the influence of environmental differences between communities. We found that taxonomic and phylogenetic turnover is higher among communities that span phylogeographic breaks. For taxonomic turnover, this result holds at the continental scale even after controlling for environmental differences among assemblages. Overall, our results indicate spatial consistency across temporal scales in processes shaping diversity, highlighting the need to consider species' recent history in the search for the drivers of diversity patterns.

CS18-08
Incorporating interspecific interactions into phylogeographic models: A case study with Californian oaks

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Phylogeographic inference has traditionally focused on testing alternative hypotheses on how the distribution of species and lineages is shaped by different spatial and temporal components of landscape heterogeneity. However, even though theoretical and empirical research has demonstrated the impact of interspecific interactions on the demography of organisms and community assembly, such ecological processes have been seldom incorporated into phylogeographic models. Here, we consider hypothetical interspecific interactions (competition, facilitation) at different phylogenetic scales (genus, section) to generate testable phylogeographic models within a spatiotemporally explicit framework. Using as a case study the Californian oaks *Quercus chrysolepis* (section *Protobalanus*) and *Q. berberidifolia* (section *Quercus*), we formulated a suite of phylogeographic models considering alternative scenarios of competition/facilitation with other congeneric taxa and tested them using genomic data. Model selection using Approximate Bayesian Computation highly supported competition over neutral or facilitation models, particularly in the taxon *Q. berberidifolia* belonging to the most speciose Californian oak clade. These results are in good agreement with ecological studies showing the importance of competitive exclusion among closely related taxa on the assembly of forest tree communities. Our study highlights the potential of integrating ecological and evolutionary processes inferred at micro- and regional scales into phylogeographic models in order to better understand the factors governing the spatial distribution of genetic variation of natural populations and refine our predictions about how entire communities, rather than specific taxa, will respond to ongoing global change.

Concurrent Session 19: Biodiversity Patterns and Maintenance

CS19-01
The variation in population dynamics across a species range is mostly about variability

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Abundance of a species is known to vary by orders of magnitude across a species range. And, although the patterns are not as simple as the "abundant center" hypothesis, there is clear spatial structure of this variation. Correlational approaches examining how abundance covaries with climate are central to the niche modelling approach. However, developing a more mechanistic theory based on population dynamics is an oft-stated goal that should lead to improved ability to extrapolate and predict species ranges into novel conditions. Using the North American Breeding Bird survey, I fit several population dynamic models including a stochastic Ricker population model and some robust estimators of population dynamic parameters to each route and explore how the population dynamic parameters covary with each other, with

abundance, and across space. I find that surprisingly abundance is weakly negatively correlated with population growth rate parameters, but is strongly negatively correlated with population variability. Using multivariate methods I show that there are three axes of variation in population dynamics across a species range (in decreasing order of variance explained): bet hedging, high r+K, r vs K. I suggest that studies of species ranges need to move beyond studying means to embracing the role of variability.

CS19-02

Relative importance of water-energy conditions on the geographical patterns of terrestrial vertebrate richness

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Biodiversity gradients are caused by multiple processes, which act together on a complex web of causality. Environmental factors related to energy and water availability are among the strongest predictors of species richness. However, their relative importance is expected to vary across space, as water should be more limiting in warm areas. We revisited the water-energy hypothesis globally for mammals, birds and amphibians, employing a novel combination of Path Analysis and Geographically Weighted Regression, therefore accounting for spatial non-stationarity on path coefficients. We explored how water-energy conditions drive species richness by decomposing the (1) direct effects of temperature, precipitation, Net Primary Productivity (NPP) and elevation on species richness; (2) indirect effects of elevation on temperature and precipitation, which in turn affects NPP and species richness; and (3) total effects, by combining the direct and indirect effects. Spatially-explicit path analysis indicates that the relationships among water-energy conditions and richness change in magnitude and direction among taxonomic groups, geographic regions and connecting paths (direct, indirect and total). Mammals and birds respond more similarly to water-energy conditions. Considering all connecting pathways, temperature has the strongest effect on richness of birds and mammals in the New World, while precipitation has the strongest effect on all three groups in the Old World. As expected, precipitation is the strongest driver of species richness of all studied groups in extremely warm areas, such as the deserts. Accounting for indirect pathways and spatial non-stationarity uncovers a complex causal network of environmental effects on spatial patterns of species richness.

CS19-03

From evolution to local ecology - A holistic explanation of regional variation in α-diversity, using the Cape flora Restionaceae

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Spatial variation in local (α) diversity is notoriously difficult to explain, and it has become increasingly evident that this is due to different processes operating at different scales. Regional (γ) diversity is shaped by immigration, speciation and extinction, whereas α diversity results from sampling this regional diversity, using environmental, dispersal and interaction filters. We explore these interactions using the Restionaceae, a dominant element in the hyper-diverse Cape flora. We show a strong archipelago-like pattern, with the highest diversity in the central region, which is characterized by high speciation and low immigration rates. This contrasts to peripheral regions with lower speciation and higher immigration rates. We complement these findings by calculating probabilistic local species pools (at a resolution of 5 x 5 km) shaped by climate (especially where the gradients are steep), dispersal rates (where the gradients are shallow) and biotic interactions. Observed species richness variation in 916 10 m diam. relevés is significantly explained by the probabilistic species pool, the largest deviations are in unusual local habitat (edaphic) conditions (e.g. poor drainage, usual bedrock, heavy soils). The full, holistic model allows quantification of all of the mentioned processes, and can be summarized as: speciation - extinction + immigration -> regional species pool; regional species pools filtered by environment x dispersal distance x biotic interaction -> local species pools; local species pool filtered by local habitat -> α diversity. Conclusion: the effect of any variable on local diversity can only be estimated by taking all other variables into account.

CS19-04

Unveiling the effect of growth rate and niche differences for species co-occurrence across and within habitats

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At the landscape scale species coexistence is strongly related to environmental suitability. However, at smaller scales, species will coexist only if they are not excluded by competitors. At this scale, coexistence theory predicts that to avoid competitive exclusion species must differ in their niches. Alternatively, if their environmental optima and niches are similar, species may coexist if they have small differences in growth rates (fitness) and cannot outperform each other. These three factors are known to interact but the outcome of this interaction is not fully understood, especially at the landscape scale. Here, we analyse the influence of environmental optima, niche differentiation and growth rates on species co-occurence. To do so, we compiled data on trait characteristics and phylogenetic distances (as proxies of niche differentiation), Ellenberg values (as a proxy of environmental optima) and growth rates under different experimental conditions (water, light and nutrients) of 121 plants and explored their influence on the co-occurrence patterns in the ca. 26,000 vegetation sampling plots of Czech National Database. Our results show that differences in environmental optima between species explain most of the co-occurrence patterns, but differences in traits and growth rate responses also show a significant effect on co-occurrence. In fact, we show that plants with similar environmental optima will co-occur more often if they have small differences in growth rates. This result is consistent across habitats confirming the theoretical expectations that predict that growth rate similarity contributes to coexistence.

CS19-05

Global-scale analysis of woody plant fossil records: a test of regional extinction and range dynamics of angiosperm woody genera through the Cenozoic

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Understanding the origin and maintenance of latitudinal diversity gradients (LDGs) is a central issue in biogeography and macroecology. Dynamics of LDGs are debated in the context of dispersal-driven dynamics and/or tropical niche conservatism, but the underlying mechanisms remain unclear. In this view, we compiled global-scale dataset of woody angiosperm fossil records, combining with phylogenetic information, physiological trait, and modern assemblage patterns, and then investigated the role of extinction and range dynamics, which reflect dispersal- and tropical-niche-driven mechanisms, in shaping LDGs through the Cenozoic. Global-scale data of woody plant fossils showed a substantial bias, especially poorly sampled in lower latitudes, therefore requiring extreme care when interpreting ecological patterns from aggregated fossil data. Nonetheless, we found a greater extinction rate in higher latitudes during colder geological ages, while in lower latitudes survival rate was consistently greater. Moreover, extinct genera in higher latitudes were relatively old and less cold tolerant, but in lower latitudes were relatively younger genera, and also these extinct genera indicated poor species richness per-genus. During Cenozoic, temperate taxa with freezing tolerance generally maintained their distribution at high latitudes, and dispersed into lower latitude and further to the Southern Hemisphere in response to Post-Pliocene global cooling. On the other hand, tropical taxa without freezing tolerance stayed at lower latitudes throughout the Cenozoic and failed to disperse to higher latitudes. These findings suggest that extinction (or survival) process and range shift, which are associated with climate niche conservatism and paleoclimate changes, play a significant role in temporal dynamics of LDGs.

CS19-06

Phylogenetic diversity of the species pool drives species sorting in insular mammal assemblages worldwide

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Evolutionary processes have long shaped the “theater” in which members of ecological communities interact. In other words, the evolutionary history of a region interact with more local ecological processes to influence the contemporary structure of communities. But how can we investigate the relative influence of such processes? First, the evolutionary history of a region leaves a signature in the taxonomic, functional and evolutionary diversity of the species pool. Moreover, the relative influence of spatial and environmental distances on patterns of species compositional turnover provide clues on the relative influence of dispersal limitations and environmental sorting on the structure of a metacommunity. As such, we can better understand how historical, evolutionary and ecoological processes interact by studying metacommunities that differ in attributes of their species pools.

Here, we used taxonomic, functional, and phylogenetic β-diversity to investigate how species pool diversity relates to species sorting and dispersal limitation in nine mammal metacommunities (i.e. archipelagos) distributed around the world. Although most metacommunities did not show strong signal of either process, we found strong evidence of species sorting in Melanesia and of dispersal limitation in Alexander Archipelago. More importantly, we found stronger species sorting in metacommunities with more phylogenetically diverse species pools. Our findings show that the evolutionary history of the regional species pool mediates the outcome of local ecological processes, and that both scale of processes must be considered to shed light on the forces generating the patterns of biodiversity we see today.

CS19-07

Dispersal and the latitudinal diversity gradient in marine fishes

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Marine fishes exhibit a striking latitudinal diversity gradient (LDG), with far more species occurring in the tropics than in extratropical regions. Speciation rates are substantially elevated in polar and high-latitude temperate regions relative to the tropics, suggesting that faster tropical speciation cannot explain the LDG in marine fish diversity. However, we do not yet understand the role of lineage dispersal over macroevolutionary timescales in generating and maintaining the LDG. The “out of the tropics” model posits that tropical taxa expand their ranges and disperse out, thereby enriching high latitude regions. However, extratropical diversification and environmental niche conservatism might be expected to influence the strength of the gradient as well as the movement of species from polar-temperate to tropical regions. We assessed latitudinal source-sink dynamics in marine fishes by estimating biogeographic transition rates and dispersals between tropical, temperate and polar regions while distinguishing between taxa with predominately shallow versus deep-water distributions. We find a strong contrast in rates between the northern and southern high latitudes, with dispersal rates associated with the Arctic being the greatest, and relatively low dispersal rates associated with the Southern Ocean, thus reflecting the Arctic’s history as an area of biotic interchange between the north Pacific and north Atlantic oceans. We also find a strong pattern of greater movement of deep-water lineages than shallow-water lineages in either direction, suggesting that environmental conservatism and the depth distribution of biogeographic corridors likely play important roles in shaping global patterns of marine fish diversity.

CS19-08

Are there universal biodiversity rules? Insights from a marine natural experimental system

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A key step towards understanding whether universal rules underlie diversity and abundance in ecological communities is to systematically compare patterns, and the processes that underlie them, across spatially, temporally, and taxonomically diverse communities. The marine lakes of Palau – independent 'natural experiments' that began when rising seas flooded inland valleys ~6000-15000 years ago – provide a rare opportunity to test whether parallel or distinct diversity patterns emerge from parallel or distinct processes. To exploit this opportunity, our interdisciplinary project team integrated expertise in marine molecular and microbial ecology, paleobiology, biogeochemistry, and macroecological modeling. We asked two overarching questions: (i) Have parallel diversity patterns emerged across organisms as evolutionarily and functionally diverse as microbes and macro-organisms? (ii) Since marine lakes are isolated from the ocean to varying degrees and differ in their habitable area, are the general predictions of island biogeography and neutral theory relevant in these systems? We find that microbes and macro-organisms display parallel beta-diversity patterns among lakes, despite contrasting limits on alpha-diversity, and that isolation and area drive relative abundance patterns across these island-like marine environments. These findings have broad implications for a general understanding of biodiversity. First, they suggest that transition zones between regional biotas may be shaped by large-scale processes acting in parallel on diverse taxa across the tree of life. Second, they suggest that predictions from influential ecological theories, such as island biogeography theory and the unified neutral theory of biodiversity, also apply in the marine realm and may represent truly universal biodiversity rules.

Concurrent Session 20: Climate Change Biogeography

CS20-01

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

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Climate change is a major threat to biodiversity and impacts on species distributions are already evident across a wide array of taxa. Species have been found to typically 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 compare the impacts of a low climate change scenario versus a high climate change scenario on terrestrial bird distributions and, subsequently, species diversity. We use SDMs for the worlds' terrestrial birds to project range changes and derive current and future community compositions. We show that individualistic responses to climate change are wide spread across the globe, but less frequent at higher northern latitudes. These individualistic responses lead to significant changes in community compositions,

affecting the PD of these communities and potentially further reducing their resilience to climate change. We find that areas where diversity patterns are changed markedly by the mid-century are significantly reduced, under the low compared to the high warming scenario, highlighting the importance of keeping global warming to a minimum level.

CS20-02
Climate change inside terrestrial protected areas worldwide

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Under climate change species ranges are dislocated and resized; species migrate poleward and towards higher elevation tracking suitable habitats. Biotic interactions and community assemblages are thereby modified rapidly, with uncertain consequences for ecosystem integrity. When species are forced to emigrate from protected to unprotected areas to track suitable habitat under climate change, species are particularly threatened with extinction and protected areas may lose conservation value, i.e. importance. Here we individually assessed the proportion of disappearing and novel climate inside 137,432 terrestrial protected areas until the year 2070. The protected areas considered in this study represent 99.9% of the world's protected area. The uncertainty of both climate change metrics was quantified including ten Global Climate Models, and Representative Concentration Pathways RCP 4.5 and 8.5. Locally novel and disappearing climatic conditions in protected areas differ considerably between the Erath's biomes. Moreover, protected area characteristics such as size, elevation, topographic heterogeneity, human pressure and biotic uniqueness were used to estimate the climate change-vulnerability of these protected areas. Future conservation action must focus on highly climate-vulnerable areas as well as areas of high conservation value now and under climate change. Climate-proof conservation strategies are needed. Our study informs climate-smart conservation policy for the local to global extent.

CS20-03
Did climate change in the past lead to increased extinction risk of mammals?

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There has been a long and acrimonious debate in the literature about the role of climate in driving extinction in mammals. This exchange has been particularly volatile in regards to the terminal Pleistocene megafauna extinction, which resulted in the loss of all mammals over 600 kg in the New World, including mammoth, mastodon, camels and horses. While this event coincided with rapid climate shifts and ecosystem reorganization in the Americas, it was asynchronous with climate in Australia and few extinctions occurred in the Old World. Thus, whether climate had a role in driving terminal Pleistocene mammal turnover remains unclear. Climate change is not novel in the Earth system; certainly, the Cenozoic experienced large-scale swings in temperature and aridity. Here, we employ an expanded perspective: using the mammal fossil record and paleotemperature proxies, we examine the influence of the global climate state, climate variability and climate changeon mammalian turnover and extinction selectivity over the entire Cenozoic. We find no evidence of higher (or lower) extinction rates with climate shifts, nor was there any evidence that larger (or smaller) bodied sized mammals were differentially affected. Our results argue that climate change in the past was not a key driver of extinction in mammals. While climate shifts probably led to changes in abundance, distribution, and morphological adaptation, most mammals were able to cope with the changing environments of the Cenozoic through these mechanisms.

CS20-04

Contemporary climatic analogs for 540 North American urban areas in the late 21st century

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A major challenge in articulating human dimensions of climate change lies in translating global projections of temperature and precipitation into local vulnerability assessments that convey the implications of climate change in intuitive ways. Climate-analog mapping involves matching the expected future climate at a location (e.g., a person's city of residence) with current climate of another, potentially familiar, location - thereby providing a place-based assessment of climate change that is broadly interpretable. For 540 urban areas in North America, we used climate-analog mapping to identify the geographic location that has contemporary climatic conditions that are most similar to each urban area's expected climate by 2080. We find that for business-as-usual emissions (RCP8.5), climate of North American urban areas will shift considerably to become, on average, most like the contemporary climate of locations 928 km away and mainly to the south, with the distance, direction, and degree of similarity to the best analog varying by region and future climate scenario. However, for many urban areas we found substantial differences between future climate and the best contemporary climatic analog, underscoring that many cities could experience novel future climates with no modern equivalent in the study domain. In addition to providing an intuitive means of raising public awareness and informing adaptation strategies, our results suggest that through interactions with infrastructure, resources, and human health, climate change will profoundly alter urban environments.

CS20-05

Shrubs constructing tundra soils

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Tundra biogeography is changing, as shrubs are significantly expanding their distribution towards higher latitudes and altitudes. In a dwarf shrub dominated tundra, we examine the impacts of shrubs on tundra soil conditions, namely soil moisture, soil temperature, and soil organic matter. As resources and direct drivers of tundra ecosystem functions, these soil factors are vital for the growth and distribution of tundra flora and fauna.

Our *in situ* data are collected from 1100 plots located in northern Fennoscandian mountain tundra. In addition to shrub cover and height, the data consist of soil conditions and snow depth measurements from two consecutive years. The soil conditions studied here are soil moisture level and change, summer and winter soil temperature, and soil organic matter analysed from both organic and mineral layers. We aim to control the influence of other environmental factors on soil conditions, such as climate and topography, by using high-resolution LiDAR (Light Detection and Ranging) based variables and structural equation modelling (SEM). SEM enables building a hypothesis based model, which takes into account the hierarchy as well as the direct and indirect relationships in our study system.

Observational studies are valuable for understanding tundra vegetation dynamics and their consequences on the surrounding ecosystem, as the dynamics may alter tundra carbon and water cycles. To the best of our knowledge, this is the first study investigating the impacts of dwarf shrubs on multiple soil conditions. This will shed light on how shrubification may affect the ecosystem foundations in dwarf shrub dominated tundra.

CS20-06

Interactive effects of climate warming and invasive pests on European forest carbon storage

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In view of a warming world carbon storage has become an increasingly important ecosystem service. In forests, carbon storage capacity depends, among other factors, on disturbance regimes which are, in turn, likely to be altered by different components of global change. Among these components, the human-induced spread of non-native pests may have strong, yet hardly explored effects. Here, we use a combination of species distribution and carbon cycle modelling to evaluate, first, the potential consequences that invasion by five different, non-native forest pest species (2 beetles, 1 nematode, 1 fungus and a *Phytophthora* from the Oomycota group) may have on European forest carbon storage; and, second, how different scenarios of climate warming may change pest invasion patterns and hence, indirectly, forest carbon storage capacity. We find that invasive pests could trigger massive reduction of carbon storage potential, though variability among species and geographical regions is pronounced. Importantly, potential negative effects of the invaders are rising under climate change either because the pests' climatically suitable ranges increase, or because these suitable ranges match the distribution of their host tree species more closely. Taken together, these results raise concern about negative feedback loops triggered by the interactive effects of climate warming and invasive pests on European forest carbon storage capacity.

CS20-07

The relationship between extinction and climate change in space and time

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How climatic variation affected past extinctions is a crucial question for understanding the role of climate in shaping biodiversity patterns, but has rarely been assessed quantitatively. Here, we use marine bivalves as a model system to identify the key mechanism(s) linking global and regional extinctions to climate variation in space and time. We analyzed the temporal variation in global ocean temperature and bivalve genus extinction throughout the Cenozoic. We found that bivalve extinction rate was strongly influenced by the rate of climate change, while the direction of climate change (warming versus cooling) and the climatic condition in itself (mean temperature) were less relevant. When comparing extinction rates across space, we further found that regions that experienced greater net changes in temperature since the Pliocene suffered great (regional) extinctions. However, a higher extinction rate did not necessarily lead to a higher diversity drop, if the spatial configuration of the climatic conditions, e.g. a shallow temperature gradient along a coast, allowed a fast recovery, via evolution and geographic range expansion. Our findings collectively highlight the importance of considering climate (and biodiversity) as dynamical in space and time, as assessments based on static pictures of the climatic conditions cannot capture the full impact.

CS20-08

Climate warming accelerates the increase in plant species richness on mountain summits

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The Earth system is impacted by accelerating anthropogenic change. Mountain summits experience some of the highest rates of warming with upward migration of species in mountains as direct expected ecological responses. We analysed repeated plant surveys from 302 mountain summits across Europe, spanning 145 years of observation, to assess the temporal trajectory of mountain biodiversity changes. We find a continent-wide acceleration in the rate of increase in plant species richness. This acceleration is a direct and immediate response to the acceleration in the rate of temperature change observed on all studied mountain regions, while other global change determinants, such as changes in precipitation and nitrogen deposition cannot explain the rate in species richness increase. The accelerating increases in species richness on mountain summits across this broad spatial extent aligns with globally accelerating trends in societal development and human environmental impacts since the mid-twentieth century known as the Great Acceleration.

POSTERS

BA-01

Use of fuzzy logic for distribution modelling of the risk of zoonotic-disease

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The study of infectious-disease risk areas is essential for designing prevention and management programs, and for understanding the factors contributing to pathogen spillover. Models describing the geographic distribution of zoonotic diseases are usually based on macroecological and human factors, and only recently the distributions of potential animal reservoirs have been considered, together with the environment, as predictor variables. However, risk areas may be determined by an extremely complex assemblage of agents whose particular contributions should be differentially calibrated in the models: 1) the history (in biogeographic terms), which is able to constrain the occurrence of a disease to certain regions of the globe; 2) the complexity of the zoonotic component, shaped by often undefined reservoirs and vectors that can either modulate the extent of the risk or constitute strict limiting factors; 3) the changing nature of factors shaping the current distribution of risks, as a consequence of globalization. Here we introduce a conceptual framework from which complex risk models can be built, through sequential steps of model integration and recalibration sustained on fuzzy logic operations. We use the risk for dengue and yellow fever as case studies. Both diseases share critical geographic particularities: 1) transmission between humans mediated by Aedes mosquito species coexist, in some regions, with spillover events from primates through a wider mosquito complex; 2) pathogens' global ranges are narrower than the extent of their vectors' distributions; 3) vectors and pathogens are currently subject to expansion toward regions previously free of disease.

BA-02

Intact but empty forests? Patterns of hunting-induced mammal defaunation in the tropics

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Tropical forests are increasingly degraded by industrial logging, urbanization, agriculture and infrastructure, with only 20% of the remaining area considered intact. However, this figure does not include other, more cryptic but pervasive forms of degradation, such as overhunting. Here, we used an unprecedented database of 3,281 mammal abundance ratios in hunted and unhunted areas to model and project the spatial distribution of hunting-induced mammal defaunation at a pantropical scale. We estimated an average abundance decline of 13% across all tropical mammal populations, with medium- and large-sized mammals predicted to suffer more severe abundance declines (27% and 42%) than small-sized species (5%). Mammal populations are overhunted (i.e. declines of at least 10%) in ca. 50% of the pantropical forest area (14 mill. km^2), particularly in West and Central African countries. We further found that 20% of the protected areas and 9-11% of the intact forests and wilderness areas, respectively, and are overhunted when the full mammal assemblage is considered. Yet, large-sized mammal populations are overhunted in more than half of the intact forest area, thereby jeopardizing the multiple ecosystem functions and services provided by intact forests. The pervasive effects of overhunting on tropical mammal populations call for a systematic consideration of these impacts in (large-scale) biodiversity assessments and underscore that forest coverage alone might not be a good proxy of ecosystem intactness.

BA-03

Can agricultural intensification explain a successful colonization? An example in Mediterranean citrus orchards

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Agroecosystems are considered a basic habitat for an important part of native Mediterranean biodiversity. However, the recent implementation of new productivity techniques has been modifying intensively these habitats. An example of this effect can be observed in the general decline of many bird species linked to different kinds of field. On the other hand, little is known about the potential effect that these changes can produce on attracting generalist native species capable to thrive in a wide range of environmental conditions. In this work, we studied the colonization of citrus orchards by two species, a medium sized bird, the common magpie *Pica pica* and a small mammal species, the garden dormouse *Eliomys quercinus*. The study area corresponded to an intensively managed orange plantation located in Sagunto (Eastern Spain), near the Mediterranean coast which has been studied since 1975. During this period bird populations were monitored by the method of constant nest search whereas dormouse presence was assessed by a combination of tree nest search and the regular checks of nest-boxes. We reported the first evidence of dormouse presence in 1999 meanwhile first magpies were found in 2006. Both species showed an important population increase after their arrival to the orange groves. This successful colonizing process was explained by the capacity of these species to adapt to new conditions such as the loss of vegetation cover, the soil compaction, the decrease in water availability caused by the change of irrigation system and the generalized use of biocides.

BA-05

Potential geographic distribution of Oligoryzomys flavescens (Rodentia, Cricetidae) as hantavirus reservoir host in Uruguay

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New World hantaviruses (Hantaviridae, Bunyavirales) may cause a severe respiratory illness called hantavirus pulmonary syndrome (HPS) with a mortality rate in humans up to 40%. They are zoonotic viruses which in America are carried by rodents of the Cricetidae family, as the only source for human infection. Oligoryzomys flavescens is classified as a complex of species whose distribution comprises part of Argentina, Brazil, Uruguay and Paraguay. In Uruguay, virologic studies on the rodent hosts and circulating viral lineages showed that HPS cases were mostly concentrated in the Southern region of Uruguay and that the main reservoir host is the yellow pigmy rice rat (O. flavescens). There is no vaccine or specific therapy for HPS, thus, knowing the favourable zones for the hantavirus reservoir host contributes with relevant information for prevention. From a set of variables related to space, topography, climate, land cover and anthropogenic factors, and the records of hantavirus positive-negative O. flavescens we applied the favourability function to estimate the risk areas for HPS cases in Uruguay. The annual average precipitation of less than 1345 mm was the most relevant variable explaining the range of infected O. flavescens. The resulting model pointed out that the favourable areas for the rodent host are located in Southern Uruguay, therefore indicating this region as the area of highest risk for HPS. Our approach integrated microbiology and biogeography methods to understand the distribution pattern of the main hantavirus rodent host and to contribute to determine the risk areas for new HPS cases.

BA-06

Biogeographical, multi-dimensional approach to analysis of relation between land use and surface water contamination: case study from the Baltic Sea basin to the Pilica River catchment

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The world is faced with problems related to quality and quantity of surface water resources due to extensive industrialization, increasing population density and a highly urbanized society. Export of nutrients to rivers and coastal zones driven by human-related activities is a major problem in river catchments and coastal marine ecosystems. The intensified anthropogenic input of nutrients, especially phosphorus (P) and nitrogen (N), to the environment and landscape from point and diffuse sources resulted in the spatial variation of the riverine nutrient export, which has been observed worldwide.

The aim of the study was biogeographical, multi-dimensional analysis of influence of land use on water quality – from the Baltic Sea basin scale – to the scale of the Pilica River catchment.

The Baltic Sea drainage basin comprises 1,720,270 km^2 in which the southern and south-western parts of the Baltic Sea basin include areas with intensive agricultural activity and others with high population density. Whereas the Pilica River catchment, which is 9258 km^2 in area and is located in central Poland (the Baltic Sea basin) in which agricultural lands account for more than 60% of its total area, and forests cover about 31% of the catchment. The remaining area consists of urban areas and other forms of land use.

The research was conducted within the framework of the following projects:

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BA-07

Forest mesophication in modern forests of New York State in relation to soil drainage and distance from Native American villages ca. 1700 CE

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Mesophication, the replacement of sun-loving fire-tolerant tree species with shade-tolerant fire-intolerant trees species, has occurred across much of the eastern USA between pre-Euro-American settlement and present. There are two main hypotheses for mesophication: loss of Native American burning upon Euro-American settlement, and reduction of drought incidence since the late-1700s. We evaluate those hypotheses using tree-data collected from 124 old-forest plots in 50,000 km^2 of New York State. Plots were selected to vary soil drainage, precipitation, temperature, slope aspect, and distance from Native American villages ca. 1700 CE. In each plot, 16 trees were recorded, four in each of four DBH classes. Species were categorized by tolerance for fire, drought, shade, temperature, and food source for Native Americans. The dominant tree species in the >40cm DBH class was *Quercus rubra*, and in the smaller DBHclasses was *Acer saccharum*. Mesophication was detected when comparing the characteristics of the >40 cm DBH trees and the 1-14.9 cm DBH trees using paired t-tests: larger trees were more useful as Native American food, more drought tolerant, more fire tolerant, contained more oak, and were less shade tolerant. There was no evidence, however, that mesophication varied across soil drainage classes. Multiple regressions indicate that species fire-tolerance was highest in sites closer to Native American villages, with faster soil drainage, higher temperatures, higher precipitation, and northerly aspects. Within soil drainage classes and for different tree DBH classes, Spearman correlations generally suggest higher abundance of fire-tolerant species closer to Native American villages.

BA-08

From reintroduction to expansion: Red squirrels (Sciurus vulgaris) colonizing urban areas in the south of Spain

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The Red squirrel is a species that came to populate historically the entire Iberian Peninsula. However, more recently the species disappeared from different areas and, currently, in Andalusia region (south of Spain) there are currently only two important populations: Sierra Nevada and Sierra de Cazorla y Segura. In the seventies the species was reintroduced in the province of Malaga (southern Spain) with the release of a few specimens in the Montes de Malaga Natural Park. Forty years later, the Red squirrel is a frequent species that has expanded its distribution area outside the Natural Park, reaching the green areas and other forest nuclei of the Malaga city. Here we present a first approximation to the current distribution of the species in Malaga. We analyze its potential distribution area through favorability models and we determine the environmental factors that have driven the expansion of the species. The presence of forest stands (mostly pines) in the urban environment and the climatic stability of the area are the main factors involved in the expansion of the species, which still has areas to colonize in the southernmost region of mainland Spain.

BA-09

Global pathogeography of dengue fever

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Dengue fever is a viral disease transmitted by mosquitoes *Aedes* in two geographically overlapping cycles: the "urban" cycle, from human to human and transmitted by *A. aegypti* and *A. albopictus*; and the "jungle" zoonotic cycle, in which the virus can be transmitted from primates. The dengue fever has experienced a historical spread from southern Asia to America and Africa; since 2010, cases derived from local transmissions have been also recorded in Europe, where *A. albopictus* is spreading with alarming speed. We present a biogeographic analysis of risk areas for dengue, based on worldwide cases reported after 2000. The output is a risk map based on the geographical convergence of favourable spatial and environmental conditions for both vector presence and virus transmission. Recent changes in the global range of vectors and disease are considered through the analysis of factors able to explain new spatial trends during the 21st-century respect to 20th-century distributions. By including *Aedes* distributions as limiting factors in our models, we corroborate that risks for new outbreaks are significant in areas currently free from reported cases; and that some outbreaks could have been mistakenly reported as endemic. Results show that some primate populations could increase significantly the chances for dengue fever outbreaks in forested areas.

BA-10

Insect and disease threats to United States tree species and geographic patterns of their potential forest impacts

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Diseases and insects arguably pose the most destructive threat to North American forests. Recently, exotic and native insects and diseases have wreaked extensive ecological damage and caused billions of dollars of economic impacts. As part of an effort to identify United States tree species and forests most vulnerable to such epidemics, we compiled a list of up to the five most serious insect and disease threats for 419 United States tree species and assigned a severity rating for each of the 1378 host and insect/disease combinations. We then combined this list with data from a spatially unbiased and nationally consistent forest inventory to assess potential ecological impacts of insect and disease infestations. Specifically, potential host species mortality for each host/agent combination was used to weight species importance values on 133,000 Forest Inventory and Analysis plots across the conterminous 48 United States which, when summed on each plot, represent an estimate of the proportion of existing importance value that could be lost on the plot. Plot estimates were then used to identify statistically significant geographic hotspots and coldspots of potential forest impacts associated with insects and diseases in total, and for different agent types. We found potential impacts could be greatest in the northern Rocky Mountains, along the Pacific Coast, and in the Northeast. Markedly different patterns were evident for insects than for diseases, and for exotic versus native insects. These results should be valuable for decision-makers determining where to target for monitoring efforts and pro-active management activities.

BA-11

Extreme events and their influence on the contemporary distribution of genetic variation

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Extreme events, including environmental perturbations, disease outbreaks, and mass mortalities are increasing in frequency. The increase of these stressors on populations can have a number of consequences, including population declines, extinction, range shifts, and evolution. With an increase in genetic monitoring of wild populations and accessibility and affordability of genomic techniques, we are beginning to accumulate the data necessary to better understand the genetic responses of natural populations to such extreme events. Recent mass mortalities in marine species have gained notable attention for their severity. We explore in detail the ecological and genetic consequences of two extreme events — which differed in their magnitude, duration, and geographic extent — on a suite of marine invertebrate species to better understand the roles that life-history, demography, and microevolution play in restructuring (or not) genetic diversity across space and through time. We find species with high dispersal potential and large population size tended to recover more rapidly than species with low dispersal potential and small population size. A keystone species with approximately 80% mortality showed evidence of recolonization, evolutionary rescue, and nearly zero loss in genetic diversity. Brooding species are yet to recolonize large stretches of coast. In a time of unprecedented rapid climate change, it is important to identify the factors that contribute to the vulnerability and resilience of diverse species to stressors arising in the Anthropocene.

BA-12

Range-restricted species are disproportionately more vulnerable to local extinction for habitat loss

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More localized species are at higher risk of extinction. In addition, more localized species tend also to have lower mean local abundances and occur more aggregated. Therefore it could be that more localized species also become locally extinct under much lower levels of habitat loss than widespread ones. Here we address this hypothesis by exploring (i) changes in the range size frequency distribution of plant communities before and after habitat loss and (ii) the relationship between range size and the probability of persisting increasing local habitat loss.

For this, we calculate species' ranges and reconstruct time series, using distribution data on vascular plant species from major international biodiversity data-sharing networks and the most recent historical land use reconstruction data for the late Holocene.

We found a systematic decline of small-ranged species and a gain of widespread ones in plant communities after habitat loss. Moreover, small-ranged species were already vulnerable to little habitat loss; their chance to persist decreased almost linearly with the proportion of local habitat remaining. On the other hand, almost all of the most widespread species persisted even near complete local habitat loss.

We conclude that habitat loss may not necessarily spell doom for many wide-ranging species. However, since small ranges dominate, the higher local extinction risk of range-restricted species and their replacement by widespread ones may inflate biodiversity loss and drive the homogenization of the global flora at already initial levels of habitat loss.

BA-13

Drone-based remote sensing for cross-scale integration of spatiotemporal vegetation dynamics

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Two main challenges hamper our current ability to understand and predict vegetation dynamics: non-equilibrium dynamics and scale dependency of patterns and processes. Currently, knowledge gaps exist on the scale at which drivers and processes act and interact. These gaps exist because of a lack of data, linking locally observed changes in plant communities and its individuals to species wide responses globally. Much ecological inference on the drivers and magnitude of vegetation change is currently based on either local field-based observations, with limited spatial extent, or broad-scale assessments of patterns based on macroecological approaches or satellite based remote sensing. Vegetation change initially manifests itself at the scale of individual plants and both approaches are suboptimal for capturing fine-scale dynamics under rapid environmental changes in the Anthropocene. Ultrahigh resolution data obtained from Unmanned Aerial Systems (UAS or drones) has the potential to close this data gap and to improve our ability to gain new insight on the drivers of vegetation dynamics in space and time. We provide an overview of how drone-based remote sensing can be used for cross-scale integration in ecology and to improve our understanding of spatiotemporal vegetation dynamics.

BA-15

Biota dynamic near the northern edge of the forest-steppe zone in Central Russian plain

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Aim: to assess a biota modern dynamic near the northern edge of the distribution of steppe ecosystems. Location: Central Russian plain, Tul'skaya, Moskovskaya, Ryazanskaya Oblast's. Methods: Field observations on vascular plant, insect, and bird distribution; retrospective analysis of land cover, vegetation cover, and distribution of plant and animal species (using field data, remote sensing, and historical maps). Results. Over the last century, the northern edge of the forest-steppe zone is stable. To the north of this zone, broad-leaved forests after logging are often replaced by self-replicating small-leaved forests, usually existing as small groves with a small number of broad-leaved trees. Many birds, especially birds of prey, have become rare. Some insect and plant species have spread to the north of the forest-steppe belt in small extrazonal steppe sites. New extrazonal steppe sites have not been identified. We assume that the broad-leaved forests have degraded both due to the leveling of the canopy in the cutting areas, and due to the reduction in the size of the groves, which leads to the drying of the microclimate. Global warming has increased this effect. At the same time, despite the warming and drying up of the climate, the steppe ecosystems do not extend to the north, because there are no corresponding soils there. Reducing the number of birds of prey reduces their role in ecosystems. As a result, at the belt to the north of the forest-steppe zone, when climate changes, an azonal biota is formed with a reduced ability to self-regulation.

BH-02

More potential biodiversity hotspots: insight from herbivorous drepanosiphine aphids

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Invertebrates have been greatly neglected in currently recognized global biodiversity hotspots which were generally inferred from the species richness and endemism of vertebrates and vascular plants. In this study, based on 4322 occurrence records of 524 species, we investigated the diversity pattern of the drepanosiphine aphids (Insecta: Hemiptera: Aphididae) and reassessed the global biodiversity hotspots. Using parsimony analysis of endemicity (PAE), NDM/VNDM and the weighted endemism methods, twelve areas of endemism were identified, nine of which were found in the Northern Hemisphere and congruent with the species richness centers. All of these diversity centers were located in mountain areas, islands and peninsulas. Seven centers fell within current global biodiversity hotspots, suggesting that the plants in these hotspots have served as umbrella species for the phytophagous insects and are beneficial for maintaining their diversity. In addition, outside of these hotspots, the southwest of Changbai Mountain–the Korean Peninsula, the coastal region of Central China, Taiwan Island, the central Rocky Mountains and the north of the Appalachian Mountain region were found to harbor high aphid species richness and endemism. The richness of the drepanosiphines' specific host plants was very high in these five regions, which was also revealed as one of the key ecological variables affecting aphid species richness by the regression analyses. Our study thereby highlights the necessity and importance of evaluation more different organisms for the identification of more potential biodiversity hotspots and consequently for protecting more biodiversity in the entire ecosystem.

BH-03
Elevational patterns of Trichoptera diversity in Hengduan Mountains

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As one of the global biodiversity hotspots, the Hengduan Mountains are located in the transitional zone between the Qinghai-Tibet Plateau and the low-land region in Southeast Asia. Due to its unique topographical features and climate, many rivers (e.g. Irrawaddy, Salween, Mekong, Yangtze) run through this region, which harbors abundant freshwater species. Trichoptera are widely distributed in mountain streams and sensitive to environmental change, they are worldwide used as indicators of water quality. In order to investigate elevational patterns of Trichoptera diversity and examine how environmental variables (e.g. spatial, topographical and physiochemical) shape Trichoptera assemblages, we collected Trichoptera assemblages in the Hengduan Mountains along an elevational gradient from 1022 to 4381m a.s.l., covering the four main drainage basins in this area. We explored the relationship between taxon richness and elevation and compared the composition of Trichoptera assemblages in these four basins. In addition, we examined the correlations between assemblage dissimilarities and distances (e.g. Euclidean, topography, river network, environmental). Our research provides a basic understanding of Trichoptera assemblage structure in the Hengduan Mountains. Furthermore, determining the impact of environmental variables (e.g. elevation and physiochemical) on Trichoptera distribution will make it possible to predict the response and range of Trichoptera in the future in the face of climate change.

BH-04
Species filtering in tropical Africa: Biogeographical filters shaping the phylogeny tree in the Gulf of Guinea Region

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How species agglutinate in biotas under different spatial setting is essential to understand speciation and extinction processes. However, this topic is better known in temperate regions, but less works has been conducted in Tropical areas.

We pursue the identification of main filters affecting the phylogenetic assemblage of species diversity and to describe their role in one of the highest biodiversity spot in Tropical Africa: the complex including the Gulf of Guinea islands, Mount Cameroon and continental Equatorial Guinea. Particularly, we ask for the contribution of three different biogeographic filters (spatial effects, altitude and sample bias) in the constitution of biotas on a tropical system.

Taxonomy matrix was compiled from 3 complementary databases (*Flora de Guinea Ecuatorial,* Gbif and RAINBIO) containing absence/presence data for 5,116 species. Phylogenetic trees were built following APGIV and PPG classifications. Gini Index and Mean Phylogenetic Distanc index were used to measure the structure of the different territories. Chao and RE indexes were used to test the effect of sampling bias on filters.

Most diverse places showed more imbalanced and uneven structure in their biotas. No relation with area or altitude but with number of species was found.

Removing basal branches produce more imbalanced phylogenies that accumulated nodes predominantly at the base. The effect is specially found in small islands, were the relation between seed plants and ferns is more balanced.

Dissimilarities in sampling effort may affect not only species richness in the areas but also phylogenetic structure being small territories more sensitive to sample effort.

BH-05

Population divergence across the Isthmus of Kra biogeographic break.

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Southeast Asia is recognized as a region of very high biodiversity, much of which is currently at risk due to habitat loss and other threats. Sundaland and Indochina are two of the four biogeographic regions in this area. Sundaland is separated from Indochina by the transition from rainforest to more seasonal forest at the Isthmus of Kra. This biogeographic break has been defined based on the distributional limits of many species. Although the majority of species have their limit around it, there are some widespread species that are distributed both north and south of Kra. In this study, we test if the pattern observed in species distributions (turnover at the Isthmus of Kra) is mirrored within species that are distributed across it. To achieve this, we look at neutral genetic variation (mitochondrial genomes and several nuclear markers) of the following small mammal species: *Hylomys suillus, Crocidura fuliginosa, Tamiops macclellandii, Callosciurus caniceps, Dremomys rufigenis, Maxomys surifer* and *Leopoldamys sabanus*. These species have different evolutionary histories, ecology, dispersal capabilities and life histories. Patterns common to these species likely indicate a deep and widespread pattern. Our preliminary genetic data indicate deep levels of divergence which are geographically consistent with the Isthmus of Kra, and suggest that a taxonomic study to review their specific status is warranted.

BH-06

Geographic pattern of self-incompatibility in prickly sow-thistle (Sonchus asper) in the Mediterranean

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The prickly sow-thistle (*Sonchus asper*) is a common weed distributed worldwide, whose invasiveness seems to depend on high seed production ability by self-fecundation. However, in the botanical literature some taxonomic descriptions of morphotypes bearing large, attractive capitula in the Mediterranean can be found. The analysis of the variability in the sexual system of the species throughout this region, by means of experimental crosses in the greenhouse, clearly distinguishes the presence of two groups. One of them include annual, biennial or perennial plants with estimated population self-incompatibility index (ISI) = 0.71-0.93 (mainly outcrossed). It is the predominant form across the central and eastern area of the northern Mediterranean and is also common in mountainous areas of the southern side of the basin. The other group include populations with ISI ≃ 0 (predictably autogamous) and exclusively comprises annual plants. It is present throughout the whole region, although is quite rare in the eastern side, being the single form in the Iberian Peninsula and western France. As expected, the differences in sexual system are significantly related to the variability in florets size, whose more significant features, e.g. ligule length and width or anther size, show bimodal distribution in the region with a clear geographical pattern. These findings indicate the need of a taxonomic revision of the species complex and allow us to propose these challenges: 1º) elucidate the incidence of self-incompatible morphotypes in the *S. asper* invasive populations and 2º) disentangle the phylogeographic relations within the Mediterranean.

BH-07

Phylogeography of prickly sow-thistle complex (Sonchus asper) in the Mediterranean

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Although *Sonchus asper* is commonly considered a typical annual, self-pollinated weed, it has been shown recently that also comprises self-incompatible large flowered morphotypes in the Mediterranean, often with biennial or perennial life cycles. That reveals that the species actually constitute a taxonomic complex that requires systematic revision and biogeographic analysis. Phylogenetic trees obtained using nrDNA ITS/ETS sequences separate two clades that clearly differ in flower size and sexual system. Bayesian clustering of AFLP fragments also discriminates small and large flower groups; in addition, it separates three clusters of plants with large flowers that show differentiated ecological ranges and well-defined distribution areas. The three clusters are highly inter-fertile, which seem to reflect preliminary speciation processes by ecological differentiation within the lineage. Interestingly, these large flowers morphotypes conform in morphology to some taxa previously described during XIXth century. The analysis of variability in noncoding cpDNA (i.e., *ndh*J-*Tab*E, *atp*I-*atp*H, and *psb*J-*pet*A) indicates that perennials retain the highest diversity in cytotypes of the complex and, in agreement with the topology of phylogenetic trees, are probably basal. It is proposed that the centre of origin for the complex is located in the southern side of the Mediterranean basin. The expansion to the north of the large flowered lineage was probably facilitated by an old connection across Sicily and during the process some isolation on the Balkan Peninsula took place. The small flowers forms seem to be little diversified in the Mediterranean and probably diverged early in the history of the complex.

BH-08

Dinaric karst subterranean diversity: old relicts in a highly dynamic environment

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The Dinaric karst, which covers the western part of the Balkan Peninsula, is a global hotspot of subterranean biodiversity. Spiders of the family Dysderidae are among the most conspicuous creatures in Dinaric caves, where they are represented by eight genera, two in the subfamily Harpacteinae (*Stalagtia* and *Folkia*) and five in Rhodinae, (*Rhode*, *Stalita*, *Mesostalita, Parastalita* and *Stalitella*), adding up to a total of 21 species. All these species are Dinaric endemics, and almost all are troglobiotic (obligatory cave dwellers). The two subfamilies show near disjunct distributions in the region, Harpacteine are restricted to the south part of the Dinarides and Rhodinae (with few exceptions) to the north part. With the aim of providing an explicit phylogenetic hypothesis of the family, we conducted a mutli-locus phylogenetic analysis combining mitochondrial and nuclear genes (COI, 16S, 28S and H3). Our results revealed a more complex taxonomic structure than currently recognized, and uncovered major overlooked diversity at the species and generic levels. Quantitative species delimitation methods confirmed the existence of many potentially new species, and revealed high levels of cryptic diversity within Harpacteinae. We further estimated divergence times using a combination of fossil and biogeographic node calibrations and reconstructed the biogeographic history of these spiders. All cave lineages showed a common pattern of long stem branches, which may hint at high levels of extinction in the history of these groups. We

hypothesize that Miocene climatic changes may have played a crucial role in shaping the extant diversity of these cave-dwelling dysderids.

BH-09

Intra-clade patterns of diversification in Nyctibatrachus, an endemic anuran genus from the Western Ghats, India

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Studying the phenomenon of biological diversification holds the key to understanding how biodiversity is produced and maintained. Very few studies have investigated the process of diversification among fauna and flora of the Asian tropics. This study makes an effort to address this gap by examining the patterns of diversification in *Nyctibatrachus*, an endemic anuran genus from the Western Ghats, a biodiversity hotspot in India. Sampling was conducted to ensure spatial coverage of the topographic and ecological heterogeneity of the Western Ghats. I obtained a time-calibrated multi-gene phylogeny for *Nyctibatrachus*. I examined the characteristics of lineage, morphological and ecological diversification in this genus by generating lineages-through-time and disparity-through-time plots, and by calculating gamma statistic, morphological disparity index and phylogenetic ANOVA. I recovered two deeply divergent clades within *Nyctibatrachus*, one consisting of lineages predominantly distributed north of the Palghat Gap, a major biogeographic barrier in the Western Ghats, and the other consisting of lineages predominantly distributed south of it. The lineages-through-time plot and gamma statistic provided evidence for an early burst in lineage diversity, while temporal patterns of morphological diversification showed signatures of an initial spurt in body size disparity in *Nyctibatrachus*. However, results for these analyses were less clear at the level of sub-clades within this genus. Additionally, though the lineage diversity of both sub-clades was similar, I observed clear differences in morphological and ecological diversity between these two sister clades. Overall, body size divergence seems to have played a crucial role in generating contrasting patterns of intra-clade diversification in *Nyctibatrachus*.

BH-10

Glaciation-based isolation contributed to speciation in a Palearctic alpine biodiversity hotspot: evidence from endemic species

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Organisms are unevenly distributed on earth and the evolutionary drivers of that have puzzled ecologists and evolutionary biologists for over a century. Even though many studies have focused on the mechanisms of unevenly distributed fauna and flora, there remains much to learn about the evolutionary drivers behind biodiversity hotspots. In the Tibetan Plateau and Hengduan Mountains, a biodiversity hotspot in the Palearctic realm, alpine uplift cannot be the driver for recent speciation (< two million years ago), researchers broadly refer to climatic oscillations driven biodiversity, however, the specific individual roles of glaciation and inter-glaciation periods in promoting biodiversity is unclear. The current study focuses on investigating whether recent speciation between two close-related avian species (White eared pheasant, *Crossoptilon crossoptilon* and Tibetan eared pheasant, *C. harmani*) was driven by glaciation-based isolation or by dispersal during inter-glaciation. To answer this question, we combined Sanger sequencing and next-generation sequencing technology to estimate population structure, phylogeny, divergence time, demographic history and potential historical distributions for *C. crossoptilon* and *C. harmani*, which are endemic to China. We found that the divergence time between these two species and within *C. crossoptilon* are both during glaciation periods. During glaciation periods, both *C. harmani* and *C. crossoptilon* experienced isolated distributions and extreme bottlenecks. The results of this study suggest that glaciation-based isolation contributed to recent speciation in the Tibetan Plateau and Hengduan Mountains, and sheds light on our understanding of the evolutionary mechanisms that contributed to the formation of Palearctic alpine biodiversity hotspots and unevenly distributed species richness.

BH-11
Monitoring Dimensions of Biodiversity in a Mega-Diverse Region of Southern Africa: from Traits to Communities to Ecosystems.

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The Greater Cape Floristic Region (GCFR) of South Africa includes marine and terrestrial biomes with species diversity rivaling mega-diverse tropical rainforests in a compact area (300x700km). Extinction risk studies suggest that GCFR species are among the most vulnerable to climate change over the next 50 years. I present a scoping proposal commissioned by NASA to develop a field campaign to measure and monitor the distribution and abundance of biodiversity with new remotely-sensed data and the rich historical data in this region. I will summarize the central questions to be addressed by this field campaign and lay out the proposed study design to integrate satellite, airborne, and in situ data collection. Our plan centers around the collection of new hyperspectral imagery from AVIRIS-NG, PRISM, and HyTES spectrometers combined with the LVIS laser altimeter. These data will be combined with existing and new observations of community composition and functional traits to enable high-resolution mapping and modeling of several essential biodiversity variables (EBVs) including species distributions, functional traits, and three-dimensional canopy structure. Given the wealth of available independent in situ data available that can be brought to bear, the GCFR is an ideal system to fully evaluate the capabilities of remote-sensing technology to characterize biodiversity patterns across diverse landscapes. In combination with the rich historical data and well-developed ecological understanding in this region, these new observations will enable detailed exploration into the mechanisms of change including the feedbacks from changing biodiversity to regional climate, disturbance, post-fire recovery, freshwater, and other ecosystem services.

BH-12
Proposal of important marine areas for the coral reefs considering genetic EBSA criteria, northward up of their distribution, and ecosystem services.

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Important marine areas defined through EBSA criteria are adopted by the Convention of the Biodiversity (CBD) and mostly evaluated based on the species level information. Including genetic information will adding new axis of the evaluation of EBSA. Here, we focused on the northward migration of the reef-building coral species from the southern part of the Japanese archipelago. The southern reefs of Japan is located on the northern edge of the coral triangle and shows a high species diversity of corals. In the recent years, these reefs are under crisis because of frequent coral bleaching caused by high temperature, bloom of crown of thorns starfish and unremitting terrestrial loads. However, increase of corals in temperate areas is

also pointed out. Thus, in this research we evaluated EBSA using genetic tool and considering future expansion of coral areas under elevated water temperature, connectivity under the present ocean current and genetic connectivity representing past connectivity in the northwest Pacific. The gradient of genetic diversity toward north differed among species. The genetic diversity of *Acropora hyacinthus* decreased but the one of *A. solitaryensis* did not. In addition, a significant genetic break is observed in some species between temperate and tropical regions. It may be caused by a low connectivity via current but the genetic break was more than what was predicted by the modeling of the current. Considering this information, we systematically choose both the southern part of the temperate region and the tropical region as important areas and it partially overlaid with existing protected area.

BH-13

Impacts of 21st century climate change on montane habitat in the Madrean Sky Island Archipelago

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The Madrean Sky Island Archipelago is a North American biodiversity hotspot comprised of ~60 isolated mountains that span the Cordilleran Gap between the Rocky Mountains and the Sierra Madre Occidental. Characterized by discrete patches of high-elevation montane habitat, these ‘sky islands’ serve as stepping stones across a ‘sea’ of desert scrub/grassland. Over this coming century, the region is expected to shift towards a warmer and drier climate. We used climate envelope modelling to predict how the spatial distribution of montane habitat will be affected by climate change. To approximate the current distribution of montane habitat, we built climate envelope models for five high-elevation species (*Ceanothus fendleri*, *Pinus strobiformis*, *Quercus gambelii*, *Sciurus aberti*, *Synuchus dubius*). The resulting models were projected under multiple climate change scenarios—four greenhouse gas concentration trajectories (RCP 2.6, 4.5, 6.0, 8.5) for each of three climate models (CCSM4, MPI-ESM-LR, NorESM1-M)—to generate predicted distributions for the years 2050 and 2070. While the climate models differ with respect to their predictions as to whether effects of future climate change will be mild (CCSM4), moderate (MPI-ESM-LR), or severe (NorESM1-M), they all agree that by as early as year 2050, under even the most conservative greenhouse gas concentration trajectory (RCP 2.6), there will be significant montane habitat loss and increased patch isolation. Our results suggest that under 21st century climate change, the Madrean Sky Islands will become increasingly isolated due to montane habitat loss. This may affect their ability to serve as stepping stones and have negative implications for the region’s biodiversity.

BH-14

Patterns of diversity and endemism in the geometrid moths (Lepidoptera: Geometridae) of the Andean region

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In South America, the Andean region differs from the Neotropical region by possessing a less diverse biota but with a high level of endemism, especially on the western slope of the Andes. Events occurred during Neogene produced a hyper-arid desert at north, and the glaciations affected the south. In this scenario, the vegetation located in high and low latitudes were forced to migrate to mid-latitudes. We analyzed geometrid moths (Lepidoptera: Geometridae) from Chile, a taxon with around 350 species and 80% endemism. We analyze the latitudinal distribution pattern of species richness by evaluating the mid-domain effect (MDE). Besides, we characterize spatial patterns of species richness through ordinary least squares (OLS) and spatial autoregressive (SAR) models and patterns of endemism through endemism analysis (NDM/VNDM). The pattern of latitudinal distribution of species richness reveals a unimodal pattern, with a peak at medium-high latitudes, but not according to an MDE. The model with the best fit that explains the richness of species is given by the climatic variables related to productivity (NPP and NDVI). The areas of endemism recovered account for small areas acting as islands in the north, and areas in both the coastal range and the Andes mountain range. The patterns found are similar to other taxa; however, the Geometridae seem to have a shift towards medium-high latitudes probably because of their affinity to native forests and cold tolerance. Even more, the endemism pattern seems to account a historical process associated with glacial cycles.

BI-01

Estimating the accuracy and biogeographical status of point-occurrence records

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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, soon to be implemented as an R package, for estimating the accuracy and biogeographical status of a given occurrence record 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. This package aims to provide 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.

BI-02

Aureoboletus projectellus (Fungi, Boletales) – an American bolete rapidly spreading in Europe as a new model species for studying expansion of macrofungi

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Aureoboletus projectellus is a bolete native to eastern North America that has recently started to spread in Central Europe and is considered as a potentially invasive species. Maximum entropy approach implemented in MaxEnt was used to estimate distribution of its potential niche in Europe. The obtained model and current data about species' geographic distribution in the European range were combined to predict direction of further dispersal and provide a list of locations requiring monitoring. According to the model, a continuous ring of favourable conditions around Baltic Sea, together with well-established bridgehead in Poland and Baltic states make the expansion in this region virtually unstoppable. The case of *A. projectellus* constitutes an excellent opportunity for testing the utility of employed model in practice and studying the dynamics of alien fungus dispersal process.

BI-03

Marine invasion rates across the tree of life

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Invasions are one of the most significant agents of biodiversity change. However, attempts to synthesize patters across broad taxonomic groups have been hampered by sampling biased and the lack of standardized methodology. The Eastern Mediterranean is receiving a large influx of Red Sea species has followed the opening of the Suez Canal. These invasive species make up a large percentage of total species in this region and have substantially modified its biodiversity. This research focuses on this unique 'natural experiment', to understand the underlying correlated of invasion success across the tree of life, taking into account imperfect detection and variability in sampling effort through time. By statistically controlling for potential biases in detection rate over a wide range of taxa, we are able to show substantial variation in the rates of invasion. Specifically, taxa can be separated into groups, such as fishes, bivalves and algae, that are characterized by a fast and increasing invasion rates and groups such echinoderms, sponges and ascidians that have low and constant invasion rates. We further find that the best predictor of invasion rates is the date in which the first species of the group was seen in the Mediterranean, with taxa that arrived early characterized by high invasion rates. Taken together, we argue that such inter-taxa comparison can shed light into the main life-history attributes and environmental correlates associated with invasion success.

BI-04

Native climatic niche explains establishment success in exotic mammals

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Biological invasions represent increasing threats to biodiversity, ecosystems, but also to human economies and health. Major effort was accordingly put in recent years to better understand why some exotic species fail to establish, but others are successful. Successful exotics have passed several filters: geographic, abiotic and biotic. One key hypothesis in this regard is that, when introduced in a new range, an exotic species initially develops in environmental conditions similar to those in its native range, i.e. within its native niche. Yet, this hypothesis has so far remained largely untested. Here, using a large dataset of 989 introductions of 177 mammal species worldwide, we show with SDM suitability and niche innerness - two indices of the relative position of the introduction sites within the species' native niche - that climate matching to the native niche is a strong predictor of establishment success. The integration of such indices in pre-border risk assessments could improve chances to prevent invasions before introduction, and possibly avoid costly eradications.

BI-05

Assessment of health and vitality of a narrowly distributed habitat in a Mediterranean island, the case of the endemic Cedrus brevifolia forests in Cyprus.

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The habitat type "9590* *Cedrus brevifolia* forests (*Cedrosetum brevifolia*)" is a narrow (290 ha) endemic habitat type of Cyprus, included in the Annex I of the Directive 92/43/EEC, characterised as a priority habitat type. Its exclusive and limited area within the Pafos forest makes it inherently susceptible to many factors threatening its very existence. We focused on the biotic factors altering the survival and the reproductive success of trees, as key drivers of ecological and dynamic processes in this habitat during outbreaks. This survey used 12 sampling plots (0.1 ha) equally distributed among four vegetation types of the habitat type 9590*. Seed predation rates by *Megastigmus schimitscheki* (Hymenoptera: Torymidae) were assessed by X-ray radiography of seeds collected randomly in each plot in 2016. Bark beetle (Coleoptera: Curculionidae) populations were monitored twice a month between April and November 2017 using two baited slit traps per plot. Seed predation rates showed variation between the 12 sampling plots (0–18.6%) but were overall found to be low. The Coleoptera *Orthotomicus erosus*, *Hylurgus ligniperda* and *Aulonium* sp. (a predator of *O. erosus*) were the most abundantly trapped species and displayed a bivoltine cycle between June and November. *O. erosus* is likely to be the most harmful biotic factor to habitat type 9590* as it was found more abundant than *H. ligniperda* in all types of vegetation (cedars and pines), while *H. ligniperda* was restricted to pines. These results provide guidelines for the management of biotic risks in this vulnerable endemic habitat.

BI-06
Understanding plague's niche in native and naturalised regions

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Yersinia pestis is the bacterial agent of plague, the infectious disease responsible for three historic pandemics that repeatedly caused massive human mortality and influenced significant societal change. Plague is now classified as a re-emergent disease with both epidemics and isolated cases occurring with increasing regularity. Currently, plague is distributed across its native region of continental Asia, with naturalised populations across Africa and the Americas. What limits the geographical distribution of plague is still unknown, with a key debate centring on whether it is limited primarily by the environmental niche of *Y. pestis* or by the environmental niche of the hosts. There is further uncertainty regarding the survival of the bacteria during inter-epizootic periods, with environmental reservoirs of plague suggested as a potential explanation. Increasing our understanding of plague's current niche can aid in better understanding pivotal historical events as well as predicting future risk under rapid environmental change. In this work, we use pathogen and host locality data and species distribution modelling to test how pathogen and host niches influence plague's distribution in native and naturalised regions at continental scales.

BI-07
Role of Invasive shrub species on soil nutrients and microbial biomass of chir pine forest in Kumaun Himalaya, India

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Soil microbial biomass constitutes 2- 5% of the soil organic carbon and plays significant role in cycling of nutrient and organic matter dynamics. Globalization has reinforced invasive alien species (IAS) *Lantana camara* and *Ageratina adenophora* to spread in Kumaun Himalaya. They are considered as a threat for plant biodiversity and nutrient cycling. This study concerns about the influence of IAS on soil nutrient and

microbial biomass carbon (C_{mic}) content among invaded and non-invaded sites in three chir pine forests in Nainital district, Uttarakhand.
Soil samples were collected with the help of soil corer from all invaded and non-invaded sites at 0-10, 10-20, 20-30 cm depth interval and their physical, chemical and seasonal biological characteristics were analyzed in laboratory. Values for soil organic carbon, total nitrogen and C_{mic} in *L. camara* (1.5-2.3%, .32-.39%, 440- 660 μg g^{-1}) and *A. adenophora* (1.6-2.2%, .25-.34%, 493-596 μg g^{-1}) invaded sites were found respectively higher than non-invaded sites (1.3-2%, .25-.32%, 423- 557 μg g^{-1}) for 0-10 cm, but no such differences were reported for 10-20, 20-30 cm depth. All sites showed considerable seasonal variation for microbial biomass carbon with maximum value in rainy and minimum in winter season.
It is observed that IAS improve soil nutrient and microbial biomass because of high specific leaf area, elevated leaf nutrient concentration, rapid decomposition and nutrient release from litter than native shrubs. Such changes are likely to cause positive feedback on invasion but further long term studies needed to understand invasion effect on different soil nutrient cycle.

BI-08

MIREN: the Mountain Invasion Research Network

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The Mountain Invasion Research Network (MIREN) has been founded in 2005 in a global attempt to tackle the emerging issue of plant invasions in mountainous regions. Since then, the six original regions have been joined by several additional partners from all over the world, numbering over twenty today. The aim of the network is to understand the effects of global change on species' distributions and biodiversity in mountainous areas, from the equator to the poles. Since the first meeting in 2005, we have expanded our initial focus on non-native plant invasions to a more general study of species redistribution under different drivers of global change, including biological invasions, climate change and land-use change. The main strongholds of the network are globally orchestrated long-term observational and experimental studies along elevation gradients. They allow us to evaluate and quantify the processes and mechanisms that are shaping mountain and cold-climate plant communities. These help us answering our core questions: 1) How are species distributions in mountains changing over time? 2) Which mechanisms influence species redistribution in mountains under global change? 3) What are the impacts of species redistribution on mountain biodiversity and ecosystems? 4) What are effective ways to manage species redistribution in mountains? and 5) What general lessons can we learn from mountain gradients about the process of species redistribution under global change?

BI-09

Towards global scenarios of biological invasions in the 21st century

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Biological invasions substantially affect ecosystems, ecosystem services and human livelihoods alike, and the impacts of species invasions will rise in the future as the rate of establishment of alien species has increased strongly during the last decades with no sign of saturation. Further, they drive species extinctions worldwide and especially in phylogenetically rich regions such as island systems that contribute strongly to global biodiversity, causing high mitigation and adaptation costs. Consequently, different international initiatives and agreements such as the United Nations Sustainable Development Goals (SDG), Convention on Biological Diversity (CBD) and Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) consider the assessment and control of biological invasions as a crucial step to sustain global biodiversity, ecosystem services and human livelihoods. Here, we present a conceptual framework for the development of scenarios and models on how alien species richness and impact might change in the 21st century. This includes the establishment of qualitative scenario narratives and the quantification of pressures and impacts for these narratives. The recent advances in data availability of biological invasions for the first time allows addressing this task appropriately. We believe that the biological invasion scenarios concept proposed here provides an important contribution for understanding - and proactively managing - the future of biological invasions.

BI-10

Extreme high temperature and precipitation seasonality are key climatic filters of invasion-modified biogeography

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Anthropogenic dispersal of alien species is breaking down traditional, native biogeographical boundaries, allowing species to occupy more potential climatic niches in their invaded ranges. Climate has therefore been suggested playing an essential role in explaining invasion-driven reorganization of biogeography. However, what remains unclear is which climatic parameters most account for invasion-redefined biogeography that is crucial for predicting future biogeographical patterns in response to accelerated rates of biological invasions and climate change. Here, based on 361 alien reptiles and amphibians in 271 native and 297 current ranges, we explored the effects of climate average, variability and extreme on the change of global biogeographical patterns by controlling for natural and anthropogenic dispersal of alien species. We revealed that geographic distance, a proxy for natural dispersal barriers, was the dominant variable contributing to native biogeographical patterns. In contrast, bilateral trade, and extreme high temperature and precipitation seasonality, which are two hallmarks of global climate change, explained more unique variations in biogeographical patterns after invasions. Our results imply that human-assisted species introductions may combine with climate change to accelerate the reorganization of global biogeographical patterns in the Anthropocene. Incorporating climate extreme and variability data may help predict range shifts of both native and invasive species and associated biogeographical patterns in response to climate change.

BI-11

Revisiting the distribution of the invasive species agave weevil (Scyphophorus acupunctatus) in Spain and predicting the future spread

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Biological invasions are considered one of the main factors of biodiversity loss on the planet. Currently these invasions are intentionally or accidentally favoured by the increase of trade and long-distance transports in our society. A certain species is considered as invasive when it is transferred through human activities beyond the limits of its native geographic range, and spread unaided within natural communities. The concern for these species is growing worldwide, because they pose a threat to the biodiversity and have a high economic cost associated to their management. This would be the case of the agave weevil (*Scyphophorus acupunctatus*) in Spain. This species feeds essentially on plants belonging to the families Agavaceae and Dracaenaceae, including *Agave americana*, an exotic species typical of the landscape in the Mediterranean basin. It was detected for the first time in Spain in 2007, in Barcelona, suffering a wide expansion throughout the Mediterranean coast. We have done a review of records and updated its distribution. With this new set of presences we have built distribution models to determine the potential areas where this species could stablish in the near future, or it may be already present but undetected. The favourable unoccupied areas may reflect locations highly susceptible for invasion. It seems likely that the agave weevil will continue colonizing new areas. Our results should be considered as a first warning of future expansion, and their use are of special interest for the design of future management plan for this species at the Iberian Peninsula scale.

BI-12

Invader species must favor other invaders

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Some bird species are considered invaders after release or escape from housholds. Monk parakeet (*Myopsitta monachus*) is an invader species with higher population on larger cities of Spain, mainly on Mediterranean coast region and in the central part of Iberian Peninsula. A previous work showed that fruits of date palm (*Phoenix dactylifera*) were the preferred food. An analysis carried out using itineraries in the city of Valencia allowed us to estimate a population of 6040 date palms in the city. Dates are grown in stems that were grouped in bunches. We estimated that each date palm contained (5.1<5.4<5.8) bunches and 76.2 (69.2<76.2<83.2) stems, with (10.7<11.4<12.1) dates per stem. We distributed the date palm in larger (>10g) and small (<10g) fruits. Since we sampled larger and small fruits the population must have contained both types of fruits. With the assumption of variation between 25%-75% of each type the date palm in the City of Valencia produce 274.2-412.7 tons of dates is produced per year. Thus, a plant invader can sustain another invader, monk parakeet. Probably, to promote an invader species (date palm) that is a basic food resource for another invader species (monk parakeet) will be a bad method to move out, in our case the monk parakeet, or at least it does not provide the conditions to evict it.

BI-13

How important is the landscape to supporting plant invasions? Distribution and abundance of invasive plants in a temporally-spatially structured urban-forest landscape

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Biological invasions it is a process of degradation of ecosystems caused by proliferation of alien species. The establishment of invaders is associated to biological traits, although abiotic variables occupying similar indicate that the species establishment may also be mediated by habitat attributes. The surface covered by *Acacia* – one of the principal terrestrial alien groups – in Arouce River (Portugal) has increased extensively, threats seriously the ecosystems. This communication discusses about four main steps of studies which incorporating plant invasion data (species distribution, habitat suitability, land-use history, geo-ecological impacts), showing results of a M.Sc. research project on the *Acacia* in Arouce River Basin (7000 hectares). The research has started developing a spatial-temporal cartography to assessment of landscape structure, using available maps and orbital images, namely 'CAF Portugal' (1965) and 'Basemap' (2014). In the field and using a GIS, was collected species abundance data, through a grid of 200x200 meters and buffers of 5x5 meters. The obtained values to individuals quantity (1831 presence record) by each landscape unit (headwaters, intermediate, terminal), were submitted to statistical treatments. The distribution pattern was determined through cross-validation by Moran's Index (0,28). The invaded area has changed from 55 to 936 hectares, where Acacias is most abundant in the intermediate area than headwaters (1200 meters). The land use most affected by the invasions were pine forests (-15%), and was obtained a positive statistic correlation to abandoned agriculture zones (1,000) and web factors (roads and water bodies), what represent the main areas subject to frequent invasion.

BI-14

Determinants and Impacts of Acacia longifolia Andrews (Willd.) Spread: A Comparative Study Between Portugal and Brazil

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The success of Biological Invasions depends both on the environmental attributes and on biological species features. Invasive species have high biological diversity and in favorable conditions, tend to expand and cover large areas. In Portugal and Brazil, the concern around this subject is recent, and decisions about management of invasive species have been taken without sufficient knowledge, generating negative unforeseen impacts. In this work, we present the phases of an ongoing PhD project that intends to model the distribution and analyze the susceptibility to invasion by *Acacia longifolia*. The tools to be used range from field surveys to laboratory and greenhouse work as well as the use of spatiotemporal models of analysis implemented in GIS Systems. *Acacia longifolia* is a coastal tree native from Southern Australia, introduced in Portugal more than one hundred years ago with the objective of assisting in the stabilization of the coastal dunes. More recently, this species was introduced in Brazil. Through evaluation of environmental attributes (climate/soil conditions, potential species distribution, socioeconomic variables), and biological species features (taxonomic and functional features), we intend to explain the distribution of this species and calibrate the models of analysis. In a second phase, considering the different distribution patterns of species and the specific environmental conditions, we intend to extrapolate the knowledge obtained in modeling the *A. longifolia* in Portugal to predict its future evolutionary behavior in Brazil. This is a rare opportunity to compare the functioning of an invasive species with a global distribution between Mediterranean and Tropical climates.

BI-15

Mechanistic niche approaches allows to explain, rather than to predict, invasive species range distributions.

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Understanding which species traits underlie the invasion success of alien species in order to predict invaders' potential distributions remains a key challenge of invasion biology. Criticisms have been levelled at forecasts of invasion risk derived from correlative distribution models, as they do not explicitly account for the mechanistic links between organism's functional traits and their (climate) environment. Here, we test whether incorporating biophysical, morphological and behavioural processes allows for accurate predictions of invasive species potential range dynamics. For about 20 bird species successfully introduced to Europe, we applied an animal energetics model (NicheMapper) that relies on a set of functional species' traits to solve heat-energy-balance equations, allowing identification of areas within the invader's niche. Invasive range occurrences were then used as an independent validation of our mechanistic model range forecasts. We found that overall, model predictive accuracy was moderate to low, as our invasion risk forecasts were prone to both omission and commission errors. Sensitivity analyses revealed a set of key functional traits strongly influencing model accuracy. For comparatively larger avian invaders, estimates of basal metabolic rates, body temperate and body mass are crucial while for smaller birds, feather characteristics such as feather length and plumage depth are important as well. Our results indicate that complex and parameter hungry mechanistic modelling approaches such as the one applied here may be better suited to uncover processes driving species invasions, rather than for obtaining highly accurate spatial predictions of where invaders are likely to establish.

BPM-01

Global-scale spatial patterns of phylogenetic endemism in birds

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Current geographic patterns of biodiversity are a consequence of the evolutionary history of the lineages that comprise them. Integrating phylogenetic and spatial information to estimate the degree of endemism of evolutionary diversity is an important goal for the management and conservation of biodiversity. There is estimated to be about 10,000 bird species in the world, among are included some of the most endangered species at risk of extinction. This study was aimed at exploring how evolutionary endemism of birds is distributed across the globe. Using comprehensive avian phylogenies and global distributional data for all extant birds, we calculated weighted endemism, phylogenetic endemism and categorical analysis of neo- and palaeo-endemism (CANAPE), using a spatial randomization to assess statistical significance. We found that both species and phylogenetic endemism peak predominantly in tropical and Southern Hemisphere island and montane regions. Nevertheless, some areas such as Amazonia and central Africa harbour more evolutionary endemic diversity than is apparent from the species ranges alone. In general, areas of significantly high levels of paleo- and neo-endemism agreed at global scale, and were concentrated in the Andes and Himalaya Mountains, Central America and Caribbean Islands, Southeast Asia and the Malay Archipelago, and East Australia. These areas posse a high value for conservation as they imply localized processes of avian recent diversification, which could be ongoing, and concentrations of relictual taxa of high historic value that at the same time have high avian genetic and functional diversity, providing sources of resilience when facing uncertain future scenarios.

BPM-02

Global patterns of lake plants between two metacommunity levels

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Biogeography and metacommunity ecology are two disciplines that share interests in investigating how historical events, dispersal, biotic interactions and environmental filtering structure biological communities at broad spatial and temporal extents. However, much uncertainty still exists in our understanding of the role of historical and climatic influences on local communities over broad extents, due in part to the lack of comparable data over large areas. Thus, we studied community-environment relationships of lake plants at two metacommunity scales using data from 16 regions across the world. More specifically, we examined a) whether the lake plant communities respond similarly to key local environmental factors, major climate variables and lake spatial locations in each of the regions (i.e., within-region approach), and b) how well can explained variability in the community-environment relationships across multiple lake plant metacommunities be accounted for by elevation range, spatial extent, latitude, longitude and age of the oldest lake within each metacommunity (i.e., across-regions approach). We found that niche filtering related to local lake-level environmental conditions was the dominant force structuring aquatic plants within metacommunities. However, our results also revealed that elevation range associated with climate (increasing temperature amplitude affecting macrophytes) and spatial location (likely due to dispersal limitation) was important for aquatic plants based on the findings of the across-metacommunities analysis. These findings suggest that different determinants influence aquatic plant metacommunities within different regions. Moreover, our study emphasized that the use of a single metacommunity scale gives incomplete information on the environmental features explaining variation in aquatic plant communities.

BPM-03

Application of monitoring tools and spatial modelling techniques for the management and conservation of threatened fauna: The case of the Dja Forest Reserve in Cameroon.

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In the tropical forests of Africa there are numerous protected areas (PAs) that are seriously threatened as a consequence of human activity. Tools are therefore needed to enable the management and conservation of wildlife within PAs. SMART (Spatial Monitoring and Reporting Tool) software allows gathering information on the presence of fauna and threats directly in the field. We analysed these data using the Favourability Function (FF) spatial modelling technique in the Dja Forest Reserve (DFR), in Cameroon, to generate risk maps for three threatened species: Western lowland gorilla (*Gorilla gorilla gorilla*), chimpanzee (*Pan troglodytes*) and African forest elephant (*Loxodonta cyclotis*). Our results show how the monitoring carried out by the rangers of the reserve and the use of this information in the generation of risk models constitute a rapid assessment tool to be used in the management and conservation of fauna of interest in the DFR. Finally, we concluded that the methodological tools provided in this study may be applicable to any other PA for conservation purposes.

BPM-04

The richness - heterogeneity relationship depends on the spatial configuration of the environment

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The positive relationship between environmental heterogeneity and species richness is a fundamental ecological pattern. In recent years, however, it was suggested that this relationship is unimodal rather than linear due to a tradeoff between environmental heterogeneity and population sizes, which increases local species extinctions at high heterogeneity levels. The prevalence of the unimodal richness – heterogeneity relationship was confirmed in both empirical and theoretical studies. Yet all previous studies were based on a single aspect of heterogeneity, environmental composition, whereas heterogeneity is also characterized by environmental configuration. Here, we used a spatially explicit meta-community model to quantify the effects of both environmental configuration (random, gradient, or patchy environments) and environmental composition (the range of a given environmental variable) on species richness. Given that species characteristics are known to affect the richness – heterogeneity relationship, our models also accounted for species' niche breadth and immigration rates. We found that environmental composition and environmental configuration had interactive effects on species richness, which in turn were affected by species' niche breadth and immigration capabilities. Across all parameter combinations, the richness – heterogeneity relationship was unimodal, but the patterns of the unimodal curve differed significantly among environmental configurations: for a given environmental composition, gradient configurations always supported higher species richness than clustered configurations, and species' niche width had an interactive effect on this pattern. We conclude that spatial configuration has profound and complex effects on how species richness patterns emerge in heterogeneous environments, and urge its inclusion in future studies or richness – heterogeneity

BPM-05

Universality in biodiversity patterns: causes of the variation of species-temperature and species-productivity relationships

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Biodiversity patterns, such as the relationship between species richness and temperature or productivity, are always defined for a particular taxon at a specific area (the entire range of the taxon or just an arbitrarily chosen region). The form of these patterns varies between taxa and regions. Weak relationship between richness and temperature or productivity is sometimes interpreted as a counterevidence against a hypothesis explaining diversity patterns by given variable. However, the strength and shape of biodiversity patterns may be affected by many effects including size of the taxon or exact delimitation of the study region. Although some of these effects (e.g. spatial scale) have been already investigated, most of them are usually ignored. Comparing (1) published data on different taxa and regions (46 datasets of species richness for a wide range of vertebrate, invertebrate and plant taxa) and (2) different (nested) clades within large vertebrate taxa globally (mammals, birds, amphibians), we evaluate the universality of biodiversity patterns and the factors affecting their strength. There is a strong effect of mean temperature and correlation between environmental variables (temperature and productivity) on the strength and slope of the richness-temperature and richness-productivity relationships. Richness-temperature relationships are stronger in colder areas, while richness-productivity relationships are stronger in warmer areas. These properties are additionally affected by taxon richness and range size in the nested taxa within vertebrate classes. Biodiversity patterns are thus not universal across all taxa or regions, and studies of diversity patterns should pay attention to the variation among observed diversity patterns.

BPM-06

Disentangling the influence of climate, soil and land cover on plant species distributions of the European Alps

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Climate is generally considered the main driver of range-wide plant distribution, with soil and land cover variables considered important at smaller spatial scales. Nevertheless, the predictive power of these three categories has not yet been empirically compared for many species and for an entire biogeographical region. The relative importance of these three variable groups for plants is indeed likely to be highly variable with expected higher importance in one or two variable groups for predicting species distributions, depending on ecological preference and taxonomic group of the species. In this study, we highlighted and compared the predictive power of the three categories of variables – climate, soil and land cover – for explaining the distribution of >2000 plant species at high spatial resolution (500m x 500m) across the European Alps. We fitted ensembles of four models (GLM, GAM, GBM and Random Forest) together with five predictors for each category to predict species distributions. We generally found climate to outperform, soil and land cover variables as predictors. Yet, large variations among species were found with respect to the performance ranking of the three variable groups. Here, we present what traits, niche preference, and species characteristics best explain the dominance in predictive power among the three variable groups. Finally, we summarize the conclusions drawn from this exercise for larger scale species distribution modelling.

BPM-07

Richness patterns and distribution of the Acre clade (Crassulaceae) in America

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The *Crassulaceae* family presents an almost cosmopolitan distribution, distinguishing four centers of high concentration of species: South-Africa, Mexico, Macaronesia and Southeast Asia. In order to know the richness patterns for one of these centers, models of distribution with macroclimatic variables (WorldClim) were performed for 180 of the 420 species that make up the Acre clade in America. For each species was applied to the MaxEnt algorithm, obtaining a total of 448 candidate models per species (each candidate model is the result of the combination of regularization multipliers and features). The best model was selected based on the omission rate and the AICc delta and later were binarized and added to obtain a richness map. Additionally, geographic records of 177 species with 5 or fewer occurrence were add to the richness map, to which it was not possible to apply MaxEnt. In the end the analysis included 357 representatives of the clade. The results show that the region of greatest richness is in the central zone of Mexico. Mexican ecoregions such as the "Trans-Volcanic Belt " or the "Valley of Tehuacan" present high values of richness. Secondarily, the Peruvian Andes region was identified as a regional center of richness, although with much lower values than those found in Mexico. At the genus, *Cremnophila* or *Lenophyllum* presents very restricted distributions compared to *Sedum* or *Echeveria*. This work helps to make conservation decisions, incorporates new knowledge about macroclimatic preferences and reveals richness patterns for one of the largest clades in the family.

BPM-08

Conditional love? Investigating interactions shifts along continental-scale water availability gradients

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Joint Species Distribution Models (JSDMs) can help disentangle the role of environment and biotic interactions in species co-occurrence patterns. These models have gained quite some popularity in the past years and can, for example, be used to generate hypothesis on the specific species interactions. However, most joint models assume that interactions between species are static. In reality, species interactions may be mediated by the environment. Recently, environmentally dependent JSDMs have been developed that allow species associations to change with the environment.

Here, we tested whether shifts in species interactions along a water deficit gradient influence the European scale distributions of species and whether the resulting pattern complies with the Stress Gradient Hypothesis. We used the recently developed context dependent JSDMs to infer the interactions of 287 grassland species in mesic and dry grasslands across a water deficit gradient in Europe. We expect that a low water deficit (i.e. low stress), negative associations (competition) will dominate while at a high water deficit, positive associations (facilitation) will become more prevalent.

Our results show that associations between the species in our models vary along a gradient of water availability at large scale as expected. This may indicate that biotic interactions between grassland species are modulated by the environment (i.e.: water availability), and that this in turn of influences their large scale distribution. Furthermore, we show how these models might be used generate and investige large-scale hypotheses on species interactions such as the Stress Gradient Hypothesis.

BPM-09

Alfa and beta diversity analysis based on endemic taxa to the Mexican Transition Zone's mountain ranges

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The Mexican Montane Transition Zone (MMTZ) is the area where taxa of the Nearctic and Neotropical regions overlap. It comprises the mountain ranges of Mexico, from the southwestern of the United States of America to Central America. Herein, we describe the richness and similarity patterns of some species inhabiting this zone based on different taxonomic groups (plants vascular, amphibians, reptiles, birds and mammals). Records of species were downloaded from the Global Biodiversity Information Facility. The diversity analyses (richness and replacement) were performed with the software Biodiverse 2.0 using a 0.5° x 0.5° grid-cell. The database includes 89,802 depurated records of 700 species of vascular plants and vertebrates. The richness of the species among the grid-cells ranges between 1 and 216. The highest values are in the extremes of the Trans-Mexican Volcanic Belt and the Sierra Madre del Sur (Oaxaca and Guerrero) with approximately 150 species, in the middle of the Sierra Madre Occidental (near Durango and Sinaloa) and in the mountain ranges of Chiapas with 130 species, and in the Sierra Madre Oriental with 120 species. The beta diversity analysis identified areas with complex biotic composition. The more homogeneous areas were assembled into three main groups corresponding to the northern, central and southern MMTZ. We also found some subgroups that match with portions of the transition zone. We identified regions with a higher species richness, as well as areas showing relative biotic homogeneity, which makes easier a hierarchical arrangement of areas in a system of provinces nested in dominions.

BPM-10
On the nature of isolation and its role in speciation and endemism

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Isolation is known to promote speciation and endemism, but theory on this is under-developed and isolation is typically both conceived and measured simplistically. We develop a framework that defines different dimensions of isolation, in both space and time, and use it to help explain both spatial patterns of endemism, and variation in speciation rates in space and time. We suggest that considerable progress can be made using this approach.

BPM-11
Influence of geographic isolation and environmental filtering on patterns of genetic differentiation in the widespread alternateflower watermilfoil (Myriophyllum alterniflorum DC., Haloragaceae)

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Knowledge about the processes determining gene flow and genetic diversity and structure of aquatic populations is essential for assessing the role of dispersal limitation, genetic drift and natural selection on metapopulation dynamics. Hence, understanding how environmental and geographic factors influence population genetic structure is becoming one of the most fundamental issues for molecular biogeography and landscape genetics. In this study, we examined the spatial genetic variation of twelve alternateflower watermilfoil (*Myriophyllum alterniflorum* DC.) populations from twelve ponds located in northwestern Spain by using nine polymorphic microsatellite loci (Myrsp1, Myrsp4, Myrsp6, Myrsp9, Myrsp12, Myrsp13, Myrsp14, Myrsp15, Myrsp16 - Wu, Yu, & Xu, 2013). Our main aims were to: i) reveal population genetic structure and gene flow patterns; and ii) assess the influence of geography and environmental dissimilarity on genetic differentiation of *M. alterniflorum* in Mediterranean pond environments. Bayesian cluster analyses of population structure were performed to determine the number of genetic clusters. Genetic isolation by geographic distance (IBD) and the importance of environmental dissimilarity on population genetic differentiation (IBE) was tested by causal modelling and multiple matrix regression with randomization (MMRR). The baseline genetic information of our work may be useful for understanding the role of geographic isolation and environmental filtering on metapopulation structuring of this widespread submerged macrophyte species.

Wu, Z., Yu, D., and Xu, X. (2013). Development of microsatellite markers in the hexaploid aquatic macrophyte, *Myriophyllum spicatum* (Haloragaceae). Applications in Plant Sciences 1: 1200230.

BPM-12

Historical antecedents on the biotic complexity of the Mexican Transition Zone throughout the 19th Century

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Abstract:

The concept of Mexican Transition Zone was established by Halffter back in 1964. In this area, Halffter recognised the superposition of different homologue distribution groups connected to each other by a shared biogeographic history. However, the geographic complexity of the Mexican biota and the idea of a spatial biotic transition had already caught the eye of several naturalists back in the 19th century, who tried to find an order within such complexity. On one side, Alexander von Humboldt explained this as the result of the contact between the northern and southern floras; Augustin de Candolle, for its taxonomic peculiarity; Alphonse de Candolle and Francis Sumichrast, for its remarkable biotic replacement; Eugène Fournier, as several groups of species that displayed a congruent distribution patterns of taxa from different areas in space and time and that are overlapped in Mexico; and lastly, Alfred R. Wallace, as the result of different dispersal events. Before the of Darwin's evolutionary theory was released, the description of different spatial diversity patterns (regionalization, diversity gradients, and taxonomic replacement, among others) coexisted without contradicting each other. After the evolution theory, the botanical and zoological regions acquired the connotation of primitive centers of origin. Later on, the wide congruent distributions (mainly the disjunctive distributions) became the main support of the hypotheses of the historical relationship among biotas, based on dispersal events.

BPM-13

The intermediate disturbance hypothesis is supported for regional communities

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The Intermediate Disturbance Hypothesis (IDH) explains species diversity of local ecological communities as a function of disturbance (and succession). Does it also apply to regional communities? We used regional species richness (γ) and occupancy-based measures appropriate to regional communities to answer that question. To help explain results, study size (e.g., number of disturbance levels) was also evaluated. Regional community data sets (125 successional time steps, 33 disturbance levels) were compiled from 24 study systems. Among-study pattern was evaluated with model selection for succession data. Within-study succession and disturbance data were evaluated using model selection and interrupted regressions. Probability that a ∩-shaped quadratic is most plausible (i.e., IDH support) was modeled as a function of study size (e.g., number of successional time steps) for empirical and simulation results. We found that categorical ranked species occupancy curves (RSOCs) were not sufficiently sensitive, and ≳ 25 species are needed for RSOCs. But models using quantitative measures supported the IDH among regional communities in succession and within the majority of study systems. Importantly, simulated data with > 8 succession time steps or disturbance levels always supported the IDH; smaller studies varied predictably and in opposite directions. Overall, the IDH was supported for regional communities, and small study sizes have likely contributed to past confusion for local communities. Future IDH research in local or regional communities should use: ≳ 8 disturbance levels or successional time steps; ≳ 25 species; quantitative measures of RSOCs; and model selection.

BPM-14

Cytogeography and altitudinal-climatic niches in diploid-allopolyploid complex of grasses: Festuca tatrae (Czakó) Degen and Festuca amethystina L.

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Whole-genome duplication (polyploidy) is evolutionary importance in plants. In grasses (Poaceae) evolution has been accompanied by frequent and repeated genome size gain and loss. Process may lead to change of habitat requirements, where polyploids can occupy intermediate niches in relation to their ancestors and have ability to colonize larger areas. However, above 'niche shift' hypothesis is currently questioned to be an exclusive rule.

Our biogeographical analysis concerns the couple of closely related grasses: *Festuca tatrae* (Czakó) Degen, with only diploid cytotype (2n=14) and *F. amethystina* L., where diploid (2n=14) and tetraploid (2n=28) plants were found. Tetraploid cytotype of *F. amethystina* is allopolyploid, originated by hybridisation with *F. tatrae*. Studied taxons have strongly different ranges. *F. amethystina* occurs in the most areas of the Central and Southern European mountains, while occurrence of *F. tatrae* is limited only to the Western Carpathians. Moreover, *F. amethystina* occurs also in lowlands, where is considered as relict. The detailed distribution and habitat preferences of cytotypes of *F. amethystina* is unknown. Hence, our study aimed to analyse cytogeography and altitudinal-climatic niches in studied complex.

The plant material was collected during the field studies in the most areas of species occurrence. Additionally plant material was acquired from herbaria. The ploidy level of individuals was estimated according to the flow cytometry method. Analysis of cytotype distribution and environmental niches was conducted with using GIS software and scripts in R.

The research was conducted within the framework of the Project of the National Science Centre, Poland, Project No. 2018/02/X/NZ8/01063.

BPM-16

Determinants of terrestrial biodiversity at different trophic levels: insight from high-resolution LIDAR data

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Understanding the determinants of biodiversity remains a fundamental question in macroecology. Measures belonging to three different categories – variation in environmental conditions, biotic interactions, and habitat continuity – are expected to be key determinants of biodiversity at the landscape to regional scale. Airborne LIDAR can provide a quantitative representation of these three categories. We aimed at investigating the relative importance of predictors in the three categories for overall diversity as well as diversity of organism groups at different trophic levels. We used generalized linear models to explain patterns of total species richness of nine organism groups (i.e. macrofungi, lichens, vascular plants, bryophytes, gastropods, spiders, hoverflies, carabid beetles, and galler and miner species) inventoried in a nationwide stratified biodiversity survey across Denmark (~42.000 km^2). The importance of predictors was accessed using AIC and cross-validation among five geographically independent regions. We find that LiDAR-based metrics alone explained 50% of the variation in total terrestrial diversity. The cross-validation score of the best model was 0.68 and indicated reasonable predictive power. The importance of environmental conditions, biotic interactions, and continuity differed among trophic levels. We conclude that LIDAR-based metrics can provide important predictors of biodiversity. Hence, our results highlight the importance of considering remotely-sensed data products in studies of species richness patterns.

BPM-17

Exploring distribution patterns of macrophyte communities in boreal lakes

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Macrophytes underpin key ecosystem functions in aquatic environments, and are thereby important in indicating the quality of freshwaters. Macrophyte communities are widely used to classify entire lakes, and community comparisons among lakes are typical in macrophyte distribution modelling. However, the within-lake spatial variation in these communities can also be substantial. We move from landscape patterns to exploring the fine-scale spatial structuring of macrophyte communities. We use spatially explicit data from two large, oligotrophic Finnish lakes to disentangle the environmental drivers of within-lake spatial patterns in macrophyte diversity. The hierarchical structure of our data enables the exploration of macrophyte species diversity and turnover at several spatial scales: (i) every survey plot of 1 to 4 m^2 is individually located, forming a spatial point data set that is clustered within (ii) line transects inside (iii) study sites (littoral zone segments encompassing 100 m of shoreline) around the lakes. Comparisons at the coarse resolution, between study sites, suggest that sheltered soft bottom shores with gradual slope host the greatest structural diversity of macrophytes, i.e. observed number of different life forms. However, the preliminary results from maximum entropy modelling show a potential mismatch between the scale of macrophyte distribution patterns and the resolution of our lake wide environmental covariates. This may impede the prediction of macrophyte communities for new locations, but we will introduce fine-scale point measurements on environmental covariates to the modelling for gaining better understanding about the spatial scale of the patterns in macrophyte distribution.

BPM-18

The role of Pleistocene island connectivity cycles and the diversification of Philippine mammals

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Island archipelagos have long piqued the attention of evolutionary biologists interested in biogeographical patterns implying processes of diversification in terrestrial vertebrates. Pleistocene sea level fluctuations have long been hypothesized to contribute to diversity between previously connected groups of islands. However, little research has focused on the factors contributing to genetic diversity within island groups. We aim to test how demographic, biogeographic and landscape genetic factors influence genetic diversity, in a previously connected group of islands, in the southern Philippines. We used a genomic single nucleotide polymorphism (SNP) dataset generated using a RAD-Seq method to investigate genetic diversity in two forest mammal species, *Bullimus bagobus* and *Haplonycteris fischeri*. We found that while population divergences predated the Pleistocene, the number of migrants per generation varied for both species. Our results also show that all geographic and ecological barriers tested contributed to genetic differentiation than distance alone, however, different barriers contributed more depending on the species.

BPM-19

DarkDivNet: a network to study dark diversity of vegetation on a global scale

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Why are some species present and others absent in a locality? To answer this central ecological and biogeographical question, we have to explore biodiversity at larger spatial scales but also consider habitat preferences of species. Species present in the surrounding have a chance to disperse to our study site. However, only a subset of them can tolerate local ecological conditions (the site-specific species pool). Moreover, several of these ecologically suitable species are still absent and form the dark diversity of a community. If we know the size and composition of dark diversity, we are better equipped to understand and protect biodiversity. DarkDivNet is a collaboration of researchers interested in dark diversity studies. We plan vegetation surveys replicated on the global scale. The information collected in the network will allow 1) to determine observed and dark diversity, species pool and community completeness, and link them to geographical and environmental gradients, anthropogenic disturbance, and interactions with soil biota (sampled with eDNA); 2) to test different methods to predict dark diversity; 3) to evaluate whether locally collected empirical information on species co-occurrences can be substituted by the use of available large vegetation databases: 4) to expand the dark diversity concept from purely taxonomy-based approaches to include the functional and phylogenetic aspects of diversity. DarkDivNet is currently open to add new participants from all over the world. We explain the structure and rationale of DarkDivNet, the guidelines for participation, the sampling protocol, and the publication plan. Contact can be made at darkdivnet@ut.ee.

BPM-20

Do United States protected areas effectively conserve forest tree rarity and evolutionary distinctiveness?

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Because forest tree species face serious threats including insect and disease epidemics and climate change, prioritizing species and forests for conservation is an essential management goal. This paper describes a species prioritization approach that incorporates both the rarity of species, because of the increased vulnerability associated with rare species, and their evolutionary distinctiveness (ED), because species with higher ED may possess rare traits. Rarity and ED scores, and scores for the two combined, were calculated for 352 North American forest tree species. A weak but significant phylogenetic signal was associated with species rarity. The scores were used to weight species importance values on approximately 130,000 forest inventory plots across the conterminous United States. The resulting plot-level estimates of conservation value were employed to identify geographic hotspots of forests with high conservation value, and to assess whether forests with protected status effectively conserve rarity and ED. Rarity hotspots were detected in California, the Southwest, central Texas, and Florida. Hotspots of ED included locations along the Pacific Coast, in the Northern Rockies, and in scattered eastern locations. Protected forest areas across the United States effectively conserve ED, but not rarity. In fact, rarity was lowest in areas with the highest protection, and highest in areas with no or unknown protected status. Multiple-use protected areas had higher ED, but not rarity, than restricted-use protected areas. Protected area effectiveness varied across the country. Such spatially explicit assessment approaches can help determine which forests to target for monitoring efforts and pro-active management activities.

BPM-21

The role of the Tapajós river in the Amazonian small mammal diversity pattern

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The Amazon region houses one of the richest biodiversity in the world, and one of the earliest biogeographic hypotheses to explain this diversity highlights the role of rivers as dispersal and/or diversification barriers. The Tapajós is an important tributary of the Amazon basin and it is not a very meandering river, thus it is expected to limit, more effectively, the gene flow among populations inhabiting the opposite borders, because represent a more permanent physical barrier. Here, we describe the small mammal's diversity of Tapajós River, and investigate its role in acting as a geographic barrier influencing the genetic distribution patterns of this community. Small mammal samples were collected on both banks, following a standardized methodology, implemented in 12 sampling points along the River, totaling 48,000 night traps. Using mitochondrial cytochrome bgene, we were able to identify 26 species-groups on the banks of Tapajós River, 10 marsupials and 16 rodents. From theses lineages, we tested the river barrier hypotheses in nine of them. Using PCA, phylogenetics and haplotypes analyzes we could not found a strong evidence that this river has hampered the gene flow among most of the lineages, since there is no genetic structure separating individuals from both banks in none of the analyses, except for *Marmosa micoureus demerarae* and *Marmosops pinheiroi*. This fact suggests that the Tapajós River is a recent and/or permeable barrier for most of the small mammal's community.

BPM-22

Distributional patterns of some members of the Phylum Ascomycetes inhabiting the Mexican montane cloud forest

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Montane cloud forests in Mexico harbour a great wealth of biological diversity. Ascomycota is one of de larger groups of fungi and it is recognized as a monophyletic group. We analysed the distributional patterns of some members of the Ascomycetes. We obtained the distributional records mainly from herbaria and field work in montane cloud forests. We assembled a database of approximately 900 records, consisting preliminarily of more than 200 species, 80 genera, 33 families, 11 orders and 5 classes inhabiting in this complex, archipelagic and relic vegetation type. The south-eastern part of Mexico has the highest number of species. The Sierra Madre Oriental and the Sierra Madre de Oaxaca contains the higher number of records with nearly 400 and 250 respectively. The states of Oaxaca and Hidalgo are the richest in species (more than 100 species), followed by Puebla ≈ 50, Tamaulipas ≈ 25, Veracruz ≈ 15 and Morelos. Some species of Ascomycetes inhabiting the Mexican cloud forest have close relationships with the canopy trees, for example Quercus, Fagus and Pinus, many of them dominant in the forest. In our study we can suggest that some species belonging to the Ascomycetes are endemic to certain diagnostic species of vascular plants. Our results show the lack of field work in the Serranías Transístmicas, mountain chains in which big portions of cloud forest occurs. We suggest that efforts must be done to explore these areas and many other areas of the Transmexican Volcanic Belt.

BPM-24
Regions of Endemism in SC USA based of selected Texas Angiosperms

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Widely used ENMs could provide more reliable information for delineating areas of endemism when combined with previous knowledge of biogeographic relationships in the region. To find areas of endemism in South Central US/North Mexico, ENMs for 60 selected species of flora Texas were produced. The region was framed by -125 to -75 longitude and 20 to 45 latitude, divided into 1 x 1degree cells, the species presence-absence matrix, based on the ENMs, was generated and analyzed using VNDM software to find clusters of correlative ENMs. The choice of species for modeling was based on the classification of chorotypes I developed and used to analyze three Texas floras: Big Bend Region (1587sp.), Edwards Plateau (1618sp.), and South TX Plains (1250sp.). Species with wide geographic ranges and ecological tolerances were dropped, and those most representative of each chorotype were chosen for generating ENMs. A special preference was given to recently revised genera and species with 30 to 300 herbarium records. Distribution data were obtained from GBIF. Suitable areas for the species were then modeled using MAXENT and 11 uncorrelated climatic variables. The models were evaluated with AUC and an omission rate. Preliminary results will be presented, while more models will be generated later and incorporated into the data frame for future analysis using VNDM. The diagnostic for each area of endemism species will be discussed in the light of their phylogenetic relationships based on literature.

BPM-25
Addressing common pitfalls does not provide more support to geographical and ecological abundant-centre hypotheses

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A long-standing hypothesis in biogeography is that a species' abundance is highest at the centre of its geographical or environmental space and decreases toward the edges. Several studies tested this hypothesis and provided mixed results and overall weak support to the theory. These studies, however, are affected by several limitations related to the sample size, the comparability among abundance measures, the definition of species geographic range and corresponding environmental space, and the proxy variables used to represent centrality/marginality gradients Here we test the abundant-centre hypothesis on 108 bird and mammal species and embrace the plural nature of the hypothesis by considering 9 geographic and ecological centrality/marginality measures. We analyse the species-specific effect sizes using a meta-analytical approach, and test whether the support for the hypothesis is mediated by species traits and data coverage. The summary effect sizes estimated for the 9 measures are largely inconsistent with the theoretical expectations and show a significant amount of residual heterogeneity. Additional factors appear important in explaining the variation observed between different species, but the results are contrary to those originally hypothesized, and inconsistent across different centrality/marginality measures and the datasets used. We show that addressing common pitfalls in previous studies does not provide more support to the abundant-centre hypothesis, with support being very dependent on the centrality/marginality measure tested, the geographic extent considered for the test, and geographic and environmental coverage of the data. The abundant-centre hypothesis so far remains an appealing speculation with little and variable empirical

BPM-26

Combining islands as study system and mechanistic models as methodological tools to understand biodiversity dynamics

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Understanding mechanisms underlying biodiversity patterns requires appropriate study systems and methods. Islands offer ideal study systems, having sparkled influential theories in both ecology and evolution. Recent advancements in mechanistic models for biodiversity dynamics are providing the tools to manipulate factors and processes at a spatiotemporal scale that is impossible in real-world experiments. Hence, combining islands and mechanistic models may prove insightful about biodiversity dynamics across scales. We present findings from spatially-explicit, eco-evolutionary, individual- and population-based models of plant metacommunities applied to oceanic islands to address different questions concerning biodiversity. In an experiment contrasting genetic traits to assess diversification trends, we found that a high degree of gene linkage causes lineages to show more niche conservatism, whereas low linkage results in populations with more flexible adaptation capabilities. When contrasting different scenarios of propagule pressure, disturbance and species pool to assess island invasibility, propagule pressure showed the strongest positive influence on the success of plant invaders. When contrasting isolation scenarios to assess its role on diversification patterns, we found that several abiotic (e.g. distance, propagule pressure) and biotic (e.g. dispersal ability and specie spool size) components of isolation increased the number of diversifying lineages and of species per diversifying lineage. These examples illustrate aspects of eco-evolutionary dynamics that are difficult to address in real-world systems. Considering that there have been an increase of mechanistic models for large spatiotemporal scales in general, we believe that applying those models to island-like systems will speed up our understanding of complex process interactions governing biodiversity dynamics.

BPM-27

Biodiversity informatics solutions for profiling occurrence data

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Occurrence data is prominent in biogeographical analysis and modeling. Yet most of the data has some kind of inaccuracy that makes it difficult to be used in one specific way or another. In this study, we present a profiling technique to apply a quality control and assessment of tree species occurrence data. We combined data from five major aggregators of occurrence data (e.g. Global Biodiversity Information Facility, Botanical Information and Ecological Network v.3, DRYFLOR, RAINBIO and Atlas of Living Australia) by creating a workflow to integrate, assess and control data quality of tree species occurrences for species distribution modeling. We further assessed the coverage – the extent of geographical data – of five economically important tree families (Arecaceae, Dipterocarpaceae, Fagaceae, Myrtaceae, Pinaceae). Globally, we identified 49,206 tree species (84.69% of total tree species pool) with occurrence records. The total number of occurrence records was 36.69 M, among which 6.40 M could be considered high quality records for species distribution modeling. The results show that Europe, North America and Australia have a considerable spatial coverage of tree occurrence data. Conversely, key biodiverse regions such as South-East Asia and central Africa and parts of the Amazon are still characterized by geographical open-public data gaps. Such gaps are also found even for economically important families of trees, although their overall ranges are covered. Only 15,140 species (26.05%) had at least 20 records of high quality.

BPM-28

Differences in Vegetation Diversity between Sites, Ecosystems, and Biogeographical Regions in Colorado

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This research was a compositional study comparing proportional floristic species diversity, as well as species richness between three organizational entities: local sites, ecosystems, and biogeographical regions in Colorado. Datasets included 72,166 vascular plant species observations (246 species) for 3724 sites (XY point locations) over a 17 year period that coincided with 55 potential ecosystems (900 m^2 resolution), and 35 small biogeographical regions that nest within 6 large biogeographical regions. Single-factor analysis of variance (ANOVA) tested the distinction of data means at a significance level of $p < 0.05$. Results indicated that mean species diversity values for local sites was different for 3% of possible ecosystem pairs, 16% of small biogeographical region pairs, and 53% of large region pairs. In contrast mean species richness was not significant for distinguishing ecosystems and was only significant for 1% and 7% of small and large biogeographical region pairs respectively. Diversity values were different between geographically separated small regions, but they also occurred between small biogeographical regions adjacent to one another in the Southern Rockies, where elevation gradients are pervasive. The average frequency of observations identified per site was less than twenty. Species diversity values included observation frequency of each species which provided insight into the variation of the identified species distribution within sites. Since species richness did not differentiate between types of species the total assemblage of species within a particular ecosystem or biogeographical unit was not discernable. This study confirms a compositional relationship between sites, ecosystems, and biogeographical regions with respect to species diversity.

BPM-29

Global diversity patterns are modulated by temporal fluctuations in primary productivity

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The pattern of unequally distributed species diversity across the Earth is generated by processes of speciation, colonization, and extinction. The balance of these processes is affected by climatic variables related to energy availability and its stability, so that high environmental productivity and its stability is linked with higher number of species. Low resource availability and its seasonal and aseasonal changes are hypothesised to reduce the number of species with viable populations, leading to higher extinction rates. We test the hypothesis that seasonal and stochastic fluctuations in productivity play a critical role in shaping the diversity patterns. We evaluated the effects of temporal productivity fluctuations on global diversity patterns of amphibians, birds, and mammals. First, we performed time series decomposition of temporal dynamics of productivity (measured as NDVI) into the components of seasonality (periodic fluctuations) and unpredictability (aperiodic random fluctuations). Next, we tested the independent effects of these variables on species richness. The results revealed that species richness is affected by temporal productivity variation, but these effects fundamentally differ depending on mean productivity level. While high productivity variation has a negative effect on species richness in regions with moderate to high productivity levels, species richness is higher in arid regions with high productivity variation. In productive areas high environmental stochasticity may increase extinction rates, whereas arid regions probably benefit from resource fluctuations which promote species coexistence via storage effect.

BPM-30

Bioregionalisation of Australian amphibians

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Australia's unique biota includes four native amphibian families containing ecologically and morphologically varied species. How or even whether these species form macro-scale communities has never been studied using detailed occurrence data. Here, we test for bioregions and describe the characteristics of the species falling within them. We used a filtered dataset of museum specimen records containing 142,336 occurrences to define bioregions across the continent. Occurrences were grouped into half-degree grid cells and used to create a presence/absence matrix. Diversity is highest along the east and northern coasts, but it does not follow a standard latitudinal diversity gradient. To delineate bioregions, we used factor analysis (FA) with a manipulation that improves FA's handling of many absences and compared the results with those obtained using partitioning around medoids (PAM) clustering. FA found five distinct bioregions, including the southwestern Australia biodiversity hotspot. The two methods differ in their bioregion assignments. Based on FA, southeastern Australia is an area of particular conservation concern with high diversity, high endemism, and the highest proportion of threatened species. The PAM results show the highest proportion of threatened species in a coastal bioregion between Sydney and Brisbane and highest endemism in southwestern Western Australia. We favour the FA solution because its support for five factors is unambiguous, and because it allows for uncertainty in assigning cells to regions. Regardless, both arrangements indicate that coastal southeastern Australia has a particularly high proportion of threatened species, likely due to extensive land-use changes in this area.

BPM-31

Spatial distribution of the eco-morphological diversity of two bird families in Colombia

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In this study, I used a revised and corrected version of the BioMap database to model the potential geographic distributions of Trochilidae and Tyrannidae species using climatic variables and the MaxEnt algorithm. In addition, implemented two measures of eco-morphological diversity: the "eco-morphological species-equivalents diversity index" (E) and the "eco-morphological groups equitability index" (E '). Each species was classified into several functional groups according to their ecology, assigning to each one a fraction of the unit according to the importance for the particular species. These fractions in each case were weighted by a morphological index that relates the interaction between bill length and weight (Trochilidae) and total length and weight (Tyrannidae). E was calculated by adding the weighted maps of all species and functional groups, while E 'was calculated using information theory, similar to the Shannon-Wienner index. The majority of zones of high diversity and eco-morphological singularity appeared in the Andean region, the Sierra Nevada de Santa Marta and the Serranía del Baudó between ≈1,000-3,000 m. However, both families showed some differences in the spatial distribution of eco-morphological diversity. Also, there were some differences in the patterns within each family between both indexes. The continuation of studies of functional measures of diversity represents a unique opportunity to continue advancing the knowledge of biodiversity in the country and bring the concepts of biodiversity and ecosystem services closer.

BPM-32

Network analysis of aquatic plant range sizes in Europe and North America

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Ecological networks in terms of species interactions have the potential to influence the ecological dynamics of species. In reality, however, most interactions within a community tend to be weak, for which only a minority of interactions will have the potential to exert such influence. Moreover, interactions are often asymmetric, both in terms of degree (i.e., number of links per species) in mutualistic and antagonistic binary networks and in terms of strength in quantitative mutualistic networks. Here, we have used a 50km x 50km grid to map occurrences of 337 and 157 aquatic plant species in North America and Europe, respectively, into a complex network. Considering each species as a node, we create a link between them if they shared at least one grid. Since a pair of species can share many cells, we will have a weighted network where the weight of each link is equal to the number of grids the species share. This approach resulted in two systems: one for the United States and another for Europe. The degree distribution P(k) can be used to distinguish the networks apart. Using this feature, we have found that the degree distribution for the United States presents an exponential behavior, i.e., P(k)~exp(-k/k*), where k* is a characteristic exponent, while for Europe the distribution was almost constant, i.e., well-defined scale like Erdős–Rényi random graph.

BPM-33

Topography and climate explain plant diversity bias of the eastern Asia - eastern North America disjunction

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Biogeographers have reached the consensus on the long-standing mystery of the Asian bias in the disjunct plant distribution between eastern Asia (EAS) and eastern North America (ENA). However, the primary causes of the disjunction and what factors shaped the floristic diversity bias still remained unsolved. We compiled data on topography, contemporary climate and historical climate changes since Last Glacial Maximum to quantify their respective contributions to the EAS-ENA plant disjunction. Topography and contemporary climate were used to assess whether differences in physiography and climate accounted for the Asian bias. We used generalized linear models to model the diversity patterns in EAS and ENA separately, the variances of which were accordingly partitioned to distinguish potential factors. Our results showed that topography, contemporary climate and historical climate changes together explained around 83% and 90% of variation in EAS and ENA on both genus and species levels, while the pure contribution of historical climate changes were less than 4% in the two regions. Contemporary climate alone contributed about 44% and 69% to the variation in species richness in EAS and ENA, respectively. Topography independently accounted for about 3.7% of the variation in species richness in topographically more complex EAS but explained only 0.4% in ENA. Topography contributed more to species richness in EAS though contemporary climate was more powerful in ENA. We concluded that historical climate changes played little role in forming the EAS-ENA floral disjunction and that topographic heterogeneity may lead to the Asian bias diversity pattern with effects from contemporary climate.

BPM-35

Components of species richness varying with latitude – A synthesis on patterns in trees, marine fish, ants, and small mammals

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The latitudinal diversity gradient (LDG) is one of the most prominent and widely discussed, yet still poorly understood macroecological patterns. Hypotheses explaining the LDG (e.g. "more individuals" or "more niches") cannot be discerned using traditional approaches, which simply correlate species richness with environmental variables co-varying with latitude (eg. temperature, energy). However, species richness is underlain by three components, which themselves can provide deeper insights into the possible processes driving richness patterns such as the LDG. 1) The regional species abundance distribution (SAD), 2) the number of individuals captured by the sample (density) and 3) the intraspecific spatial clustering of species (spatial aggregation). For instance, if "more individuals" is the main driver, the SAD and spatial aggregation should remain constant along the gradient, and only the numbers of individuals determine the richness pattern. Here, we dissect latitudinal gradients of species richness in trees, reef fish, ants and small mammals into these underlying components by deriving metrics from alpha- and gamma-scale individual based rarefaction curves. Contrasting patterns of 1) the probability of interspecific encounter PIE (evenness measure), 2) rarefied richness S_n (estimator controlled for sample size) and 3) beta diversities of PIE and S_n (reflective of the degree and type of spatial aggregation), our results from plot-level data help to draw a more differentiated picture of the LDG in these groups. Across taxa, we find little evidence for the more-individuals-hypothesis. Our preliminary results point to refinement of hypotheses and models that can help to deeper understand these patterns and their underlying drivers.

BPM-36

Phylogenetic conservatism and biogeographic affinity influence woody plant diversity-climate relationships in eastern Eurasia

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The mechanisms underlying the latitudinal gradient in species diversity remain a central yet controversial issue in biology. Climate has been suggested to be the primary determinant of species diversity. However, the evolution of species diversity-climate relationships remains poorly understood. Here, using newly compiled database containing distribution maps of 11,422 woody species from 176 families in eastern Eurasia, we investigated how biogeographical affinities (i.e. tropical vs. temperate affinities) of families influenced the effects of climate on species diversity of woody plants. Furthermore, we evaluated phylogenetic signals in the geographical patterns of species diversity of families and the species diversity-climate relationships. We found that contemporary winter coldness dominated species diversity of tropical families, while Quaternary climate change dominated that of temperate families. Species diversity patterns of closely-related families were more similar than those of distantly-related families and significant phylogenetic signals characterize the slopes of the relationships between species diversity patterns and climate. Our findings indicate significant phylogenetic conservatism in family-level species diversity patterns and their relationships with winter coldness and annual precipitation, and the evolution of contemporary species diversity-climate relationships in plants may have involved conservation of their ancestral niches.

BPM-37

Phylogenetic diversity in grassland communities across Europe

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Plant species richness is largely dependent on local environmental conditions, but it may result also from evolutionary processes, either from rapid speciation or from gradual accumulation and preservation of species over time. However, there is no comprehensive analysis of phylogenetic diversity for European plant communities so far. Here, we attempt to map phylogenetic diversity in local plant communities of different grassland vegetation types across Europe, namely dry, mesic, wet and alpine grasslands. Our study is based on extensive dataset of vegetation plots provided from the European vegetation archive, which we filtered to meet our criteria on plot size, date of recording and geographical distribution. These data have the advantage that species co-occurring within the plots share the same environmental conditions. For each vegetation plot, we calculate phylogenetic diversity based on the largest available dated phylogenetic tree. We explore how spatial patterns in phylogenetic diversity coincide with the distribution of plant species richness, and how they vary along latitudinal and macroclimatic gradients.

BPM-38

Spatial variation of host plant communities as inferred from diet profiling of full beetle assemblages using metabarcoding

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The composition of species assemblages of herbivores may be determined by the distribution of their host plants. However, the role of trophic interactions in driving diversity patterns is rarely addressed at the level of communities and large spatial scales because of the difficulties to determine the host choice. In particular, leaf beetles (Chrysomelidae) are narrow diet specialists feeding on one or a limited number of plant species, and thus niche effects on leaf beetle distributions might be more linked to trophic interactions than to other constraints (e.g. climatic). Here we explore the use of metabarcoding to reconstruct the assemblage of host-plants on which leaf beetles have been feeding in 20 different localities across a North-South transect in the Iberian Peninsula. PCR amplification of the plant DNA in beetle guts were conducted following a metabarcoding approach targeting the trnL intron of the chloroplast genome directly from total DNA extracted from individual beetles. PCR amplification and subsequent Illumina sequencing on pooled DNA extractions from species-rich beetle assemblages each represented one of the 20 localities. The plant assemblage of each locality was recovered from read counts. Species counts, turnover and nestedness patterns were assessed at the host plants level. This additional layer of information can be integrated into the niche vs. neutral debate in order to determine the role of the distribution of plant species on the geographic ranges of the herbivores and, thus, understand the factors that control large-scale species distribution patterns.

BPM-39
Biogeography of the Western Ghats

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The Western Ghats (Ghats) are a discontinuous mountain range that run parallel to the Western coast of peninsular India (Joshi and Karanth, 2013). These mountains are an old and extremely biodiverse tropical range with multiple areas of high biodiversity (hotspots). There are two conflicting hypotheses to explain high biodiversity levels within the tropics, the museum and the cradle hypotheses. The museum hypothesis conjectures that the tropics are areas of high biodiversity due to species accumulation over geological time while the cradle hypothesis attributes high diversity to recent rapid diversification (Pennington *et al*., 2015). We question the origin of tropical biodiversity through examining these hotspots and wonder whether they follow the cradle/museum hypothesis. The Ghats were formed between 160 and 90 mya (Briggs, 2003)and are old compared to other tropical mountains, e.g., the Andes (66-4 mya) (Hoorn *et al*., 2010). This indicates that their flora may contain elements which conform to the museum hypothesis of tropical hyperdiversity (Pennington *et al*., 2015), meaning the Ghats are appropriate to test this hypothesis. We can better explain the origin of tropical hyperdiversity by using a phylogenetic approach, comparing my studies from the Ghats to studies from geologically younger mountains (e.g., the Malay Archipelago and the Andes). This will be done using herbarium genomics (through genome skimming and hybrid bait capture) to complete taxon sampling for species native to the Ghats.

BPM-40
Getting off the right foot: integration of spatial distribution of genetic variability for aquaculture development and regulations, the European perch case

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Knowledge of spatial genetic variability (i.e. differentiation and diversity) patterns is key information for conservation, management, and production strategies of species. It allows improving conservation actions, translocation regulations, and farming productivity. However, these improved strategies are often considered when issues are observed. By taking into account lessons from the past, we investigate the genetic variability of *Perca fluviatilis*, a fish species at a nascent stage of its aquaculture, in order to promote a sustainable aquaculture. We characterise the genetic variability across 84 West-Palaearctic sampling sites using four mitochondrial sequences and eight microsatellites. By considering this variability, we aim to provide (i) guidelines for conservation and efficient regulations of the movements of the species within its natural range and (ii) a genetically-based population structure that could act as an impetus for further production improvement. Our analyses show an uneven distribution of the genetic variability across the species range. Based on genetic differentiation, we identify five large geographic scale clusters: European plain, Danube and Alpine Foreland, Western and Northern Fennoscandia, Eastern Europe and Balkans. These main clusters are further subdivided into several subgroups when analysing population structure with microsatellites. Mapping of genetic diversity highlights several hotspots across the species range. This spatial pattern of intraspecific diversity implies to develop specific and appropriate regulations of translocations. Moreover, we observe similarities between geographic differentiations in genetics and in zootechnical performances previously reported. We ultimately propose potentially efficient regulations for policy-makers and intraspecific regulations for further investigations of population-specific performances in aquaculture.

BPM-41

Distributional patterns of the Order Polyporales (Fungi: Basidiomycota) in Mexico

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The Polyporales is a diverse group of Agaricomycetes including roughly 1800 described species. They are key players in the carbon cycle, and the white-rot members of the order are among the most efficient lignin decayers in the biosphere. A database was assembled from three main sources: a) Specialized literature: papers published in peer-reviewed journals with an emphasis on taxonomic studies; b) Public databases of government environmental agencies, or databases associated with mycological collections, both private and public; c) Mycological collections: distributional records were obtained directly from specimens deposited in the main Mexican herbaria. The gathered database consists of 14,995 records of Polyporales belonging to seven families, 119 genera and 290 species. The species that has more records is *Pycnoporus sanguineus* with 1014. The states of Veracruz, is the richest in species (137 species), followed by Jalisco 134 and Oaxaca 109. The central and southeastern parts of Mexico have the highest species numbers, mainly corresponding to the Trans-Mexican Volcanic Belt and the Sierra Madre Oriental.

BPM-42

Knocking on the trap-door: Unraveling the species boundaries and evolutionary history of western Mediterranean ctenizid trap-door spiders

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The trap-door genus *Cteniza* is an ancient yet poorly diverse lineage that, along with the Aegean *Cyrtocarenum*, is the only European representative of the mygalomorph family Ctenizidae. It includes three species circumscribed to the Maritime Alps, Calabria and the Tyrrhenian islands. The taxonomy and distribution ranges of the species, however, are contentious.Trap-door spider taxonomy has been traditionally hampered by a conservative morphology, with few yet highly polymorphic variable traits. Molecular based approaches have gained popularity to establish species boundaries in groups of conflicting taxonomy. However, trap-door spiders usually show highly structured populations, which challenge the basic tenets of quantitative delimitation methods. Here, we use a target multi-locus approach along with relaxed clock models to unravel the history and delimit species in *Cteniza*. Additionally, we generate RADseq data to investigate fine-scale population genetic structure. Our study uncovers higher species diversity that previously assumed and confirms deep mitochondrial structuring of trap-door spiders. Furthermore, we suggest that *Cteniza* diversification was driven by the opening of the Western Mediterranean Basin and that the continent was secondarily colonized from the islands. Some biogeographic relationships recovered are at odds with the geology and geographical settings, which may hint at frequent lineage extinction events during the evolution of the genus.

BPM-43

Using the fuzzy logic in the distribution modelling of competitive interactions.

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The interspecific interactions are affected by the environment in which they take place. Focusing on competitive interactions, three biogeographical situations are predicted to occur into the contact areas of two similar ecologically species: 1) the sympatric coexistence, when an optimal environment for both species provides high abundance of resources that minimizes the effect of competitive interactions, 2) the autoecological segregation, when the pressure of a bad environment is stronger than biological interactions, and 3) the sinecological segregation, when in sub-optimal areas one species, better adapted to this environment, could exclude the other by competition. Favourability models and fuzzy logic methods could be used to explain these biogeographical interactions. Considering low, high and intermediate favourability areas using 0.2 and 0.8 thresholds: 1) the sympatric coexistence could occur in those areas with high favourability for both of them, 2) the autoecological segregation could be the main situation in those areas with low favourability (at least for one species), and 3) the sinecological segregation could occur in areas of intermediate favourability for one species and higher for the other. In this study we have used the contact zones of the parapatric distribution of *Vipera* species in the Iberia Peninsula. Using a presence/absence matrix for each species and a set of environmental variables in a UTM 10x10 Km grid cell we have obtained favourability models that were subsequently compared. Our results are consistent with the evolutionary scenarios inferred for the species and their dispersal through the Iberian Peninsula and colonization processes.

BPM-45

Ecology of diversification in mammals changes with phylogenetic scale

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Why some regions act as the engines of species diversity, while others act as diversity museums or sinks remains unresolved. Multiple mechanisms have been hypothesized to govern these dynamics, but their interactions and relative importance have yet to be uncovered. Here, we evaluate five classes of prominent mechanisms that govern the dynamics of species diversity in mammals (including the effects of climate, geography, topography, and regional competition). We find that the dynamics transition from an unbounded diversification toward slowdowns and equilibrium diversity. The unbounded expansion seems stochastic and dependent on multiple mechanisms. The slowdowns, however, depend primarily on regional competition between related species for resources, which seems to suppress the diversification process. Eventually, the dynamics converge toward equilibrium diversity, determined by regional climate, energy, and productivity. Highly productive regions (esp. the tropics) tend to be densely packed with species and clades, while the opposite holds for low-productive regions (esp. the temperate). These results held across multiple taxa within mammals (Carnivora, Artiodactyla, Chiroptera, Eulipotyphla, Primates, Rodentia) when controlling for different sources of possible errors. They demonstrate the intuitive, though rarely considered, possibility that multiple mechanisms together influence diversification. But their relative effects and their interactions vary systematically across scales, producing scale-dependent diversity dynamics.

BPM-46

What distinguishes (and does not distinguish) vernal pool habitats on both sides of the Strait of Gibraltar?

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Vernal pools habitats are known hot spots of biodiversity in Mediterranean climate areas. They host original plants specifically adapted to fluctuating soil flooding and drought. The Strait of Gibraltar has a 14-km length and separates Iberian peninsula (Europe) from northern Morocco (Africa). Geological events have involved land bridges and effective sea barriers for the flora of both sides of the Mediterranean. The aim of this study was to evaluate the role of the Strait of Gibraltar in vernal pool habitats on the basis of their floristic composition and ecology of their plant communities. We also examined the molecular varibility of certain characteristic vernal pool species belonging to *Isoetes* and *Baldellia*. Vernal pool habitats showed a similar vegetation zonation in growth forms, including isoetid, batrachiid, and helophytic vegetation, on both sides of the SG. Water nitrate concentration was higher in Moroccoan vernal pools, which are characterized by *Isoetes velata* subsp. *adspersa* and *Ranunculus saniculifolius* communities. Iberian vernal pools had lower water nitrate content, and were characterized by *Isoetes velata* subsp. *velata* and *Ranunculus peltatus* communities. Molecular results, derived from the ITS region, supported the entity of two taxa within *Isoetes velata*, which currently are recognized as *Isoetes velata* subsp. *velata* for Iberian populations and *Isoetes velata* subsp. *adspersa* for Moroccan populations. Besides, *Baldellia repens* populations from Morocco, appeared to be genetically distinct from their European counterparts, which also supported the taxonomical differentation between *Baldellia repens* subsp. *repens* (Morocco) and the european *Baldellia repens* taxa (eg. *B. repens* susbp. *baetica*).

BPM-48

Foraging specialization and niche overlap in Australian songbirds

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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.

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.

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. 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.

BPM-50

Analogous responses of tropical and temperate pond metacommunities to environmental, spatial and temporal factors

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Metacommunities are structured by a complex set of processes involving historical, environmental and spatial components. Here we contrasted patterns of species sorting across a large diversity of taxonomic groups (from phytoplankton to vertebrates) in temporary ponds of Costa Rica and the eastern Iberian Peninsula. Given the low temperature gradient in the tropical area, we expected species sorting to be less important in this system. However, variation partitioning of the thirty ponds sampled twice during a hydroperiod in each area revealed similar relative percentage of variation explained for most groups within both geographical zones: Bird and phytoplankton assemblages showed a greater influence of the environment compared to space, probably related to higher dispersal abilities (either active or passive, respectively). Despite large differences in diversity of amphibians and reptiles between the two areas, their distributions were highly spatially structured as expected from their reduced dispersal capacities. Aquatic macroinvertebrates, with a wide variety of ecological strategies, showed higher differences between both metacommunities in terms of relative spatial and environmental effects, the latest being stronger in the temperate area. Temporal effects, i.e. differences between sampling periods were significant but weak, and higher in the temperate system where we found also the highest environmental effects (except for the herpetofauna). Finally, the percentage of explained metacommunity variation was higher in the temperate compared to the tropical system, probably because of the stronger environmental filters and the lower diversity.

CB-01

Conservation Priority Comparison of Two Major Valleys on Central Taurus Mt. via Alpha Beta Diversity Analysis

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Central Taurus mountain range is located in the Mediterranean region and part of the Alp-Himalayan chain which hosts the highest number of endemic plant species in Turkey. The area is among Earth’s most important biodiversity hotspots "Mediterranean Basin Hotspot-Priority Corridor", including two Important Plant Areas (IPA). Central Taurus mountain range starts from the Mediterranean coast and rises up to 3000 meters; containing diverse ecological regions as a cumulative result of topographic variations, climatic conditions, and geological features. Due to its millennia-old civilization history and recent human activities such as mass tourism, intense agriculture; the area has been subjected to high-level anthropogenic degradation. Here we put forward comparative plant diversity of two major valleys via alpha, beta diversity measurements in an analytic manner which will help decision makers for the selection of priority sites to be protected. Shannon Wiener diversity index is used for the species diversity measurements of plant communities and beta diversity of different communities was analyzed via Whittaker Differential Equation.

CB-02

Predictive biogeography at work: a Mediterranean-island perspective

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The Western Mediterranean region is a dynamic biogeographic setting, with a complex history of Neogene tectonics where vicariance and dispersal intertwined to yield high endemism. Millennia of human-induced extinctions and translocations have impacted heavily on native biotas. Thus, sound conservation can only stem from understanding the processes generating local biodiversity across a wide range of insular ecosystems.

A quantitative measure of insularity as a species-specific trait allows assessing vulnerability of islanders, as well as invasiveness of continental taxa. In an explicit phylogenetic context, it is then possible to infer the tempo and mode of insular evolution. However, there are at least three obstacles: uneven taxonomic inflation across archipelagos (at both species and genus level), phylogenetic artifacts (ranging all the way up to systematic error), and invoking ad hoc scenarios (usually based on assumed paleogeography or mythical events). Eventually, it is clear that Holocene extinctions vary widely, with strong phylogenetic, ecological and temporal effects.

Conservation guidelines emerging from this perspective are relevant to sort out what is endemic and what is introduced, how to evaluate priorities for species conservation, what needs to be done in order to preserve the biogeographic category of islands, and when and how to address ecosystem restoration.

CB-03

Problematic of administrative and biogeographical boundaries. The case of Genista umbellata, a threatened endemic taxon.

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A second locality in the Valencia territory has been detected from ibero-african endemism threatened *Genista umbellata* (“susceptible” according to a valencian catalogue of threatened plant life and in danger of extinction according to UICN). It’s about of the population more northeast of world and the biggest number of individuals in the Valencian community that has almost tripled in “Hondón de las Nieves”. The only known population known at present.

Census of this new population was made with high precision GPS and differential correction in `post process. After the field work it observed that the new locality is of anthropogenic origin, which is a consequence of a ecological restoration. Furthermore, it is verified that the propagation of species around the perimeter surrounding the restoration is being produced explosively because it has counted a large number of individuals of medium size, as well as seeding whose origin is in the mother plants. This shows the problems and the scarcity with regards to the regulation of borders inside the same country for the exchange of the taxons plants, as the genetic quality and contamination that it could produce after its reproduction in garden centers and subsequent use in restorations.

Lastly, it's proposed, the possibility of as well as catalogues of threatened plant life of each autonomous community to make a mechanism of coordination that was more a biogeographical perspective and not based on administrative borders.

CB-04

ECOPOTENTIAL – Protected Areas and Earth Observation

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Protected Areas have been set-aside and accepted by the society for the purpose of conserving valuable landscapes, ecosystems and species. Besides these spatial investments, linked with restrictions for use and access, extensive financial investments have been done in order to develop and install sensors for Remote Sensing of nature and of the human environment. Large amounts of Data are gathered through Earth Observation additionally on the ground (in-situ). ECOPOTENTIAL is blending Earth Observation with a set of internationally recognised European Protected Areas distributed over a range of Biogeographical Regions.

ECOPOTENTIAL is focused on ecosystems that are sensitive to change such as in mountainous, arid/semi-arid or coastal and marine environments. The categories of Protected Areas cover a wide range of administrative categories in order to address different levels of legal frameworks and implementation.

CB-05

Bare ground is expanding in unprotected areas of the Maasai Mara ecosystem

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Degradation of the last remaining “wilderness” areas in the world is of big concern, and different management approaches are applied for protection. Here, we report a remote sensing approach to assess the effect of the different protection regimes.

The iconic Kenyan savannah, known as the Greater Maasai Mara constitutes the northern part of the Mara-Serengeti Ecosystem. It is famous for being the last natural ecosystem with migration of millions of large mammals. Especially the wildebeests passing the big Mara River to access the rich grass savannah in Mara is legendary.

This ecosystem is under pressure from increasing human populations, intensifying land-use, and climate changes. Declining wildlife populations and increasing human-wildlife conflicts are progressively being reported.

The Greater Maasai Mara is divided into three categories of land administrative units: (1) unprotected, (2) semi-protected community-based conservation with regulated livestock grazing and tourist camps, and (3) fully protected national reserve without livestock.

To assess the impacts of these different management regimes on the ecosystem we have quantified the land-cover and vegetation dynamics over the past 32 years based on classifications of Landsat Images.

Our results show accelerating degradation of natural vegetation with significant loss of woodland and grassland, and expansion of bare ground within unprotected land. There is only minimal directional land-cover and vegetation changes for both types of protected land.

Our study thus indicates that protection of land either as national reserve or as private conservancy opposes degradation of natural vegetation in East African savannah ecosystems.

CB-06
Biogeographical applications for management and conservation of the endangered Northern Bald Ibis in Morocco and Spain.

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Over the last century, the Northern Bald Ibis (*Geronticus eremita*) had suffered an extreme decline in its population size and distribution range. At present its natural populations are confined to the Agadir region, in Morocco, considering as critically endangered. The aim of this study is to characterize past and present breeding areas in Morocco to support from conservation biogeography the current conservation efforts. We used a presence/absence database obtained from bibliography and a set of environmental variables to obtain favourability models. A purely spatial descriptor of the cohesion trend in the distribution was use regarding its history and population dynamics. Another model was built using only environmental variables to identify those areas which are favorable for the species without the effects of the spatial trend. Northern Morocco and the Atlantic coast were considered as the most environmentally favorable areas for the species, whereas the eastern Mediterranean coast and the Middle Atlas region were the most spatially favorable areas. Due to numerous local extinctions the spatial trend was broken and the dispersal of individuals is ineffective. With the arrival to Morocco of individuals coming from introductions in Spain a new spatial structure along the Atlantic coast could arise, if these individuals establish new colonies, which should be taken into account in the conservation programs of the species. The close monitoring of the species is required to validate the new spatial structure, which seems to occur because new individuals from Agadir are moving northwards from their original colonies for the first time.

CB-07
Measuring the meltdown: drivers of geographical extinction and decline in Chinese vertebrates

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With large area, diversified topography, and varied climates and habitats, China has a high degree of species diversity and is considered as an important biodiversity center in the world. However, many species, especially those within vertebrates, are considered highly threatened and some are identified as Extinct or Regional Extinct according to the China Biodiversity Red List. Here, we conducted the first extensive analysis to systematically investigate the patterns and processes of extinction and threat in Chinese vertebrates. In particular, we addressed the following four questions by focusing on Chinese birds, snakes and amphibians. First, is extinction risk randomly distributed among families in Chinese vertebrates? Second, which families contain unexpected more threatened species than would be expected by chance? Third, which intrinsic traits or extrinsic factors or any of their combinations determine the geographical extinction and decline in Chinese vertebrates? Finally, what should we do to protect vertebrate species from extinction and how to set regional conservation priorities? We found that extinction risk of Chinese vertebrates was nonrandomly distributed among taxonomic families and species. By using a large number of intrinsic traits and extrinsic factors, we identified that different factors determine the geographical extinction and decline in Chinese vertebrates. For instance, small range size and small elevational range were important predictors of extinction risk in Chinese amphibians. Our results suggested that vertebrate species should be conserved with different strategies. Conservation actions should also focus on preventing human threats for the effective preservation of the geographical diversity of Chinese vertebrates.

CB-08

Implementing "half-earth" framework, influences protected ranges in marine and terrestrial ecosystems: A case study with the USA and IUCN

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The idea that "Nature Needs Half" or "Half Earth" suggests that if humanity protects half of the natural landscapes on the planet, the ongoing mass extinction will be reduced, and ecosystem services should be promoted. Recent communications have identified the pros and cons of such a proposal, but no clear way forward has yet been described. In this work, we present a proposal to treat the Half-Earth framework as a goal setting iterative cycle, rather than a fixed goal. In a cyclical manner the best available science needs to promote environmentally conscious policies. We argue policies should incentivize environmentally sustainable economic development and ultimately inform how much area any individual country can reasonably set aside for conservation purposes. The interaction between science, policy, and economic development should be carefully balanced between social and environmental justice. We show that the Half-Earth goal is achievable, and present data from the United States management of marine and terrestrial protected areas. Our exploration of American conservation history reveals that conservation and environmental protects efforts have not been partisan issues and should not be (at least in the US). We show that the US is very close to achieving a 50% goal for marine protected areas but has stagnated in protecting terrestrial areas.

CB-09

Long-term effects of wind farm operation on bird communities. Different locations involve different effects in a major migratory bottleneck.

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Wind energy has gained prominence among renewable resources and wind farms remain one of the most widely used technologies for the production of energy throughout the world. It is known that wind energy facilities affect flying animals through collision and displacements or exclusion. Most studies have focused on raptors or other large bird species, but limited information exists on the effect of wind farms on small birds. Another aspect that requires further study is the long-term changes in habitat use, mostly due to the lack of information. In this study we have monitored bird communities in the vicinity of a wind farm in a mountainous habitat in southern Spain, immediately after installation and 6.5 years post-construction. The wind farm is located near the Strait of Gibraltar, one of the most important migratory routes in the Palaearctic where the highest mortality rates have been reported. We found differences in the recovery of habitat use between raptors and non-raptors. Raptors showed an upturn in numbers but non-raptors abundance fell significantly. Taking into account the expected growth in wind farms in the coming years, it would be necessary a greater attention to the long-term effects of this energy in bird communities after the initial environmental impact assessments.

CB-10
Modelling the lake selection of white-headed duck Oxyura Leucocephala in central Spain.

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Since the white-headed duck settled in two lakes, Zoñar and Rincon in 1977 this species has increased its occupancy of the lakes occupied in mid southern part of Spain. Fish presence is a negative factor to white-headed duck, but in central Spain there are a higher number of lakes, mainly temporary, where there is no fish. In this area, the white-headed duck breeds in a small number of lakes, thus other factors will be necessary to explain the presence of this duck species. We have used 31 biotic and abiotic variables including the geographic location as a control measure, but 6 variables were unavailing by collinearity problems. Therefore, a Hier-Part analysis was carried out. Each analyzed group contained less than nine variables. Thus, seven groups were employed. Six groups had at least a significant variable. Among them: the number of islands that contained reed and water waste. The last analysis using the significant variables showed that probability of white-headed duck occupying a lake increases when the lake presents islands or shorelines covered with vegetation, mainly reeds or canes.

CB-11
Vertebrates' taxonomic and functional diversity are well represented in Iberian protected areas

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The Iberian Peninsula hosts a network of protected areas that harbour half of Europe's biodiversity. Traditionally, protected areas have been designed focusing mainly on taxonomic diversity, ignoring other diversity components such as functional diversity. The main goals of this study were to evaluate whether the Iberian network of National and Natural parks includes a good representation of: i) terrestrial vertebrates' taxonomic and functional diversity; ii) endangered species; and iii) functional groups defined by dietary requirements. We used species distribution and functional trait data (obtained from the literature) for all terrestrial vertebrates to calculate taxonomic and functional diversity measures for each park. Observed diversity values were compared with those obtained from a random assembly of species from the park's surrounding area, using several pools defined by different distance buffers from the parks' borders. Our results suggest that Iberian parks host a good representation of the regional taxonomic and functional diversity, with the only exception being found for birds, as this group's functional diversity is usually lower in protected areas than expected by chance. Further, National and Natural parks include a good representation of endangered species and also of some functional groups. Although, our results show a general good representation of Iberian taxonomic and functional diversity in existent protected areas, this does not guarantee the future persistence of Iberian biodiversity due to potential impacts driven from climate and land-use change.

CB-12

Modeling distributions of Arctic mammals for effective conservation

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The Arctic marginal sea areas will be important as future transportation routes, however there is only a limited amount of information about the ecosystems and their vulnerability to marine traffic. This is due to the scarce survey data, especially along the Northeast Passage. Here we made an effort to reveal the habitat characteristics of polar bears, ringed seals and walruses and modeled their distributions in the Kara Sea along the Siberian shelf area. We tackled the data shortage by introducing a methodology for modeling different types of survey data jointly to increase the accuracy of the model predictions. The data consisted of *in situ* species sightings made by researchers but without information about the detection probability. Sightings were modeled as a point process, which was explained with known environmental conditions and unknown survey effort and spatiotemporal random effect. Polar bears and ringed seals were well explained with ice cover and distance to the coast, and additionally polar bears were explained with the predicted abundance of ringed seals highlighting their dependence on their main prey. Both species may be present, when sea ice covers over a half of the study cell, whereas polar bears stay further away from the coast than ringed seals do. Walruses were abundant in the coastal areas but their habitat characteristics came with high levels of uncertainty. Furthermore, we could predict the seasonally varying species distributions and give probabilistic assessments about species abundance along the main traffic lines and in areas of natural resource excavations.

CB-13

How to make the theory of source-sink dynamics operational at biogeographical scale? Applications to butterflies' conservation biology

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The species geographical range presents an internal complexity due the different conditions in which a species can occur in the territory, some parts acting as sources and others acting as sinks. This is usually hidden from the observer's eye. Modelling of the species distribution can be used to assess the differential favourability of different parts of the species ranges. We can reasonably assume that environmental favourability for species occurrence is related to their demography, although testing this assumption would require broad-scale birth and mortality rates that normally are not available. We modelled the distributions of the 222 Iberian butterflies using Favourability functions and 92 environmental variables. We obtained a significant environmental favourability model for each butterfly. We identified the potential sources and sinks in the distribution area of each butterfly species using their respective favourability and presence–absence maps, considering as sources only those areas with high favourability where the butterfly is present, and sinks only those areas with low favourability where the butterfly is present too. For each grid cell, we computed its consideration as source or sink for every species. Most of the sources areas are located in the mountain systems (Central Pyrenees, Cantabrian Range, Central Range and Baetic Range). Sinks are less spatially structured, but they are concentrated in the eastern part of the study area (Alicante and Murcia provinces), and the Doñana National Park, in the southwestern part. Butterfly conservation strategies should be different in each kind of areas.

CB-14

Evolutionary history predicts the response of tree species to forest loss: A case study in peninsular Spain

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Evolutionary history can explain species resemblance to a large extent. Thus, if closely related species share combinations of traits that modulate their response to environmental changes, then phylogeny could predict species sensitivity to novel stressors such as increased levels of deforestation. To test this hypothesis, we used 66,949 plots (25-mradius) of the Spanish National Forest Inventory and modelled the relationships between local (plot-level) stem density of 61 Holarctic tree species and forest canopy cover measured at local and landscape scales (concentric circles centred on the plots with radiuses of 1.6, 3.2 and 6.4 km, respectively). Then, we used the output model equations to estimate the probability of occurrence of the species as a function of forest canopy cover (i.e. response to forest loss), and quantified the phylogenetic signal in their responses. Most species showed a lower probability of occurrence when forest canopy cover in the plots (local scale) was low. However, the probability of occurrence of many species increased when forest canopy cover decreased across landscape scales. We detected a strong phylogenetic signal in species response to forest loss at local and small landscape (1.6-km) scales. However, phylogenetic signal was weak and non-significant at intermediate (3.2-km) and large (6.4-km) landscape scales. Our results suggest that phylogenetic information could be used to prioritize forested areas for conservation, since evolutionary history may largely determine species response to forest loss. As such, phylogenetically diverse forests might ensure contrasted responses to deforestation, and thus less abrupt reductions in the abundances of the constituent species.

CB-15

How many amphibian species are there and where?

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Advances in geoprocessing and satellite imagery boosted our knowledge of the Earth's physical environment, but many pieces of the Earth's biodiversity puzzle are still lacking. Conservative estimates indicate that we know less than 20% of all living species of the planet. Mapping the missing pieces of the biodiversity puzzle can help scientists and decision makers to identify where on Earth we should put more boots on the ground. We used information on description dates of 6,500 amphibian species to build time-to-event models across grid cells globally. We incorporated species-level information on body size, geographic range size, and taxonomic effort to estimate the percentage and number of undescribed species, and the amount of time needed to complete amphibian species descriptions worldwide. Our findings show that species-rich regions are the most rewarding places for future amphibian discoveries, particularly the tropical/subtropical moist forests and mangroves in the Neotropics, and tropical/subtropical dry forests in the Afrotropics. In addition, mangroves, tropical/subtropical savannas, and deserts/xeric shrublands are the regions with the lowest rates of species description. At the current rate of species descriptions, these latter regions might require more than one century to complete species discoveries.

CB-16

A study on prey resource compositions of herbivore wild animals in the Hustai National Park Mongolia and their competitions for the resources

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The Hustai National Park (hereinafter called HNP) in Mongolia was certified as a wildness area by the government in 1992 to reintroduce Takhi. It is a habitat for them as well as red deer, Mongolian gazelle, wolves, and others.

After the wildness area certification in 1992, grazing and capturing of wild animals in HNP has been prohibited, and the inhabiting number of wild animals keeps rising. By transect researches of the past, it is proved that Takhi and red deer inhabit overlapping areas. It seems more likely that prey resources are competing against each other. Also, it is proved that the understory vegetation in a land shall be changed when herbivore wild animals become overcrowded. So, it is important to clarify compositions of prey resources for such herbivores in HNP in order also to manage national parks.

This study aims to clarify compositions of prey resources in the Hustai National Park as well as to make more clearly feeding frenzies between species, by the investigation of vegetative plotting.

CB-17

Biogeography of Nepeta hispanica, a plant growing on gypsum habitat islands across the Iberian Peninsula

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Gypsum soils form island-like habitats across the world, and they support peculiar plant communities. *Nepeta hispanica* Boiss. & Reut. is an herbaceous geophyte that lives in xeric environments mainly linked to gypsum-containing soils in Spain and Morocco. It is morphologically similar to *N. ucranica* L., distributed in eastern Europe and Asia. In the Iberian Peninsula, conditions favourable to *N. hispanica* are found near large river basins, which were endorheic seas during the Paleogene. In this research, we investigated the biogeography of *N. hispanica* at multiple scales. First, we evaluated the relationship between *N. hispanica* and *N. ucranica* in the context of a phylogenetic analysis of the genus *Nepeta*. Second, we conducted a phylogeographic analysis of Iberian populations of *N. hispanica* based on plastid DNA sequences of the *trn*S-*trn*G and *psb*J-*pet*A regions. The aim was to reconstruct historical connections and relationships, and to evaluate the degree of isolation among populations growing on island-like gypsum habitats. In addition, since *N. hispanica* is an endangered species in the Spanish Red List, a risk assessment was done, and a Species Distribution Model was inferred to help find new populations and to predict the future of this species under different climate change scenarios.

CB-18
SPATIAL PATTERNS IN HABITAT SPECIALIZATION OF EUROPEAN BIRD COMMUNITIES

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The level of habitat specialization is informative in terms of animals' space use and life-history evolution. In the context of global change, we are witnessing how specialists are slowly declining. Under this scenario, identifying the areas where specialist species are aggregated and understanding the ecological constrains that might shape their distribution has become an important issue, not only for their conservation but also to understand the ecological implications of specialization. In this sense, we test whether specialist communities are more likely to succeed in milder and stable environments or in harsh less predictable environments. For that purpose, we used data from the EBCC atlas of European breeding birds and for each of 50x50 km grid cells calculated several community specialization indexes (CSI). We used generalized least squares models to relate these measures to geographic and climatic variables across Europe. We identified two areas, Scandinavian peninsula and the southernmost lowlands of Russia, where bird communities are highly specialised. Moreover, high level of specialization was registered in montane regions of Europe. Concerning climatic variables, we found that specialist spatial distribution was significantly affected by extreme temperatures and lower level of precipitation. Our results thus suggest that European specialist birds tend to be successful in harsh environments. Thereby, preserve these sensible environments from further perturbations might be the key for the specialist conservation. Furthermore, the presence of one "hotspot" of specialization in the Russian lowlands serve as example of how important might be inclusion of such understudied eastern Europe regions into continent-level analyses.

CB-19
Drastic landscape change on Shola Sky Islands indicates rapid fragmentation and isolation of montane grassland habitats and its birds, more than forests

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Tropical montane habitats, including the shola sky islands in the Western Ghats, host several threatened taxa of which, the global distributions are restricted to these mountain-tops. The rapidly increasing human footprint and the spread of invasive alien plants have already resulted in the local extinction of several taxa. Here we examine the entire shola sky islands ecosystem to estimate the extent of habitat loss and to create a baseline of land use in this rapidly changing landscape. We further examine the occurrence of a montane-grassland specialist bird, Nilgiri Pipit across its global distributional range, to understand the impacts of habitat fragmentation. We used a combination of LANDSAT and Sentinel imageries from 1973, 1995 and 2017, with 840 ground truth points across the ecosystem. We find substantial landscape modification in the large high elevation plateaus (7-60%) over the last four decades while changes are muted in the other parts. The loss of grasslands to timber plantations (particularly Acacia) predominates (23.4%) the modification of this landscape, and, continues today at a rapid pace. Contrary to popular belief, shola forests have been relatively stable, implying that most timber plantations were established on grasslands—traditionally classified as "unproductive wastelands". The existing grasslands are highly fragmented with only a few (<10) large remnant grassland patches that harbour Nilgiri Pipits today. The large-scale local extinction and the reduction of the global distribution of this threatened, sky-island endemic species (~400 sq.km) is an indicator of impacts of the continuing spread of invasive species.

CB-20

Combining remote sensing data and habitat suitability models to monitor species' extinction risk through the IUCN Red List

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The IUCN Red List is the most authorative and widely used framework for assessing the relative extinction risk of species. The criteria contain quantitative thresholds relating to the size, trends and structure of species' distributions and populations. Data on these parameters are, however, sparse and uncertain for many species, and unavailable for others leading to their classification as Data Deficient. Here we propose an approach combining data on land-cover change and species-specific habitat preferences, population abundance and natal dispersal distance to estimate key parameters and hence IUCN Red List categories. We demonstrate the applicability of our approach for birds and mammals globally (~15,000 species), generating predictions fairly consistent with published Red List assessments, but more optimistic overall. We predict 3.5% of species (400 birds and 125 mammals) to be more threatened than currently assessed, and 19.4% of Data Deficient species (8 birds and 108 mammals) to be at risk of extinction. However, incorporating habitat fragmentation sub-criterion reduced the proportions 1.2-1.8% and 3.2-10.4% (depending on the quantitative definition of fragmentation applied), highlighting the need for improved guidance to Red List assessors on applying this aspect of the Red List criteria. Species that are predicted to be more at risk than currently evaluated should be prioritized for reassessment. Our approach can be used to complement traditional methods of estimating parameters for Red List assessments, and can provide an early warning system to identify species potentially warranting changes in their extinction risk category based on periodic updates of land cover information.

CB-21

Landforms increase plant biodiversity at Rokua Global Geopark, Finland

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Global biodiversity loss is a matter of urgent concern. Thus, better understanding of local biodiversity drivers, such as abiotic environmental heterogeneity, is crucial for conservation management. Although geodiversity (the abiotic richness of the earth's surface) is recognized as an important determinant of biodiversity, this has rarely been explored at local-scale. In this study we seek answers to two main questions: (1) are there differences in biodiversity between distinct geofeatures (or landforms, such as kettle holes, beach ridges or lake shores) and control sites (i.e. null model, or sites without any distinct geofeatures), and (2) how does biodiversity vary among different geofeatures. To gain answers to these questions, we examine several indices of vascular plant species diversity and rarity in levels of alpha, beta and gamma diversity in relation to ten different geofeatures and a control habitat. The study area is located at boreal vegetation zone, at Rokua UNESCO Global Geopark area which is dedicated for geoconservation and geotourism. Based on our results, most of the geofeatures harbored greater biodiversity than the control sites. Additionally, different geofeatures sustained various amounts of biodiversity. Our results encourage

exploring and integrating geodiversity and biodiversity in further studies, especially with geofeatures in the focus. Furthermore, the value of geodiversity in local and global conservation planning is enhanced.

CB-22

Current potential non-breeding range of the Golden-winged Warbler (Vermivora chrysoptera)

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The Golden-winged Warbler (*Vermivora chrysoptera*) is a species of interest for conservation due to the decline of its populations in recent decades. In response the GWWA has conducted surveys in Latin America since 2009 aiming to improve the knowledge of its range and ecology. We modelled the GWW non-breeding range with historic and new field data, and a series of climatic and environmental variables implementing the MaxEnt algorithm. Our results suggest that current range, estimated from new field data and several environmental variables, fills scantily (< ≈20%) the potential habitat suitable for the species predicted by a model based on historic data and pure climate. This pattern was exacerbated when models were restricted to current forest remnants (≈9–11%), and instead, areas covered by croplands emerged as of potential relevance (≈63–70%). It is necessary to advance our knowledge on the importance of this type of "Anthrome" for the survival of the GWW during the non–breeding season and its migration to and from Boreal regions, which may contribute to clarify its true potential contribution for the conservation of this species.

CB-24

Conservational genetic evaluation of Emei Shan liocichla (Liocichla omeiensis)

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The Biodiversity is unevenly distributed on the world and the endemic organisms are the key part of conservation. It is essential to evaluate the population structure and gene flow pattern of endangered species in conservation; however, we almost have no these information of lots of endemic species. Hence, we employed next generation sequencing technique to develop microsatellite and then estimate the population structure and migration pattern of Emei Shan liocichla (*Liocichla omeiensis*). *L. omeiensis* is an endemic passerine bird mainly distributed in Hengduan Mountain, a biodiversity hotspot in southwest of China. Due to the disturbance of human activities in recent years, the habitat of *Liocichla omeiensis* is more fragmented, and its population keeps declining, therefore it was listed as "vulnerable" by the IUCN. With 64 samples from six fragment populations, we carried out the RAD-seq for developing microsatellite, and identified 24 novel microsatellite loci. The main results as below: (1) There was gene flow between populations. (2) STRUCTURE and PCoA both showed that all samples should be one genetic unit. (3) Mantel test suggested that these populations did not comply with "Isolation by Distance" model. (4) The effective population size is 340. These results implied this endemic species need to be protected urgently, and rejected the preconceive that *Liocichla omeiensis* does not migrate horizontally, which enlightened us that in conservation, we could regard all populations as one conservation unit. The current project shows us the importance of using genomic technique in conservation.

CB-25

Biogeographic patterns of population structure and dynamics of a serotinous conifer, knobcone pine (Pinus attenuata)

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There is great concern that populations of fire-adapted species exist in a decadent state and are at risk of local extirpation due to 20th century fire (i.e. senescence risk). Concurrently, increasing fire activity is prompting concern that short interval, repeated fire poses a risk to young stands before trees reach reproductive maturity (i.e. immaturity risk *or* interval squeeze). Conceptual models assessing vulnerability to both risks exist, yet there is a lack of empirically-based studies that examine how these risks varies geographically across the range of a fire-adapted species. We used geospatial data on fire occurrence (1900 to 2015) and a systematic sample of re-measured forest inventory plots across the range of a serotinous conifer, knobcone pine in southwestern Oregon and California, U.S.A., and assess immaturity and senescence risk based on: 1) fire history; 2) geographic variability and changes in stand-scale population structure, and 3) patterns of local colonization, extirpation, and population change. Most knobcone pine populations exist in a mature, decadent state, newly initiated stands were relatively rare, and repeated short-interval fires (<15 years) occurred across <1% of the species' range. Approximately 12% of the re-measured plots experienced extirpations over the ten-year period, but new colonizations (less than half of which were associated with fire) were almost double extirpations and resulted in the cumulative expansion of knobcone pine. We provide a geographic framework for assessing range-wide population structure and dynamics of fire-dependent species and highlight the potential for alternative pathways of persistence for serotinous species under anthropogenically altered disturbance regimes.

CB-28
Disentangling the factors affecting the expansion of large carnivores in Europe

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In the last few decades, large carnivores have made a dramatic recovery across Europe and nowadays almost all mainland European countries have at least one permanent and reproducing population of large carnivore. Different possible factors have been proposed to explain this recovery, as the implementation of national and international conservation laws such as the EU Habitats Directive and Bern convention, abandonment of agricultural land and change in perception of society towards these species. With this work we want to investigate the relationship between the drivers of the expansion of three of the European large carnivore's species (the wolf, the Eurasian lynx and the bear). Specifically, we aim to assess the relative influence of land cover change and human population density through the development of multitemporal species distribution models. We built the multi-temporal SDMs based on GLMM lasso approach. We used the NUTS2 regions as random effects in order to account for the different local management, the diverse perception of the species by local community, and possible context-specific responses to the different predictors across Europe. We predict how the species probability of presence changed in Europe between 1992 and 2015, building SDMs related to the entire timeframe, and re-projecting the distribution at different time steps within the temporal window considered.

CCB-01
Aridity and land use negatively influence a dominant species' upper critical thermal limits.

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Understanding the physiological tolerances of ectotherms, such as thermal limits, is important in predicting biotic responses to climate change. However, it is even more important to examine these impacts alongside those from other landscape changes: such as the reduction of native vegetation cover, landscape fragmentation and changes in land use intensity. Here we integrate the observed thermal limits of the

dominant and ubiquitous meat ant *Iridomyrmex purpureus* across aridity, land cover and land use gradients spanning 270km in length and 840m in altitude across northern New South Wales, Australia. Meat ants were chosen for study as they are ecosystem engineers and changes in their populations may result in a cascade of changes in the populations of other species. When we assessed critical thermal maximum temperatures (CT_{max}) of meat ants in relation to the environmental variables we detected a negative aridity effect on CT_{max}, a negative effect of land use intensity, and no overall correlation between CT_{max} and CT_{min}. We also found a negative relationship with warming tolerance of *I. purpureus* and landscape aridity. Our findings suggest that as land use intensity and aridification increase, the physiological resilience of *I. purpureus* will decline. A reduction in physiological resilience may lead to a reduction in the ecosystem service provision that these populations provide throughout their distribution.

CCB-02

Potential distribution of Picea (spruces, Pinaceae) in Mexico during the Last Glacial Maximum.

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In Mexico, three species of *Picea* considered as endangered by the Official Mexican Standard NOM-059-SEMARNAT-2010 are distributed, all of them are restricted to the north of the country, in the Sierra Madre Oriental and Occidental. However, these species may have had a larger distribution during the Last Glacial Maximum (LGM), 22000 years ago when the temperature was colder. The objective is to reconstruct the potential distribution of *Picea* in Mexico during the UMG using the ecological niche models. The results show that the three species could have a wider distribution during the UMG, at lower altitudes, and southern latitudes, this due to the predominance of colder temperatures. In the past, the potential distribution of *P. chihuahuana* could have been 1.6 times greater than at present (it has been reduced by 38.8%), for *P. mexicana* 5 times more (it was reduced by 80.8%) and P. martinezii 14 times larger (93% reduction). It is also observed that *P. chihuahuana* presents favorable conditions mainly in the Sierra Madre Occidental, *P. martinezii* in the Sierra Madre Oriental, while *P. mexicana* encompassed both mountain ranges and was linked by a corridor located in the southern part of the Altiplano Mexicano. These species were an important component of the vegetation, and in the present, they are a relict of the last deglaciation. According to the response observed in these species, it is very likely that they will disappear in the future due to global warming, if new conservation strategies are not developed

CCB-03

Predicting climate change impacts on bears (Ursidae) species' distributions in America

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Changes in climatic conditions greatly influence the geographic distributions of the species and are likely to continue to affect species in the future, however the change that is taking place today is occurring at an unprecedented rate. Predictions about how these changes will affect the biodiversity are necessary to carry out conservation planning. Bears are large carnivores that play an important role in the ecosystem since they are charismatic and umbrella species, but they are facing serious threats and are experiencing massive declines in their populations and geographic ranges around the world. We assess the potential impact of climate change on the geographic distribution using species distribution models of three species of bears that inhabit America (*Ursus americanus, U. arctos* and *Tremarctos ornatus*) under two climatic data sets (current and future 2070). Our results indicate a likely strong reduction in species' distributional areas especially in *U. americanus* that was predicted to decrease more than 60% its distribution, *T. ornatus* may lose 50% and *U. arctos* 70%, but particularly in this last species may increase its distribution because areas that are currently unsuitable, in the future it will change suitable under climate scenarios. We identified areas that are most vulnerable to climate change effects, which can and should focus priorities for protection of this ecosystem, and it is important to analyze the changes that will be occur in the composition of species communities as well as the ecological interactions.

CCB-05

Bumblebee Venom: A potential early indicator of Climate change

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Hymenoptera is a diverse insect group with members exhibiting different life styles and inhabiting different ecological niches. Among Hymenoptera are bumblebees which are the closest relatives of honeybees and are one of the two members of the family Apidae. It is estimated that there are 250 species of bumblebees around the world, and to our knowledge, there are 30 in the western Swiss Alps. They are important pollinators of naturally produced and cultivated plants. Here, we propose to analyze an adaptive trait - the venom - of bumblebees, a key defense tool for these species. Bumblebee venom is a complex biofluid composed of unique mixtures of proteins and peptides, exclusively and dynamically tailored for the need of the species and is a clear example of convergent evolution. The aim of the study is to detect any possible variation in venom properties along environmental gradients and use these findings to assess potential venom response to climate change. We have collected *B. pascuorum* populations from different elevational gradients from the Western Swiss Alps (930-1360-1700m). Venom proteins were identified by using shot-gun proteomic approaches. This data will be correlated with ecological modelling approaches. Potential correlations identified between changes in venom composition and structure and changes in environmental conditions will be ultimately used to develop a potential venom-based system of early indicator of climate change.

CCB-06

Projected Eastern Hemlock Redistribution in Maine using Climate Scenarios

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Introduced invasive pests and climate change are perhaps the most important and persistent catalyst for changes in forest composition. Infestation and outbreak of the hemlock woolly adelgid (HWA, *Adelges tsugae*) along the eastern coast of the USA, has led to widespread loss of hemlock (*Tsuga canadensis* (L.) Carr.), and a shift in tree species composition towards hardwood stands. Maine's forest dominated landscape and position at the leading edge of the HWA invasion provides an excellent opportunity to use spatially explicit models to predict future range shifts of the foundation tree species, eastern hemlock in Maine.

Given the importance of climate variables in predicting the current distribution of eastern hemlock (Dunckel et al. 2015), forecasts of future range shifts are possible using data generated through climate scenarios. The NASA Earth Exchange (NEX) Downscaled Climate Projections (NEX-DCP30) dataset was used to model future shifts in the geographic range of eastern hemlock throughout the state of Maine. The results clearly describe a significant shift in eastern hemlock range with gains in total geographic area that is suitable habitat.

CCB-07

Predicting climate change effects on global vegetation patterns using a trait-based approach

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Dynamic Global Vegetation Models are used to quantify future changes in vegetation. These models use plant functional types (PFT), assuming that all species within a PFT respond similarly to different kinds of change, and that among species relationships remain similar. However, some species might be more resilient or resistant to change, and others might adapt faster to cope with change. To overcome this inflexibility, trait-based modelling has been introduced, where plant traits rather than PFTs are related to climate. Most prevalent advantages of this method are that 1) among and within species variation is included, and 2) uncertainty of model predictions is reduced, as vegetation processes are more realistically modelled. As this results in more realistic models and predictions, trait-based modelling is especially suitable for predicting future changes in plant communities.

In this study, we aim to quantify the effect of climate change on global terrestrial biome distributions in terms of plant traits and biomes, and indicate areas of major change. First, we predict current distributions of plant height, specific leaf area, and wood density using ensemble forecasting. Here, trait community means were related with climate variables, soil properties, and fire frequency using four different models. Second, we cluster trait combinations to biomes using a Gaussian mixture model. Effects of climate change are predicted using space-for-time substitution: future plant traits are predicted under different climate scenarios, which might result in predicted biome change. Locating future biome changes will help allocate large-scale conservation efforts with regard to climate change effects.

CCB-08

Oscillayers: A framework for the study of climatic oscillations over Plio-Pleistocene time scales at high spatio-temporal resolution

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Understanding how species responded to Plio-Pleistocene climate oscillations is of great utility in understanding the evolution of organisms and can provide guidance on how extant species will respond to future anthropogenic climate change. However our ability to discern how climate fluctuations have affected the evolutionary response of organisms in terms of speciation, extinction and adaptation is limited due to the lack of global-scale climatic datasets with high temporal resolution spanning the Plio-Pleistocene. To fill this gap I here present, *Oscillayers*, a framework for the generation of global-scale and region-specific bioclim datasets, facilitating the study of climatic oscillations during the last 5.4 million years at high spatial (2.5 arc minutes) and temporal (10 kyr time periods) resolution. This multi-step procedure builds upon interpolated anomalies (Δ layers) between bioclim layers of the present and the Last Glacial Maximum (LGM) that are scaled relative to the Plio-Pleistocene global mean temperature curve, derived from benthic stable oxygen isotope ratios, to generate bioclim variables for 539 time periods. Evaluation of the scaled, interpolated estimates of paleoclimates against independent General Circulation Models (GCMs) for three time periods (6 ky, 120 ky and 3 million years ago) showed good agreement. *Oscillayers* thus provides new perspectives for studying spatio-temporal patterns of evolutionary and ecological processes at high temporal and spatial resolution.

CCB-09

Effects of climate and phylogeny on thermal limits in Chilean Liolaemus.

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Biological responses to climate can be the outcome of phenotypic plasticity, population dynamics, or adaptive evolutionary processes. Even though there are examples of rapid evolutionary processes it remains open to question whether thermal traits evolve sufficiently fast to keep pace with species physiological requirements under climate change. We used physiological and climatic data in combination with a time calibrated phylogeny to analyse the relationship between climate, species thermal limits and preferences and phylogenetic distances across a sample of 37 species of chilean *Liolaemus* lizards. We found that current climate change is several orders of magnitude faster than the fastest evolutionary rate of change detected for thermal traits. Physiological adaptation to climate change would require evolutionary rates that seem unprecedented in the history of the clade. Therefore, adaptation to global warming by increasing physiological temperatures seems unlikely. Thermal traits show little phylogenetic signal with the exception of preferred body temperature and field body temperature. A correlation between weight and field body temperature is only apparent when controlling for phylogenetic effects, showing that phylogenetic autocorrelation can mask the relationships between variables (and therefore create a false negative).

CCB-10

Registry of rare aquatic birds as an indicator of droughts attributable to climate change

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Within the predictions of the impact of climate change in Spain is the arrival of new species from Africa, forecasts that should materialize in an increase in the number of observations of rare birds from the African continent.

In our country, we have the work done by the Rareness Committee of the SEO, whose reports are published periodically in the magazine Ardeola, published by this company. The objective of this communication is to evaluate the available information on rare aquatic birds of African origin observed in mainland Spain and the Balearic Islands, describe trends in the number of homologated records and investigate their relationship with the incidence of meteorological events such as droughts attributable to the change climate. The initial results for the period 1985-2016 indicate that there is a significant increase in the number of rare bird species and their appointments in our country, considering in this work as rare birds 12 species of aquatic birds. It is tested as hypothesis that this increase may be due to extreme weather events of droughts in the African continent that may favor the arrival of birds seeking alternative wetlands. To characterize the droughts attributable to climate change, the values of the SPEI index have been used. It is also explored to what extent this increase in the observations of rare birds in our country may be related to a greater observation effort because of an increase in birdwatchers.

CCB-11
Butterfly richness in the Iberian Peninsula and Global Warming: the short-term future

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Using an updated account of occurrence data on the butterflies (Lepidoptera: superfamily Papilionoidea) of the Iberian Peninsula referred to a grid of 50 x 50 kilometers we estimated the degree of completeness of the inventories and the observed species richness. The observed richness was modelled on the basis of climate variables while controlling for the density of sampling effort and area, and the results extrapolated to a reasonable near-future scenario (50 years). As far as temperature played a central role in the models fitted to present data, expected future species richness was systematically predicted to decrease across the whole area.

CCB-12
Determination of forest microclimate from remote sensing proxy variables

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Bioclimatic models forecast redistribution, assemblage change and extinction risk for many species as a result of the anthropogenic climate change. However, these predictions mostly stand on coarse interpolated climate measurements and neglect microclimate heterogeneity relevant for terrestrial habitats. In our study, we point out that even within a 20-ha temperate forest, annual average temperature varied nearly 1° C, even more in temperature extremes. Contrary to expectations, there was found minimal variability in geomorphometric characteristics, suggesting a dominant role of the forest canopy cover in modifying its interior environment. Such a relationship was confirmed by assessing canopy openness properties based on an analysis of hemispherical photographs. However, hemispherical photographs provide purely discrete information about local forest canopy architecture, and are difficult to scale up. Therefore, we discuss several alternative forest structural metrics derived from UAS laser scanning as spatially continuous and highly detailed proxies of near-ground temperature. Though our results show a medium strength of statistical relationship (probably because of partial stochasticity of microclimate and other explanatory predictors), we consider the remote sensing of microclimate proxy variables capable to improve future bioclimatic modellig.

CCB-13
Mapping the range-wide pattern of disappearing and novel genotypes of balsam poplar in future climates

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A central challenge to predicting climate change effects on biodiversity is integrating information on intraspecific variation, specifically population-level local adaptation to climate. Directly assessing how climate change will disrupt current patterns of local adaptation can provide nuanced information about population's exposure to climate change – including where climatically adaptive genotypes may disappear from the landscape, where new novel genotypes may emerge, and how far populations would need to migrate to minimize genetic differentiation. To address this challenge, we used models of genetic differentiation of balsam poplar (*Populus balsamifera*) populations to predict the range-wide geographic

patterns of local genomic change, disappearing current genotypes, and future novel genotypes by 2070. High local genomic change, and disappearing current genotypes are predicted to occur along the northern and eastern range edges, while future novel genotypes are expected to emerge in the extreme eastern and northern portions of the range. In contrast, the center portion of balsam poplar's range is predicted to have low levels of local genomic change as well as low future novelty. Distances to future locations that minimize genomic offset were shortest in the southern and northern parts of range, but increased toward the eastern range edge. Our work combining genomic information with spatial models provides insights into the tradeoffs population's may face in future climates and illustrates the value of integrating intraspecific variation with predictions of climate change effects on biodiversity.

CCB-14

Coral diversity hotspots tend to shift to subtropical marine ecoregions under climate warming

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The accelerated bleaching events in recent decades have brought coral reef ecosystems under spotlight. However, coral diversity, a major indicator of coral reef health, has been underemphasized with limited quantitative studies. Here we adopted a robust modeling framework to project diversity change of the whole coral group into next three centuries, with species distribution models on 531 species (covering 11 genera) based on 32000 occurrence data. We show that: 1) coral species richness is declining in tropical marine ecoregions and rising in subtropical ecoregions within all studied time periods. Species turnover rates are generally high. Net species richness gain and loss can be roughly delimited by the latitudinal parallels around 15-20 degree (N/S), depending on time scales and greenhouse gas emission scenarios. 2) Tropical corals in the Western Pacific tend to shift their ranges to higher latitudes both northward (around Japanese islands) and southward (southern Australian and New Zealand marine ecoregions), while Caribbean corals generally loss suitable habitats with little new supply in higher latitudes; 3) Under RCP4.5 greenhouse gas emission scenario, coral species turnover rate peaks in the next century and then slows down, while under RCP8.5, it keeps at a high level in all the coming three centuries. It seems inevitable that lots of coral species will shift their ranges to higher latitudes, which causes fundamental changes in coral diversity patterns and community assemblies. Our results suggest the necessity of a global scale scheme of coral conservation and proactive actions (e.g. assisted migration).

CCB-15

Extinction can be also a creation phase: the conceptual framework of perfugia and the 'trailing-edge' relicts

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During the species range restriction, populations are typified inter alia by a reduced gene flow and smaller size. However, they can also be driven by the creation of new relationships with changing abiotic and biotic factors. The extinction phase can then be paradoxically a dynamic period when the ecological foundation can be laid for the future long-time species persistence in the region in microrefugia. The concept of 'trailing-edge relicts' (young relict populations) and 'stabilized relicts' (old relict populations) clearly corresponds to the above processes. Younger 'trailing edge' populations often occur near the core range of the species and have recently become isolated. In contrast, the oldest 'stable' climate relicts have persisted for a long time over changing climate conditions. To distinguish between the sites with young and old relict populations, we propose the Latinised term 'perfugium'. During unfavorable changes in the region, species extinction occurs and increasing numbers of isolated localities are established. These can be termed

perfugia. Over time, unsuitable abiotic conditions, degenerative genetic processes or the lack of adequate (new) ecological configurations can result in extinctions. The occurrence of the species in the region becomes possible only in microrefugia – perfugia with the highest refugial capacity. The conceptual schemes given in our presentation summarise and develop the patterns which occur during species range shift. We highlight the importance of sites harbouring 'trailing-edge' young relicts in the future long-term persistence of the species, as old relicts.

CCB-16

Assessing the vulnerability to climate change of six Iberian soil moss species through field and mesocosm experiments

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Bryophytes are useful bioindicators of the state of ecosystems. Their sensitivity to pollution and climate is linked to their dependence on thermal and hydric environmental balance. They also play an important role in the ecosystems, providing several key ecosystem services such as regulation of the water cycle, carbon sequestration or soil stabilization. Thus, they can inform about climate change-driven variations in ecosystem functioning. We developed a protocol to assess the growth of non-vascular cryptogams (bryophytes and lichens) in both field and growth chamber conditions. This protocol involves measuring conductance and remote sensing indices, which allows us to estimate in situ the period of effective growth of bryophytes or lichens in relation to environmental conditions (temperature and humidity). We applied this protocol to six common Iberian soil moss species with different environmental preferences, as representatives for the whole soil moss community. We characterized their fundamental climatic niche through their response curves to changes in temperature and water availability in field and controlled conditions. Then, we compared their fundamental niches with their realized responses to temperature and precipitation during their growing season in the geographical space considered. Based on this, we reconstructed the relationship between fundamental and realized niche for each species, and projected it to future climatic conditions to determine their vulnerability to climate change. We use these results to identify potentially vulnerable groups of Iberian moss species, to pinpoint particularly sensitive geographic areas, and to forecast changes in ecosystem service provision by Iberian soil moss communities. p { margin-bottom: 0.25cm;

CCB-17

Linking biogeography and evolution: environmental variation and evolutionary dynamics of phenotypes in wild bird populations

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Natural selection is the main mechanism and most powerful explanation for adaptive evolution, and environmental variation is the main fuel that feeds the engine of natural selection. From a microevolutionary perspective, evolution can be detected within populations where natural selection acts on the expression of phenotypes. We are starting to unravel how and what agents of selection can cause evolutionary adaptation within a temporal perspective. However, our knowledge is rather limited towards very few species that are experiencing particular environmental conditions. In addition, and unsurprisingly, biogeographically dispersed populations of the same species can respond differently to the same agent of selection, i.e. climate change is expected to have different evolutionary responses depending on the environmental conditions that every population experiences. Here we illustrate how evolutionary dynamics of phenotypes and biogeography can be married using species distribution models built with the favourabilityfunction. We use own and bibliographic-based data gathering more than 1400 estimates of evolutionary traits in wild European populations of birds. We found that selection gradients increase as environmental favourability increases for secondary sexual traits in pied flycatchers (*Ficedula hypoleuca*). At multispecies level, we also found that both evolvability and selection gradients of multiple phenotypes are linked to environmental favourability in a non-linear way: selection and evolvability decreases at both ends of environmental favourability. We suggest how intra- and inter-specific interactions within populations might explain these patterns. More importantly, we present a new methodological approach to link both fields of research and discuss its limitations and benefits.

CCB-18

Predictive biogeography of soil bacteria in mountain environment

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Soil bacteria forms a large proportion of biodiversity, yet little is known of their biogeography. Further, very few forecasts of influence of changing environment on soil bacteria exist. Here, we aim to fill these gaps by applying spatial modelling techniques on a bacterial metagenomics dataset representing soil samples from 265 sites in mountain environment and covering wide environmental gradients (e.g. elevation 425-3119 m.a.s.l.). Targeting V5 region of the 16S rRNA gene, bacterial DNA of the soil samples were sequenced in Illumina HiSeq 2500 platform. The resulting paired-end sequences were clustered to operational taxonomic units (OTUs) both using close-reference (QIIME with gg_13_8 database from Greengenes as a reference) and De Novo approaches (custom scripts with SILVA rRNA database as reference for taxonomic annotation). Close-reference approach identified 15’769 OTUs, while De Novo clustering resulted in 75’009 OTUs. Taxonomic annotations for the OTUs were found at least until family level for most identified OTUs. Based on a subset of the data, edaphic factors (e.g. soil pH and moisture) were found as most influential in driving distribution and abundance of bacteria. Number of OTUs decreased with elevation. Bacteria also responds to climatic factors, and changes therein, according to our

preliminary habitat suitability models: with warming temperature, most bacterial genus and orders benefit from warming with increased habitat suitability within our study area. Increases in suitable habitat occurs especially in higher elevations, resulting in positive change in richness of bacterial genus, and strong change in community composition of both genus and orders in higher altitudes.

CCB-19
Environmental correlates of food web structure

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The study of food webs started as early as the 1920s. One of the many areas of research explores the relationship between aspects of the environment and the structural characteristics of the food webs. Yet published studies have focused mainly on the study of food webs in specific locations or ecosystems and a general synthesis of the relationships between food web structure and environmental variables is still missing. We list several of the patterns identified in food web ecology and explore the circumstances in they might or might not be verified. We also note that despite the high number of studies, strong geographical bias exists towards Europe and most are fine-scaled, encompassing short temporal periods and focusing on marine ecosystems. Therefore, there is still limited capacity to generalise patterns regarding the relationship between food web structure and environmental variables.

CCB-20
Evaluating the influence of bioclimatic variables on the potential distribution of allium sativum in the Philippines

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Anthropogenic climate change is projected to alter the geographic distribution of crops. However, there have been few studies modeling the impact of climate change on the distribution of crops in the Philippines. Detailed and reliable information about the potential distribution of crops could provide important information that could help to evaluate the impact of climate change, and be used as basis in formulating appropriate science-informed adaptation policies, strategies, and measures. This study identified the key variables highly correlated with the distribution of economically important crop in the Philippines: *Allium sativum*. Maximum entropy approaches using the Maxent modeling algorithm was used to predict the potential distribution of *Allium sativum* under A1B emissions scenario for the year 2030, 2050, and 2100, using the occurrence records from the Philippine Statistics Authority and bioclimatic variables with 30" resolution from WorldClim datasets. The relative importance of the environmental variables was evaluated using Jacknife tests. The robustness of model predictions was evaluated using the AUC statistics. The results show that the more influencing variables are temperature annual range and precipitation seasonality. The model performed better than random with an average test AUC value of 0.75. It is forecasted that *Allium sativum* will likely suffer from the future climate.

CCB-21

A multi-trait assessment of species' vulnerability to climate change along a tropical elevational gradient

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Anthropogenic climate change threatens biodiversity worldwide. The vulnerability of species and ecological communities to climate change is determined by species' sensitivity and adaptability to the changing conditions. Many studies focus solely on species' climate niches as a proxy for species' sensitivity, while other vulnerability components are not considered. We aim at a comprehensive estimate of the vulnerability of species to climate change based on species' climate niche breadth, mobility, dietary and habitat specialization and want to test how vulnerability to climate change varies across ecological communities. We applied this framework to a forested elevational gradient in southeast Peru (300 to 3600 m a.s.l.) and estimated climate niche breadth (based on current occurrences), mobility (based on wing pointedness), dietary specialization (based on bill width) and habitat specialization (based on habitat preferences) for more than 200 frugivorous bird species. We assessed species- and community-level vulnerability by each of the four components separately and by an integrated vulnerability measure across the four components. We expect an increase in climate and habitat niche breadth with increasing elevation because species with large ranges are expected to increase in importance at high elevations. In contrast, dietary niche breadth and mobility could decrease with elevation because frugivorous species, on average, may feed on more fruit types and be more mobile in lowland than highland communities. Hence, different components of vulnerability may dominate in lowland and highland bird communities, suggesting that species' vulnerability to climate change is driven by distinct factors in different ecological contexts.

CCB-22

Bottom-up: Exploring climate change effects on habitat suitability for the deep sea fauna of Isopods (Crustacea: Isopoda)

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The deep sea is the largest ecosystem on our planet, harboring complex, often poorly known communities. The order Isopoda is a highly diverse and specie-rich group of deep sea crustaceans, with many species reported from the abyssal benthos. Represented in a wide range of trophic levels, the clade is considered as a network hub, connecting modules and communities. Despite its relevance for the maintenance of deep sea biodiversity, understanding of how anthropogenic climate change will affect this clade and its habitat remains unknown. Here ,we generated ecological niche models for 80 species of deep sea isopods to forecast how suitable habitats will shift considering environmental changes over the remainder of this century. Occurrence data were obtained through sampling in the North West Pacific as well as Ocean Biogeographic System and Global Biodiversity Information System. Models were calibrated using two distinct environmental datasets, seven feature classes and nine regularization multipliers, resulting on 126 models per species. Model selection was done based on statistical significance, prediction ability, and model complexity. Final model projections were built under three distinct extrapolation settings and evaluated based on overall model variability. Preliminary results indicated multidirectional distributional shifts, but considerate poleward distributional shift, characterizing the Arctic Ocean as a highly risked habitat considering future climatic scenarios. This is the first time climatic change effects are investigated

in deep sea fauna of isopods. Future steps include measuring geographical and environmental suitability centroid shifts of individual species, and investigate its impacts at the community level.

CCB-23
Is all niche space created equal? A novel framework for measuring variation in performance across the climatic niche

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Most applications of ecological niche models assume relationships between climate and various metrics of species' performance that are rarely tested explicitly. For example, the assumption that occurrence density corresponds with climatic suitability is widespread in species distribution modeling studies. However, recent work questioning the validity of these assumptions has made clear that we need to develop a better understanding of these relationships. In particular, understanding how climate and niche position modulate species' performance is critical to forming more accurate and detailed predictions of species' responses to climate change. Here we present a novel framework for measuring variation in performance across the climatic niche of a species. In this framework, we draw transects in climate space that guide field site selection in order to ensure that the full breadth of niche conditions are sampled. This is followed by field surveys at those selected sites to measure the performance metric of interest. We have applied this framework to selected North American pines (genus *Pinus*), and present preliminary results describing variation in individual growth and climate sensitivity across the niche of ponderosa pine (*P. ponderosa*). We advocate that this is an important step toward developing more detailed and accurate predictions of climate change's impacts on species' distributions.

CCB-24
Rare and widespread: target-enrichment approaches reconstruct the origins of the Rand Flora pattern in Camptoloma (Scrophulariaceae)

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Groups that have a widespread (geographically discontinuous) distribution but represented by a few species are intriguing. Are these groups of ancient origins that diversified slowly or did they undergo extinction? Did they recently achieve their distribution but had no time to speciate? The Rand Flora pattern is an enigmatic plant distribution in which unrelated species from different families are found along the margins of the African continent and adjacent islands, relating floras of distant regions such as Arabia, South Africa and Canary Islands. A notable example of this distribution is the genus *Camptoloma* (Schrophulariaceae), with only three species separated by thousands of kilometers: *C. canariensis*, endemic to the Canary Islands, *C. lyperiiflorum*, endemic to Somalia a Socotra; and *C. rontundifolia*, which only occurs in Namibia and Angola. In order to disentangle the origins of such distribution, we used a phylogenomic approach in which we combined target enrichment with custom probes and genome skimming to sequence c.1492 orthologous low-copy nuclear loci (c.3,7 Mbp). We employed supermatirx and multispecies-coalescent approaches to estimate phylogenetic relationships within the genus and close allies, and then used it to infer a spatiotemporal framework. Our results demonstrate the utility of our custom probes in providing resolution at both within species and family level. The widely disjunct distribution of *Camptoloma* was achieved during the Pliocene, through a combination of global climate change, widespread aridification and extinction. This suggests that species can persist and maintain a geographically restricted distribution for millions of years without further speciation or dispersal.

CCB-25

Toward community predictions: multi-scale modelling of mountain breeding birds' habitat suitability and landscape preferences

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The fact that the world is losing biodiversity due to human activities is widely acknowledged. In this context, landscape composition like mountains is key for population persistence and biodiversity conservation. Modelling can be used in this regard, to support monitoring and prediction of biodiversity changes. The main theoretical problem behind modelling rare species is the risk of overfitting the models due to low numbers of occurrences being modelled by a large number of environmental variables. One proposed solution to this problem is to apply small (bivariate) models with only two predictors at a time and then combining all small models into a single final ensemble model. Identifying the best scale of environmental variables can be interpreted as the best effect of environment variables on species distributions. Thus, it becomes urgent to develop new framework that assess the effect of environmental variables at the appropriate scales on species distribution. To identify the best radius for each focal variable and for each species, we fitted univariate models and ensemble of small bivariate models (ESM) were constructed in R with the bird data and the final set of the variables. Univariate analyses showed that the AUC of the majority of univariate models for each group of species varied and the richness maps showed that the lowland networks are most suitable for most species. Our analysis revealed significant important of focal variables in patterns of habitat suitability and show that ensemble of small model, is the best way for modelling species with detection difficulty.

CCB-26

Individual-Based Models Predict Loss Of Range And Genetic Diversity In Cold-Adapted Amphibians With Climate Change Due To Dispersal Constraints

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Two prominent questions in ecology regarding climate change are how biodiversity will be redistributed over the landscape and whether potentially adaptive genetic diversity will be lost. Forecasting models that only include climate data are limited because they predict potential species distributions that may not be realized due to dispersal limitations, and they are unable to evaluate if genetic diversity in the southern range will be lost. Projecting how species respond to change is particularly important for amphibians because range shifts are likely limited by their dispersal abilities. We used MigClim to forecast range shifts and loss of genetic diversity for six North American cold-adapted amphibians. Predicted range sizes were reduced compared to climate-only models. Dispersal distance or dispersal rate was the most important parameter, as opposed to age at dispersal or number of dispersal years, depending on species. Because the evaluated parameter space for each species was identical, this indicates that geographic position or initial range size influence range shift dynamics. Second, we ran simulations for only the southern populations of each species to evaluate whether adaptive variation will be retained for the species by dispersing individuals as ranges shift. Southern ranges experienced > 50% net range reduction within the model across all species, indicating that the range was reduced at a rate that was faster than individuals could migrate northward within the current range. This generation of more sophisticated models enabled us to determine large range reductions and loss of genetic diversity are expected for cold-adapted amphibians.

CCB-27

Not only climate change, also predictor numbers and correlations drive species out of their simulated ranges

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Uncertainties from the choice of model algorithms, global circulation models and emission scenarios are increasingly accounted for in future projections of species distributions. However, other key aspects of model design, like complexity of the fitted models or the structure of the predictor variables included, have received little attention until very recently and are typically handled based on simple rules of thumb. Here, we conducted a thorough sensitivity study on the role of 1) the number of predictors, 2) the predictor intercorrelation, and 3) the SDM calibration complexity on projected species range change for different model algorithms. Using distributional data of 34 widespread European tree species from the ICP Forest inventory and based on four different model algorithms (GLM, GAM, GBM, RF), we analyzed the effects of varying these three model aspects. Our analyses reveal that increasing the number of predictors initially yields higher TSS scores which tend to plateau off once 4-5 variables have been added. Moreover, higher correlation among predictors is associated with a decrease in mean TSS. On the other hand, future range loss is strongly driven by correlation between predictor variables. Representative concentration pathway and temporal horizon are also important determinants of species range loss, but their effect may be weaker than predictor intercorrelation. Our results indicate that predictor choice and model complexity are key sources of uncertainty in predictions of species range change and require careful handling.

CCB-29

Geodiversity : buffering plant communities against rapid climatic change

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Significant increases in global temperatures are predicted, likely to exceed 2°C by the end of the century. In the Arctic, much greater warming is expected and, importantly, warming of the magnitude predicted globally by the end of the century has already been experienced in certain areas. In response to such rapid warming, individual organisms are forced to adapt, migrate or face extinction. Geodiversity has been shown to be related to biodiversity, such that conserving the abiotic may be important in conserving plant communities. The role of geodiversity in mitigating against climate change has not been assessed empirically, however. Using a large network of vegetation plots across the Arctic (each surveyed at least twice over a 27-year period) as well as global distributions of productivity, methods to assess the role of geodiversity in buffering plant communities against recent climatic change are presented here. Geodiversity metrics will be derived at various scales, using the ArcticDEM as well as UAVs to explore the impacts of both micro- and broad-scale topography. These will be related to the distributions of both individual species and plant communities within each plot, as well as to pan-Arctic patterns of primary productivity. Crucially, analyses will be temporal - focusing on respective changes through time. It is hoped that these results will help us to understand the nature of vegetative responses to climate change, as well as providing valuable information for the designation of protected areas.

FB-01

Functional diversity and redundancy in Hong Kong mangrove crabs: biogeographic causes and future scenarios

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The Pearl River estuary, and Hong Kong in particular, are among the most densely populated regions on the planet, but they are also a biodiversity hotspot, due to their geographic location. At the geographical boundary between the tropical and temperate areas, they host both tropical habitats and temperate species. Hong Kong is very close to the northernmost limit of distribution of mangroves, hence why there is only a modest number of tree species present. The assemblages of invertebrates associated with mangroves are, however, among the richest on the planet, both in term of taxonomic and functional richness. Here we present a first attempt of using functional diversity indexes to characterise mangrove crab richness and redundancy in Hong Kong forests. Our aim was to characterise the health and resilience of particular forests, to be selected for conservation efforts, and to identify species that have particularly important roles in the ecosystem. Our results confirm that Hong Kong is a biogeographical cross-road, with over 10% of mangrove decapod species at their northernmost, or southernmost, distributional limit. In the light of climate change, and its implications for the geographical distribution of populations, we can conclude that, although rather diverse and redundant, Hong Kong mangroves are particularly vulnerable environments. Our functional diversity approach, coupled with the study of biogeographical patterns of the mangrove crabs of Hong Kong, proved to be a powerful tool in describing patterns of diversity and redundancy and in forecast their future trends, particular in the light of climate change.

FB-02

Effect of elevational gradient and experimental warming on VOC-mediated plant–insect interactions in alpine meadow ecosystems of the Himalayas

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Global average temperature has been increasing at an unprecedented rate since the early 20th century, and predicted to increase further by 2-3°C within the next century. The effect of climate warming on plant–insect interactions could be profound. While numerous studies reported changes in phenological patterns and range shifts, breaking synchrony between plants and their insect partners, relatively less is known about effects on chemicals that mediate interactions between them. Warming could affect biosynthesis and volatility of plant Volatile Organic Compounds (VOCs) crucial in such interactions, ultimately affecting community and ecosystem processes. Tropical montane ecosystems such as the Himalayas are especially vulnerable because the increase in average temperature there is higher than global average. Presently, little is known about warming effects on plant–insect interactions in such ecosystems. Focusing on four Himalayan alpine meadow plant species, we investigated the effect of elevational gradient (3000, 3500, 4000 m asl; temperature decreases with increasing elevation), and *in situ* warming experiments at a single elevation, on floral VOCs. We found significant intraspecies variation in floral VOC profiles across elevations, and also between warmed and control plants. However, despite intraspecies variation across elevations, VOCs of the same species clustered together and away from VOCs of other species. Further, we observed no clear trend in pollinator visitation rate across elevations. Our results imply that despite variation VOC profiles due to environmental factors, the floral VOC identity of each species is preserved, and pollinators can identify its flower as long as the community structure is maintained.

FB-03
Range limits and interpopulation variability in North American river otters

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Understanding species responses to environmental change is necessary to preserve biodiversity in an increasingly anthropogenically modified world. For species with broad ranges, local adaptation may be as critical as species-level adaptation to maintaining distributions, but potentially causes populations within a species to have differential responses to change. The North American river otter (*Lontra canadensis*) is a freshwater carnivore whose range covers much of North America. Despite extensive (and successful) reintroductions, relatively little is known about factors associated with otter persistence and the potential extent of local adaptation. We used species distribution models (SDMs) and 3-dimensional morphometrics to explore range limits and interpopulation morphological variability in river otters to determine whether the factors that affect species range limits are also associated with local adaptation. We paired otter occurrences with WorldClim climate and MODIS environment variables, then constructed Maximum Entropy models using the R package "ENMeval". We then examined morphological differences in skull shape between populations across physical and environmental gradients. We found that climate was not a strong predictor of otter presence and that there is a large amount of variation in skull shape across the species range. We will further identify whether differences in skull morphology trend with environment variables that define range limits. Overall, this study informs our understanding of otter environmental tolerances and how morphological variation might contribute to local adaptation and otter persistence. These results may inform whether certain populations will undergo more stress than others when changes occur, and how to mitigate that stress.

FB-04
A large-scale biogeographical analysis of European rabbit damage to agriculture in Spain

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Many small and medium-sized mammal species cause widespread and economically significant damage to crops all over the globe. Most research on pest species has focused on accounts of the magnitude of damage locally, while there are much fewer studies at large geographical scales, or on analysis of the ecological and anthropogenic factors correlated with crop damage by mammal pests. We used the Favourability Function (FF) to model the potential distribution of European rabbit (*Oryctolagus cuniculus*) damage throughout Spain based on ecological and anthropogenic variables. Rabbit damage data was gathered from news on the online media (reports, forums, hunters' and farmers' websites, and blogs). Damage was mainly concentrated within the central-southern regions of Spain. Our model revealed that areas more favourable for larger rabbit losses were characterised by scarcity of natural vegetation, presence of main railways and highways, and by friendly environmental conditions for rabbits. From our analysis, we suggest that roads and railway lines act as potential corridors along which rabbits can spread. Currently, the application of modelling techniques with management purpose is limited, but FF models can provide easily available rapid assessment tools to highlight the most vulnerable regions to wildlife pest. In conclusion, this approach can be valuable for assessing drivers of wildlife pest damage at biogeographical scale, and can be used to propose methods to reduce human–wildlife conflicts.

FB-05
Alternative strategies drive strong brain size bimodality in variable habitats

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Habitats that undergo large environmental fluctuations present a unique ecological challenge by exposing organisms to a breadth of biotic and climactic conditions. Enhanced encephalization (i.e. large brain size relative to body size) has been suggested as a potential solution because it equips species with an increased ability to mount flexible and varied behavioral responses in the face of frequent or unexpected change. However, our global analysis of over 1500 non-migratory birds shows that the Earth's most variable habitats, those at high latitudes that are characterized by high seasonality and low predictability, are preferentially occupied by not only the largest, but also the smallest relative brain sizes. Here, we explore how diet and reproductive output interact with brain size and environmental conditions in order to understand how small brains can facilitate persistence in these challenging habitats. We find that small-brained species in variable environments tend to specialize on difficult to digest, consistently available resources and produce many offspring per year – characteristics that are not obtainable for larger-brained species. While access to consistent resources may increase survival across environmental fluctuations, high reproductive output would allow recovery from high mortality suffered during particularly difficult conditions. Our results reveal that the link between brain size and environmental variability is more complex than previously thought and demonstrate that these opposite strategies are equally equipped to cope with some of Earth's most challenging habitats.

FB-06
Functional biogeography of four saxicolous species of the fern genus Asplenium across two European biogeographic regions

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Functional biogeography uses functional traits (individual features that inform us how species adapt to environmental conditions) to draw how forms and functions of organisms are distributed across space and time. This is an emerging science, which has looked virtually nothing at ferns, so far. The Iberian Peninsula is a good scenario to develop this sort of studies, because two biogeographic regions are well represented: Mediterranean and Atlantic. The main differences between them are the arid period and a less amount of rainfall in the former. Thus, it is presumable that ferns exhibit an increasing gradient of functional productivity when comparing Mediterranean and Atlantic populations. In this study, we wanted to test this hypothesis by measuring three functional traits related with foliar productivity (LMDC, LT, SLA) in four saxicolous species of *Asplenium* that spread through both biogeographic regions. Our results show statistically significant differences among these traits across the bioclimatic regions considered. We have found higher values of LMDC and LT in the Atlantic region, whilst SLA is higher in the Mediterranean region. These results don't adjust to the expected, as productivity is generally related with high SLA and low LMDC and LT values. The mean maximum temperature of the warmest month is the variable that better explains the observed data. Surprisingly, the annual rainfall seems not to play an important role. Our results could be explained by the particular habitat of the saxicolous ferns: verticality and absence of soil prevent retention of rainfall, while productivity is promoted with temperature.

FB-07

Biogeographical identification of demersal fish communities in the Spanish Mediterranean Continental Shelf (50-800 m)

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During the MEDITS Project, the quantity of sampling stations (2188 hauls), and the number of species listed to be inhabiting the Mediterranean Sea (269 during the sampling period 1994-2012), display significant variations in distribution (42 chorotypes and 13 patterns of gradual variation in time and space) and in terms of abundance (num/km^2) per year.
This study describes the assemblages and distributions of demersal fish species under a qualitative point of view, using innovative techniques for the spatio-temporal analysis of distribution data.
We found that the spatial structure of the Mediterranean fish community was determined by abiotic factors such as depth and temperature, the biogeographic community structure, and extremely cold conditions in both 1996 and 2001. These assemblages can be identified with defined groups of species regarding the environments where they live.

FB-08

Agro-biogeography of Chocolate in Colombia: CacaoBIO expedition

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The center of origin of chocolate is in the Northern Andes of South America in the Amazonian forest where the largest number of wild species of cocoa can be found. Since peace was established following years of conflict in Colombia, vast areas of untouched forests in the Amazon of Colombia have been occupied illegally and cut down at an alarmingly rate. Consequently, wild cocoa species that have been growing in these regions for hundreds of years, are at a risk of disappearing altogether. To prevent this from happening, we need to identify the wild species growing in these locations, investigate the environment and conditions in which they thrive in, and explore ways in which they can be exploited for agricultural purposes. To do so, new agro-biogeography approaches are required. This study focuses on the largest current bioprospecting research project of cocoa in Colombian cover a large number of Amazonian species. I combine the latest ensemble modelling techniques, biodiversity, geographical and socio-political aspects to forecast agro-biogeography maps and identify areas in Colombia where cocoa had not been collected. The results led to recognize potential agronomical traits of wild species of cocoa. They also contributed to enhance our knowledge on how to use agro-biogeography for biodiversity and conservation.

FB-09

Biogeography of foliar nutrient resorption efficiency in relation to nutrient limitation of woody plants

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Nitrogen (N) and phosphorus (P) are the most common nutrients limiting terrestrial plant growth. It has been believed that the growth of plants living in the old soils, such as those at low latitudes, is more likely limited by P than N, while those growing in young soils at high latitudes tend to be limited by N more than P. Plants have developed various nutrient conversation strategies to adapt to infertile habitats. Nutrient resorption is another such strategy by which plants re-translocate nutrients from senescing plant organs, especially foliar, to new tissues. According to the relative resorption hypothesis, plants should resorb proportionately more N when they are N limited, relative to P, and vice versa. A latitudinal gradient of nutrient resorption efficiency can thus be expected to emerge globally, given that plants should resorb proportionately more N than P at high latitudes, but more P than N at low latitudes. Using three independent datasets of foliar N and P of woody plants, we tested whether there existed such a biogeography of plant nutrient resorption. The results showed that the resorption efficiency of N vs P generally increased towards the Poles but decreased towards the Equator, consistent with the latitudinal variation in green-leaf N:P ratio, another indicator of plant nutrient limitation types. Moreover, the relative resorption efficiency decreased with increasing precipitation and temperature, or decreasing aridity. These spatial patterns suggest that plant nutrient internal recycling can be regulated by climatic regimes and soil developmental stages across broad biogeographic scales.

FB-10

Are montane areas associated with the evolution of higher pitched acoustic calls in Malagasy bright-eyed tree frogs (Mantellidae: Boophis)?

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We investigate the evolution of acoustic signals in the genus *Boophis* from the Malagasy/Comoran family Mantellidae. *Boophis* are a group of arboreal frogs that breed in riparian habitats and are characterized by loud advertisement calls. We provide a new molecular phylogeny with increased taxon sampling (100 species-level units), and genetic loci sampling (ten total), and our results confirm a much higher level of phenotypically cryptic species richness than previously estimated. We find strong statistical evidence that rapidly-cascading stream inhabiting *Boophis*species evolve calls with higher frequencies (i.e. pitch) relative to those that breed in ponds or slow moving, quiet streams. Our results reveal that species occupying montane forests have higher pitched calls, suggesting an association with steep, high-gradient slopes that create rapidly-cascading streams. Overall, these results also suggest a potential role of sensory bias in the evolution of mating signals resulting from loud stream interference selecting for higher dominant frequency calls in fast stream-breeding *Boophis*.

FB-11

Ecogeographic correlates of phenotypic diversity: addressing the thermal melanism hypothesis in Eurasian vipers

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How environmental conditions of species´ distribution range shape phenotypic diversity is a major question in evolutionary biogeography. The coloration of ectotherms is functionally linked to their thermal environment, and is therefore potentially under a strong environmental influence, where dark-colored individuals may profit from a thermal advantage. However, this hypothesis has only been tested within species, thus failing to address its relevance for macroevolutionary diversification. Eurasian vipers constitute an ideal model for testing this hypothesis, as they range across highly variable environments and ecosystems, and they exhibit remarkable variation in dorsal coloration. We used phylogenetic comparative methods to test for associations between dorsal pattern and range characteristics (latitude, altitude, climate) across 40 evolutionary lineages of Eurasian vipers. We found a positive effect of precipitation on the degree of pigmentation, and a positive effect of temperature and negative of altitude on the number of dorsal marks. However, the multivariate evolutionary association between dorsal pattern and range characteristics occurred in a direction that contradicted our predictions: species with a higher pigmentation index and lower number of dorsal marks were characterized by distribution ranges of low altitude, high temperatures and high precipitation. Our results do not lend support to the hypothesis that a thermal advantage may be driving the evolution of dorsal pattern in Eurasian vipers, and suggests that phylogenetic inertia and ecological functions, like crypsis or aposematism, might be more influential in shaping phenotypic diversity in this trait.

FB-12

The geography of sodium limitation in terrestrial food webs

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Twenty five elements are required to construct most living organisms. Sodium is unique in that it is metabolically unimportant for plants, but vital across consumers like animals and fungi. As a consequence, plant consumers like herbivores, detritivores, and pollinators must increase their sodium supplies 100-fold above that found in their food. When you consider that sodium supplies also have a geography, this suggests that the populations that make up terrestrial food webs may be limited, and food webs structured, in ways that track sodium geography. We test this hypothesis using both comparative studies, and distributed experiments across 54 North American grasslands. We show the persistent and consistent signature of increasing sodium limitation along geographical gradients of decreasing sodium supply.

FB-13

Global palm functional traits provide new biogeographic insights into plant-frugivore interactions and life history variation in a pantropical keystone plant group

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Understanding how functional traits have shaped the ecological and evolutionary assembly and macroecological patterns of clades is of key interest in the emerging field of functional biogeography. However, the lack of integrated and harmonized species traits information (known as the Raunkiaeran shortfall) has hindered progress in biogeography, especially our understanding of tropical plant groups. Here, we show how newly compiled, global trait information of palms (Arecaceae), a pantropical animal-dispersed keystone plant group with >2,500 species, allows the quantification of biogeographic, phylogenetic and allometric variation in life histories and the relationship between palm assemblages, their fruits and associated frugivore assemblages. Specifically, we demonstrate a comprehensive biogeographic and phylogenetic coverage of palm species traits and show how morphological traits (e.g. measures of fruit, leaf and stem size) reveal key ecological strategies within the group (e.g., canopy vs. understorey or different growth forms). Moreover, we infer that frugivore body sizes are strongly correlated with palm fruit sizes at regional scales, highlighting the role of frugivores in shaping palm assemblages. Our results highlight the importance of functional traits in understanding macroecological and biogeographic patterns of plant-animal assemblages at the global scale.

FB-14

Biodiversity change: does function follow richness?

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Understanding how ecosystems are changing in response to anthropogenic pressure is essential for appropriately managing and conserving ecological systems into the future. Loss of species diversity is widely cited as the greatest threat to the stability, resilience, and functioning of ecosystems. Underpinning this assertion is the assumption that species diversity is an appropriate surrogate for the aspects of species identity and interactions that confer those properties, broadly referred to as functional diversity. However, empirical studies document a wide array of relationships between functional and species diversity, and responses of both aspects of diversity to different environmental perturbations are poorly documented. Establishing the relationship between functional and species diversity is further impeded by methodological concerns about the ability of functional diversity metrics to capture change independent of species richness (number of species). Using multiple large-scale biodiversity datasets for both plants and vertebrates, we assess the ability of functional diversity metrics to detect change through a null model approach, assessing i) metric behavior, and ii) variation in the form of the functional diversity-species diversity relationship across biomes.

FB-15

Context-dependent tree species effects on soil nitrogen transformations and related microbial functional genes

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Although it is generally accepted that tree species can influence nutrient cycling processes in soils, effects are not consistently found, nor are the mechanisms behind tree species effects well understood. Our objectives were to gain insights into the mechanism(s) underlying the effects of tree species on soil nitrogen cycling processes, and to determine the consistency of tree species effects across sites. We compared N cycling in soils beneath six tree species (ash, sycamore maple, lime, beech, pedunculate oak, Norway spruce) in common garden experiments planted 42 years earlier at three sites in Denmark with distinct land-use histories (forest and agriculture). We measured: (1) net and gross rates of N transformations using the ^{15}N isotope pool-dilution method, (2) soil microbial community composition through qPCR of fungal *ITS*, bacterial and archaeal *16S*, and (3) abundance of functional genes associated with N cycling processes—for nitrification the archaeal and bacterial ammonia-monooxygenase genes (*amoA* AOA and *amoA*AOB, respectively) and for denitrification, the nitrate reductase genes *nirK* and *nirS*. These results are compared with research we conducted in British Columbia, Canada, addressing similar research questions in an environment with less anthropogenic N deposition. This research aims to address the question: When can consistent mechanisms behind tree species effects be observed across continents?

FB-17

Integrative systematics in the genomics era: Unravelling the taxonomy and evolutionary history of a grasshopper species complex

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Systematics has traditionally relied on morphological characters to interpret and classify biological diversity. The integration of genomic data with phenotypic and ecological evidence, improves taxonomic delimitation and helps to disentangle complex evolutionary histories. Here we provide an example of how traditional approaches have led to species designations that are neither corroborated by high throughput sequencing data nor by the quantitative integration of genomic information with other sources of evidence. Our model system is a recent (Quaternary) evolutionary radiation of montane grasshoppers of the subgenus ***Dreuxius* (genus** *Omocestus*. Most taxa are distributed in allopatry, often isolated on mountain tops. In particular, we focus on ***Omocestus antigai*** and ***O. navasi***, two sister taxa of the complex that inhabit the Pyrenees, pre-Pyrenees, and Catalan Pre-Coastal Range. These two taxa were originally described based on subtle phenotypic differences and distinct habitat associations (alpine vs. Mediterranean-montane habitats). However, mitochondrial markers have failed to recover reciprocal monophyly of the two-putative species. To test species boundaries and understand the factors that contributed to lineage divergence, we integrated phenotypic information (morphometric analyses) and genome-wide SNP data (ddRADSeq) for 95 specimens representing 16 populations of both species across their entire known distribution. Our phylogenomic, species delimitation, and Bayesian clustering analyses rejected the hypothesis of two taxa and suggest instead that all sampled populations constitute a single species with a deep hierarchical genetic structure along a west to east gradient. Our results exemplify the power of integrating new genomic tools and quantitative phenotypic and ecological data to resolve taxonomic problems.

FB-18

Filtering processes in European grassland plant communities revealed through functional traits and dark diversity

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Filtering processes in the assembly of plant communities acting over broad spatial extents are still poorly known. Using a dataset of more than 300,000 grassland vegetation plots from the European Vegetation Archive, functional characteristics of species, and the concept of dark diversity, we study underlying filtering processes in European grasslands. We hypothesise that grassland species actually occurring within local communities are functionally less diverse than species belonging to corresponding dark diversity under strong environmental filtering (e.g. drought or cold stress). In contrast, under benign environmental conditions competitive exclusion may cause realised communities to be functionally more diverse (over-dispersed) when compared to their dark diversity, or there can be no significant difference in this regard. To test these hypotheses, we specifically address the following study questions: (1) What are the patterns of functional diversity in European grasslands viewed from the perspective of dark diversity under (1.1) strong environmental filtering and (1.2) benign environmental conditions? (2) Which environmental (or other) conditions can explain the patterns found? To assess the dark diversity of European grasslands we estimated the regional species pools using co-occurrence matrices. Trait composition and functional diversity of the realised plant communities are compared with their dark diversity within four separate datasets: dry, mesic, wet, and alpine grasslands. The differences are expected to vary systematically across Europe, in relation to gradients of temperature and water availability, which we test using GIS data on macroclimate.

FB-19

Effects of habitat fragmentation on functional diversity of plant communities on land-bridge islands

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Trait-dependent responses of species richness and composition to habitat fragmentation have been recognized, but how functional diversity response to habitat fragmentation is still poorly understood. In this study, we examined how habitat fragmentation affect functional diversity pattern on land-bridge islands. Six functional traits were measured for 76 tree species on 29 land-bridge islands in the Thousand Island Lake region, China. We calculated five metrics of functional diversity (functional richness (FRic), functional evenness (FEve) and functional divergence (FDiv), mean pairwise functional distance (MPFD) and mean nearest functional distance (MNFD)) and analyzed how they shift along island area. We tested the effects of habitat filtering by a null model approach. FRic increased with island area; while FEve and MNFD decreased with island area. FDiv and MPFD didn't show a clear pattern along island area. For most of the 29 study islands, the standardized effect sizes of FRic, FEve and FDiv values were significantly negative. The assemblage of 76 woody plant species was clustered well into three functional groups, and their species richness was all increased with island area. The relative abundance of group B increased with island area, while group C decreased with island area and group A tended to increase with island area without significance. On these land-bridge islands, strong habitat filtering was structuring plant communities. Functional richness and functional similarity increased with island area, and additional species on larger islands tended to be functional similar with species on smaller islands, which could be attributed by the distribution of functional groups.

FB-20

Resource pulse increases polypore species richness

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To counteract population declines and local extinctions it is necessary to increase the resources available for species, which can be done through ecological restoration. If the restoration is conducted as one-off action on a large area it resembles a natural resource pulse, which should lead to increased abundance of individuals, accompanied possibly by increased species richness. Species-energy relationship and underlying theory allow creating predictions about how different features of resource pulses affect species richness. We conducted a large scale, controlled, randomized and replicated field experiment to study the effect of resource pulse on polypore species richness in a previously managed boreal forest landscape. We manipulated the amount and distribution of dead wood (i.e. resources available for the species), and explored the effects on polypore assemblages on added and natural dead wood during nine years after manipulation. Resource pulse increased polypore species richness mainly through increased abundances: a large resource pulse resulted in higher number of abundances and species than a small resource pulse. Also, heterogeneity of the resource plays a significant role: for a given number of occurrences added dead wood contained *less* species than natural dead wood, which is most likely due to low diversity of the added dead wood. Resource pulses strengthened the populations primarily of common species. However, these species play a major role in nutrient cycling and other ecosystem functions driven by wood-decaying fungi.

GCB-02

Butterfly biodiversity trends accross Europe

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Data from long term monitoring schemes has proven fundamental for the assessment of the effect of habitat and climate change on biodiversity, and have already supported highly valuable research. This also is the case for Butterfly Monitoring Schemes (BMS), wich have been implemented in several European regions, using a common standardised methodology. The sECURE project aims to study how global change restructures species assemblages of butterflies through environmental filtering, niche partitioning, spatial and stochastic processes and the relative importance of these underlying mechanisms. Under this scope, we use the eBMS data available for many countries in Europe.
We present the results of using this compiled dataset to examine the spatial patterns and temporal trends of butterfly abundance, alpha and beta biodiversity as well as species turnover across Europe.

GCB-03

Postglacial recolonization of North America: integrating niche models and corridor modeling to study species' range dynamics over geologic time

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Understanding the factors that influence and shape species' distributions is a central topic in biogeography. As climates change, species either cope with these changes through evolution or plasticity, or shift their ranges to track the optimal climatic conditions. Ecological niche modeling (ENM), quantifies the niche of the organism by using occurrences and environmental data to estimate species' potential distributions. ENMs are often criticized for failing to take into consideration species' dispersal ability. Here we attempt to fill in this gap by combining ENMs, dispersal and corridor modeling to study the range dynamics of North American spadefoot toads over the Holocene. We first estimated the current and past distributions of spadefoot toads, and then estimated the past distributions from when the last major geologic process occurred (Last Glacial Maximum - LGM) to present day. Then, we estimated how each taxon recolonized North American by using dispersal and corridor modeling. By combining these two modeling approaches we were able to 1) identify the LGM refugia used by the American spadefoot toads, 2) further refine these projections by estimating which of the putative LGM refugia have contributed to the recolonization of the North America via dispersal, 3) estimate the relative influence of each LGM refugia to the current distribution. The models were tested using previously published phylogeographic data. This effort aims to pave the way towards a new approach in studying species' range dynamics by combining ENMs and dispersal modeling over time.

GCB-04

The thermal performance of Hong Kong mangrove crabs: a key to understand their future species distribution

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Mangrove crabs are important ecosystem engineers, affecting the mangrove community through their feeding and burrowing activities. Since they colonize tropical and subtropical intertidal forests they are often subjected to a high thermal stress. With global warming, the average global temperature is increasing, and extreme weather events are becoming more frequent. These two combined factors have the potential to change the geographical distribution of mangrove crabs, through populational range shifts. The Southern China Sea coasts, and Hong Kong territory in particular, are biogeographical boundaries between temperate and tropical marine and coastal populations and are critical areas where to study the influence of thermal physiology on the latitudinal distribution of crab species. Our objective was to investigate the lethal temperatures (LT) of ten representative mangrove crab species common in Hong Kong, and to discuss the implications of global warming in terms of possible shifts in their geographical distribution. Our preliminary results show differences in LT among the most common families of crabs in mangroves, with Ocypodidae coping better with higher temperatures, followed by Grapsidae, while Sesarmidae were characterized by lower lethal temperatures. In particular, and although some of the studied sesarmids show geographical distributions centered at different latitudes, they did not show significant differences in LT. Our data show that some of the mangrove crabs of Hong Kong face temperatures close to their thermal limits, and we hypothesize that further increases in temperature would affect their fitness and, ultimately, their distributional range across the coast of Southern China.

GCB-05

Thermal tolerance and climate change vulnerability in alpine water beetles

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Facing the threat of global warming requires accurate predictions of how species will respond to future environmental changes. Despite the fact that high-altitude systems will experience some of the fastest rates of warming on the planet, projections of the impacts of climate change on alpine freshwater biota are still scarce, especially for Mediterranean mountain ranges. We estimated the vulnerability to ongoing global warming of two threatened water beetles (*Agabus nevadensis* and *Hydroporus sabaudus sierranevadensis*; family Dytiscidae) endemic to alpine lagoons of Sierra Nevada national park (south Spain) by combining thermal tolerance data with predicted changes in maximum summer temperatures. First, we estimated the upper thermal tolerances of both taxa and their acclimation capability by laboratory experiments, and then we obtained thermal safety margins (TSMs) for each species. We found that both species did not show acclimation capacity after long-term exposure (one week) at different temperature treatments, which indicates a reduced capacity to adapt to future warming conditions. These species had TSMs of 10.3–12.2 °C based on current maximum summer temperatures. However, species' current distributions will

experience maximum summer temperatures very close to their thermal limits (TSMs of 3.8–5.7) by the year 2100. Our results show that both endemic taxa are highly vulnerable to climate warming, given their reduced capacity to maintain present populations under climatic warming and the lack of suitable future environments in this mountain range.

GCB-06

African vegetation change since the last glacial maximum: climate versus pastoralism

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Prehistoric vegetation change on the African continent is not well understood, especially surrounding the controversial termination of the African Humid Period, circa 5500-3500 years before present (BP), when important changes in land use for animal production were simultaneously underway. In order to improve our understanding of continental-scale vegetation trends, we reconstruct changes in the climatic envelope of selected vegetation biomes from the last glacial termination (~20,000 BP) to the modern day, using fossil and modern pollen datasets. We map and compare vegetation reconstructions with broad climatic trends, as well as the development of animal production and hunting land uses. Our results show that the extent and establishment of vegetation classes in climatic space responded closely to changes in northern hemisphere summer insolation prior to the Holocene climatic optimum (~9,000-10,000 BP), but responded non-linearly during the past 9,000 years, as pressure from land use increased. We overview possible climatic and anthropogenic drivers of these changes, and discuss the role that animal production could have played. Furthermore, our mapped analyses highlight geographic areas where more data coverage is necessary in order to improve reconstructions of vegetation change.

GCB-07

Savannas at the forest boundary: an understudied biome at risk

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High rainfall savannas are poorly understood and threatened globally. Such savanna ecosystems span 800 - 2000 mm annual rainfall across the seasonally dry tropics. Often misclassified as degraded forests, these diverse ecosystems are vulnerable to policies of afforestation and fire suppression. Rising atmospheric CO_2 lessens the competitive ecological advantage of the C_4 grasses that characterise the ground layer, increasing the risk of woody encroachment. High rainfall savannas in Africa are considered the world's remaining agricultural frontier, and 50% of the equivalent Brazilian savannas have already been converted for agriculture and plantation forestry. However, across these vast regions of Africa, Madagascar and Asia little is known of their ecology; a knowledge gap detrimental to their conservation and management. Historically, research in African savannas has focused on arid and semi-arid savannas, such as environments typified by the Serengeti. Over my PhD, I aim to develop a new understanding of the ecology and biogeography of high rainfall savannas focusing on Africa and Asia, with fieldwork in little studied regions of Cambodia and Mozambique. I will combine investigations of ground layer plant species diversity focusing on grasses and forbs to understand how variation in overstory vegetation structure (ie. tree density and size) aligns with ground layer diversity where different groups of ground layer species can be common, e.g. grasses, N fixing forbs, and underground trees. I will examine whether savannas from different biogeographic regions with structural similarity show similar patterns of ground layer diversity to determine the resilience of these ecosystems to structural change.

GCB-09

Global change impacts on the ecosystem services provided by mountain dung beetles

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One of the current key issues in ecology and conservation is to understand how global change can affect biodiversity and ecosystem services (ES). Many ES are delivered by insects, among which stand out those performed by dung beetles (DB). DB feed and breed on (and under) the excrement, and by burying it they contribute to soil mineralization, aeration, and nutrients available, etc.

In an ongoing project funded by Fundación Biodiversidad and Universidad de Alcalá (Spain), we aim to determine how temperature increase and habitat management can affect three ES: dung removal, seed dispersal and nutrient supply to the soil. In addition, we will identify the morphological and behavioural DB traits that are associated with these ES. Two types of experiments will be carried out, one in the laboratory, using tacclimatized chambers to simulate future temperatures, and another in the field. DB will be placed together with cow dung, evaluating the loss of excrement after 72 hours (dung removal). Artificial seeds will be placed in the dung, and will be counted at the end of the experiment (seed dispersal). Soil samples will be taken to measure nutrient concentration. These three ES will be measured in the field in a similar way, but comparing the differences between open areas and forested areas. Also, DB communities will be sampled using pitfall traps placed in sun and shade. This project will provide information for the development and implementation of land management and conservation policies that maximize diversity, functioning and sustainability of mountain agro-forestry systems.

GCB-10

Compositional shifts in Spanish forests during the last decades: ecological patterns and responses to global change

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Spanish forests have endured significant changes during last decades. Traditional land uses abandonment, afforestation policies and climate change can be mention as the main drivers of shifts in forest distribution areas. However fewer is known regarding how these drivers are affecting the forest ecological dynamics related with species compositional shifts.

Based on the information from different Spanish Forest Inventory cycles, the aim of this work is to analyze plausible trends and drivers of compositional shifts during the past 30 years. For this, the dynamics of tree recruitment and richness of different forest types as well as the relation of the patterns observed with biotic and abiotic factors are studied.

First results show a national increase of 2.92% of mixed plots. It is also noticeable that pure plots are more sensitive to change than mixed ones. Thus, 41.34% of pure plots did not show any recruitment in the next cycle and 12.34% of them showed mixed recruitment. Furthermore, within mixed plots, mixed coniferous forests tend to be the most stable and less sensitive to change over time

The detected increase in species richness also reinforces the upward shift in composition and the trend towards higher degree of mixture in Iberian forests. This trend seems to be related to forest recovery and naturalization after recent changes in traditional land uses. The preliminary results point to pure forests undergoing dynamic processes towards more stable and mature successional stages.

GRB-01

Saturniid and sphingid moths as novel models for the study of insect diversity and macroecology

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Insects are the most speciose group of terrestrial organisms and are strongly affected by global environmental and climatic changes. They exhibit a remarkable variety of forms and life history trait combinations not represented among vertebrates and are responsible for many ecosystem services and disservices. Yet, our knowledge of their diversity and distributions, as well as our understanding of their evolution and diversification dynamics through space and time, remains fragmentary.

We have identified a group of herbivorous insects – the Saturniidae and Sphingidae, two sister families of moths – that represent an unparalleled insect model. This group comprises about 5000 species and has been thoroughly documented worldwide, through comprehensive DNA barcode libraries, hundreds of thousands of occurrence records in databases, and a broad documentation of their life histories. Thus, they offer for the first time an opportunity to study patterns of diversity and distribution at a global scale in insects, together with their underlying macroevolutionary processes.

Here we present the comprehensive database built by our research group and the different approaches – such as integrative taxonomy, biogeographical analyses, phylogenomics and analysis of traits– that we combine to address key questions about the macroecological patterns and the evolutionary history of these moths. We expect that it will shed light on the processes governing the extant diversity of insects and help us understand how global changes will affect them, how they may adapt to these changes, and how can act to conserve their species and preserve their roles in our ecosystems.

GRB-02

The Macroecology of Microbes and Macrobiota from eDNA

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Environmental DNA (‘eDNA’)—which provides a common currency for studying biogeographic patterns and processes from microbes to macrobiota—could be the foundation of a unifying macroecological framework. However, conceptual and methodological challenges remain substantial. The CALeDNA network aims to address these challenges while also increasing public understanding of biodiversity and research. Multiple 1200 km coastal and inland transects allow us to test patterns of community richness and similarity across all major clades in the tree of life, against a backdrop of extreme environmental variation from deserts to temperate rainforest, from the mountainous Sierras to the seas, and in urban, agricultural, and natural reserve areas. eDNA distribution is heavily influenced by silt proportion, and persistence of eDNA is predictable at the habitat scale. California eDNA exhibits familiar beta diversity patterns; presence and richness of organismal families are frequently predictable by habitat, elevation, temperature, and human impact. Macrobiotic and microbial eDNA diversity may be modestly correlated within habitats but less-so across habitats. Network analyses suggest the species with highest centrality and degrees are parasites, and that the correlations of parasites with community features indicate their specific functional roles. eDNA for diverse systems is still in its infancy, and precision monitoring will require filling in the tree of life with DNA barcode references so all clades can be tracked. Quantifying how patterns of diversity, and their underlying processes, scale spatially and temporally are among the most long-standing and challenging problems in biogeography and macroecology. eDNA brings us to the brink of unifying solutions.

GRB-03

Competitive interactions between cousin species, a biogeographical approach with Iberian martens

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The stone marten (*Martes foina*) and European pine marten (*Martes martes*) are two medium-sized mustelids with a high biological and ecological similarity, which live in sympatry over a wide range in Europe. Competitive interactions between both species have been studied at local and regional scales with different results. Here we analyse how competitive interactions may change geographically along species' distribution ranges under the biogeographical context of Iberia, the south-western boundary of the species' European range distribution. We use a biogeographical approach to identify those areas where environmental features allow for coexistence or promote competitive exclusion. We have modelled their distributions based on presence/absence data from the Iberian mammals' atlas (10x10 UTM grids), and a set of predictor variables (spatial, topographic, climatic and land cover). The modelling procedure was based on the favourability function and we used fuzzy operations. According to our results, environmental features allow for coexistence in a wide area from Pyrenean Mountains to occidental Cantabrian Mountains. Competitive exclusion by pine marten takes place in a wide area along the north-western Iberia, while the main areas of competitive exclusion by stone martens occurs in a narrow belt along the southern limit of the main favourable areas for the pine marten, located in a wide band along northern Iberia. Our analytical approach provides patterns of biogeographical relationships between competing species. This approach combined with field studies at local and/or regional scales may be useful to a better understanding of ecological interactions between competitors.

GRB-04

Along came the spider: Patterns of population structure and determinants of genetic diversity in Iberian spiders

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Genetic diversity and population structure vary widely among species and provide essential information to understand the evolution of species and assist with their conservation – genetic diversity may inform on the viability of populations, while intraspecific gene flow may help to determine management strategies. Likewise, understanding shapes genetic patterns (functional characteristics such as body size, fecundity, dispersal ability or distribution ranges) is paramount.

Spiders are an excellent model taxon to investigate genetic diversity because they are abundant, diverse and ubiquitous predators, and therefore play a key role in trophic networks and ecosystem functioning. They have a plethora of functional traits and different dispersal abilities and ecological strategies and are easy to collect. Here, we use a community level approach to unveil the patterns and identify drivers of genetic diversity and population structure among spiders across a latitudinal gradient.

For our study, we collected spider specimens in 16, 1 ha plots of white oak forest, distributed across six Spanish National Parks by using semi-quantitative sampling protocols. We identified 376 spider species belonging to 40 families from 8,521 adult specimens. From the collected specimens, we generated 3,081 DNA barcodes, corresponding to 99% of the species and 5 individuals per plot. We calculated nucleotide diversity and *Fst* indexes for all populations to test the relationship between variables such as dispersal ability, body size, guild or microhabitat and the observed genetic diversity and population structure patterns, and here we show some preliminary results.

GRB-05

Climate change and facilitation: can nurse plants save native plants?

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The Chilean mediterranean ecosystem(32° to 40° S) is characterized by having an altitudinal climatic gradient, where the increase in elevation decreases the temperature and rainfall increases. It has been described that the grouping of shrub trees produce particular microclimatic characteristics and at the same time, positive effects on the recruitment of trees under the species such as Quillaja saponaria, Lithraea caustica, Colliguaja odorifera and Baccharis linearis . On the other hand, climate change can be considered an environmental variable in the context of the altitudinal gradient of central Chile, coinciding with future predictions of an increase in temperature and a decrease in rainfall. This allows to use the altitudinal gradient as a natural experiment, where the transplant of communities of higher elevation to low elevation simulates the conditions of change in the climate. In the present work, we hypothesized on whether, in this environmental gradient, facilitation significantly decreases what is expressed in a decrease in the diversity between the total diversity of species and the diversity of environments. Through the use of manipulable field experiments, transplant of seeds from conditions of 2000 m to 1000 m of elevation, simulating the change in temperature and humidity, and comparing the germination and growth in open sites and under shrubs. Part of the results indicate that the facilitation could be a factor of maintenance of some species, but not of the total diversity of species of the community, while some species fail to survive new environmental conditions.

GRB-06

Disentangling the effects of dispersal, niche and biotic interactions in shaping species distributions of amphibious marine snakes (Reptilia: Laticauda)

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Species distribution modeling (SDM) is an important technique to study diverse questions in biogeography. SDMs are correlating the occurrence records of a species with its environmental (usually, climatic) variables to estimate species distributions. Although the effects of climate on species distributions have been studied for a long time, the effects of dispersal and biotic interactions have attracted less attention. Here, we are estimating the species distribution of sea kraits (Reptilia: *Laticauda*), which are amphibious marine snakes specialized in feeding on eels and live in South-East Asia and Pacific. First, we estimated the sea krait species distributions in both marine and terrestrial environmental domains. We found that when the two domains are being modeled separated, the distribution estimates are overpredicted; however, when both domains are taken into account, then the species distribution estimates are more restricted. Hence, we can conclude that when studying amphibious species, is important to take both environmental domains into consideration. Second, we tested whether a) biotic interactions are being important in shaping species distributions, and b) whether biotic interactions improve the accuracy of species distribution estimates. We found that biotic interactions are a significant influence in shaping sea krait species distributions, and that inclusion of biotic interactions into SDMs results into more accurate models. Hence, we can conclude that when available, biotic interactions should be included in the models. Finally, we tested whether sea kraits distributions are corresponding to the niche availability or dispersal ability. We found that the most suitable pixels for all species are found

GRB-07

Drivers of regional and local diversity of Amazonian stream Odonata

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Large Amazonian rivers may act as barriers for animals with low dispersal ability, limiting their distribution to certain interfluves. Consequently, the distribution of these taxa would be less affected by macroclimatic gradients. Whereas high-dispersal taxa would be less constrained by large rivers and may track suitable climates. We evaluate whether Zygoptera and Anisoptera, two Odonata suborders with different dispersal abilities, show different distribution patterns across Amazonian interfluves. We further assess the relative importance of macroclimatic and habitat factors in their community assembly. We used network modularity analyses to identify biogeographic species pools and spatial buffers to define metacommunity species pools. Then, we used Structural Equation Models to estimate the relative importance of multi-scale factors on species richness patterns. Zygoptera communities are more similar in species composition within than between interfluves, suggesting that large Amazonian rivers indeed limit the distribution of Zygoptera species. Conversely, the distribution of Anisoptera extends across Amazonian interfluves. Seasonality has a strong positive effect on Zygoptera (r=0.17 to 0.22) and Anisoptera richness across scales (r=0.47 to 0.51). In addition, habitat integrity is negatively correlated with the regional species richness and abundance of Anisoptera and positively correlated with Zygoptera local richness. The contrasting effects of habitat integrity on Anisoptera and Zygoptera suggest that the former is favored in open habitats whereas the latter is so in forests. Despite these differences, both suborders appear to follow similar community assembly mechanisms in Amazonia, with a strong climatic control across scales and an effect of habitat filters on local communities.

GRB-08

Predicting the magnitude of residual spatial autocorrelation in species distribution modeling

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In species distribution modeling, biogeographers are essentially concerned with spatial data. This means that variables, be they biological or environmental, are most likely to possess an amount of spatial autocorrelation (SAC) with varying degrees. It is widely recognized that SAC has profound influences on the basic assumptions, performances, and inferences of species distribution modeling. Although many spatial prediction methods have been developed in order to reduce the degree of spatial autocorrelation in model residuals (rSAC), we are still far from understanding what the main sources of rSAC are and under what circumstances the magnitude of rSAC increases. Here, we reviewed previous studies (> 100) to identify diverse factors that potentially induce the presence of rSAC in species distribution models. It turned out that five categories of factors are worthy of note: ecological data and processes, scale and distance, missing variables, sampling design, and assumptions and methodological approaches. In addition, by reanalyzing Bini et al.'s (2009) data from 97 different biogeographical systems, we found that, when spatial eigenvector mapping was applied, the magnitude of rSAC increased significantly as a linear function of the average Moran's I of independent variables in each system ($R^2 > 0.40$, $p < 0.001$). There should be more indicators of the magnitude of rSAC than this, but we believe that our finding serves as a

meaningful start to search for them. Further investigations are recommended to continue to identify the degree to which rSAC becomes detrimental to the process and outcomes of species distribution modeling.

GRB-09

Predicting spatial patterns in the beta diversity of lake macrophytes across decades

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Temporal aspects are often underrepresented when studying global change and effects of human activities on biodiversity patterns, especially in the aquatic realm. Human activities can cause various changes on beta diversity patterns and these patterns can reveal biodiversity loss or biotic homogenization. We aimed to discover if vascular aquatic macrophyte communities show different spatial patterns in beta diversity in relation to human impacts across decades. We used presence-absence data of aquatic macrophytes from five different decades (1940s to 2010s) from small boreal lakes. We decomposed the total beta diversity to species replacement and richness difference components and utilized generalised dissimilarity modelling to analyse spatial patterns in these components in relation to environmental gradients. In addition to the generally used environmental variables, we used land use variables derived from base maps. Vascular aquatic macrophyte communities showed only slightly different patterns in beta diversity in relation to human impacts across decades. Species richness difference was more dominant than replacement component in each decade. Altitude and pH were the most important variables in each decade. As altitudinal gradient in this study area is not particularly steep, position in the landscape, reflecting both connectivity and lake characteristics, probably explains the patterns found in beta diversity. We found that land use was not particularly important in explaining the beta diversity in our study area. Our findings provide important information for aquatic biodiversity assessment and conservation research in boreal areas and beyond.

GRB-10

Inferring species ranges from the geographical distribution of SNPs under selection

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All across the distribution range of a species, independent individuals have to confront contrasting ecological requirements relying on the genetic variation that evolution supplies. Using as a model the lizard *Psammodromus algirus*, whose range extend over most of the western Mediterranean region, we show that by scanning the genome of only five populations located along an environmental gradient close to the center of the species distribution, we are able to adequately infer its whole distribution range. We characterized the fractions of the genome under selection and we used them as input in a genotype-environment association model. Then we extrapolated this model to unsampled populations constituted by unsampled (but plausible) genotypes. By using this approach, we created a very accurate reconstruction of the geographical locations where the species as a whole could inhabit, given their genotypes: the resulting inferred distributional map showed an 85% overlap with the 'real' one (i.e. the species range according to published sources), and it also adequately predicted its latitudinal boundaries. Assuming that the genome is the ultimate and only determinant of a species' range, we have developed a very simple model that explains the vast majority of a species distribution. So that, given that genomes constitute very specific instructions manuals even at broad levels, we have shown that it is possible to define entire geographical distributions from only a few SNPs under selection detected only in a few populations far away from its distribution boundaries.

GRB-11

Measuring of forest microclimate, we explain bryophyte species occurrence at fine spatial scale. Remote sensing factors are also useful for due to high correlation with measured microclimate.

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Bryophytes are thought to be sensitive for local microclimate and micro topography in spatial scale of centimetres or metres Interestingly, this presumption is poorly supported by systematic measurement and research. We empirically tested the presumption in heterogenous landscape of forested, bryophytes rich sandstone national park in Czech Republic, Central Europe. Using automated dataloggers we continuously measured forest microclimate on 198 sites for 2 years with time resolution of 30 minutes. We calculated various microclimate and sub meter resolution DEM derived parameters for each site. We recorded bryophyte species on each site.

We found measured microclimate factors are important for bryophyte species occurrence (random Forest models) and community composition (distance-based RDA). Most important factors are growing degree days (5°C – 20 °C), duration of period with temperature extremes (below 0°C, above 25°C) and local rain events (soil moisture peaks). Potential solar radiation, Wetness index and Vertical distance to channel network are the most important DEM derived factors.

Factors derived from fine resolution DEM are very good proxy for measured microclimate and can be used to explain bryophyte community composition instead of in situ measured microclimate. DEM derived factors are unable to substitute/predict microclimate information about duration of frost, which is important for bryophytes.

In our study, we confirm presumption, bryophytes are affected by microclimate and micro topology on one hand. On the other hand, we found almost complete amount of variability explained by microclimate we were able to explain using fine scale DEM derived factors and vice versa.

GRB-12

Altitudinal distribution patterns and conservation status in a Mediterranean hot spot: the Betic Ranges (Southern Spain)

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The Betic Ranges conform the most important hot spot for flora in the Mediterranean Basin and constitute an extraordinary natural laboratory for testing hypotheses related to endemisms biogeographic patterns. Here, our aim was the study of the altitudinal distribution of Betic endemic flora and its conservation status. For that purpose a list was prepared with information about the endemic Betic taxa, their altitudinal distribution (100 m belts) and IUCN threaten categories. To quantify the conservation status, UICN categories were pondered following a log scale. Our results show the existence of an altitudinal gradient for 432 endemic taxa. The altitudinal distribution of the endemic flora follows a mid-height hump-shaped curve, with the maximum number of taxa located in the range of 1000-1100 m, obtaining a distribution graph quite similar to a Gaussian bell. Excluding the effect of the area the same curve is obtained, although with the maximum it moves to the range of 1300-1400 m. This model could be consequence of the low isolation of the lowlands, the geometric constrictions in Sierra Nevada summit areas and the effect of other phenomena that could be present at random, such as the presence of peculiar habitats (cliffs, springs…) or substrates (gypsum, dolomite, serpentine…). The pattern obtained when we considered risk units is similar to the obtained for taxa, with a maximum value in altitude of 800-900 m.

GRB-13
THE EXCEPTION AS A RULE: GROUND BEETLES ALONG MEDITERRANEAN ELEVATION GRADIENTS

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The elevation gradient of decreasing species richness is one of the oldest diversity patterns established in biogeography. Either unimodal or continuously decreasing, it has been documented in many different taxa on mountains from several geographical regions. At the same time, as in most rules in ecology, a few exceptions have also been found, with certain cases that either show no response to or even an increase of species richness with elevation. Here, we show that some exceptions might constitute a rule, in the sense that the same taxa consistently exhibit deviant elevation patterns, at least in the same geographical region. We have explored ground beetle (Coleoptera: Tenebrionidae and Carabidae) communities on different mountains of southeastern Mediterranean with an elevation reaching around 2,000 m a.s.l. We found that the mostly herbivorous Tenebrionidae follow a 'reverse unimodal' pattern while the mostly carnivorous Carabidae tend to increase with elevation. These trends are similar for both species richness and abundance. For ground beetles, at least, habitat structure seems to be the major determinant of diversity patterns. Furthermore, beta-diversity among sites is mainly shaped by the turnover component, indicating different local communities adapted to different habitats. Sparse evidence from other Mediterranean mountains suggests that the 'deviating' response of ground beetles to elevation should be the rule rather than an exceptional case of the particular systems studied. It remains to be seen whether these trends are also found in other biomes and if they persist along broader elevation ranges.

GRB-14
Altitudinal variation induces a negative distribution abundance relationship for woody plant species in the mountains of China

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The generally recognized positive species distribution and local abundance relationship (DAR) has facing increasing challenges from recently reported neutral and negative patterns, and the underlying mechanisms remained controversial. With the data from 728 woody plant species of 1105 forest plots in 57 mountains across China, we confirmed this positive relationship between the local abundance and occupancy (LDA) within a mountain or across all mountains, and revealed a generally negative relationship between woody plants' range size and mean abundance (RDA). Moreover, the negative RDA correlation decrease significantly ($r^2=0.593$, $P<0.01$) with increasing altitude, while the positive LDA correlation keeps roughly stable ($r^2=0.037$, $P=0.09$). Both distribution metrics are positively correlated with species niche breadth (measured by elevational extent), and negatively linked with niche position (across the domain of China). We tested the effect of niche breadth, niche position and metapopulation characteristics for the altitudinal patterns of species distribution at two spatial scales, i.e. local occupancy and species range. The ROA model mainly supports the niche breadth hypothesis, showing an increasing interpretation power with the increase of elevation; however, the LOA model is dominated by a stable effect of local abundance (supporting metapopulation dynamics hypothesis) and an increasing role of niche position, along with increasing elevation. Our study doubts the generality of a positive DAR in a heterogeneous environment, highlights the effect of scale coupling in the pattern, and suggests that elevational variation might complicate the DAR patterns via habitat availability.

GRB-15

Do we need statistically independent indices?

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Several indices of biodiversity were shown dependent on each other and on species richness. As argued, this disqualifies these indices where we compare species-rich with species-poor regions or periods. A partitioning of the indices into different components has been suggested to solve the problem along with an introduction of new indices. Species richness is considered as an index of biodiversity in our report. We argue that the values of the indices that carry complete information on spatial biodiversity pattern are necessarily mutually dependent in the statistical sense. This dependence, however, does not prevent us from drawing correct inferences on biodiversity pattern of two regions with different species richness. Finally, we demonstrate how to draw the proper inferences based on the combination of three indices, i.e., Jaccard index, Simpson beta and Species Richness. We particularly focus on inferences about long-term time-series and successional sequences. This research addresses only the indices that do not utilize abundances.
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GRB-16

Biomic specialization as a tool in macroevolution: testing the resource-use hypothesis

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Vrba's resource-use hypothesis and the related habitat-theory suggest that a key to present-day macroecological patterns is found in the past: in the long-term history of turnover (speciation and extinction) of clades, and in the changes of palaeoclimate and other geological settings within the areas where clades evolved. In our work, we test several subsidiary predictions of this hypothesis on swallowtails (Lepidoptera: Papilionidae) using the degree of biome specialization (BSI) for each species, which is based on its global geographical range within different climate zones (biomes). These observed data have been contrasted to a null distribution of BSI values generated from 10000 Monte Carlo simulations of our data. Our results were consistent with the resource-use hypothesis' axioms, showing more species restricted to a single biome (BSI=1) than expected by chance and the higher incidence of specialists in most of the biomes situated in the extremes of the climatic range.
Furthermore, the Papilioninae and Parnassiinae subfamilies showed differential specialization across biomes; Papilioninae shows a worldwide distribution with species adapted to a wide range of biomes although most of the species are markedly tropical in association with equatorial rainforests and, secondarily, tropical deciduous woodlands, while Parnassiinae constitute a temperate Holarctic clade, with a significant association to steppes and, secondarily, to sclerophyllous and tropical woodlands. This appears to be the result of divergent biogeographic and evolutionary history associated to climatic fluctuations and orogenic events during the Cenozoic, which affected ancestral Papilionidae lineages

GRB-17

Using plant community attributes to identify bioclimate indicators along an elevational gradient in a sub-Antartic environment

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Variation in vegetation with altitude has been widely used as an ecological indicator to identify bioclimatic belts. However, there is still little knowledge of the changes in plant-community composition and plant diversity in sub-Antartic ecosystems along climate gradients. Our study was focused along altitudinal gradient (0-800m) on Isla Navarino (Chile). Clustering analysis identified four community types: a) mixed forest of *Nothofagus betuloides* and *Nothofagus pumilio* (0-300 masl); b) pure forests of *Nothofagus pumilio* (350-550 masl); c) *krummholz* forest of *Nothofagus pumilio* (500-550 masl); and d) tundra vegetation of *Bolax gummifera* and *Abrotanella emarginata* (above 600 masl). Plant richness followed a hump shaped from mid to high elevations. The highest species turnover was reached at the tree line (550 to 600 masl) where *Nothofagus* forest gives way to tundra. The identification of bioclimatic belts based on changes in plant community attributes and the calculation of biotemperature along the altitudinal gradient suggests the following plant communities bioclimatic indicators: oroantiboreal mixed forest of *Nothofagus betuloides* and *Nothofagus pumilio*; oroantiboreal pure forest of *Nothofagus pumilio*; hemi oroantarctic *krummholz* of *Nothofagus pumilio*; and oroantartic tundra of *Bolax gummifera* and *Abrotanella emarginata*.

GRB-19

A meta-analysis of niche breadth – species richness associations

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Although narrow niche breadth has long been assumed as either an explanation or an outcome of high species richness, it gained only equivocal empirical support. This may be the result of scale and methodology differences between studies, which in turn reflects different possible mechanisms that drive this association. We suggest two such mechanisms: (1) climatic - where low seasonality at lower latitudes enables species to specialize in specific environmental conditions, which results in high species richness, and (2) community assembly - where species rich sites forces species to specialize, in order to allow co-existence. For each of these mechanisms we expect to find different patterns of richness-niche breadth correlations.

Under the climatic mechanism we expect associations between species richness and niche breadth over large scales, specifically across climatic gradients, and only when using environmental measures (e.g. habitat breadth). While the community assembly mechanism would yield such associations mostly over small scales, across many types of richness gradients, and when using both environmental and functional measures (e.g. diet breadth). Thus, distinguishing the scale dependence, and the niche breadth type may shed light on the underlying processes.

We conducted a meta-analysis on studies that report the correlation between niche breadth and species richness. We found (1) negative correlation between species richness and niche breadth; (2) species richness has a stronger effect on niche breadth compared to latitude; (3) lack of any effect of scale or type of niche breadth. These results suggests that community assembly processes drive niche breadth patterns.

HP-01

Palaeobiogeography of the porcelaneous larger benthic foraminifer Borelis de Montfort (Alveolinoidea)

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Genera of larger benthic foraminifera with wide distribution and high dispersal potential, such as the porcelaneous *Borelis* de Montfort (Alveolinoidea), provide the opportunity to evaluate the effect of palaeogeography on shallow-water marine species (palaeo)biogeography. The features diagnostic at species level of *B. melo*, *B. curdica* and *B. pulchra* were assessed by shell architectural analyses of fossil and modern isolated specimens using the micro-computed tomographic system. Stratigraphic, taxonomic and palaeobiogeographic approaches suggest migration and speciation of *Borelis* species starting from the early Oligocene in the Pacific area. Two lineages characterised by absence/presence of Y-shaped septula were found in the Oligocene-early Miocene in the Tethyan ocean. *Borelis inflata*, *B. pulchra* and *B. pygmaea* lack Y-shaped septula. In the Pacific region, the long-lasting *B. pulchra* is still widespread. The first species bearing Y-shaped septula, *B. philippinensis*, appeared in the Rupelian of the Indo-Pacific. Its middle Miocene descendant, *B. schlumbergeri*, lives in the Indo-Pacific. Westward migrants reached the Mediterranean during the Miocene and gave rise to *B. melo* and *B. curdica*. These species became isolated from the Indo-Pacific by the middle Miocene eastern closure of the Mediterranean basin. The upper Miocene *Borelis* specimens occurred in the last shallow-water coral-reef settings in the Mediterranean. These settings were refugia for *B. melo,* which subsequently disappeared during the Messinian Salinity Crisis. Before the Pliocene closure of the Central America Seaway, the Pacific *B. pulchra* reached the Caribbean area from where it colonized the western Atlantic coasts.

HP-02

Small mammal population and assemblage dynamics at the Rancho La Brea Tar Pits

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Inferring interactions among species within past communities is complex, and requires understanding how such dynamics are structured by environmental change and community context, as well as the process of fossil deposition. We explore niche dynamics, species interactions, and community structure with multi-trophic paleo food webs through time and along climatic gradients, using fossil mammal and vegetation data from the Rancho La Brea (RLB) tar pits in Los Angeles, CA. We first determine community composition and deposition time of the assemblages recovered from multiple asphaltic deposits at RLB.

We then assess variation in relative abundances among small mammals through time and use isotopes to infer changes in dietary niche breadth of several focal taxa (ground squirrel *Otospermophilus beecheyi* and rabbits (genus *Sylvilagus*)). Finally, we integrate mammalian and plant data and simulations to build a preliminary model of the consumer-resource interactions that structure the community.
The fossil deposits date to between ~30 ^{14}C ky BP and >49 ^{14}C ky BP and capture a typical late Quaternary small mammal fauna of rabbits, squirrels, cricetid mice, kangaroo rats, and woodrats. Relative abundances among taxa differed substantially between deposits and the isotopic niche breadth of both squirrels and rabbits was narrower in the younger deposits. δ^{15}N became increasingly positive through time in both ground squirrels and rabbits, potentially associated with increasing aridification. We are now exploring which consumer-resource interactions most strongly structured the community through time.

HP-03

Recovering the evolutionary footprint through bioregionalization analyses: in search for the best methods.

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Wallace proposed bioregions as broad territories defined by a common history that generates a distinctive biota. Despite the recent blossoming of research on bioregionalization, few studies focus on the evolutionary distinctiveness of the delineated regions. Here, we seek the best approach to pinpoint historically defined regions. We develop a simulation of diversification within a spatially explicit context and classify the resulting scenarios with different regionalization methods: a distance-based method and three network approaches (Map Equation and two versions of a method based in the inference of stochastic block models -SBM1 and SBM2-). In the first one a distance matrix of pairwise phylogenetic beta diversity between geographic cells is classified by UPGMA. Map equation and SBM1 classify a network with phylogenetic nodes directly as nodes of the network of distribution. SBM2 incorporate historical information as 'tags' in the network. Finally, we compare the classified regions with the ones expected based on the simulated, 'known' history. The distance-based method and SBM2 are the best methods in recover history, but the difficulty in obtaining an objective hierarchy of regions of the first one makes SBM2 a better option. SBM1 have similar results and is the only method able to detect the recent dynamics of the species. Finally, Map Equation recover only isolated parts of the history. These results provide a preliminary framework in the selection of regionalization methods, which depends on the final goal: the identification of units defined by a common deep history or by more recent processes.

HP-04

Including phylogenetic information into network based bioregionalizations

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Community detection techniques —borrowed from network theory— are gaining in popularity to delineated bioregions. By treating presence-absence matrices as bipartite networks, these methods can identify groups of sites sharing similar species, and which are those species, simultaneously (i.e. bioregions and their associated faunas/floras). Additionally, they allow to detect hierarchies and overlaps within and among regions. Despite this rich information, community detection techniques have been unable to incorporate phylogenetic information, and such information might be of crucial importance to, for instance, unravel historical processes. Recent advances in the field permit nowadays to incorporate more sources of information into community detection exercises, which may constitutes a natural way to consider phylogenetic relationships among species. Here, we develop a methodology to incorporate phylogenetic information into network bioregionalizations based on higher order networks and the community detection algorithm so-called Infomap. Higher order network configurations can include dependencies among nodes beyond observed links, which in our case allows to directly incorporate phylogenetic dependencies between species. Infomap groups nodes (i.e. species and localities) if a random walker stays for a long time visiting

them, thus incorporating phylogenetic information is possible by, for instance, constraining the random walker to stay longer times among related species. We tested different higher order configurations using simulated data. Our results showed that the best performing configurations can accurately identify bioregions and the portions of the phylogenetic tree associated to them. This rich and valuable information should help to delineate bioregions while delving into the historical processes behind them.

HP-05

Tracking human impact on island ecosystems with ancient DNA

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Island ecosystems generally experience significant changes after human settlement. Coastal and lowland ecosystems are often the first to be explored and occupied, and thus being impacted from the earliest stages of human colonization. In the Canary Islands, the first human colonizers were frequently coastal dwellers whose diet was highly reliant on marine resources, and historical accounts make reference to significantly populated nuclei on lowland valleys. Therefore we would expect vegetation from these lower coastal areas to be significantly transformed. Assessing the early impacts and effects of human activities on lowland vegetation may be challenging due to the lack of suitable study sites. In the Canaries, low elevation areas are also the driest, reducing the options of finding high-quality proxy records of past vegetation (e.g. sediments with plant microfossils) that are often better preserved under wetter conditions. In addition initial human occupation in coastal areas may have developed into permanent urban settlements, thereby limiting the access to sites and the availability of materials providing long-term records. Through a combination of palaeoecological proxies we attempt a more reliable reconstruction of lowland environments before and immediately after human arrival to the islands, and the consequences of the transformation of these plant communities through time. In particular, the application of palaeoenvironmental DNA analysis for the first time in the Canary Islands will complement the lack of evidence from other conventional proxies and offer new insights on the long-term dynamics on these otherwise under-studied ecosystems.

HP-06

Genetics and fuzzy logic unravel the historical biogeography of European rabbit subspecies in the species' native range

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The European rabbit Oryctolagus cuniculus is native to the Iberian Peninsula (IP), where the two known rabbit subspecies occur. Previous studies have suggested that O.c. cuniculus distribution extends towards the north-east of the IP, while O.c. algirus is restricted to south-western regions; a transition area crosses the IP from the north-west to the south-east. Here, we revisited rabbit subspecies distribution to define with greater precision historical distribution areas, identifying the potential expansion cores and evaluating the spatial interaction between both subspecies expansion waves. We used different diagnostic loci located on mitochondrial and nuclear DNA to classify in any of the subspecies 4500 rabbits from 197 populations distributed throughout the IP. Using populations where all the rabbits were either O.c. cuniculus or O.c. algirus, we determined the spatial structure of the two molecules independently, by using a trend surface analysis based on favourability functions. We then combined the different spatial structures using fuzzy logic operations. Two areas in the Guadalquivir and Ebro valleys were identified as respective expansion cores. In comparison to previous studies, we found an increase in the distribution range of O.c. algirus to the northwest and a shift of the transition zone eastwards in its northern area. Our results suggest that competitive exclusion may have a greater role than expected in regulating the expansion of both subspecies. The spatial structure of these genes reflects, and thus may be used to unravel, the historical biogeography of these subspecies, provided that we possess appropriate analytical tools, such as fuzzy logic.The

HP-07

Climatic niche evolution and paleo-climatic change in the Wheatears and Chats

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In order to cope with changing climatic conditions, many species have been observed to shift distribution. However, alternatively species can respond by physiologically adapting to new conditions, i.e. changing their climatic niche. Although previous studies have observed that shifts in climatic niches appear to correspond to periods in time associated with major changes in climatic conditions, these have been largely descriptive and to our knowledge no study has explicitly tested for a consistent relationship through time. As such it remains unclear under what conditions and over what time period species are likely to undergo niche shifts. Using a group of 71 bird species, the Wheatears, Chats and allies, from the family of Old World Flycatchers (Muscicapidae) as a case study we test whether there is a relationship between rates of climate change and niche evolution. We combine climatic niche quantification methods and dated phylogenies for living species to infer the past rates of niche evolution using a variable rates model. Making use of the mammal fossil record and a tooth-based paleoclimate proxy, we infer terrestrial climatic conditions for the last 20MY in the regions where the studied bird species occur today. If climatic niche evolution is driven by climate change, we expect a positive relationship between rates of climatic niche

evolution and paleo-climatic conditions. Our results will have important implications for understanding the evolution of niches as well as predicting species responses to climate change.

HP-08

Global Succulent Biome phylogenetic conservatism across the pantropical Caesalpinia Group (Leguminosae)

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To investigate the origins and global diversification patterns in arid habitats, the pantropical Caesalpinia Group (Leguminosae) was used as a case study. This group of c. 225 species principally occurs in the Succulent Biome, but a subset also occurs in savannahs and warm Temperate areas (deserts and prairies), and are found as shrubs, trees, lianas or herbaceous plants. In addition to reconstructing the biogeographic history of this group, diversification rates were investigated to examine whether they vary as a function of long-distance dispersal, evolution towards new biomes or changes in plant habits. A molecular dataset with all 27 genera and 74% of species of the group was used to reconstruct a time-calibrated phylogeny, using two fossil calibrations. Ancestral areas occupied by this group were reconstructed, as well as the ancestral states for plant habit and biomes. Biome/habit co-evolution was also examined, and various tests of niche conservatism were carried out (including simmap permutation and testing for phylogenetic signal). Our results suggest that the clade most likely appeared in the Paleocene period, and was likely a tree/shrub species in the Succulent Biome, either from South America or Africa. Intercontinental dispersals events were estimated to occur most frequently in the Succulent Biome. The age and persistence of the group, combined with a single evolutionary rates regime, suggests long-term stability and resilience of the Succulent Biome. The frequent intercontinental dispersals within this biome points to niche conservatism acting to shape diversification of this clade on a global scale.

HP-09

Historical biogeography of Centipede Snakes of the genus Tantilla (Serpentes: Colubridae)

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The centipede snakes of the genus *Tantilla* are a diverse group of small- to medium-sized, New World snakes, uniquely specialized as predators of centipedes. *Tantilla* presently contains over 60 described species, making it the third most speciose snake genus in the world, widely distributed from Argentina to the central United States. The clade's species diversity and expansive distribution would seem to position *Tantilla* as a tempting subject for biogeographers. However, such inquiries have been hampered by a poor understanding of the interspecific relationships within the genus. Indeed, no published studies have yet examined the molecular phylogenetics of *Tantilla*. In order to explore the biogeography of this group, we generated nuclear and mitochondrial DNA sequences from genetic material sourced from the field and natural history collections. Here we present the first molecular phylogeny of *Tantilla,* which we use to

explore range evolution of the genus across space and time. In this presentation we present results of biogeographic inference (ancestral area reconstructions) and temporal framework for diversification (analyses of variation in rates of lineage accumulation) for the genus, and we discuss our results in the context of the broader biogeographic history of the Americas.

HP-10

Characterization and value enhancement of the priority gypsum habitats in Castalla and Villena (Alicante, Spain).

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Presence of gypsum-rich soils in the province of Alicante, mostly linked to the outcrops of Keuper, justifies the distribution of the gypsum habitat, in which we find scrub formations with an important endemic character and which are specially interesting for Biogeography. In this study, two gypsum fields, Els Campellos and Los Cabecicos, are proposed for their characterization in the municipalities of Castalla and Villena (Alicante, Spain) respectively. The aim of the study is to contrast the presence of exclusive species and plants with preference for gypsum soils in these two localities. Field work, GPS and GIS have been fundamental tools to carry out this corological study at a detailed scale. This analysis reveals the diversity and floristic richness of the habitat, considered as priority by the European Directive 92/43 / EEC, better known as the Habitat Directive, under the code 1520* *Iberian gypsum vegetation* (*Gypsophiletalia*), with the presence of species such as *Gypsophila struthium* L. in Loefl. subsp. *struthium*, *Teucrium libanitis* Schreb. and *Senecio auricula* Bourg. ex Coss. The evolution of the vegetal formations that colonize these gypsum areas, which include endemic, rare or threatened species, has ben conditioned by a differentiating factor: the existence of an environmental protective figure. Whilst in Los Cabecicos (Villena) there's a micro-reserve of flora, Els Campellos's diapir (Castalla) lacks environmental protective measures.

HP-11

Molecular phylogeny of Peperomia (Piperaceae) in the Pacific suggest two parallel radiations of Peperomia on the Hawaiian Islands

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Peperomia is one of the most species-rich genera globally (ca. 1600 species). Though primarily distributed across the world's continental tropics, *Peperomia* have also colonized and diversified across the islands of the Pacific Ocean, which collectively harbor about a tenth of its global diversity. Nevertheless, despite their evolutionary success on Pacific islands, the evolutionary relationships and patterns of dispersal among Pacific taxa are unclear. In addition, larger island archipelagos such as Hawaii and Fiji have been hypothesized to play host to independent radiations derived from single colonization events, but the monophyly of endemic taxa on these archipelagoes remain to be tested. To better resolve the evolutionary relationships of Pacific taxa, we sequence full plastomes for over 80 Pacific taxa using a genome skimming next-generation sequencing approach. Using this phylogeny, we find a complex history of colonization across the Pacific by four main lineages. Furthermore, we find that the endemic taxa (23 species) of the Hawaiian Islands has been derived through diversification of two of these colonist lineages. While the Hawaiian flora provides examples of spectacular radiations from single colonist ancestors (e.g., silverswords, lobeliads), and genera derived from multiple colonization events (e.g., sandalwoods), to the best of our knowledge, we present the first documented case of parallel radiations from two independent colonization events on the Hawaiian Islands. Our results emphasize the importance of expanding the

biogeographic lens through which many island lineages are typically viewed, and raise an interesting new dimension to the assembly of oceanic island floras.

HP-12

Multi-lines of evidence deny fast post-glacial northward forest migration in China

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It was commonly regarded that no forests were distributed north of the Yangtze River and the current temperate forests in northern China were resulted from fast northward migration from southern China. We systematically compiled pollen data from 69 sites north of the Yangtze River, as well as available phygeographical data of dominant tree species, in order to figure out how three dominant forest types, pine, oak and birch, have been developed in northern China. Niche model and phylogeographical data suggested that mountains north of the Yangtze River could have served as refugia for dominant temperate tree taxa. Biomization model suggested that western China, with its east–west mountain chains, experienced a faster forest migration rate than that experienced in middle and eastern China, possibly due to mountain refugia. Even in eastern to middle China, the current distribution of the species originated primarily from the spread of local refugial populations, instead of long-distance migration, implying a quite slower migration rate than ever expected. This type of continental-scale biome migration could also balance fragmentation in species range-shifts. Different from pine and oak, climate changing ratio were the main driving factors for *Betula* migration, while the succession to *Quercus* and *Pinus* occurs during the mid-Holocene when climate maintains stable, implying that future fast climate warming will cause expansion of birch forest at the cost of pine and oak.

HP-13

Biogeographic history and diversification of the Western Mediterranean vipers, Vipera aspis and V. latastei-monticola

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Past paleogeographical and climatic events have shaped biodiversity patterns of the Western Mediterranean Basin. Vipers (Viperidae) are highly susceptible to range shifts and demographic processes driven by climate changes. Previous works have identified genetic structure for the Western Mediterranean vipers, *Vipera aspis* and *V. latastei-monticola*; however, the evolutionary and ecological processes that might have triggered their diversification remain poorly understood. This work aims to reconstruct and compare the biogeographic history and diversification of these vipers, combining phylogeographic, paleoclimatic and ecological niche analyses. Specifically, we study: (1) genetic structure and diversity, and time of divergence; (2) ecological niches divergence through time; and (3) location of refugia and responses to Pleistocene climatic oscillations. Bayesian inferences were performed over mitochondrial and nuclear sequences (five genes) from 351 specimens, covering species distributional ranges. Paleoclimatic and ecological analyses were based on 3,687 records and climatic variables. Mitochondrial structure evidences a late Miocene-Pliocene diversification process in this group. Two, four and three main lineages that diversified during the Pleistocene are recognized within *V. aspis*, *V. latastei* in Iberia and *V. latastei* in North Africa, respectively. Ecological tests suggest an allopatric speciation process, although some lineages show signals of ecological divergence. Paleoclimatic reconstructions suggest that major lineages likely

responded differentially to Pleistocene climatic periods. Climatic stable areas likely acted as refugia for linages since mostly fit genetic structure and diversity within them. Our multidisciplinary approach allows proposing a biogeographical scenario for the evolution of these species, signaling areas for conservation that might be representative to other taxa.

HP-14

Mountains as evolutionary arenas: emerging approaches, paradigm shifts and their implications for the future of plant phylogeography in the Tibeto-Himalayan region

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Recently, the “mountain-geobiodiversity hypothesis” (MGH) was proposed as a key concept for explaining the high levels of biodiversity found in mountain regions of the Tibeto-Himalayan region (THR), comprising the Qinghai–Tibetan Plateau, the Himalayas, and the biodiversity hotspot known as the “Mountains of Southwest China”. In addition to the MGH, which covers the entire life span of a mountain, a complementary concept, the so-called “flickering connectivity system” (FCS) was recently proposed for the period of the Quaternary. The FCS is putting a focus on connectivity dynamics brought about by repetitive climatic changes during the past ca. 2,6 million years, emphasising that fragmentation and allopatric speciation are not the sole factors for accelerated evolution of species richness and endemism brought about by climatic oscillations and accompanying shifts of elevational belts. I will provide a review of the current state of knowledge concerning geological uplift, Quaternary glaciation, and main phylogeographic patterns of seed plant species in the THR, and view these in the light of a more generalised framework provided by the MGH, FCS, and emerging paradigm shifts brought about by ecological niche modelling and trait-based considerations.

HP-15

Testing alternative bathymetric models to link the magnitude of Messinian sea-level fall and genomic differentiation in a Mediterranean-Turanian grasshopper

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The closure of the Strait of Gibraltar during the Late Miocene led to an abrupt sea-level drop till the partial desiccation of the Mediterranean Sea (Messinian Salinity Crisis, MSC, ~5.96-5.33 Ma). Despite different biogeographical hypotheses have been proposed to explain how this event contributed to the expansion and exchange of biota across the Mediterranean region, most empirical studies rely on informal comparisons of geographical concordance between phylogenetic and paleogeographic reconstructions. Here, we integrate mitochondrial and genome-wide nuclear information with fine-scale bathymetric models within a spatially-explicit landscape framework to examine the link between the magnitude of the Messinian sea-level change and the evolutionary and demographic trajectory of *Mioscirtus wagneri*, a Mediterranean-Turanian grasshopper inhabiting hypersaline grounds. Our landscape genetic approach revealed that population genetic structure and lineage distribution was best explained by a scenario of ~500 meters sea-level drop originating a land-bridge connecting the Iberian Peninsula and Africa, which elucidate the paraphyly of Iberian subclades and the close phylogenetic relationship of southwestern Iberian and north African populations. The highest levels of genetic diversity observed in the easternmost populations suggest a westward expansion of the species linked to the increased availability of suitable habitats during the MSC. According to post-Messinian large-scale fragmentation of hypersaline habitats, our demographic reconstructions inferred dramatic declines in effective population sizes across all populations. Overall, our study highlights the power of bridging population genetics, phylogenomics, and paleogeographic reconstructions to infer the processes shaping the distribution of genomic variation at different evolutionary scales.

HP-16

Historical biogeography of Southeast Asia aquatic biotas

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In Southeast Asia (SEA), Sundaland is considered as one of the most important and threatened biodiversity hotspots. One of the major drivers for diversification in the area, "hypothetically", is the cycle of sea levels fluctuation that repeatedly isolated and merged the major islands of Sundaland during the Pleistocene. This research aims to explore the diversification and biogeography of Sundaland, particularly regarding the impact of eustatic sea level fluctuations towards the distribution of molecular lineages of freshwater fishes within the palaeodrainages' boundaries in the area. Pre-existing sequence data from several locally widespread species from genus Dermogenys, Hemirhamphodon, Nomorhamphus (Beloniformes, 266 individuals); Clarias (Siluriformes, 88 individuals); and Channa (Perciformes, 535 individuals) were mined from GenBank and BOLD system, and were analysed using different set of markers for each order. Maximum likelihood trees were reconstructed using RAxML followed by species delimitation using GMYC, ABGD, mPTP and RESL algorithms; divergence time estimates and phylogenetic relationships using the GMYC model as implemented in *BEAST2; and completed by ancestral state reconstruction (ASR). Our study evidences a high proportion of cryptic diversity and a diversification burst during the last 1.5 mya with 70% of the speciation events occurring during this period. Early result of ASR analysis shows more transitions between palaeodrainage-within Island than between island-within palaeodrainage. This result challenges the earlier hypothesis of eased dispersal among islands during sea level lowstands. Further ASR analysis is carried out to examine the most probable scenario for the diversification and biogeography of freshwater fishes in the region.

HP-17

From the Middle East around the Mediterranean to Europe: historical biogeography of Anthriscus sect. Cacosciadium (Apiaceae)

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Anthriscus sect. *Cacosciadium* comprises seven plant taxa that are recognized as separate species or subspecies of a widespread *Anthriscus sylvestris*, occurring from eastern Asia to western Europe and to northern Africa, with isolated localities in the mountains of tropical East Africa. In Europe, this complex includes five taxa that exhibit a remarkable ecological diversity inhabiting both primary and secondary lowland habitats as well as primary alpine screes and mountain shady forests. We have investigated the biogeography of this group using dated phylogenetic trees inferred from nuclear rDNA ITS sequences (148 georeferenced plant samples) and three plastid intergenic spacers: *rpoB-trnC*, *trnS-trnG* and *trnH-psbA* (102 samples). Our data suggest Middle Eastern origins of the genus and its sect. *Cacosciadium*. However, plastid phylogeny demonstrates that the migration of *A. sylvestris* sensu lato to Europe did not occur through the Anatolian and Balkan peninsulas but around the Mediterranean through northern Africa to western Europe and then eastwards. ITS data and morphology—the occurrence of bristled fruits in southeastern Europe and Asia Minor and their absence in northern Africa and western Europe—suggest secondary gene flow from Asia to Europe when these two populations got into contact. The ecological diversity of this complex in Europe is very recent as various taxa share the same pool of plastid DNA haplotypes.

HP-18

Extinction patterns of insular mammals from the Late Pleistocene till today

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We analysed the number and percentage of extinctions of endemic mammal species, body mass distributions of endemic mammals, island size and the timing of the first human arrival for 35 palaeo-islands from 10 archipelagos worldwide. Our data show that all islands lost their heaviest mammal species, as predicted. Maximum body size ranged from above 1000 kg for the Philippines to above 1 kg for the Mediterranean. No mammal heavier than 100 g survived on the Canaries, while the Galápagos lost all their native mammals. In some cases, notably in Madagascar, smaller-sized species were decimated as well. The number of extinctions is positively correlated to island size, in accordance with predictions following from the species-area relationship, whereas the percentage of extinctions in relation to total number of endemics is negatively correlated to island size. Almost 80% of insular extinctions occurred after the first human arrival, with the highest percentages during the Late Pleistocene (34.5%) and the Modern Era (31%). This indicates a dramatically increased rate of extinctions in the Modern Era, considering the substantially longer time span of the Late Pleistocene (at least one order of magnitude difference). Increased globalisation with substantial anthropogenic habitat alteration in combination with alien introductions likely underlies this pattern. The gradual increase in extinctions of native mammals through the Holocene, with a peak (31%) in the last 500 years, is suggestive of a slow scenario ("sitzkrieg", contrary to "blitzkrieg").

HP-19

Distributional changes of the felid guild following the Pleistocene megafaunal extinction

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During the Pleistocene, meso-carnivores such as the cougar (Puma concolor), were potentially outcompeted by larger-bodied felids such as Homotherium and Smilodon. Extinction of these more massive hyper-carnivores at the terminal Pleistocene likely opened new habitat/niche space. Here, we examine if cougars began to exploit eco-space presumably vacated by the extinctions of the mega-felids. We employed a MaxEnt and Ecospat ecological niche modeling (ENM) approach using felid occurrences from the Neotoma Paleoecology Database and paleo-climactic records from the Community Climate System Model. We produced ENMs of New World felids for the late Pleistocene, mid-Holocene, and historical/modern time periods. ENM predictions were compared in environmental-space (as opposed to geography) for to test for niche stability in cougars across the Pleistocene-Holocene boundary. Comparisons were also made between cougars and extinct felids to test for cougar niche expansion into those previously occupied niches. Preliminary results suggest that niche stability was observed in cougars between the Pleistocene and mid-Holocene, but surprisingly niche contraction was the predominant observation into the Holocene. Further contrary to expectations, we find that cougars did not re-fill the niche space vacated by the mega-felids following their extinction. Our findings suggest that niche stability is not as common as presumed in many modern ecological analyses. Further, cougar ecological niches do not appear to have been constricted by interactions with other large felids during the Pleistocene.
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HP-21
Filling knowledge gaps in global plant geography over two centuries

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Accurate knowledge of species distributions is vital for biogeographical research. Despite the fact that we have vast databases of occurrence information, there remain gaps in our knowledge regarding the distribution of plant species. Surely, we have been filling in these gaps over time, but it is unclear the rate at what which we are accumulating knowledge, which gaps are being filled and which remain unresolved. Using plant family and floristic kingdom maps compiled by botanist Joakim Frederik Schouw in 1824, along with a biogeographical text from 1822, we examine the accumulation of phytogeographical knowledge over the last 172 years. Schouw's historical phytogeographical maps are the first known global plant distribution maps, and are the synthesis of the works of early biogeographers and explorers such as Linnaeus, Humboldt, de Candolle, and Wildenow, and contain both distributional and richness data. We compare these historic maps to contemporary estimates of the distribution of families and floristic kingdoms based on expert maps and occurrence databases such as GBIF and BIEN. The comparison will allow us to evaluate how biogeographical knowledge on distributional ranges, species richness estimates, and climatic limits of families have changed over time. Finally, we will quantify knowledge accumulation to estimate how close we may be to filling in these phytogeographical knowledge gaps.

HP-22
Avian blood parasite prevalence is governed by bird community assemblies and colonization histories

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The prevalence of parasites can be influenced by the communities of their hosts. Cosmopolitan host-parasite interactions, such as vector-transmitted haemosporidians (blood parasites) of birds, provide opportunities to investigate how host communities drive parasite prevalence. Over space, haemosporidian prevalence may be higher in warmer lowlands compared to colder highlands with more limited vector abundance. Similarly, bird species in geologically younger regions may experience lower parasite prevalence and pressure due to the lag time of parasite/vector colonization. We tested these hypotheses for haemosporidians in bird communities along an elevational gradient (200-3700m.a.s.l) on the tropical island New Guinea, and between two comparable bird communities in mountains of different geological ages. We found a mid-elevational peak of haemosporidian prevalence, primarily driven by differences in bird communities between elevations. Mid-elevation communities were occupied by multiple bird species with higher haemosporidian prevalence than low- and highland communities. However, parasitism in individual bird species did not show a mid-elevational peak, confirming that haemosporidian prevalence across space is not driven by individual species but by the composition of the community. As predicted, we found significantly lower parasitism levels in comparable bird species communities in the geologically younger than older mountain areas, in support of a lag time in vector colonization. Our findings suggest that haemosporidian prevalence across space is shaped by the communities of bird species, and that birds moving into geologically younger regions may temporarily escape blood parasites.

IB-01

The early spider catches the woodlouse: Early colonization and island hoping partially explain the diversification of Dysdera ground dweller spiders in the Canary Islands

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Species diversification on islands, either adaptive or not, have provided experimental model systems to investigate speciation and characterize drivers of eco-phenotypic differentiation. In this framework, a fundamental aspect to understand speciation mechanisms is to determine the patterns of geographic formation of lineages. Unfortunately, phylogenies of islands radiations are frequently either incomplete or outgroups are poorly sampled, compromising our ability to reconstruct the colonization pathways and the ancestral distribution ranges.
The genus *Dysdera* includes more than 250 species of nocturnal, ground-dwelling spiders mostly circumscribed to the Mediterranean basin and the northeastern Atlantic Macaronesian archipelagoes. The genus stands out among spiders in including species with different levels of dietary preferences, ranging from generalist to obligate woodlouse feeders. The trophic preferences have evolved independently several times.
Here we present the results of a multi-locus, target gene phylogenetic analysis of the most thorough sample of island endemic and continental species of *Dysdera* conducted to date. We further estimate divergence times using multiple calibration points and reconstruct biogeographic history. Our results indicate that (1) *Dysdera*colonized the different archipelagoes multiple times, (2) the Canary islands were colonized early in their subaerial geological history, (3) Canarian endemic lineages split from common ancestor before the diversification of extant western Mediterranean species and (4) intra-island colonization played an important role in *Dysdera*diversification in the Canaries, although the numerous events of local diversification also revealed opens the door to the involvement of other processes such as microallopatric events or ecological speciation.

IB-02

Testing species boundaries and phylogeographic patterns in the nocturnal ground-dweller Dysdera spiders of the Canary Islands by means of DNA barcoding

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The use of DNA barcodes, i.e. standardized, small fragment of DNA used as species identifier, has greatly contributed to ease identification and discovery of new candidate species. Divergent DNA barcodes may hint at the existence of potentially overlooked species that should be further tested using phenotypic data and additional nuclear markers. However, because of the low genetic divergences, and short time for complete lineage sorting, adaptive radiations and other forms of rapid diversification has been shown to pose challenges to the use of single marker delimitation approaches.The genus *Dysdera* is among the most diverse spider groups in the Mediterranean Basin, where more than 250 species have been described. The genus has colonized and highly diversified in the Macaronesian archipelagoes, in the eastern Atlantic Ocean. Approximately, 50 endemic *Dysdera* species has been recorded in the Canary Islands, and

additional ones await formal description.We have generated more than 500 barcodes obtained from a thorough sampling of *Dysdera* individuals, collected across most terrestrial ecosystems in the islands. We use these data to specifically address (1) whether morphologically diagnosable species are also delimited by DNA barcodes, (2) whether DNA barcodes reveal the existence of previously overlooked lineages and (3) whether widely distributed species share common geographic patterns of intraspecific genetic divergence within the archipelago. Results of this analysis will help us to accelerate the inventory of *Dysdera* species and to identify within-island vicariant events, improving our understanding of one of the most dramatic example of island diversification among spiders.

IB-03
Are island endemic species more specialised?

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Due to their small global range and *in situ* speciation, island endemics are often considered to be specialist species, and, as such, at risk from environmental change and competition from introduced species. However, high-elevation islands contain very steep environmental gradients, and island endemics can occupy large elevational ranges and have high local abundances. Thus, it is possible that endemic species are generalists, able to tolerate changing environments.
We are using a range of approaches to test the hypotheses that endemic species are more specialised than non-endemics and exotics. One, reported here, uses plant trait data from the island of La Palma (Canary Islands), measuring specialisation as clustering in trait space. We also categorise the island geographically into environmental zones and combine this with presence–absence data to test the idea that range-restricted endemics (those restricted to a single zone or habitat) are more specialised than wider-ranging endemics.

IB-04
Dispersal ability shapes the strength of diversity-environment relationships in spider communities on oceanic islands

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Studies seeking to explain local diversity patterns have typically relied on historical constraints, and niche-related and neutral processes. However, the relative contributions of these processes are difficult to disentangle; community assembly resulting from multiple interactions between them. A promising approach to understand these interactions is to deconstruct diversity patterns using group-specific traits, such as dispersal ability, that has been proved useful for quantifying the importance of niche and neutral processes.

Herein, we investigate the role of environmental factors on the local diversity patterns of spiders with varying dispersal abilities. Our study took place in Macaronesia where we sampled six plots in pristine forest and in arid habitats in two islands in each of the archipelagos of the Azores, Canary Islands, Madeira and Cabo Verde. Our main question was whether habitat type, landscape heterogeneity (dispersal cost and slope diversity) and productivity (temperature and NDVI) affect local diversity. We classified spider species into frequent ballooners (high-dispersal), occasional ballooners and rare ballooners (low-dispersal). Habitat type better explained local diversity of low-dispersal than for high-dispersal species. We found that the local diversity of low-dispersal species was positively related with temperature and NDVI, while none of the environmental variables affected the local diversity of high-dispersal species.

Overall, our results suggest that local energetic constraints are important in structuring the communities of low-dispersal spiders in Macaronesia, while mobile species seem to be not or less affected by local conditions. Our findings add to a growing body of evidence highlighting the need of using dispersal traits for macroecological analyses.

IB-05

Chorotypes of Darwin’s finches

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Islands that never were in touch with the continent are valued systems for studying the distribution of species. The Galapagos Archipelago is an emblematic place to investigate colonization, extinction, and speciation processes. Darwin’s finches are a well-established group of birds, whose variability and adaptability have allowed the group to be present on all the islands and adapt to many habitats. Although many studies have been carried out with Darwin’s finches regarding their biogeographic origin, their distribution patterns inside the archipelago have not been analyzed. To describe and explain the distribution of the 17 species of finches over the 16 islands or islets, we classified the species into nine statistically significant groups of similar distributions, that is to say, chorotypes. Chorotypes consist of two different components: the geographic (islands) and the biotic (species) element. The different geographic elements allow us to arrange the islands into a central and a peripheral biogeographical sectors. The chorotypes derive from colonization, speciation and extinction processes. Therefore, these patterns evidence the history of this group of birds. However, the configuration of these types of distributions of Darwin’s finches can also reveal the geological history of the Galapagos Islands. On the other hand the results achieved allow us to group species and create management unites that can make easier their use and conservation. In consequence, the results here obtained cannot only be considered as useful biogeographic units to provide a context for evolutionary studies, but they can be used for conservation managements.

IB-06
Patterns of distribution of Galapagos Archipelago's seabirds

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Islands which have never been in touch with the continent are systems with the greatest value to study the distribution of species. The Galapagos Archipelago is an emblematic place to delve into island biogeography's knowledge. From amongst its fauna, birds are one of the most studied groups, with 80% of the resident species being endemic. Nevertheless, regarding seabirds, some questions remain unsolved due to their pelagic characteristics. An example of this is the Elliot's storm petrel, which despite being an endemic subspecies the breeding localities are still unknown. In this study, we focus on this group of species (seabirds) in order to describe and understand their distribution patterns. We have grouped them into statistically significant sets of species with similar distribution — chorotypes. We considered the presence/absence of species at island level, and we took into account the 50 seabird's species recorded until present in the archipelago. Three approaches were applied: we studied all seabirds, vagrant species, and breeding species. We obtained 8, 7 and 9 chorotypes, respectively, demonstrating patterns of distribution shared by different species. These results allow us to group seabirds into chorotypes, to finally generate management units in order to facilitate conservation plans. On the other side, with respect to seabirds that reach accidently the archipelago, this method highlight groups of species that share potential colonization processes.

IB-07
Niche evolution in the adaptive radiation of Hawaiian Tetragnatha spiders

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Adaptive radiation provides the ideal context for exploring the interaction of ecological and evolutionary processes in generating biodiversity. The Hawaiian *Tetragnatha* (long-jawed) spiders constitute a remarkable adaptive radiation, with approximately 50 known species across the archipelago, displaying a striking variety of morphologies and ecological affinities. The adaptive radiation consists of two clades: one which spins orb webs to capture prey, and another (the "Spiny Leg clade") which hunts actively. While the evolutionary history of the Spiny Leg clade has been well characterized, very little is known about the relationships within the web-builders, nor is it known whether the two clades originated from the same colonization event. We present the most taxonomically comprehensive phylogenetic hypothesis for Hawaiian *Tetragnatha* to date, based on four mitochondrial and six nuclear markers, and including representatives of every known Hawaiian species. We find some clades that are confined to a single island, with high rates of morphological and ecological diversification within the clades, while at the same time, convergent evolution of certain phenotypes appears to have occurred in multiple lineages. Conversely, one clade shows high levels of niche conservatism, with all of its species confined to dry forest habitats across the islands. We also find evidence that the web-builders and Spiny Leg clade do not form a clade together, and therefore likely arose from separate colonization events. Our results indicate a complex history of contrasting evolutionary processes leading up to the present-day diversity of Hawaiian *Tetragnatha*.

IB-08

Are organisms with dispersal traits better colonizers within oceanic archipelagoes?

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When studying species dispersal, it is often assumed that species with specific traits -such as winged animals or plant diaspores with hooks, pappus or nutritious tissues- are better dispersed than unspecialized species and thus tend to have wider distribution ranges. However, recent studies have challenged this assumption. It has been described that plants with structures associated with specific long-distance dispersal vectors show only a small or negligible advantage. This finding raises two interesting questions: Do winged animals display a significant advantage for colonisation? And secondly, are mobile animals better colonisers than plants? To answer these questions, we analysed animal (Coleptera, Sauropsids and Mammals) and plant (Angiosperms) traits and distributions across the Canary Islands. We found that dispersal traits have played a more important role in animal dispersal than in plant dispersal. More surprisingly, we found that despite lacking voluntary movements, plants have been at least as effective inter-island colonizers as animals.
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IB-09

Pinning down the origins of an island adaptive radiation implementing a combined approach using transcriptomic and genomic data

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Adaptive radiation is a trademark of island evolution, usually explained as the result of ecological opportunity. With more than 50 endemisms on the Canary islands, the Mediterranean ground-dwelling genus *Dysdera* stands as one of the most extreme cases of island diversification within spiders. Inferring a well-supported phylogeny is fundamental to identify the number of colonization events and testing whether the island endemics constitute a case of adaptive radiation. Gene target approaches suggest that *Dysdera* forms two main clades, one including species from the Western Canaries (younger islands) and a second with species from the Eastern Canaries (older and highly eroded). However, relationships between these clades and with continental relatives remain unresolved.
To improve the phylogenetic resolution we sequenced the transcriptomes of 9 Canarian species, and combined with publicly available data, we built up a molecular matrix of a thousand arthropod-specific single-copy orthologous genes. Transcriptomics, however, is hindered by the need of well-preserved specimens. To circumvent this limitation, we sequenced low-coverage genomes from key species stored in museum collections and added their molecular data to the matrix using the aTRAM pipeline, which retrieves raw reads corresponding to genes and assemble them. I will present a time-scaled phylogeny using this hybrid phylogenomic approach addressing an extreme example of island colonization and later diversification.

IB-10

From forest to driest: The multi-scale role of habitat heterogeneity in shaping spider communities on oceanic islands

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Islands have long been used as natural laboratories to test hypotheses about dispersal, adaptation and speciation. Much research has focused on understanding how island age, isolation and size determine the richness and composition of species communities, yet we have just started to explore the importance of environmental and habitat variability on species diversity and composition at different spatial scales. In our study, we used the Macaronesian archipelagos and spiders (a taxon with disproportionate effects on invertebrate communities and ecosystem functioning) as our model system and taxon, respectively, to assess the effect of habitat complexity and stability on species diversity and composition. We tested the hypotheses that, due to the buffering or stabilising effect of forest on microclimate: 1) community turnover is more important in dry areas than in forest areas; and 2) this should be true at both regional and local scales. Our results showed that the contribution of beta diversity to gamma diversity was greater in dry areas than in forest areas at three out of the four analysed spatial scales. We also found that not only was the species turnover (and its replacement component) generally greater in dry areas than in forests at the local level, but it was greater than expected at the local (within plots) and regional (between plots) scales. Our findings highlight the need to consider the different spatial scales at which habitat heterogeneity – and associated factors – act on community assembly and structure.

IB-11

Comparative analysis of phylogenetic and trait fields on island bird species worldwide

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Many non-exclusive mechanisms, both deterministic and stochastic ones, could affect the diversity and the distribution of species on the earth. The outcome of these processes could be reflected in the phylogenetic structure and distribution of traits in the assemblage. The degree of phylogenetic trait conservatism could also affect the pattern observed in these structures. The speciation events evidently cause clustered phylogenetic structure, but the distribution of traits depends on the trait conservatism even under this

situation. When the traits are conserved, environmental filtering should lead to a clustered phylogenetic structure while competitive interactions between co-existing species should result in the opposite pattern. On the other hand, environmental filtering can generate phylogenetic overdispersion when traits from distantly related taxa have converged in response to similar environment. Thus, the simultaneous examination of phylogenetic and trait structures of assemblage might be quite useful. Although the ordinal analysis of phylogenetic structures is carried out at the level of assemblage, this could prevent the examination of the effects of species-specific features on the community assembly. The concept of phylogenetic and trait fields allows us to directly compare the phylogenetic and trait position of species within an assemblage. In the present study, we used global distribution data, phylogeny, and trait data to quantify the phylogenetic structure and trait distribution of insular bird assemblages. Insular system is ideal for investigating how the evolutional and ecological processes influence species assembly. Our results suggest the synergetic effects of both evolutional and environmental as the force structuring the assemblages.

IB-13

The long-lost relatives: Phylogenomics solves the Euphorbia balsamifera Macaronesian riddle

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Biogeographic relationships between the Canary Islands and northwest Africa are common among plants, often explained by oceanic dispersal and geographic proximity. Sister-group relationships between Canarian and Eastern African/Arabian taxa are more rare, and correspond to a disjunct "Rand Flora"-type distribution spanning thousands of kilometers on opposite sides of Africa. One hypothesis is that the Macaronesian component of the Rand Flora originated from a recent dispersal event from a northwestern African population that went later extinct, leaving a large spatial "gap" between the east and western disjunct taxa. Yet, no phylogenetic evidence supports this event. The sweet tabaiba, *Euphorbia balsamifera* consists of three subspecies: *balsamifera*, a lineage centered in the Canary Island with a few scattered enclaves along the coast of Morocco and Western Sahara, Western Sahel *sepium* and Eastern African/Arabian *adenensis*. Using target enrichment with genome skimming of nuclear and plastid genomes (HybSeq), we reconstructed phylogenetic relationships within this taxon. Preliminary results across *E. balsamifera*'s distribution range suggested a recent colonization of the Canary Islands from northwestern Africa. One advantage of HybSeq is the possibility to use the same genomic resources to expand taxonomic coverage. New fieldwork in coastal Morocco, Western Sahara and across the Canary Islands, has allowed us to complete population sampling within subsp. *balsamifera*. Using multispecies coalescent approaches and Bayesian dating we infer the direction and timing of colonization events between northwest Africa and the Canary Archipelago. We also reconstruct colonization events between islands within the Canarian Archipelago and compare phylogeographic patterns with other Macaronesian-African disjunct taxa.

IB-14

Speciation and extinction shape phylogenetic structure of island bird assemblages worldwide

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How the speciation and extinction contribute to shape the global diversity pattern is one of the most fundamental questions in macroecology. Oceanic islands are ideal for investigating how these processes influence species assembly, because the assemblage on islands are known to possess more endemic species and show higher extinction rates especially in birds. In this study, we aimed to assess the effects of speciation and extinction on phylogenetic structure of co-occurring species. We also linked island characteristics, functional traits and human activity with the events of speciation and extinction. We used

distributional data of whole bird species with their phylogeny to identify the species endemic to and extinct on the islands. The effects of island characteristics and species traits on the extent of speciation and extinction were evaluated by generalized linear mixed models (GLMMs). We selected body size, diet, habitat and mobility as bird traits. The area, isolation, elevation and temperature, etc., were used as the environment factors of each island. As a result, some endemic species on tropical islands were linked with extreme phylogenetic clustering, indicating recent diversification. Moreover, the extent of speciation increased with area, isolation, climate stability and body size, while extinction was associated with smaller and more isolated islands and larger species. We demonstrate that island bird assemblages are shaped by speciation and extinction dynamics, which are influenced by island characteristics and species traits. Our findings could also be useful for conservation prioritization of threatened insular species

IB-15
Phylogenomics of Melanesian Forest Frogs: Biogeography of a Pacific Island amphibian radiation

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The direct developing frogs in the family Ceratobatrachidae have a unique insular distribution along the eastern margin of Southeast Asia. Within this group, the Melanesian Forest Frogs of the genus *Cornufer* extend to the distributional limits of anurans into the oceanic islands of the Pacific, but are conspicuously absent throughout much of Southeast Asia, ranging only into eastern Indonesia. To date, analysis into the biogeographic history of *Cornufer* has been inhibited by small genetic datasets that have been unable to resolve their phylogenetic relationships. Here, we provide a phylogenomic approach, using a anuran-specific exon capture probe set, to resolve their evolutionary relationships and test biogeographic hypotheses regarding their dispersal and diversification throughout the archipelagos they inhabit. Our analyses provide new insights into vertebrate colonization patterns of Southeast Asia from the fringing archipelagos of the western Pacific, and uncover deterministic evolutionary patterns that underlie the assembly of island frog communities.

IB-16
Global island biogeography of land snails

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The status and trends of global biodiversity are traditionally assessed with a taxonomic bias towards charismatic vertebrate groups, despite the fact that invertebrates constitute the vast majority of animal species. Land snails contribute to recent global extinctions by an ample 36%, according to the IUCN Red List. The vast majority of these have been witnessed on islands, but, to date, estimations of global snail insular diversity are based on scattered and widely patchy records. Here, for the first time, we attempt to a) develop a centralized record of the island snails of the globe and b) investigate their biogeographic patterns at a global scale.

We recovered full species lists from existing literature and available species checklists for 756 islands scattered across 83 archipelagos. Geographic coverage mounted to *ca*. 5% of global mainland area. We compiled a species database including *ca*. 46% of all known species (11069/24000) and 24% (114/476) of all known land snail families. Eighty-nine percent of these are archipelagic endemics, with a subset of 73% located on single islands.

The high proportion of species richness yielded from a small fraction of global land area signals a potential underestimation of worldwide land snail diversity. The exceptionally high endemism documented here, along with the well-known excessive extinction rates advocate the utility of global invertebrate biogeography towards a better understanding of the biodiversity crisis.

IB-17

An empirical assessment of variation in relative dispersal ability among widely distributed Philippine snakes

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Long-distance dispersal is a fundamental process shaping species distributions, and biogeographers ever since Wallace and Darwin have pondered the abiotic and biotic factors influencing dispersal ability. The Philippine Archipelago is an ideal system for comparative studies of dispersal, because it includes more than seven thousand oceanic islands, most of which by definition have never been connected to continental landmasses. Additionally, land bridges connected clusters of these islands into multiple Pleistocene aggregate island complexes (PAICs), which have remained disconnected from each other throughout their geological history, necessarily requiring numerous bouts of oceanic dispersal to account for the resulting geographic range evolution of widespread Philippine taxa. To investigate whether some organismal traits are associated with dispersal ability, we inferred chronograms for eight clades of widely distributed snakes of varying age and taxonomic scales, and employed stochastic mapping to infer historical range evolution with an assessment of relative dispersal ability/performance for each clade. We examined whether macrohabitat (arboreal, terrestrial, or fossorial), taxonomic group (family-level), ancestral distribution, or body size is associated with relative dispersal ability, and we relate prevailing trends in variation in species diversity throughout this iconic island archipelago.

IB-18

Contingency and determinism in simulations of the island progression pattern

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Terrestrial clades in volcanic hotspot archipelagos (e.g., Hawaii) frequently exhibit a phylogenetic pattern whereby the deeper branches of the radiation are represented on the oldest islands, and the youngest islands have a subclade of more recently diverged taxa. In this study, I use a spatially explicit macroevolutionary simulation in R to explore which conditions are minimally required for (simulated) clades to exhibit patterns consistent with the island progression pattern. I find that in the absence of competitive exclusion, phylogenies consistent with the island progression pattern frequently emerge, and that island age, configuration, and taxon dispersal probabilities are important predictors of the phylogenetic patterns that emerge. However, also noteworthy is the extent to which simulations with identical starting conditions and parameters can lead to divergent patterns, including a wide range of taxon diversity and distributions. This study highlights the limitations of our ability to infer community ecology processes from phylogenetic patterns.

IB-19

Analysis of community phylogeny along elevation gradient in subtropical island Taiwan supports "Out of Tropical Lowland" hypothesis

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Understanding the mechanism of species assembly in response to temperature is challenging; however, information about phylogenetic relatedness among species in the community may provide some important insights. Two opposing hypotheses are tested here: “Tropical Niche Conservatism” (TNC) predicts that as temperature decreases, the mean clade age of species in a community tend to be younger as niches are temperature-constrained, causing certain lineages to continuously adapt to temperate climate. A contrasting “Out of Tropical Lowland” (OTL) hypothesis signifies a rapid migration of randomly distributed tropical lineages to mountains where they diversified slowly, therefore lacking younger lineages. Taiwan offers a strong case for the observation of community assembly due to its young geological age, diverse climatic range and steep elevation gradient. In this study, we focus on determining underlying assembly mechanisms in the woody flora of Northeast Taiwan, a region characterized by heavy rainfall and frequent cloud coverage with elevation-influenced climate ranges from tropical to warm temperate. By analyzing nearly 300 vegetation community plots, we found that with decreasing temperature toward higher elevation, phylogenetic relatedness of species within the community decreases and the mean family age (MFA) increases. This pattern is coherent with the OTL hypothesis and is further supported by findings that show MFA correlates to factors such as lowest minimum temperature of the coldest month. By applying phylogenetic methods to community distribution, our results tell us more about Taiwan's community assembly mechanisms, providing new information about the biogeographical and evolutionary source of species in plant communities at different elevations.

MB-01

Role of geographical and environmental factors in global-scale distribution of marine benthic protists and meiofauna

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Small-sized organisms, both unicellular ("microbes") and multicellular (e.g., microcrustaceans), are ubiquitous and play the key role in global functioning of the biosphere. However, geographical patterns of their diversity and composition are unclear, and the relative role of spatial, historical and ecological factors in structuring their assemblages is poorly known due to lack of empirical data. We studied the global distribution patterns of the three key groups of marine benthic organisms: heterotrophic flagellates, ciliates and harpacticoid copepods, basing on the comprehensive databases compiled from many sources. Two groups of factors potentially driving these patterns were considered: 1) geographical (spatial distance and geographical isolation by landmasses, hydrological barriers etc.), and 2) environmental (average annual sea surface temperature (SST), annual SST variation, and average salinity). There was the significant correspondence between ciliates and harpacticoids in geographical distribution patterns, while these patterns for flagellates were quite distinct from other groups, both in terms of species richness and composition similarity. For flagellates, only the environmental variables (mainly SST) were significant, while they explained as little as 7-8% of variations in taxonomic composition. For ciliates, both geographical and environmental variables were significant, explaining together 16-24% of compositional variations. Harpacticoids demonstrated the most predictable pattern, with 61% explained by geography, 9% - by environment, and 8% - by spatially structured environmental variations. Thus, protists (flagellates in particular) exhibit a stronger response to environmental factors (mainly temperature) than to geographic distance or barriers for dispersal; while the harpacticoids' global-scale distribution suggests clear geographical dispersal limitation.

MB-02

Modeling the spatial distribution of whale shark in the Atlantic Ocean

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The whale shark *Rhincodon typus* has been considered as endangered by the IUCN and included in their red list. This species can be impacted by the activities of the industrial purse seiner fleet targeting tropical tunas. Tunas tend to aggregate around all types of floating objects, including whale sharks. The objective of the present study is to analyze and model the spatial distribution and environmental preferences of whale shark based on fishing observations in the Atlantic Ocean. The most suitable variables for the distribution model were selected using the multGLM function of the fuzzySim R package. This function performs a selection of variables based on multicollinearity, the false discovery rate, and stepwise selection using Akaike's information criterion. The selected variables were then used to build models with the 15 algorithms implemented in R package sdm version 1.0.46: BIOCLIM, BIOCLIM.DISMO, BRT, CART, FDA, GAM, GLM, GLMNET, MARS, MAXENT, MAXLIKE, MDF, RF, RPART and SVM. The potential distribution of the species was calculated as the mean of the predictions of each algorithm weighted by the discrimination capacity, measured as the area under the receiver operating characteristic curve (AUC). We also calculated the variance between the predictions of different algorithms, as an estimate of the discrepancy or lack of consensus among model predictions. Our results highlight the region jus south of the Gulf of Guinea as the most suitable for whale sharks, under current environmental conditions. We also predict the locations of these suitable environments under future projections for the Atlantic Ocean.

MB-03

Indo-Pacific origin and global distribution patterns of the agar-producing marine algal genus Pterocladiella (Gelidiales, Rhodophyta) inferred from multigene datasets

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Pterocladiella is a red algal genus comprising 24 species from temperate and tropical seas. Some species are economically important as sources for agar and the production of agarose. Our aim was to investigate the species diversity and evolutionary biogeography of the genus to understand the pattern of global distribution of the genus. We analyzed five markers (mitochondrial *cox*1, *cob* and plastid *psa*A, *psb*A, *rbc*L) from about 200 taxa, including type specimens of equivocal species. Species delimitation were investigating with coalescent analyses and revealed that *Pterocladiella* contains at least 37 species, 13 more than previously recognized. In our five-gene phylogeny, *Pterocladiella* was monophyletic and composed of eight distinct groups that are either geographically structured or globally distributed. Three species, *P. caespitosa*, *P. feldmannii*, *P. hamelii* from South Africa and Madagascar, consistently resolved outside the major clade, suggesting a Western Indo-Pacific origin of *Pterocladiella*. The main diversification events occurred in the Central (18 spp.) and Western Indo-Pacific (11 spp.). Most species have limited ranges within a marine ecoregion. However, several species were discontinuously distributed over several ecoregions: *P. bartlettii* from Chile, Guadeloupe, Guyane Française, Madagascar, Malaysia, New Caledonia, Singapore; *P. caerulescens1* from Malaysia, Philippines, Singapore, Vietnam, Hawaii; *P. caerulescens2* from New Caledonia, Western Australia, Madagascar, Sri Lanka; *P. media* from the northeast Pacific, Brazil; *P. musciformis* from Costa Rica, Mexico, Vietnam; and *P. capillacea* from the Pacific and Atlantic oceans, Mediterranean Sea. We present our biogeographic analyses and molecular clock estimates to explore and dynamic of dispersion and diversification of *Pterocladiella* species.

MB-04

Global Distribution Patterns Of The Hawkfishes (Pisces: Cirrhitidae): What We Know And What We Should Know

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Hawkfishes (Cirrhitidae) are small to medium-sized fishes (one species to 60 cm) found in tropical and subtropical/warm temperate insular and coastal waters on relatively shallow coral and rocky reefs; some species to depths of 30-100m. Virtually all species are benthic and utilize thickened lower pectoral rays to perch or wedge themselves in place, either in coral heads, upon rocks, or in wave-swept habitats such as the spur and groove zone of coral reefs or deeper tide pools and reef fronts of rocky reefs. Some are polychromatic and all are presumed to be protogynous hermaphrodites. Thirty-three species are currently recognized and represented in 12 genera of which seven are monotypic. Thirty-one species are distributed in the Indo-Pacific Region, including three in the Eastern Pacific, while three species occur in the Atlantic. At least three species have pronounced disjunct distributions within their respective ranges, two species range from the Red Sea to the Pacific coast of the Americas, and seven species are considered endemic. While knowledge of species distributions is useful for examining patterns of diversity across geographic ranges, how they got that way remains largely unknown. The need for phylogenetic and phylogeographic analyses is emphasized.

MB-05

Phylogeography and population structure of the European sardine using a draft genome assembly and low depth sequencing data

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The European sardine (*Sardina pilchardus*, Walbaum 1792) is a species widely distributed in the North Atlantic and the Mediterranean. Besides having a significant commercial relevance, sardines are also an interesting model for studying molecular adaptation to temperature and salinity gradients. In order to characterize the genetic diversity and the level of population differentiation, we generated a genomic data set consisting of a draft genome of the European sardine (N50: 25 kb) and resequencing data (1.5 X depth) for 60 individuals from 12 sampling locations in the Mediterranean and Atlantic, including the archipelagos of Madeira and Azores. We show how this minimal sequencing approach is cost-effective for non-model organisms with small to medium genome sizes, providing robust inferences of population genetic statistics within a reasonable time frame and allowing for an easy scaling-up of the number of analyzed samples.

MB-06

The physiological responses behind F. serratus biogeographic distribution: phenotypic differentiation and niche underfilling.

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The change occurring in the oceans in the last decades is influencing physiological and ecological processes of diverse taxonomic groups, which eventually may affect their ranges of geographical distribution. Species could adjust their physiological responses to local conditions, via acclimatization or local adaptation, which could facilitate the persistence of species of southernmost populations. This study aims to determine the effect of different environmental factors on the vital rates of different life-stages of the brown macroalgae *Fucus serratus*, and the inter-population variability in the response. Overall, in adults, no variability in growth and survival was found among populations in response to increases in seawater temperature, except for one of the southernmost populations, which presented higher survival physiological threshold than the other populations. The large decoupling between thermal tolerance and environmental temperature experimented in the field suggest a niche underfilling in *F. serratus*. In early stages, the temperature during emersion reduced survival and growth, but this effect was dependent on the origin population, with more pronounced effect in benign conditions of marginal populations. The phenotypic inter-population differentiation observed in early stages, support the detected differential survival of adult thalli, suggesting that both seawater and air temperature are relevant for the understanding the current distribution of species and forecasting *F. serratus* distributional shift and could explain the niche underfilling detected in adults. Although we found differences in the response of populations to environmental factors, this physiological divergence is not enough to cope with the rapid climate change along its southern limit of distribution.

MB-07

Biogeographic regionalization in the Tropical Eastern Pacific, a new hotspot for marine invertebrates

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The Tropical Eastern Pacific (TEP) and its constituent provinces have been defined so far using primarily distributions of bony fish taxa and physicochemical factors that delimit species distributions. Integrating additional sources of data—such as marine invertebrate distributions, phylogenetic species, and population genetics—will provide a fuller understanding and may reveal alternative hypotheses for biodiversity patterns in the marine realm, including designation of hotspot areas. Here we compare phylogeographic patterns of nine species of jellyfish (*Stomolophus* spp. and *Chrysaora* spp.) with biogeographic barriers and genetic discontinuities. To infer multi-scale biogeographic patterns, we estimated pairwise phylogenetic distance, F_{ST} and molecular variance (AMOVA) among and between described taxa collected at 25 locations from across the entire TEP. Our findings revealed numerous cryptic species, whose distributions support the TEP biogeographic regionalization and designation as a hotspot. However, the intraspecific genetic structure shows geographic discordance among the well-known phylogeographic boundaries. We suggest that are other factors, such as life history and ecology of species which are important determinants of population dynamics and shape the biogeography in the TEP.

MB-08

Combining physiological threshold knowledge and species distribution models in predicting the future distribution of intertidal macroalgae along a latitudinal climatic gradient

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The species distributions are determined by climate change and the analysis of the factors involved in such distributions have always been considered as a key issue in ecology. Thereby, species distribution models (SDMs) are a useful tool for predicting species range shifts in response to global warming. For making robust predictions in this area, we can combine the SDMs and the physiological threshold knowledge of the studied species. Through growth and survival manipulative experiments simulating thermal gradients, we obtained the thermal thresholds of some foundational macroalgae, which are proxies of the fundamental thermal niche. To predict the distribution of these macroalgae we used the distributional records of species and environmental layers with ecological influence over the species in the Maxent software. Finally, both approaches, correlative and mechanistic, were combined in order to obtain more robust predictions of the intertidal macroalgae distributions along the European Atlantic coast. In this way, the predictions in a climate change scenario are improving to meliorate the accuracy of conclusions in terms of marine biodiversity conservation.

MB-09

Underestimation of projected suitable habitat ranges due to niche unfill in cold-tolerant seaweeds

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The prediction of the geographic distribution of species is based on the projection of the current realized niche of environmental tolerance. Predictive models assume equilibrium of the species' distribution with their environment to project suitable and unsuitable sites and conditions. However, the unfill of niches is a common observation and might lead to underestimation of available habitat ranges. In this study we compared the realized niche, derived from correlative Species Distribution Models (SDM), with fundamental niches, derived from experimental data from available literature. We investigated seaweed species distributed in the southern hemisphere with reported lower survival temperatures of ≤ 0°C to identify potential invaders into Antarctic regions. We showed that in a large share of the total investigated species the fundamental niche is not filled and the species can tolerate higher as well as lower temperatures than in their realized distributional range. Unoccupied low temperatures in current distributional ranges are hence not necessarily a representation of physiological thresholds but might occur due to other biotic or abiotic limitations as e.g. lack of settling substrate in low-temperature environments. This finding has implications for predictions of possible invasions because available settling substrate may remain undetected by correlative SDMs. There might be more invasive seaweed species into Antarctica than expected from correlative SDMs, which could pose a threat to Antarctic biodiversity. Combining physiological data and correlative SDMs can help to discover areas with ambiguous invasion risk.

MB-10

Niche conservatism goes back to ancient multicellular algae.

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The extent to which temperature-tolerance is conserved during evolutionary time has fundamental consequences for the current and future geographical distribution of the species. The evolution of physiological tolerance to cold and drought seems restricted in multicellular fungi, plants and metazoans that show phylogenetic niche conservatism (PNC), thus predicting widespread constraints on adaptation under a changing climate. Nevertheless, how far PNC dates back in geological time remains unknown. We tested the conservatism of Upper Survival Thresholds (UST) to temperatures across the phylogeny of green, red and brown macroalgae, which present three independently evolving lineages with green and red seaweeds dating back to the Neoproterozoic (at about 1200 Ma), while brown seaweeds originated in the Mesozoic and are therefore comparatively younger. We gathered the USTs for 280 species from physiological experiments and related them to a tree using phylogenetic signal analysis. Closely related species are more similar in their UPSs than expected by chance. The strongest support was for an OU-model of stabilizing selection towards an optimum thermal limit. Moreover, thermal tolerances remained relatively stable through time, with most variation accumulating recently. Tolerance to heat is conserved across the phylogeny of macroalgae, extending the discussion of the conservatism of ancestral niches to the earliest multicellular organisms.

MB-11

Why deep in the NW Pacific? - Depth difference of deep-sea octocoral (Cnidaria, Anthozoa) between the NW Pacific and the NE Pacific Ocean.

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Octocoral (Cnidaria, Anthozoa) is sessile marine organisms with wide distribution which inhabit every depth range in the ocean from tidal zone to hadal zone (>6000m), and any latitude from tropical to the polar region. There are not so many species which distribute both in the NW Pacific and the NE Pacific. Very few studies have been comparing the species biodiversity of corals between this two Ocean area. Matsumoto et.al.2007 mentioned that ten octocoral species (one soft coral and nine gorgonians) exist both Sagami Bay (Japan, the Northwest Pacific) and the Northeast Pacific in the record.
In this study, we will examine and discuss the difference of depth distribution of cold water octocorals between the North West Pacific and North East Pacific. Both the data of the taxonomically examined materials for the taxonomical publication purposes and the museum database were used for the detailed comparison.

MB-12

Distribution patterns of the family Tellinidae (Mollusca: Bivalvia) along the West African coast

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The Tellinidae family is composed by a high diversity of species of the class Bivalvia. For this reason, we have chosen this group for the analysis of distribution patterns along the West African coast, where the current knowledge on marine fauna has significant gaps. The main subject of this study is to analyze whether these species are distributed in chorotypes, or whether, on the contrary, they follow a gradual distribution pattern along the latitudinal range. The role of several environmental factors in the pattern detected is also analyzed. The analysis is based on the calculation of the similarity between species distributions and their subsequent classification using UPGMA. The presence of chorotypes has been tested by analyzing the significance of the resulting groups according to the Macoqui method. These chorotypes have been analyzed using fuzzy logic, and characterized with environmental variables through correlation and correspondence analyses. We identified 7 chorotypes that include 36 species. Other 13 species seem to follow a continuous pattern of distribution. The closeness of upwellings and of large-river mouths is shown as attractor for most of the chorotypes, although there are species that seem to be favored by the distance to these nutrients sources. This is a preliminary analysis to which species from other bivalve families will have to be incorporated, together with a more detailed analysis of the possible explanatory factors. We propose the use of historical descriptors with environmental factors, such as the evolutionary closeness between taxa included in the same chorotype.

MB-13

How do put we borders in the open sea?, the case of swordfish from Atlantic Ocean

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Swordfish (*Xiphias gladius*) is an important like-tuna species that sustain an important fishery that used longline from Atlantic Ocean. ICCAT (the International Commission for the Conservation of Atlantic Tuna) recognizes two stocks of swordfish from the Atlantic, one for the Northern Hemisphere and another for the Southern Hemisphere. In this area the North Atlantic Oscillation (NAO) and East Atlantic pattern (EA), are the main sources of climate variability affecting to the oceanographic variability. The main aim of this study was to test the possible effect of the NAO and EA about the landing of the two stocks of Atlantic swordfish. The landing data are collected by ICCAT. We obtained explicative multiple significant models, for each stock. In both cases our results indicate that EA and partially NAO explain the variability observed in the swordfish landing from both stocks. We obtained R^2= 0.47 in the north stock case and R^2=0.44 in the south stock case. EA have a greater explanatory capacity in both cases. ICCAT put the limit border between both stocks in the 5º north; however this limit cannot explain why the stock South is affected per EA and NAO. Our results are in agreement with other authors that put the borders in between 10º and 20º N. Therefore, a more to the north border would explain our results. Moreover, it could involve depth changes in the evaluation of both swordfish stocks.

MB-14

Different environmental predictors drive habitat suitability in three endemic breeding seabirds of Chile.

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The Juan Fernandez Petrel (Pterodroma externa), Stejneger's Petrel (Pterodroma longirostris) and Masatierra Petrel (Pterodroma defilippiana) are three endemic seabird species that nest sympatrically in two oceanic archipelagos in Chile: Juan Fernandez Islands and Desventuradas Islands. However, their distribution at sea out of the breeding season varies greatly in extension and geographic location. In this study, we used ensemble species distribution modelling to estimate the relative contribution of selected environmental variable on the habitat suitability of these three species along their geographic range. We employed presence-only data obtained from two different sources: seabirds at sea censuses carried out in the South Eastern Pacific and the GBIF database. Five predictor variables that are known to be important for marine organism's distribution were used: chlorophyll concentration (mean), sea surface temperature (mean), sea surface salinity (mean), current velocity (mean), and bathymetry slope. Our results show a high value of model fits for the three species (AUC values between 0.71 to 0.92). The most important predictor for P. externa was sea surface salinity (50%), while sea surface temperature was found to be the most important predictor for P. longirostris (37%) and P. defilippiana (59%). These results show the relative importance of these two environmental variables that may explain the differences in the non-breeding distribution of this Pterodroma species. Knowing the environmental variables that characterize the distribution areas, are important to reinforce conservation actions, such as the creation of important bird and biodiversity areas (IBAs) for migratory seabirds.

MB-15
Tracking a massive arrival of mauve stinger jellyfish (Pelagia noctiluca) on the coast of Malaga (Spain)

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Recent studies have pointed towards the possibility of an increase in blooms of jellyfish in a global scale in recent decades. Blooms are perceived with great concern by socio-economic sectors and citizens in coastal Spain and elsewhere, due to the negative effects and economic losses that these blooms may cause. This study shows how a citizen science initiative, based on a smartphone app (Infomedusa) was used to monitoring a bloom of mauve stinger jellyfish (*Pelagia noctiluca*) occurred between the 30th July and 8th August in the coast of Malaga. Jellyfish firstly appeared at medium densities in the east coast of Malaga province, soon evolving to high density swarms near the shoreline. After some days, the swarm core arrived to the beaches on the west side of the province, where it remained for some time, reaching also the coastal municipalities in the mediterranean side of Cadiz province. Future studies will be carried out to determine more precisely the reason why these phenomena may be occurring with increasing frequency in the Alboran Sea.

MB-16
Historical dynamics and oceanographic processes explain the spatial distribution of species richness patterns of reef fish Caribbean Sea

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Caribbean Sea has undergone different geological and water circulation modifications before reaching its current structure. Insular and continental land masses have emerged in a continuous and irregular process over time. These changes have affected the marine biodiversity from population structure to diversification patterns (*i.e.* species formation through sea level changes). Reef fishes in the Caribbean Sea are widely distributed from the continental shelf to the insular systems showing patterns of species similarity that have allowed delimit biogeographical provinces. However, the mechanisms behind the actual species richness spatial structure of Caribbean fishes are unknown. The present work assessed the source-sink hypothesis, taking into account extinction-colonization processes, as an explanation for the Caribbean fishes distribution. For this purpose, a database of reef-fishes presence was collected from The Tropical West Atlantic (TWA) that includes tree biogeographical provinces: north, central and south. The degree of nestedness was assessed using the T (temperature), BR (discrepancy) and NODF indices. In addition, the degree of nestedness was evaluated taking into account geological (time of formation of the area) and oceanographic (direction of the currents) processes. Results showed a significant degree of nestedness in reef-fishes distribution. A nested structure was also evidenced considering geological and oceanographic processes. Therefore, it is concluded that source-sink dynamics affect species distribution patterns of reef-fishes in the Caribbean Sea, through colonization of the new formed areas and using currents for dispersion.

MB-17
Biogeography of the Coastal Fishes of Socotra Archipelago: Challenge to current ecoregional concepts

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A recent study of the present authors highlighted the coastal fish diversity of Socotra Archipelago as the highest of any comparable site in the seas surrounding the Arabian Peninsula. The study suggested that substantial gaps exist concerning the distributional biogeography and ichthyogeography of the wider Gulf of Aden–Socotra–Somalia region, prompting the present study. Influential global mega-studies included inferences about the possible marine biogeographic and ecoregional position of the archipelago, which in terms of fish distribution data were primarily based on outdated faunal accounts. The study (a) updates existing ichthyogeographic knowledge according the latest regional faunal and assemblage data; (b) infers the comparative position of Socotra according to a variety of biogeographic classification hypotheses, including three most influential ecoregional and ichthyogeographic schemes (Spalding 2007, Marine Ecoregions of the World, MEOW), Briggs & Bowen 2012, and Kulbicki et al. 2013); (c) verifies the hypothesis that the wider Gulf of Aden does not represent a consistent "ecoregion" in terms fish assemblage composition; and, (d) proposes an ichthyogeographic consensus classification of the archipelago and its adjacent ecoregions. With regard to the MEOW the present study suggests – inter alia – that Socotra should not be included in the same province (18.) as the Red Sea ecoregions (87., 88). The Gulf of Aden ecoeregion needs to be partitioned because its north-eastern and south-western parts are not related more closely to one another than to other ecoregions. The unique position of Socotra warrants it a status as ecoregion in its own right.

MB-18
Differential biogeographical factors affecting distribution of the fin whale (Balaenoptera physalus) in the Western Mediterranean Sea inferred from opportunistic sightings

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Due to the environment where cetaceans live and their migration habits, monitoring their distribution is difficult. Currently, many opportunistic sighting reports are available, which provide a source of potentially useful. The Fin whale (*Balaenoptera physalus*) is a cosmopolitan species with resident populations in the Mediterranean Sea. The aim of this study was to analyse differential habitat use of Fin whale in relation others cetaceans. Here we used a dataset with opportunistic observations of cetaceans to disentangle the differential distribution of fin whales when comparing with other cetaceans. The results show a spatio-temporal pattern in habitat use of fin whales, showing a higher preference to use the waters over the slope of the Gulf of Lion in summer than other cetaceans in the area. This finding confirms that the Gulf of Lion is an area of importance for this species and suggests that the slope of the continental shelf could be particularly important. Opportunistic sightings provide useful information which makes them an alternate tool for biogeography studies when systematic studies are not available.

NB-01

The environmental framework in a set of tropical and temperate temporary ponds: limnological comparisions during a flooding season

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The environment is like a template where the communities fit following their ecological requirements, its precise understanding allowing to have an accurate knowledge of the community. In order to characterize the environment in a set of temporary ponds from two different climates and biogeographical regions: Neotropical region (Guanacaste, Costa Rica; Seasonal Tropical climate) and Mediterranean region (Valencia, Spain; Mediterranean climate); we selected 30 ponds at each region and visited the ponds three times: at the beginning, middle and end of the flooding period.
These climates share a dry season enough to dry the ponds but differ in many other features. We measured *in situ* several abiotic and biotic environmental variables (depth, water transparency, oxygen, pH, conductivity, temperature, vegetation cover) and collected water samples in order to analyze plankton and benthos, pigments, nutrients and ions. Some other landscape variables (altitude, size and morphometry of the pond and hydrographic basin; soil use and terrestrial vegetation cover around the ponds) were gathered using GIS. Our results show that most environmental variables did not show great seasonal variability in tropical ponds, whereas some variables such as temperature, pH or vegetation can notably discriminate seasons, in Mediterranean ponds. Variables as oxygen and vegetation cover, particularly floating macrophytes showed the larger differences among regions.

NB-03

Biogeography and Evolution of the Atacama genus Cristaria (Malvaceae)

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The Atacama Desert, located on the western side of the Andes in northern Chile, harbours a range of endemic species adapted to hyperarid habitats. In the framework of a large-scale project on landscape and biotic evolution of hyperarid environments, we aim to understand the origin and diversification of plants in the Atacama Desert. Diversifications have been shown to be surprisingly recent for some Atacama clades, which is at odds with the high age assumed for this desert. Here we estimate divergence times of the group to test whether the split between these two genera is correlated to Andean uplift or to other potential drivers. Furthermore, we evaluate the monophyly of the genus *Cristaria* (ca. 21 species) and *Lecanophora* (ca. 5 species; Malvaceae) and its position within Malvoidae especially in relation to other Andean genera from the tribe Malveae. We show the results of a molecular dating analysis of the Atacama endemic *Cristaria* based on three plastid DNA-regions. *Cristaria* was retrieved as sister to *Lecanophora*, the latter distributed in Argentina east of the Andes, both forming well-supported clades within tribe Malveae. The split between these two genera is dated to the early Miocene (ca. 20 mya), which slightly predates the time proposed for the major phase of the southern Andean uplift and therefore only weakly supports a vicariant scenario in the divergence of these two genera.

NB-05

Revealing controls on distribution and microhabitat use of Anolis lizards in a changing island landscape

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In these times of rapid environmental change and species extinction, understanding the drivers governing species' abundance and distribution is more important than ever. The goal of this work is to further our understanding of what drives variation in species' abundance and microhabitat use through space, particularly in the context of rapid land cover change. Using the little explored anole fauna of the Honduran island of Utila as a natural ecological laboratory. By pioneering emerging technologies in airborne remote sensing for predicting animal abundance and distribution, the project is designed to improve our ability to predict species' ecological responses to habitat conversion and identify key ecological interactions between habitat structure, microclimate, and species' distribution. Pilot work has revealed a distinct habitat preference in the endemic Anolis bicaorum and has noted an increased range and habitat usage of the invasive Anolis sagrei. Data collected on operative temperature from morphologically accurate 3D models (fitted with ibutton data loggers) and at a plot scale (20 x 20m) is being coupled with leaf area index from hemispherical photography and UAV imagery. This may be the key in determining whether habitat usage and distribution is primarily due to habitats being more thermally favourable for these ectotherms. Alternatively, whether factors such as habitat structure, derived from UAV imagery and standard plot vegetation metrics are a driving factor. This work is allowing us to improve our understanding of Utila's Anolis fauna, promote its conservation and demonstrate how emerging technologies can help us understand and preserve the natural world.

NB-06

Amazonian bamboo forests: are they all of the same?

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Tropical forests dominated by arborescent bamboos (*Guadua weberbaueri* Pilg and *Guadua sarcocarpa* Londoño & Peterson) occupy large areas in southwestern Amazonia. These so-called bamboo forests are commonly treated as a single formation in scientific literature but they also show many interesting biogeographical particularities. This paper presents early results of our studies on this matter, based on the combined use of different study methods. Our field surveys suggest spatial dissimilarities both in the bamboo plants and in the forests that they characterize. DNA analyses of samples collected from different locations confirm genetic inconsistencies in *Guadua* bamboos across their distribution area. Landsat TM/ETM+ image mosaics, compiled separately for each of the years from 1984 to 2017, display the overall distribution of the bamboo forests in southwestern Amazonia as a rather compact formation. Further, these data reveal the presence of large temporally separated bamboo patches, which become visible due to the bamboo's time-synchronous flowering and die-off. In all, our early results reveal numerous spatial details in the Amazonian bamboo forests in different spatial scales, from genetic differences and conspicuous landscape ecological patterns to distinctive flowering waves and other biogeographic variations.

NB-09

A biogeographic tale of an incertae sedis lineage: A new species of Atopophrynus from Ecuadorian Andes

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Genus *Atopophrynus* is considered incertae sedis within Brachycephaloidea, with a single species (*A. syntomopus*) known from Cordillera Central in Colombia. Herein, we describe a new species from the northern Andes in Ecuador, based on genetic and morphological evidences, and discuss about their historical biogeography. Phylogenetic tres and chronograms were reconstructed with mitocondrial DNA (COI and 16S genes) by bayesian and máximum likelihood analyses. Biogeographic patterns of the new species and its relatives were analyzed by constructing a dispersal-extinction-cladogenesis (DEC) model for geographic range evolution with RASP. Phylogenetic trees reveals that *Atopophrynus* is related with ancient lineages embedded within genus *Cycloramphus*, supporting previously hypotheses that Cycloramphidae is polyphyletic. The new species has a restricted distribution related with montane evergreen forest in the Amazonian slopes of the northern Andes in Ecuador. It was recovered as the sister lineage of *Cycloramphus acangatan*+*C. boraceiensis*+*C. eleutherodactylus*, all of them distributed along the Southeastern Atlantic forest in Brazil. Interestingly, the new species is part of one of the most ancient clades within Anura, with a southamerican origin in about 73-77 Mya, and a geographic speciation by vicariance in the northern Andes. Further work is necessary to understand the phylogenetic relationships and taxonomy of the group.

NB-10

Wandering rivers and the central Amazonian biogeography since the late Pleistocene

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Central Amazonian rivers are thought to have been dispersal barriers and triggers of vicariant speciation for terrestrial biota since the river network consolidated in the Pliocene. However, geomorphology and sediment chronology suggest that rivers have migrated widely even during the last 50,000 years. The Juruá and the Madeira rivers have been tributaries of the Purus river, and the Japurá river was detached from the Rio Negro river and became a tributary of the Amazon river possibly only 1000 years ago. Consequently, the major tributaries of the Amazon river cannot have been as strong dispersal barriers as has been assumed thus far. The river captures and avulsions have continuously redrawn dispersal barriers for terrestrial biota, which causes one to reinterpret the biogeographical scene of central Amazonia.

NB-11

Species-level processes drive species richness patterns in the largest clade of Neotropical lianas (Bignonieae, Bignoniaceae)

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Species richness can be defined as an aggregate variable when recovered by stacking the geographic range of different species. Therefore, processes constraining species range limits could be the main drivers of species richness patterns. We evaluate the impact of species-level processes in structuring richness patterns

in the tribe Bignonieae. We test the congruence of species ranges and richness responses to predictors using the extreme deconstruction principle. We also evaluate if such congruence varies according to subsets of species with distinct ecological or evolutionary attributes using the richness deconstruction approach. We modeled and partitioned the variance of the overall tribe richness pattern (386 species), as well as the richness of each subset of species with different attributes and species ranges using three sets of predictors: climatic, edaphic, and spatial components. We correlated components of variation partitioning of species ranges and richness to evaluate how they respond to predictors. We found that species ranges and the overall Bignonieae richness pattern respond similarly to predictors (r = 0.96). The same pattern was observed when the correlations were replicated for the richness of species subsets defined by different attributes. Although some species attributes (i.e. lack of herbivory protection, small to medium range sizes, late-diverging species) reduced the congruence between ranges and richness responses (r = 0.51 to 0.70), species-level processes acting on species ranges appear to be the main drivers of Bignonieae richness patterns. The distribution of overall tribe richness is associated with the current distribution of forest and savanna ecosystems in the Neotropics.

NB-12

A view from above: Unmanned Aerial Vehicles (UAVs) provide a new tool for assessing liana infestation in tropical forest canopies

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Tropical forests store and sequester large quantities of carbon, mitigating climate change. Lianas (woody vines) are important tropical forest components, but reduce carbon uptake. Their recent increase may, therefore, limit forest carbon storage with global consequences for climate change. Liana infestation is traditionally assessed from the ground, which is labour-intensive and difficult, particularly for upper canopy layers. We used a UAV with a three-waveband camera to collect imagery for 150ha of forest. By visually interpreting the images, we assessed liana infestation for 14.15ha for which ground-based estimates were collected simultaneously. We compared the UAV estimates with those from the ground to determine the validity, strengths and weaknesses of using UAVs as a new method for assessing liana infestation.

UAV estimates of liana infestation correlated strongly with ground estimates at individual tree and plot level, and across multiple forest types and spatial resolutions, improving assessment for upper canopy layers. Importantly, UAV-based surveys were considerably faster and more cost-efficient than ground-based surveys. UAV imagery can be easily captured and used to assess liana infestation at least as accurately as traditional ground data. This novel method promotes reproducibility of results and quality control, and enables additional variables to be derived from the imagery. It is more cost-effective, time-efficient and covers larger geographical extents than ground-surveys, enabling more comprehensive monitoring of changes in liana infestation over space and time. This is important for assessing liana impacts on global carbon balance and for forest management where targeted and effective liana management can enhance carbon sequestration.

NB-13

Leaf morphometric variation and biogeographic inferences of a Neotropical species

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Blepharocalyx salicifolius relationship over Neotropical Myrtaceae is complex and is supposed to be sister group of Myrtaceae from the new world or considered to be of highly interest in the resolution of evolutionary relations in this important taxonomic group. This species is widely distributed in the main Neotropical biomes, it is highly plastic, and combines two ecological characteristics that are dominant in the Neotropics: bee-pollination and bird dispersal. We hypothesized that this species would present biomes-structured leaf plasticity, which would correspond to a biogeographic structure observed in an independent phylogenetic analysis resulting from a broad genetic sampling of this species. To do so, we analyzed eight foliar morphometric variables of this species using data collected from different biomes to explore possible ecological structuring within morphological polymorphism. We performed correlation analyses between variables, tests of variance between means, outline (shape) analysis and principal component analysis (PCA). We also performed the leaf outline reconstruction forms of this species inferred from Elliptic Fourier analysis. The modeling leaf shapes correspond virtually to the major phylogenetic lineages observed for *B. salicifolius*. There was no evident structural difference among biomes, however the combination of some leaf characters appears to be selected under certain environmental conditions. Based on morphometric analysis, we give analytical support to the high foliar plasticity of *B salicifolius* and indicate a model of leaf shape. Our work is a step forward to clarify the taxonomic and biogeographic aspects of this species.

PE-01

Towards a stomata based atmospheric CO2 reconstruction using Pinus and Abies Holocene remains in the Iberian Peninsula

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A number of species (i.e.: *Quercus*, *Betula*, *Pinus*, *Tsuga*…), which leave/needle remains have been preserved in different deposits along the Earth and, therefore, they have been used to reconstruct past atmospheric conditions. Still, plant atmospheric responses are species and site specific, and calibration with present or recent past material is needed prior to estimate any atmospheric parameter. Recent palaeobotanical researches in the Pyrenees and in the Iberian Central System, conducted under a coordinated project funded by the Spanish Ministerio de Ciencia, Innovación y Universidades (CSO2015-65216-C2-1-P/2-P), have given light to numerous *Abies alba* and *Pinus sylvestris-uncinata* type Late Pleistocene needle remains. Here we present the preliminary stomatal-atmospheric CO_2 calibration performed on *Pinus uncinata*, *Pinus sylvestris* and *Abies alba* altitudinal transects sampled during 2013 and 2017 on six Pyrenean populations (Irati–Navarra, Mata de Valencia–Lérida, Virós-Lérida, Maçarent de Cabrenys–Gerona, Montseny–Barcelona), and an additional *P. sylvestris* Central System population (Cotos – Madrid). Five to nine needles per altitude, sampled every 100 m altitudinal increase (from 900 to 2600 m a.s.l.) were macerated and skilled to analyse cuticle parameter (stomata density, stomatal length, stomatal band width and length and pore length) responses to CO_2 atmospheric partial pressure changes.

PE-02

Paleo-occupancy models reveal species detectability and occupancy in the pollen record

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The late Quaternary fossil record contains abundant, broadly distributed data to investigate how species and communities respond to climate change. However, inconsistent sampling and differential preservation of fossil specimens can pose obstacles to our ability to create accurate reconstructions of past communities. We leverage occupancy modeling methods and the fossil pollen record from 531 sites across eastern North America. We simultaneously estimate the abundance and detectability of fossil pollen taxa in a spatially and temporally explicit manner that accounts for imperfect detection. In this modeling framework, we examine the spatial structure of site occupancy and species detection across the Eastern U.S. We then use model comparison techniques to determine the physical geography, soil, and climate variables that most affect the detectability of pollen taxa. We found that all variables examined contribute significantly to the detectability of most species during most time periods in the late Quaternary fossil pollen record. Specifically, maximum temperature of the warmest quarter, average yearly potential evapotranspiration, and average yearly actual evapotranspiration are consistently important observation covariates to determine detection probabilities. The ranks of models containing different covariate combinations (ordered by their AIC) are highly consistent across taxa. However, the power of covariates to account for detection probability degrades through time. This work will advance the integration of ecological and paleontological sciences by allowing us to better identify when a species is truly absent from a fossil site versus when it has gone undetected, i.e. detection probability is low, allowing us to produce more robust ecological models.

PE-03

New data about pollen and fire regime in Cantabria (Northern Spain) from the Late Glacial to the present

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The evolution of mountain landscapes during the Late glacial and the Holocene is explained by a multifarious interaction system between society and the environment, where fire has played an essential role. Cantabria (Northern Spain) is one of the European regions with more known Palaeolithic sites, and some of these records enable the study of climate and vegetation dynamics over time. In this communication, we present new data from two Cantabrian sedimentary records. The first one, *El Cueto de la Espina* peat bog (1130 m a.s.l.), covers from the Neolithic period (5.880 Cal years BP) to the present, and microscopic charcoal (examined on pollen slides) and macro-charcoal (>150 μm) were analysed. Microscopic charcoal provides information about the fire regime at a regional scale, while the origin of macro-charcoal particles is more local. The results indicate the existence of several fire peaks during the Neolithic. From the second location, *La Molina* peat bog (484 m a.s.l.), which covers the Late glacial (18.000 Cal years BP) and the Holocene, new pollen and macro-charcoal data are presented. In this location, macro-charcoal particles were detected since the Late Glacial and the intensity of the fire regime increased with the beginning of the Holocene. The fire regime was more intense than in *El Cueto de la Espina*, probably due to the lower altitude and a greater accessibility by humans. The pollen spectra suggest an open landscape at the end of the glacial period.

PE-04

A human role in Andean megafaunal extinction

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A new fossil pollen, *Sporormiella*, and sediment chemistry record from Lake Llaviucu, Ecuador, spanning the period from 16,280 - 9000 years Before Present, provides a high-resolution record of paleoecological change in the high Andes. The deglacial transition from super-páramo through páramo, to Andean forest is traced, with near-modern systems being established by c. 11,900 years ago. *Sporormiella* is used as a proxy for megafaunal abundance, and its decline to background levels is inferred to indicate a local extinction event at 12,800 years ago. About 1800 years prior to this extinction charcoal becomes a regular sedimentary component in this very wet valley. An early date for human activity in the valley is suggested, with the direct implication of humans in the extinction of the megafauna.

PE-06

Deep-sea biotic response to oxygen variability and Pleistocene global changes: paleoecological and macroevolutionary dynamics in a marginal sea

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The Sea of Japan is a marginal sea, connecting to adjacent seas by four shallow straits (water depths <130 m). Marginal seas are ideal for studying biotic responses to large-scale environmental changes as they often are sensitive to glacial-interglacial and stadial-interstadial climatic cycles as well as longer scale changes. However, only a limited number of studies cover time periods beyond the last two glacial-interglacial cycles. Here we present a two million year record of benthic biotic response to paleoceanographic changes in the southern Sea of Japan, based on ostracode assemblages at the Integrated Ocean Drilling Program (IODP) Site U1426 and U1427. Results show that (1) orbital-scale faunal variability have been influenced by eustatic sea level fluctuations and oxygen variability, and (2) faunal composition showed distinct difference between the post-MBE and pre-MBE (Mid-Brunhes Event) periods. Long-term oxygen variability in the bottom water has been the major control impacting the marginal-sea biota. The MBE was a major disturbance event in deep-sea ecosystems, as several studies have recently reported major faunal events during the Mid-Pleistocene in various oceans and seas. Benthic ecosystems in marginal seas are sensitive and vulnerable to both short-term and long-term climatic changes.

PE-07

Biome and functional ecosystem changes during the late-glacial to Holocene transition

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The rapid climate warming during last-glacial to Holocene transition resulted in rapid biotic responses in northern Europe. Plants quickly re-established and expanded after the Scandinavian Ice Sheet retreated. Assuming that the environment filters plants based on their traits and ability to thrive under various conditions, we use species' indictor-values and functional traits to reconstruct past biomes. We use detailed macrofossil data from Kråkenes, Norway, to investigate changes in functional traits from the late-glacial to the early Holocene (ca. 14-9 ka years).
Results show that a stable arctic-montane biome during the glacial period started to change around 12 ka yrs ago successively into a boreo-arctic montane, wide-boreal, boreo-montane, boreo-temperate, and wide temperate biome ca. 9 ka yrs ago (approximately 2500 years). At the same time ecosystem functioning changed consistently. Late-glacial assemblages are characterized by herbaceous taxa, and Younger Dryas - Holocene transition and early Holocene assemblages are characterized by long lived plants with increasing seed mass. Woody taxa rapidly expanded in the early Holocene.
Being of a similar magnitude, the late-glacial to early Holocene transition maybe analogous to changes observed in the modern arctic with melting glaciers and permafrost thaw.

PH-01

Phylogeography of the mountain endemic chameleons of the Cameroon Volcanic Line (Chamaeleonidae: Trioceros)

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The Cameroon Volcanic Line (CVL) possesses the highest diversity of species within the genus *Trioceros* within Central and Western Africa. Species delimitation and gene flow between *Trioceros* populations have been poorly studied and the chronology of their colonization of the mountains of the CVL has never been assessed. We used molecular data, two mitochondrial genes (16S, ND4) and one nuclear gene (RAG1), to understand *Trioceros* species diversification in the CVL. We used two coalescent-based species-delimitation approaches, Bounded-error Probabilistic Polynomial time (BP&P) and spedeSTEM, to estimate species diversity and identified several Operational Taxonomic Units (OTU). Our results suggest that *T. serratus* and *T. montium* both represent complexes of multiple species and that the subspecies within *T. quadricornis* will require revision. The results of our dated phylogeny estimated in BEAST2 concur with a biogeographic hypothesis stating that ancestors of the *Trioceros* clade migrated toward Central Africa from eastern Africa during late Eocene, and mountain endemics began diversifying in the CVL during late Miocene-Pliocene. Interspecific divergences between CVL *Trioceros* lineages are estimated at approximately 6 to 10.0 Mya. Multiple overlapping geographic events (altitudinal gradient, microclimate and/or geomorphological changes) most likely account for speciation patterns in CVL-endemic *Trioceros*.

PH-02
Taxonomical implications of the phylogeography of Sonchus bulbosus

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Sonchus bulbosus (L.) N.Kilian & Greuter is a Compositae species whose taxonomic position has been modified several times. Currently, it is included in genus *Sonchus*. This species is a scapose and stoloniferous perennial herb with vertical rhizomes usually bearing subglobose tubers and high level of vegetative multiplication. *S. bulbosus* spreads all over the Mediterranean Basin, and inhabits sandy coastal soils, temperate and fresh forests and, occasionally, rocky substrates that show isolated populations. *S. bulbosus* comprises three subspecies: the typical subspecies, *S. bulbosus* subsp. *bulbosus,* which lives in all the area, *S. bulbosus* subsp. *willkommii* (Burnat & Barbey) N.Kilian & Greuter, endemic to the Balearic Islands, and *S. bulbosus* subsp. *microcephalus* (Rech.f.) N.Kilian & Greuter, restricted to the eastern side of the Mediterranean Basin. The typical subspecies has unbranched scapes bearing a single and big flower head, while the other two subspecies usually show scapes with up to nine branches and small flower heads, showing quite similar habits. The taxonomic entity of the different subspecies, the centre of origin of the whole species and the most probable migration routes were assessed by using AFLP molecular markers. We found that the putative origin of this species occurs on the eastern side of the current distributional area and that central Mediterranean populations showed the lowest genetic diversity. We also discuss the biogeographical significance of the high morphologically similarity between subsp. *willkommii* and subsp. *microcephalus*.

PH-03
Finding the lost Quaternary refugia of Cistus monspeliensis in Europe

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Glacial refugia are key elements to understand the recent biogeographic history of species, and they are expected to harbour high levels of genetic diversity. However, sometimes the location of refugia is not well established despite the sampling of numerous populations. An example is the rockrose *Cistus monspeliensis* in the Mediterranean Region. Low levels of genetic diversity led to a hypothesis of recent expansion of this plant from a few refugia, but the location of these persistence areas are unknown to date. In this study, we aimed to find Mediterranean refugia of *C. monspeliensis* starting from previously published data. On the one hand, genetic sampling was increased to improve the resolution of phylogeographic reconstructions, but we failed to find potential refugial areas using this approach. On the other hand, we decided to sample new populations in potential refugial areas inferred by projection of species distributions models (SDM) to past periods. Habitat availability over the last 120,000 years showed potential refugia for *C. monspeliensis* in some areas of the westernmost Iberian Peninsula (Portugal) and northwestern Africa (Morocco). These areas were sampled and included in the phylogeographic study. As a result, we found that populations in coastal Portugal harbour the highest genetic diversity of the Mediterranean Region, which supports this area as a Quaternary refugium for *C. monspeliensis*. In sum, we propose the use of SDM techniques to guide sampling in phylogeographic studies.

PH-04

Dispersal limitations and historical factors determine the biogeography of terrestrial protists

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Assessment of the spatial distribution and diversity of free-living protists remains an open and unresolved question among the scientific community. Recent studies show that some groups of microbial eukaryotes present limited dispersion, sometimes even narrow endemism and contradict the paradigm of cosmopolitan distribution illustrated by the tenet "everything is everywhere, but, the environment selects". However, most studies aimed at demonstrating or contradicting this paradigm, and very few have evidenced phylogeographic processes driven by allopatric speciation. In this study, we investigated the spatial distribution of mitochondrial lineages (based on COI, i.e. partial cytochrome oxidase subunit 1 sequences) within the *Hyalosphenia papilio* complex of cryptic species. This testate amoeba morphotype is supposed to be distributed all over the Northern Hemisphere complex and has been shown previously to host a wide diversity of cryptic species whose distribution is geographically limited. We determined the distribution of these mitochondrial haplotypes on the Northern Hemisphere, based on sequences obtained through data mining in GenBank plus our own data. Our data support the hypothesis that patterns of phylogenetic diversity and distribution are congruent with the history of Holarctic *Sphagnum* peatland range expansions/contractions in response to Quaternary glaciations. This suggests that historical processes may contribute in the diversification of terrestrial protists and are partly responsible for their very high overall diversity.

PH-05

Geographic basis of genetic variation in Woodworth's Fanged Frog, a 'widespread' endemic Philippine species with a peculiar, 'range-restricted' distribution

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With a few exceptions, the geographic distributions of most northern Philippine amphibians fall into two categories: (1) micro-endemics restricted to a particular location or habitat type, and (2) widespread species found throughout the Luzon Pleistocene Aggregate Island Complex (PAIC; Luzon + Polillo + Catanduanes + Marinduque). Woodworth's Fanged Frog (*Limnonectes woodworthi*) is unique in that its distribution, although widespread from North to South, is restricted to eastern Luzon, the Bicol Peninsula and islands off Luzon's east coast. Because of its anomalous distribution, and because previous studies have suggested that *L. woodworthi* constitutes a complex of multiple species, we undertook a range-wide study examining the geographic basis of genetic variation. We analyzed 152 16S mitochondrial DNA sequences, collected from across its range and, contrary to our expectations, we found only shallow levels of divergence among mitochondrial DNA haplotypes, suggesting that *L. woodworthi* genuinely may represent just one species. Interestingly, genetic variation corresponds to phenotypic variation detected along the east Luzon North-South transect, suggesting that this axis should be evaluated for indications of early stages of speciation (vs. clinal variation). The disparity between the characterization of the species as a widespread ecological generalist but with a range-restricted distribution raises questions concerning factors that may limit species distributions. Comparative studies with other, co-distributed native Luzon faunal region amphibians is fertile grounds for future research.

PH-06

Diagnostic plant species of three main Pannonian and Western Pontic steppe grassland types: do they share intraspecific genetic diversity patterns and their phylogeographical history?

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Steppe grasslands have dominated vast European areas throughout the Quaternary, but are nowadays rare habitats in Central and Southeastern Europe. The remaining dry grasslands are important refuges for rare and endangered species and, therefore, of high nature conservation relevance. However, little is still known about the local continuity of their species composition and biogeographical history: potential source areas for the (re-)colonisation of the Pannonian region from glacial refuges are assumed in the Western Pontic region, along the Black Sea coast and/or on southern slopes surrounding the Pannonian Basin. Therefore, we ask if characteristic steppe species, representing three phytosociological grassland orders, show varying genetic constitutions, i.e. diverging response to glacial survival and/or postglacial expansion.

Based on a comprehensive set of relevés a preceding classification of Pannonian Festuco-Brometea grasslands (Willner et al. 2017) determined diagnostic species of Brometalia erecti (B), Festucetalia valesiacae (F), and Stipo-Festucetalia pallentis (S). We selected twelve species for our cpDNA sequence analyses, to investigate phylogeographical structure and genetic diversity.

We identified differing intraspecific histories: diagnostic F-species, like *Eryngium campestre*, *Salvia nemorosa*, and *Stipa capillata*, showed similar patterns with shallow large-scale structuring, possibly

indicating high levels of expansive gene flow. Such a pattern was only rarely found in species representing other grassland orders (exception *Filipendula vulgaris*, B). Otherwise, a large-scale split between – and therefore, independent histories of – the Pannonian and the Western Pontic/Caucasian grasslands was observed (e.g. *Astragalus onobrychis*, F; *Linum tenuifolium*, S) as well as more species-specific patterns, like in *Trifolium montanum* (B) and *Poa badensis* (S).

PH-07

A phylogeographic study of the influence of chromosome number variation in the microevolution of species (Carex gr. laevigata, Cyperaceae)

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Carex (Cyperaceae) is one of the most species-rich angiosperm genera and has experienced a relatively rapid diversification. The investigation of such radiation is sometimes hindered by taxonomical problems related to homoplastic morphological features, cryptic species and/or hybridization processes. It is the case of the *Carex laevigata* group (sect. *Spirostachyae*), which comprises four species (*C. laevigata*, *C. binervis*, *C. camposii* and *C. paulo-vargasii*). This group is mainly distributed in the Western Mediterranean, with two species reaching NW Europe, and shows an interesting pattern of chromosome number variation apparently related to geographic distribution. Recent molecular phylogenetic studies based on nuclear and plastid markers showed unresolved phylogenetic relationships within the group. In order to elucidate the systematics and evolutionary processes underlying *Carex* gr. *laevigata* and its chromosome number variation, we have designed a large-scale phylogeographic study. First, a phylogenetic tree based on RAD-seq data will be obtained from more than 180 specimens of all species to elucidate the influence of hybridization or introgression. Secondly, as chromosome numbers are available for most of the samples, analysis on correlation patterns between chromosome number, species distribution and diversification of the group will be carried out. Finally, ecological evolution of the group will be analysed by characterizing the climatic conditions on each sampled population. Moreover, this bioclimatic data will allow us detecting any possible predictor variable for chromosome number.

PH-08

Detecting cryptic diversity based on genetic distances and spatial distribution of evolutionary lineages

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The spatial distribution of evolutionary lineages within Linnaean species can aide the identification of cryptic diversity. Allopatric distribution of divergent evolutionary lineages with no morphological differentiation is usually considered an indicator of speciation, either complete or in process. Therefore, the analysis of the relationship between genetic and spatial distances (Isolation-By-Distance) in evolutionary lineages of a given morphological species can be used to identify putative cryptic diversity and the role of allopatric and sympatric speciation processes. Here we investigate the existence of cryptic diversity in Iberian leaf beetles using molecular and spatial distribution data of 4533 individuals belonging to 203 Linnaean species. We detected evolutionary isolated lineages based on cox1-5' using the Generalized Mixed Yule Coalescent (GMYC) model. While 80.1% of the Linnaean species showed an unequivocally correspondence with a single GMYC group; several GMYC groups were identified within 25 Linnaean species and, thus, were considered potential cryptic species. The hypothesis of cryptic diversity was rejected when no gap was observed between the intra and inter-GMYC genetic distances (n=9). When inter-GMYC distances were significantly larger than intra-GMYC distances; the spatial distribution of evolutionary lineages was either sympatric (n=11) or allopatric (n=3); showing that sympatric divergence may be more common than expected although allopatric divergence with posterior range expansion would be also plausible. Our study exemplifies how the analysis of genetic and spatial distances within and between GMYC groups allows identifying potential, hidden processes of speciation leading to the existence of cryptic diversity.

PH-09

Niche conservatism and topographic complexity explain divergence among squamates in Madagascar.

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Allopatric speciation is associated with closely related species maintaining similar ancestral ecological preferences (phylogenetic niche conservatism, PNC) wheras parapatric speciation is associated with the evolution of differences in the ecologies of closely related species (phylogenetic niche divergence, PND). Speciation processes among squamates of Madagascar are widely debated. Here, we investigate the impact of PNC/PND and topography-driven isolation in the speciation of Malagasy squamates. First we measured niche overlap using the RTR null biogeographic model to test whether observed niche overlaps were higher (PNC) or lower (PND) than expected by chance alone. Then, we tested for an association between PNC/PND and morphological divergence with increasing elevation. Finally, we tested whether elevational differences were higher for allopatric pairs than for parapatric pairs. We found that two of 17 allopatric pairs had PNC and two of 19 parapatric pairs had PND. Remaining allopatric pairs were found to have a significantly higher tendency towards a PNC signal than the remaining parapatric pairs ($p<0.05$). We found a significant positive association of increasing morphological divergence between allopatric taxa with increasing elevation ($p<0.01$, $R2= 0.5018$) but not parapatric taxa. We observed significantly higher differences in elevation between allopatric pairs than parametric pairs ($p<0.01$). Our results support the expectation of PNC being associated with allopatric speciation and PND with parapatric speciation. We demonstrate a decoupling of conservatism of broad ecological preferences and divergence due to local microclimatic adaptations. We propose that topographic complexity may have promoted allopatric speciation in Madagascar and that investigating ecological adaptations at different scales is critical to better understand speciation processes.

PH-10

Crossing the Speciation Threshold: Evolution in a Complex Archipelago

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Ever since Darwin and Wallace, island populations have been pivotal in understanding how new species evolve. The birds of Sulawesi, Indonesia, represent an ideal study system to examine evolutionary processes across islands and species. A region of complex biogeography and high endemism, the systematics of Sulawesi's fauna remains poorly understood. We have been looking at genetic patterns in bird populations across southeast Sulawesi, using mitochondrial genes ND2 and ND3. The genetic work is supported by analyses of morphology and song. Different species show different patterns of isolation, as certain species can more easily cross between islands, inhibiting the development of reproductive isolation. The patterns of isolation suggest that wingspan is not the only important aspect of bird biology which determines movement. Awareness of the drivers of isolation may help predict which populations are most likely to undergo allopatric speciation, leading to a greater understanding of Sulawesi and other biodiversity hotspots. We hope our discoveries will inform conservation efforts of the unique ecosystems they reveal.

PH-11
Molineriella Rouy, a Mediterranean grass genus

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Molineriella Rouy belongs to *Gramineae*, one of the largest plant families. Although several studies have focused on the biogeography of grasses, low attention has been given to *Molineriella*, a Mediterranean genus with its centre of diversity in the Iberian Peninsula. *Molineriella minuta* (L.) Rouy, *M. australis* (Paunero) E.Rico and *M. laevis* (Brot.) Rouy inhabit ephemeral pastures, mainly on sandy, siliceous substrates. Nevertheless, they occur in different geographical areas. *M. minuta* can be found in S Europe, Anatolia and NW Africa; in the Iberian Peninsula, specifically, it scatters all over most of the territory. *M. australis* appears in NW Africa and SW Iberian Peninsula, and *M. laevis* lives in NW Africa and most of the Iberian Peninsula. A total of 1,300 vouchers from 21 herbaria were studied to generate detailed descriptions and distribution maps by using ArcGIS ver. 9.3.1. This work provides enough information to disentangle the entity of the study taxa and to enhance the comprehension of the biogeography of this interesting grass genus.

PH-13
Temporal dynamics and biogeographical connections of the Antarctic flora: insight from phylogeography of the endemic moss Syntrichia sarconeurum Ochyra & R.H.Zander (Pottiaceae)

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The Antarctica is the region with the most limited terrestrial habitats and the highest isolation from other land masses. Due to extreme environmental conditions shaped by low temperatures, strong winds, drought, etc., its terrestrial life is very limited. It was widely assumed that the extant biota must have (re)colonised the continent after the Last Glacial Maximum (LGM; ca. 22–18 kya). However, this view is challenged for instance by relatively high share of regional endemic species and, lately, by first results of phylogeographic studies. The temporal dynamics and biogeographical connections of the Antarctic flora, however, remain poorly understood. Here, we present first results from our project focused on understanding evolution and past range dynamics of endemic Antarctic mosses. We examine the phylogeographical structure of one of most widespread species, *Syntrichia sarconeurum* (and its closest extra-Antarctic relatives), using a range-wide sampling and molecular tools including Sanger sequencing and target enrichment next-generation sequencing approach (ongoing). Our first, multilocus sequence data indicate several genetic breaks within the Antarctic with a major boundary separating the Antarctic Peninsula along with Dronning Maud Land from eastern zones of the continent. Remarkably, these two major lineages also display different exterior connections with South America and Australia, respectively, and molecular dating indicates their different temporal perspectives (back to Tertiary). The phylogeographical pattern of *S. sarconeurum* populations clearly indicates their long-lasting isolation in highly fragmented Antarctic terrestrial habitats and thus strongly supports a persistence of the Antarctic flora and complex evolutionary history of species marked by repeated dispersal and colonisation events in a long time horizon.

PH-14

Glacial climate drives speciation in an insular humid forest

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Understanding the drivers and dynamics of speciation within oceanic islands is fundamental to achieve a process-based understanding of the assembly and structure of island communities. While there has been much interest in the non-neutral drivers of divergent evolution within islands, such as natural selection, there has been less focus on neutral drivers, such as geographic isolation. Here we take advantage of a well-characterised beetle community within an insular humid forest ecosystem to explore the dynamics of speciation by geographic isolation. Our focal laurel forest ecosystem in the Anaga peninsula of Tenerife is effectively continuous in distribution, but presents spatial variation in climate, associated with topographical variation. These variations have the potential to create barriers to gene flow when (i) they fall outside or in the edge species environmental tolerances and (ii) species dispersal ability limits movement between environmentally favourable areas even at the small geographical scale. We have generated RAD sequence data for a flightless beetle species typical of the laurel forest, the weevil Acalles globulipennis, sampled across a 15 km transect of forest. Our results reveal a demographically complex, yet environmentally subtle speciation dynamic, where geographic isolation, secondary contact and hybridisation have played out over the space of only a few kilometres. This dynamic has community-wide implications for landscape responses to Quarternary climate change.

PH-15

Phylogeographic history of the Killarney fern, Vandenboschia speciosa (Hymenophyllaceae)

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Vandenboschia speciosa is a Tertiary relict Macaronesian-European endemic fern. Both phases of the life cycle (sporophyte and gametophyte) are perennial, can propagate vegetatively, and have different ecological requirements; so mixed and independent phase populations occur and their distributions depend on the generation. In this study we determined the phylogeographic history of *V. speciosa* using DNA sequences, from plastid (*trn*H-*psb*A intergenic spacer) and low-copy nuclear (*gapCp* gene) markers, in combination with species distribution modelling (SDM). According to our results, there is no structuring of genetic diversity between both phases. We found 9 plastid haplotypes which showed a structuring in two geographical regions, the northern haplogroup (Azores, Brittany, Czech Republic, Ireland, Luxemburg, Vosges, Wales) and the southern one (Andalusia , Canary Islands, Madeira, and Italy). We also detected a contact zone in the Cantabrian Cornice (Iberian Peninsula). *GapCp* showed no geographic structuring. Dating analysis suggested *V. speciosa* lineage dates back to the beginning of the Serravallian (13 Ma), and that two historical events determined the diversification of the lineages and their isolation in the shelters of the European western coast: 1) the salinity crisis of the Messinian, when the two main gene lineages diverged (north-south; 5.1 Ma); 2) the establishment of the Mediterranean climate, when the two haplogroups diversified (south: 3.52 Ma, north: 2.58 Ma). According to SDM, the impact of glaciations was greater in the northern distribution area. Demographic and SDM analyses suggested that the presence of the species in central Europe was due to postglacial expansive processes (<10 Ka, Holocene).

PH-16

Phylogeographic analysis of Diplazium caudatum (Cav.) Jermy by using plastid sequences

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Diplazium caudatum is a Tertiary relict Macaronesian-European endemic fern which grows in warm and very humid environments. Currently it is distributed in Andalusia (Spain) and in the Macaronesian archipelagos. The objective of this work was to establish the evolutionary relationships between the populations/genetic lineages of *D. caudatum* and to know the geological-climatic events and the population processes that explain their distribution. For this, we used DNA sequences from the plastid marker *trn*S-*trn*G intergenic spacer, and species distribution modelling. We found 10 plastid haplotypes. The regions with the highest number of haplotypes were the Azores and Madeira. All regions, except Andalusia, share the two ancestral haplotypes; the rest are exclusive of the different regions, with the greatest variation among populations. The beginning of the lineage of *D. caudatum* occurs about 19 Ma, during the Miocene, while the divergence of its haplotypes goes back to 1.82 Ma, at the end of the Pliocene and the beginning of the Pleistocene. The evolutionary history of *D. caudatum* is marked by a decrease of its distribution area during the end of the Tertiary and the Pleistocene by the climatic deterioration and the glaciations. The distribution of genetic lineages is explained by long distance dispersal processes and genetic drift. The species probably disappeared from the continent with the appearence of the Mediterranean climate during the Pliocene, remaining as a relict in the Macaronesian archipelagos, where it diversified giving rise to different genetic lineages. Later the species recolonize Andalusia, remaining as relict in the Sierras de Algeciras.

PH-17

Comparative phylogeography of the two widely distributed birds across the North Hemisphere

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Comparative study on phylogeography of sympatrically widespread birds would more clearly demonstrate geographical variation and ecological dependence of geo-climatic impacts on contemporary population genetic pattern. We studied the phylogeography of magpies (*Pica pica* species complex) and Great Tits (*Parus major* species complex). The results based on two mitochondrial genes showed six geographical lineages in magpies and five in Great Tits. Some major lineages were consistent in the two species associated with the prominent geographical features such as arid region in central Asia and Qinghai-Tibet Plateau. Simulations on historical population dynamics showed expansion in all geographical lineages of the two species, indicating a consistent population flunctuation responding to the last glacial maximum. However the time to the most recent ancestor was varied in lineages. Our results indicate congruent impacts of geographical features and the last glacial cycle in Pleistocene on the lineage diversification and population dynamics. However, some isolated lineages have been preserved and the evolutionary times differed among lineages depending on geographical complexity and species property in their ecological requirements.

PH-18

Phylogeographic data and its potential application in delimiting phylogeoregions in Sino-himalaya

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Biogeographic regionalization can help to better understanding evolutionary history and process of plant diversity in certain area, but in the lowest unit of regional division, the traditional method is relatively difficult to objectively determine these units. Phylogeographic research can reveal the historical evolution of the geographical pattern of population and the processes of its formation, as well as historical events that affect the genetic structure of populations. Therefore, phylogeographic data should be helpful in delimiting the lowest unit of regional division. In this paper we analyzed the pedigree structure of some endemic groups such as *Parasyncalathium souliei*, *Marmoritis complanatum*, the results showed that their phylogeographic structure basically can be divided into three phylogeoregions i.e. Northern Hengduan Mountain, South Hengduan Mountain and SE Tibet, which basically coincides with the current floristic division. It also proved that the 29^{0}N latitude is North-South floristic boundary of Hengduan Mountain and the Mekong–Salween watershed is the West-East floristic boundary of south-east Tibet and Hengduan Mountain. This data may provide valuable evidence for phylogeographic regionalization using chloroplast genetic data in a common, widespread endemic species from the Sino-Himalayas.

PH-19

Genetic analysis of Androsace cylindrica DC populations: genes in the cliff.

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Cliffs and other rocky environments are relevant for plant evolution. They usually present high degree of isolation allowing for a differentiation of populations and thus promoting endemism. At the same time those habitats might act as an evolutionary sink for some plants. *Androsace cylindrica* DC is a protected Pyrenean narrow endemic plant growing exclusively in calcareous cliffs. In order to better understand the genetic structure and its history, we conducted AFLPs and sequenced 4 cpDNA regions using 119 individuals from 25 localities covering the entire current distribution area. Besides, we measured morphological traits currently applied as characters to separate the 3 accepted subspecies. The results show a clear phylogeographical pattern at cpDNA haplotype level indicating very limited seed dispersal. At nuclear level this structure blurs up at population scale but is still significant at a wider regional scale. Populations are often isolated but dense patches which maintain intermediate values of genetic diversity. This diversity tends to decrease in the peripheral localities. Regarding morphology, the results are not completely consistent with subspecies circumscription because we also detected a geographical signal which could be linked to the East-West climatic gradient in the distribution area of *A. cylindrica*. Overall, with our results we (I) update the subspecies classification, (II) reveal different potential events of past disjunctions in Western Pyrenees and refugia at the current Ordesa National Park and (III) discuss the actual population distribution under different evolutionary scenarios.

PH-20

Phylogenomography of the Green Crested Lizards (Bronchocela): with insights on spatial and temporal evolution

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Southeast Asia has experienced a dynamic geological and climatic history, influencing the spatial and temporal distribution of the flora and fauna across classic biogeographic barriers, such as Wallace's Line. The region includes four well-known biodiversity hotspots: Indo-Burma, Sundaland, the Philippines, and Wallacea. One conspicuously common faunal element, a group that spans all four regions, is the widespread Green Crested Lizards of the genus *Bronchocela*. Their widespread Southeast Asian distribution makes them a well-suited model organism to investigate patterns of spatial and temporal evolution across Southeast Asia. Here we use a phylogenomic dataset to: (1) assess species boundaries within the genus; (2) test hypotheses pertaining to the spatial and temporal patterns of diversification throughout the continental and oceanic components of their distribution; and (3) use past geological reconstructions to test *a priori* hypotheses relating to biogeography. Preliminary results reveal that species diversity within *Bronchocela* is vastly underestimated, that widespread oversea dispersal and colonization have been predominant modes of range expansion in *Bronchocela*, and, finally, that Green Crested Lizards support the Dual Umbilicus hypotheses of the invasion of the Philippines—albeit along novel, seldom reported biogeographic conduits.

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BPM-40	Lola	Toomey
MB-18	Estefanía	Torreblanca Fernández
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BA-13	Urs	Treier
IB-16	Kostas	Triantis
CB-21	Helena	Tukiainen
CS1-08	Hanna	Tuomisto
CS17-06	Luis	Valente
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BPM-31, CB-22	Juan	Verhelst
CS16-15	Ole	Vetaas
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CS15-14	Sara	Villén-Pérez
S1-2	Alfried	Vogler
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