Conference Program and Abstracts

8th Biennial Conference of

The International Biogeography Society

Tucson, AZ, USA

January 9th – 13th, 2017

The International Biogeography Society
8th Biennial Conference
Tucson, Arizona, USA
Jan 9-13, 2017

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WELCOME TO IBS 2017 TUCSON!

We would like to welcome all participants of the 8th Biennial Conference of the International Biogeography Society – to be held at the University of Arizona and the Tucson Marriott University Park, Tucson, Arizona from January 9-13, 2017. The 2017 meeting will have three symposia on "Modeling large-scale ecological and evolutionary dynamics", "Experimental macroecology", "Building up biogeography - process to pattern" and a special session that focuses on the meeting location "Biogeography of Southwestern North America". Together, these symposia and the several regular sessions in the program will cover the diversity of research areas and interests of the Biogeographic community worldwide.

The IBS, founded in 2001, is the world's leading scientific society of biogeography and provides the primary forum for biogeographers worldwide. Biogeography, the study of the geography of life, has a long and distinguished history, and one interwoven with that of ecology and evolutionary biology. Traditionally viewed as the study of geographic distributions, modern biogeography now explores a great diversity of patterns in the geographic variation of nature - from physiological, morphological and genetic variation among individuals and populations to differences in the diversity and composition of biotas along environmental, geographic, continental and global gradients. Given its interdisciplinary and integrative nature, biogeography is now broadly recognized as a unifying field that provides a holistic understanding of the relationships between the earth and its biota. Our abilities to develop more general theories of the diversity of life, and to conserve biological diversity may well rest on insights from the field of biogeography. The IBS has the following mission: (1) Foster communication and collaboration between biogeographers in disparate academic fields scientists who would otherwise have little opportunity for substantive interaction and collaboration; (2) Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers; and (3) Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world's biota.

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General Information

Symposia

Concurrent Session Presentations

Mini-Talk Session Presentations

SCHEDULE OVERVIEW

Monday 9 Jan	Tuesday 10 January	Wednesday 11 January	Thursday 12 January	Friday 13 Jan
Workshops and Field Trips	Welcome Symposium 1	Symposium 2	Concurrent Sessions 5-8	Field Trips
	Break	Break	Break	
	Symposium 1, cont’d	Symposium 2, cont’d	Concurrent Sessions 9-12	
	Lunch	Lunch	Lunch	
	Concurrent Sessions 1-4	Symposium 3	Concurrent Sessions 13-16	
	Break	Break	Break	
	Mini Talks	Symposium 3, cont’d	Awards	
Welcome Reception	Discussion Groups	Poster Session B	Closing	
	Poster Session A	Banquet		


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Workshop & Field Trip Overview
Monday 9 January

8:30	**Workshop 1:** An overview of new surface and satellite-based climatologies available for biogeographers and ecologists: confidence and uncertainty assessments. ENR2-S210		**Workshop 4:** Introduction to Network Analysis in Biogeography ENR2-S215	**Workshop 5:** Introduction to the analysis of messy data ENR2-S225	
9:00					**Field Trip 1:** Desert Museum
9:30					
10:00					
10:30					
11:00					
11:30					
12:00					
12:30	**Workshop 3:** Integrating and cleaning biodiversity data: Workflows to model ranges and merge associated ecological, phylogenetic, and trait information. ENR2 -S210	**Workshop 2:** Analyzing paleoecological data: Best practices and current resources ENR2-S120B			
13:00					
13:30					
14:00					
14:30					
14:45					
15:00					
15:30					
16:00					
16:30					**Field Trip 2:** Tumomoc Hill
17:00					
17:30					
18:00					
18:30	Welcome Reception/Registration (Tucson Marriott University Park)				
19:00					
19:30					
20:00					

DAY 1 SCHEDULE OVERVIEW

Tuesday 10 January

8:30 Welcome / Intro

9:00 Symposium 1: Modeling large-scale ecological and evolutionary dynamics
Crowder Hall - University of Arizona
9:30

10:00 Coffee Break

10:30 Symposium 1, Cont'd
Crowder Hall - University of Arizona
11:00
11:30

12:00 Lunch - Offsite (not included)
12:30
13:00

13:30
14:00
14:30
14:45
15:00

Concurrent Session 1 (CS1)	Concurrent Session 2 (CS2)	Concurrent Session 3 (CS3)	Concurrent Session 4 (CS4)
Biogeography of the Anthropocene	Historical and Paleo-biogeography	Gradients, range-limits, and beta-diversity	Functional Biogeography
Canyon ABC Room	*Madera Room*	*Pima Room*	*Sabino Room*
Tucson Marriott University Park	*Tucson Marriott University Park*	*Tucson Marriott University Park*	*Tucson Marriott University Park*

15:30 Coffee Break

16:00
16:30
17:00

Mini Talks 1 (MT1)	Mini Talks 2 (MT2)	Mini Talks 3 (MT3)	Mini Talks 4 (MT4)
Climate Change Biogeography	Biodiversity Patterns and Maintenance	Conservation Biogeography	Gradients, range-limits, and beta-diversity
Canyon ABC Room	*Madera Room*	*Pima Room*	*Sabino Room*

17:30 Discussion Groups 5:30 - 6:30 *in the Ventana room*
18:00

18:30 Poster Session A / Reception / Appetizers / Cash Bar
19:00 *Ballroom (Combined Canyon/Madera/Pima/Sabino rooms - Tucson Marriott University Park)*
19:30
20:00

PROGRAM SCHEDULE

Wednesday 11 January

8:30	Symposium 2: Experimental Macroecology *Crowder Hall*
9:00	
9:30	
10:00	Coffee Break
10:30	Symposium 2, cont'd *Crowder Hall*
11:00	
11:30	
12:00	
12:30	Lunch - Offsite
13:00	
13:30	Symposium 3: Building up biogeography - process to pattern *Crowder Hall*
14:00	
14:30	
14:45	
15:00	
15:30	Coffee Break
16:00	Symposium 3, cont'd *Crowder Hall*
16:30	
17:00	
17:30	Poster Session B / Reception / Appetizers / Cash Bar *Ballroom: Pima/Madera/Sabino Combined*
18:00	
18:30	
19:00	
19:30	Banquet *Arizona Historical Society*
20:00	

DAY 3 SCHEDULE OVERVIEW

Thursday 12 January

8:30	**Concurrent Session 5** **(CS5)** Biodiversity Patterns and Maintenance *Canyon ABC Room*	**Concurrent Session 6** **(CS6)** Conservation Biogeography *Madera Room*	**Concurrent Session 7** **(CS7)** The geography of species associations *Pima Room*	**Concurrent Session 8** **(CS8)** Historical and Paleo-biogeography *Sabino Room*
9:00				
9:30				
10:00	Coffee Break			
10:30	**Concurrent Session 9** **(CS9)** Biodiversity Patterns and Maintenance *Canyon ABC Room*	**Concurrent Session 10** **(CS10)** Biogeography of South-western North America *Madera Room*	**Concurrent Session 11** **(CS11)** Global Change Biogeography *Pima Room*	**Concurrent Session 12** **(CS12)** Biological Invasion *Sabino Room*
11:00				
11:30				
12:00	Lunch - Offsite (not included)			
12:30				
13:00				
13:30	**Concurrent Session 13** **(CS13)** Biodiversity Patterns and Maintenance *Canyon ABC Room*	**Concurrent Session 14** **(CS14)** Island Biogeography *Madera Room*	**Concurrent Session 15** **(CS15)** Climate Change Biogeography *Pima Room*	**Concurrent Session 16** **(CS16)** Models and drivers of biogeographic patterns *Sabino Room*
14:00				
14:30				
14:45				
15:00				
15:30	Coffee Break			
16:00	Awards Dissertation Award - *Carsten Meyer* MacArthur & Wilson Award - *Jessica Blois* Wallace Award Presentation - *Margaret Davis*			
16:30				
17:00				
	Closing *Pima/Madera/Sabino Combined*			
17:30				
18:00				
18:30				
19:00				
19:30				
20:00				
20:30				

AWARDS

AWARD CEREMONY/PLENARY SPEAKERS

Date: January 12, 2017 4:00 pm – 5:30 pm
Location: Pima/Madera/Sabino Rooms – Marriott Hotel

IBS DOCTORAL DISSERTATION AWARD

Awardee: Carsten Meyer

Established in 2013, the Doctoral Dissertation Award aims at promoting new knowledge and new energy in the field of biogeography by recognizing and publicizing outstanding doctoral work in the field of biogeography.

The Early Career Committee and the IBS Board is pleased to announce that this year's recipient of the Doctoral Dissertation Award is Carsten Meyer.

The IBS Board notes with thanks, the work of the Doctoral Dissertation Award Committee: Fabricio Villalobos (Chair), Joaquin Hortal, Michael Dawson, Richard Field, Naia Morueta Holme, Jonathan Kennedy, Carolina Tovar, Ludmila Rattis, Leticia Ochoa, Dov Sax.

Abstract

Limitations in global information on species occurrences

Carsten Meyer

PhD thesis, Biodiversity, Macroecology & Conservation Biogeography Group, University of Göttingen, Göttingen, Germany; cmeyer2@uni-goettingen.de

Detailed information on species distributions is crucial for answering central questions in biogeography, ecology, evolutionary biology, and conservation. Millions of species occurrence records have been mobilized via international data-sharing networks, but inherent biases, gaps, and uncertainties hamper broader application. In my PhD thesis, I present the first comprehensive analyses of global patterns and drivers of these limitations across different taxonomic groups and spatial scales. Integrating 300 million occurrence records for terrestrial vertebrates and plants with comprehensive taxonomic databases, expert range maps and regional checklists, I demonstrate extensive taxonomic, geographical and temporal biases, gaps and uncertainties. I identified key socio-economic drivers of data bias across different taxonomic groups and spatial scales. The results of my dissertation provide an empirical baseline for effectively accounting for data limitations in distribution models, as well as for prioritizing and monitoring efforts to collate additional occurrence information.

THE MACARTHUR AND WILSON AWARD

Awardee: Jessica Blois

This award – named in honor of Robert H. MacArthur and Edward O. Wilson - is sponsored by *Frontiers of Biogeography* and was created to recognize an outstanding, comparatively early career scientist that has made notable, innovative contributions to the discipline of biogeography. The International Biogeography Society Board is pleased to announce that this year's recipient of the MacArthur and Wilson Award is Dr. Jessica Blois.

Dr. Blois is clearly one of the top researchers in the new generation of biogeographers. Her research integrates neo-and paleo-ecological approaches to understand the abiotic and biotic processes that control the patterns of species distributions and diversity through space and time. Dr. Blois blends deep expertise in ecology and paleo-geographic data with creative research design, field and laboratory work, and rigorous statistical analysis and modeling to advance our understanding of species and ecosystem responses to large and rapid environmental changes. In a series of groundbreaking papers, Dr. Blois' innovative work has demonstrated key mechanisms and outcomes of climate species interactions and biodiversity dynamics over millennia. Her use of state-of-the-art statistical tools and datasets has provided the community with new guideposts for tackling challenging diverse problems in an era of rapid global change. Her first authored papers in top journals as well as her excellent record of collaboration support this recognition.

The IBS Board notes with thanks, the work of the MacArthur and Wilson Award Committee: Carl Beirkuhnlein, David Currie, Jonathan Price, Jack Williams and Vicki Funk (chair).

Abstract:

Biogeography in a Changing Environment: Perspectives from the Late Quaternary

Jessica Blois

UC Merced, United States

A central goal of biogeography is to understand the factors influencing spatial patterns of present-day species and communities; an added goal of paleobiogeography is elucidate the long-term dynamics of those patterns and their drivers. The Quaternary fossil record in particular provides the opportunity to link present-day biogeographic patterns to the ecological and evolutionary factors structuring them across space and time. In this talk, I will discuss three projects that explore the recent biogeographic history of communities and thus provide a long-term context for recent and future biodiversity change: 1) richness and evenness through time in late Quaternary mammals; 2) stability of significant associations between taxa through time; and 3) the relative influence of climate on vegetation assemblages. Overall, my work shows that both the basic patterns we see on the landscape today, and the influence of various factors that may structure those patterns, have been variable across millennia. My work highlights two areas for future progress in paleobiogeography: better reconciling the different meanings of 'history' (ecological vs. evolutionary) and disentangling the drivers that underlie the signals of variability versus cohesion seen in many fossil records.

THE ALFRED RUSSEL WALLACE AWARD

Awardee: Margaret Bryan Davis

The Alfred Russel Wallace award was established by the International Biogeography Society in 2004 to recognize a lifetime of outstanding contributions by an eminent scholar in any subdiscipline of biogeography. The IBS Board is pleased to announce that Margaret Bryan Davis will be the next to join the distinguished list of recipients of the Alfred Russel Wallace Award.

Professor Emeritus Margaret Bryan Davis of the University of Minnesota has a long and distinguished career of outstanding contributions to biogeography, and deserves credit for placing paleoecology squarely in the mainstream of biogeography and ecology. Her papers combine magisterial reviews and thoughtful syntheses with a long series of carefully designed and elegant empirical studies aimed at addressing specific, focused questions.

Professor Davis' work established many of the current tenets of Quaternary biogeography: that species shift ranges in response to climate change, these changes are individualistic, and that as a consequence communities are transient. Other ideas, such as the role of pathogens in forest history and the timescale of migrational lags, remain on-going topics of research and productive debate. Her ideas opened up new fields of fertile investigation that continue today, including postglacial patterns and rates of plant migration, the transience of ecological communities, stand-scale forest history, the mid-Holocene hemlock decline in eastern North America, and how pollen data record vegetation.

A mark of a truly great scientist is the ability to reconsider, and revise or even reject, strongly held views. Margaret Davis welcomed critiques, and demonstrated that conceptual breakthroughs were not always as effective as hoped. She stood her ground and asked difficult questions, but when others provided compelling evidence, she yielded. Professor Davis was rigorous, critical, and set high standards for the field, always with a focus towards doing the best science and getting closer to the truth. She inspired countless young scientists by her professional example, as well as by the quality of her work and thinking.

Professor Davis had – and continues to have – few equals in combining rigorous, analytical approaches with broad, discipline-spanning syntheses.

The IBS Board notes with thanks, the work of the Wallace Award Committee: Ingolf Kuhn, Mark Lomolino, Jonathan Losos, Susanne Renner, Kathy Willis, and Dov Sax (chair).

SYMPOSIA

SYMPOSIUM 1: Modeling large-scale ecological and evolutionary dynamics

Organizer: Robert Colwell
Date: January 10, 2017 9:00 am – 12:00 pm
Location: Crowder Hall, University of Arizona

S1-1

Modeling spatial and temporal patterns of ecological resilience: is the past a key to the present?

Kathy Willis[1], David Benz[2], Lydia Cole[3], Marc Macias Fauria[3], Peter Long[4], Alistair Seddon[5], Carolina Tovar[6], Beccy Wilebore[7]
[1]Royal Botanic Gardens Kew
[2]University of Oxford, Oxford, United Kingdom
[3]Rezatec
[4]University of Oxford , Oxford, United Kingdom
[5]University of Bergen, Bergen, Norway
[6]Royal Botanic Gardens, Kew, London, United Kingdom
[7]Royal Botanic Gardens, Kew, Surrey, United Kingdom

Willis and colleagues present the results of two recently published approaches (Cole et al., 2014; Seddon et al., 2016) where they have attempted to assess the relative sensitivity of ecosystems to environmental perturbations from decadal to millennial timescales. They ask whether the same regions that appear to be sensitive to environmental perturbations over the past decade also demonstrate the same patterns over much longer timescales. Focusing on a South American case-study region, they then examine various biotic and abiotic factors that might lead to the patterns identified and the legacy of temporal factors in determining apparent current levels of ecosystem resilience.

2014. Cole, L.E.S., Bhagwat, S.A., Willis K.J. Recovery and resilience of tropical forests after disturbance. Nature Communications, 5, 3906 doi:10.1038/ncomms4906
2016. Seddon, A.W.R., Macias-Fauria, M., Long, P.R., Benz, D., Willis, K.J. Sensitivity of global terrestrial ecosystems to climate variability. Nature, 531, 229-232. doi:10.1038/nature16986;

S1-2

Turning back the clock: building pre-settlement baseline vegetation datasets for calibrating and testing dynamic vegetation models

John Williams[1], Andria Dawson[2], Simon Goring[3], Chris Paciorek[4], Charles Cogbill[5], David Mladenoff[6], Stephen Jackson[7], Jason McLachlan[8]
[1]University of Wisconsin-Madison, Madison, WI, United States
[2]University of Arizona
[3]University of Wisconsin-Madison, Madison, Wisconsin, United States
[4]University of California Berkeley
[5]Independent
[6]University of Wisconsin
[7]US Geological Survey
[8]University of Notre Dame

North American forests have been transformed by human action, challenging both paleoecologists and global change ecologists who use contemporary ecosystems as a baseline for past or future inferences. As part of the Paleoecological Observatory Network (PalEON) project, we present new gridded (8x8km) reconstructions of historic forest composition, stem density, and biomass for 28 tree taxa in northern US forests for the pre-settlement era (ca. 1700 to 1890 CE), based on Public Land Survey (PLS) data. These PLS-based reconstructions include multiple corrections for potential surveyor biases, including spatially varying correction factors to accommodate sampling design, azimuthal censoring, and biases in tree selection. In combination with PRISM data, we demonstrate shifts in tree-climate relationships over the last two centuries due to historic land use and climate change. We employ these pre-settlement vegetation reconstructions, in combination with networks of fossil pollen records drawn from the Neotoma Paleoecology Database (www.neotomadb.org), to calibrate the STEPPS pollen-vegetation model and reconstruct forest composition in the northern US over the last two millennia. STEPPS, as a hierarchical Bayesian model, includes estimates of uncertainty in parameter estimation and state variable reconstruction. The next stage of work is to use these paleovegetation reconstructions to initialize, validate, and improve the simulations of terrestrial ecosystem models; this work is underway.

S1-3

After the mammoths: modeling mammal communities through the terminal Pleistocene megafauna extinction

Felisa Smith[1], Catalina Tomé[1], K. Sara Lyons[2], Emma Elliott Smith[3], Seth Newsome[4], Thomas Stafford, Jr.[5]
[1]Department of Biology, University of New Mexico
[2]Department of Paleobiology, Smithsonian Institution
[3]University of New Mexico
[4]University of New Mexico, Albuquerque, NM, United States
[5]Stafford Research

Biodiversity loss is a major concern and may have serious consequences for the functioning of modern ecosystems. Recent studies seeking to understand the consequences of the decline in large mammals on ecosystems overlook that this natural experiment has already occurred. Millions of large-bodied mammals were widespread across the Americas as recently as 13-14ka; after the arrival of humans, all terrestrial mammals larger than 600kg went extinct. While the cause of the megafauna extinction remains contentious, little work to date focuses on the ecological consequences on surviving mammals. Here, we examine the effect of the extinction in local fossil communities preserved in Hall's Cave, Edwards Plateau, Texas. This site has unparalleled century-scale temporal resolution over the past 20ka, allowing characterization of communities before and after the extinction. Using geologically short time intervals and comprehensive faunal lists, we reconstruct mammal associations and body size distributions over time. We find changes in the statistical moments associated with climate change and the extinction. Employing the null model program PAIRS reveals interesting temporal patterns in the co-occurrence of species through the terminal Pleistocene and Holocene. We find that ancient ecosystems were more tightly linked than modern ones and with more significant species associations. Unlike modern communities, both positive and negative ecological interactions were important. In particular, ancient carnivores were more tightly associated with their prey base than are modern species. Our results suggest that many fundamental aspects of mammalian communities were changed with the loss of megafauna at the terminal Pleistocene.

S1-4

How novel is too novel? Using the paleo-record to define the limits on projections of biodiversity under future climate.

Matt Fitzpatrick[1], Jessica Blois[2], Diego Nieto-Lugilde[3], Kaitlin Maguire[4], John Williams[5]
[1]University of Maryland Center for Environmental Science
[2]University of California-Merced, Merced, California, United States
[3]University of Córdoba, Córdoba, Spain
[4]United States Geologic Survey, Boise, United States
[5]University of Wisconsin-Madison, Madison, WI, United States

Models that combine species data with abiotic predictors are often used to forecast future biodiversity patterns. Given the expected novelty of future climate, the temporal transferability of correlative models is often questioned. The expectation is that transferability will decline as climatic novelty increases relative to the period in which the model was fit. This raises two questions: (i) how well will models perform under novel future climates and (ii) will some models be more transferable than others? Using the paleo-record and model intercomparisons, we determined relationships between model performance and climatic novelty over the last 22k years, which we used to make

inferences regarding model transferability to the future. We found that transferability declined with increasing climatic novelty until a threshold was reached where model performance remained marginally better than random. Under future climatic novelty, the utility of empirical models may be greatly reduced starting mid-century, with models that consider species assemblages outperforming single-species models. Our comparison of past and future climatic novelty suggested that the magnitude of future climatic novelty in eastern North America may be less than that in experienced in the past, with precipitation-related variables being most strongly associated with both past and future climatic novelty.

S1-5

Macrogenetics: quantifying global genetic diversity dynamics under past and future global change

David Nogues Bravo
Center for Macroecology, Evolution and Climate, Denmark

Understanding the anthropogenic impacts in biological diversity and its future fate under future global change are among the major scientific challenges to overcome in the 21st century. Genetic diversity has been identified as a key component for biodiversity integrity due to its capacity to influence processes across population, species, community and ecosystem levels, and being a key component of the Biosphere to adapt to environmental changes. However, whilst the distribution and responses of ecosystem and species diversity to global change have been deeply investigated in the past decades, the global distribution of the intra-specific genetic is the most unknown among the three levels of biodiversity. I will show here new developments, and results, on the past, present and future dynamics of intra-specific genetic diversity under global anthropogenic change.

S1-6

Modeling ecological and evolutionary processes mechanistically across temporal and spatial scales

Thiago Rangel[1], Robert Colwell[2], Neil Edwards[3], Philip Holden[4], Carsten Rahbek[5]
[1]Universidade Federal de Goiás, Brazil
[2]University of Connecticut, Storrs, CT, United States
[3]The Open University, United Kingdom
[4]The Open University, Milton Keynes, United Kingdom
[5]CMEC Univ. of Copenhagen, Copenhagen, Denmark, Denmark

We introduce a process-based, biogeographic model that simulates dispersal, range fragmentation, geographical isolation, allopatric speciation, evolutionary adaptation to climate, the effects of interspecific competition on distributions, and climate-driven extinction of species. The model is driven by a spatially explicit, paleoclimate model for temperature and precipitation patterns in South America over the past 800Ka. Using the model, we rigorously define and aim to identify regions of especially active species origination (cradles), unusual persistence (museums), and high rates of extinction (graveyards).

SYMPOSIUM 2: Modeling large-scale ecological and evolutionary dynamics

Organizers: Miguel Matias, Imperial College London, Miguel Araujo, CSIC
Date: January 11, 2017 8:30 am – 12:00 pm
Location: Crowder Hall, University of Arizona

S2-1

Using an experimental macroecological approach to assess climate change impacts on plant populations and communities: experiences, insights, and ways forward

Vigdis Vandvik
University of Bergen , Bergen, Norway

Predicting the rate, magnitude, and consequences of ecological responses to unprecedented rates of global environmental change present a pressing challenge for today's ecologists. Both macroecological and localized experimental approaches are making important contributions to our understanding of how biodiversity and ecosystem functions and services are impacted. However, these approaches differ in scope, strengths, and more fundamentally, also in the underlying ecological questions asked. Differences in outcomes and predictions from different approaches have led to discussions and concerns over their comparability and even validity for answering the pressing global change questions, but also to calls for integrated approaches. I will share experiences and insights from such an integrated approach; replicating experiments to assess climate change impacts on grassland ecosystems across regional-scale climate gradients in Western Norway. Our work illustrates challenges facing experimental macroecologists, but also how these approaches can further our understanding of the ecological responses to climates change – focusing on context-dependencies, time-scale issues, the interplay between direct and indirect effects, and interactive impacts of temperature and precipitation change.

S2-2

Experimental community ecology: making sense of tropical rainforest food webs by manipulation of species in situ and in silico

Vojtech Novotny
Biology Centre, Czech Academy of Sciences, Biology Centre, Czech Republic

Plant-animal food webs in tropical rainforests are renowned for their extraordinary diversity that can reach 100,000 species-to-species interactions within a single ecosystem. Experimental manipulations seem to be one of the more feasible approaches to the study of dynamics of such complex systems, including the age-old question of bottom-up versus top-down control of plants, herbivores, predators and parasitoids in the food webs. These manipulations include precision removals or introductions of individual species as well as "black box" treatments of entire taxa, guilds or trophic levels. We illustrate the possibilities, and problems, of such experiments using studies of plant-insect-vertebrate food webs in tropical forests of Papua New Guinea, and discuss promising avenues for future research.

S2-3 From local to latitudinal scales: using replicated experiments across latitude to improve understanding of biodiversity and invasion

Amy Freestone
Temple University, United States

One of the clearest patterns in ecology is the latitudinal diversity gradient whereby species richness increases toward the equator in most taxonomic groups. The striking and predictable difference in species richness across latitude raises the question of whether the relative influence of ecological processes that maintain these patterns are independent of latitude, or if they change predictably across the globe. Through the emerging field of experimental macroecology, with studies that employ replicated experiments across biogeographic gradients, we are now well positioned to address these questions. I will draw from terrestrial and marine examples and my own research on coastal marine invertebrate assemblages of North and Central America to demonstrate that community processes can differ across the globe, and across latitude in particular, and have important consequences for patterns of biodiversity. I will then discuss the application of this approach toward improved understanding of global patterns of biological invasions, a primary driver of global change. By highlighting the most exciting advances in large-scale replicated experimental approaches as well as the challenges that face us, I will argue that we are well poised to mechanistically link local-scale dynamics with macroecological patterns and apply this expanded knowledge to address some of our largest environmental challenges.

S2-4

Body Size and Biogeography: Predicting Gradients of Diversity from Microbe to Macrobe

Michael Kaspari
Dept. of Biology, Dept. of Biology, Norman, OK, United States

A mature, robust biogeography is one whose processes and properties apply predictably to taxa whose individuals vary 10^{17} in body mass. This is a staggering number that beggars comprehension, underlying our current difficulties and increasing the demand for a scaling approach. I use scaling logic to develop an argument for the keys to a rapprochement between microbial and macrobial ecology. The argument focuses on how body size covaries with diversification, dispersal, and extirpation, and the resulting spatial extents at which they operate. I use this nascent theory to generate predictions for the slope of biodiversity gradients and test this theory with a survey of forests, from alpine to tropical. I conclude with how such an approach can open up new experimental avenues of biogeographical research.

S2-5

Testing the Core-Periphery Hypothesis in the Wood Frog: Genetics, Stress, Body Size, Disease, and Behavior

Leslie Rissler[1], Erica Crespi[2], Sarah Duncan[3]
[1]National Science Foundation, Alexandria, VA-Virginia, United States
[2]Washington State University, United States
[3]University of Florida, United States

The Core-Periphery Hypothesis (CPH) is a broad macroecological generalization used to explain biogeographic patterns of species' range distributions. However there are relatively few empirical studies that test and support the CPH, although much of this ambiguity in support could be due to differences in definitions of "core", i.e., geographic vs. environmental. Here we use the wood frog (*Rana sylvatica*), whose distribution spans 40 degrees of latitude, to test various predictions of the CPH. In this talk, we synthesize several of our published and unpublished analyses including biogeographic studies on patterns of genetic diversity, physiological stress levels in adult males at breeding ponds, adult and juvenile life history traits, disease prevalence, and anti-predatory behavior of tadpoles and metamorphs. Populations were sampled in multiple years and across the eastern clade's range spanning those at the southern limit in Alabama through the eastern United States to those at the northern limit in Nova Scotia. We also used common garden and reciprocal transplant experiments to tease apart geographic and environmental influences on response variables. In summary, genetic diversity patterns are most closely associated with historic patterns of environmental suitability. Physiological stress levels vary widely both spatially and temporally. Body size follows the inverse of Bergmann's Rule, and individuals from more southern populations had lower activity levels than those of more northern populations. The work is presented in a broad theoretical context to encourage synthesis across various fields within a biogeographic framework.

S2-6
Dynamic macroecology: beginning with a small scale view

Sarah Supp[1], Shane Blowes[2], Maria Dornelas[3]
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Macroecology is a potentially powerful tool that seeks to identify and understand general, emergent patterns in abundance, distribution and diversity of species, across space and time. But pattern dynamics are rarely examined in perturbed systems. Combining macroecological approaches with insights from smaller-scale datasets and experiments may help researchers gain a more complete understanding of biodiversity change - e.g., what mechanisms drive response in different biodiversity metrics, how are metrics interrelated, and what magnitude of response should be expected? I discuss using time-series data from a long-term ecological experiment in southeastern Arizona and from the global-span BioTIME database to assess how different aspects of biodiversity change through time (species composition and abundance, species richness, evenness, SAD, SAR, and STR), and what processes could be driving that change. I argue that macroecological approaches to understanding diversity change should include multiple measures of biodiversity that include species- and community-level responses and that incorporating experimental data may help macroecology make the shift from identifying static patterns to understanding the processes that lead to pattern stability or variation through time.

S2-7
Can experiments inform macroecology? Returning to the definition of macroecology.

Brian McGill
School of Biology and Ecology & Mitchell Center for Sustainability Solutions, University of Maine, United States

It has long been a tenet of macreocologists that our subject area is by definition too large for experiments to be feasible, leaving ecology as a primarily observational field. But recently there is a growing push to incorporate experiments in macroecology. Were the founders wrong? I examine the feasibility of incorporating experimentation by returning to the basic definitions of what is macroecology and "large scale". I identify what types of experimental macroecology are possible within current definitions and conversely what types of experiments would require a change to the definition of macroecology to include them.

S2-8
Experimental Macroecology: a framework to understand global changes

Miguel Matias
Imperial College London, Ascot, Berkshire, United Kingdom

Global environmental changes have caused major impacts on biodiversity. Predicting the consequences of such changes is compromised by major gaps in knowledge about how biological systems function and interact with physical and socioeconomic factors. One of the emergent trends to address these issues is the development of experimental studies covering broad biogeographical and environmental gradients. This research focus prompted changes in the way ecologists design, finance and execute their research to tackle global environmental issues. In this keynote, I will provide an overview of the Symposium "Experimental Macroecology" and discuss key areas that may be prioritized in future studies. The integration of ambitious experimental initiatives together with macroecological approaches will be key to enabling us to predict responses to global change, thus improving our ability to predict changes in biodiversity across space and time and future implications for human welfare.

Keywords: global change, biogeography, macroecology, experiments, biodiversity

SYMPOSIUM 3: Building up biogeography - process to pattern

Organizers: Miguel Matias, Imperial College London, Miguel Araujo, CSIC
Date: January 11, 2017 1:30 pm – 5:30 pm
Location: Crowder Hall, University of Arizona

S3-1

On the Inference of Pattern and Process in Ecology

John Harte
UC Berkeley, UC Berkeley, Berkeley, California, United States

Ecosystems around the planet display pervasive patterns in the scaling of species richness with area, and in the distributions of i. abundances across space and across species, ii. metabolic rates or body sizes across individuals, iii. species richness across higher taxonomic categories, and iv. edges across nodes in trophic networks. A theory of ecology based on the maximum entropy principle, predicts the forms of these patterns. Using data from hundreds of ecosystems, the predictions have been shown to be in good agreement with the patterns observed in relatively undisturbed ecosystems. Systematic failures of the theory in ecosystems that are responding to anthropogenic stresses, or are undergoing rapid diversification or succession provide insight into the processes that govern ecosystem dynamics.

S3-2

Adding temporal dimensions to infer local processes from macroecological patterns: examples using elevational gradients, avian geographic ranges, and fossil mammals

Susanne Fritz[1], Alison Eyres[2], Shan Huang[1], Jussi Eronen[3], Catherine Graham[4], Katrin Böhning-Gaese[1]
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[4]Stony Brook University, United States

In recent years, the integration of molecular phylogenies with macroecological patterns such as large-scale variation in species richness across continents has boomed, and fans claim that the added historical or temporal information increases our understanding of underlying mechanistic processes. However, is this really the case? If biogeographic history, macroevolutionary processes or past environmental dynamics are considered in macroecological studies, they are usually reduced to a "footprint measure" that sums up accumulated change prior to today, e.g. the amount of evolutionary history represented by a phylogenetic lineage. Even with such simplified approaches, I will show how such studies can increase our understanding of local community assembly, with the example of an elevational gradient of South American birds. Going further, I argue that next-generation biogeography and macroecology should go beyond such first approximations, because recent advances would allow explicit consideration of both space and time in combined analyses. I draw on two examples to illustrate these ideas. Firstly, citizen science can provide enormous temporally explicit datasets of species' occurrences today. These offer huge opportunities in measuring seasonal or short-term temporal dynamics of species' ranges and diversity patterns, as I will show for bird assemblages in Australia. Secondly, paleontological databases are rapidly growing and nowadays reflect the deep-time history of taxa and environments well. I use the mammalian fossil record over the last 23 million years to illustrate deep-time dynamics of macroecological patterns, pointing out directions how these can or cannot provide information on local and regional processes.

S3-3

Reconcile the mechanistic view and the statistical view: A case study of diversity-range size relationship

Xiao Xiao[1], Brian McGill[2]
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The last two decades have seen an increase of macroecological and biogeographical models that are neutral or statistical in nature. While these models can often make surprisingly accurate predictions for ecological patterns with minimal inputs, they are somtimes questioned for explicitly omitting major ecological mechanisms. In this talk, I will argue that the mechanistic and the statistical views of ecological patterns are not necessarily mutually exclusive. Instead, statistical models can serve as important stepping stones, used to identify the necessary and/or sufficient conditions under which the patterns arise. I will illustrate this point using an example where we examined the relationship between spatial distribution of biodiversity and species range size. Across continents and taxonomic groups, we have found that biodiversity is almost always highly correlated with the distribution of broad-ranged species, even when the species are randomly distributed in space. On the other hand, species with small ranges are much more aggregated than statistical expectation. By implementing a statistical null model, we are able to disentangle the signal in the spatial biodiversity pattern that arises purely from the range size distribution, and refine the question that remains to be answered.

S3-4

Inferring origination, dispersal and extinction processes from the fossil record

Daniele Silvestro[1], Mathias Pires[2], Tiago Quental[2], Nicolas Salamin[3]
[1]University of Gothenburg, Sweden
[2]Universidade de São Paulo (USP)
[3]University of Lausanne

Fossil data provides the most direct evidence of the evolutionary history of organisms, documenting the temporal and spatial dimensions in which extinct and extant lineages exist. Yet, the inevitable incompleteness of paleontological record often hinders our ability to infer key evolutionary processes such as speciation, dispersal, and extinction and to understand the underlying mechanisms that drive them. We present an analytical framework to analyze fossil occurrence data while explicitly modeling the preservation processes to estimate the dynamics of geographic range evolution and extinction. In an attempt to improve our understanding of the process of range evolution, we explore models where dispersal rates respond to abiotic factors (e.g. climate change), and biotic factors (e.g. ecology of the organisms). We illustrate the analytical framework with several empirical examples from the mammalian fossil record. Our results show that origination, dispersal, and extinction rates are more variable, both through time and in space, than often assumed in macroevolutionary models, suggesting that fossil-based analyses may help constructing more realistic models in neontological analyses.

S3-5

Is behaviour too far down the rabbit hole or can we build a better rope?

Sally Keith
Center for Macroecology, Evolution & Climate, Copenhagen, Denmark

Understanding the processes that determine the distribution and diversity of species is essential to gain fundamental scientific insight and to predict the response of species to novel environments. However, it is not clear how deeply we must venture into process to achieve these aims. In 1972, MacArthur said that the “economics of species behaviour” is one of the “four essential ingredients of all interesting biogeographic patterns”, yet we rarely incorporate such ecological depth. One area where incorporating behaviour could be particularly beneficial is in understanding the role for species interactions in biogeography. Direct behavioural observations at 13 sites across the central Indo-Pacific show that trophic and competitive interactions amongst coral reef fishes are plastic through space and time. This context-dependency presents a significant challenge for linking interactions to biogeographic patterns and I suggest a more explicit focus on behaviour could offer a way forward. For instance, which cues motivate individuals and how flexible are the resulting behaviours? Using this approach, we might be able to predict how behavioural changes in different environments will affect interaction outcomes.

But as we travel further down the rabbit hole, we must ensure we can return. To build a better rope, we need to integrate behavioural, community and macro- ecology. One option is to interweave behavioural data collected across large geographical extents with process-based models. This approach could enable us to scale up from individual behavioural processes to distributional patterns and start revealing the role for species interactions in biogeography.

S3-6

The problem and promise of macro-evolution in biogeography

William Pearse
Utah State University, Utah State University, Logan, Utah, United States

The field of community phylogenetics has made great strides in linking process and pattern in the fields of biogeography and community ecology. Increasingly, studies examine the evolution of functional traits that underlie biogeographical processes. Macro-evolutionary biologists have developed sophisticated models to model such traits, but often they do not perfectly align with the kinds of cross-scale questions biogeographers want to ask. I will outline where existing approaches are well-suited for cross-scale questions, and outline some new approaches I am developing that may be of use wheen they are not.

S3-7

Connecting pattern and process for deep time evolution

Luke Harmon
University of Idaho, Moscow, Idaho, United States

Comparative methods, which use the structure of phylogenetic trees to learn about evolution over deep time, have advanced rapidly over the past decades. A suite of new methods and software can now be applied to a wide range of questions about speciation, trait evolution, biogeography, and many other topics. At the same time, the connection between broad-scale patterns and actual microevolutionary process often remains murky. In this talk, I will review approaches to connect pattern and process for the evolution of species' traits. I will then suggest how these tools might be usefully applied to better connect short-term processes among populations to long-term patterns of range evolution.

S3-8

Quantum biogeography: making use of unpredictability in species distributions

A. Marcia Barbosa[1], Joseph Bull[2], Raimundo Real[3]

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[2]University of Copenhagen, Denmark
[3]Universidad de Málaga

Species' geographical distributions are not static: at a larger or smaller scale, at a quicker or slower pace, individuals are in constant movement, and maps cannot accurately illustrate all of the places where a species does or does not occur. So, complete information about a species distribution concerns not only where individuals occur, but also of how likely they are to occur there. As such, we propose establishing an analogy between the distribution of species and that of quantum particles, whose exact locations are only known at the moments when they are observed, and whose true distribution is represented by a wavefunction that summarizes the probability of their location in space. Assuming and incorporating this uncertainty, which is inherent to species distributions, into a favorability function analogous to the wavefunction, may allow significant improvements in macroecology and biogeography. By providing a worked example with practical applications, we show that applying concepts from quantum physics may improve understanding and prediction of species distributions, and thus contribute to a deeper knowledge and better management and conservation of biodiversity. We propose that considerable theoretical advances could eventually be gained through interdisciplinary collaboration between biogeographers and quantum physicists.

CONTRIBUTED TALK SESSIONS

Concurrent Session 1: Biogeography of the Anthropocene (CS1)

Session Chair: Adam Algar
Date: January 10, 2017 1:30 pm – 3:30 pm
Location: Canyon ABC room, Marriott Hotel

CS1-1 Changing climates, extirpations, and niche models

Jenny McGuire[1], Edward Davis[2], Michelle Koo[3]
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[2]University of Oregon
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Studies have questioned the ability of ecological niche models (ENMs) to transfer knowledge about species distributions from one climate regime to another. This problem is important as the world struggles to predict biological responses to ongoing anthropogenic climate change. ENMs could be used to predict future ranges if results are transferable. We demonstrate that ENMs trained using modern climate data do not perform well when hindcasting Last Glacial Maximum (LGM, ~21 ka) fossil distributions of 40 extant species of mammals. Using Huberty's one-tailed z-test, we find that only 13% of species have sensitivity greater than 0.6, meaning that hindcast distributions predict more than 60% fossil localities containing specimens of that species. In the end, the fossil specimens of half the species modeled fall nearly entirely outside of the hindcast range, suggesting a strong mismatch between their LGM and modern environmental occupation. We further find that those species whose niches are strongly controlled by precipitation are those for which the models often do not perform as well. However, this is not necessary because paleoclimate predictions are inaccurate for precipitation. In examining *Microtus californicus*, the California vole, we find independent evidence that this species has lost precipitation-linked variation from the LGM until today. Since we are in a time where extirpations are the norm, these resulting niche constrictions may mean that we frequently overpredict distributions as we project them forward in time.

CS1-2

Cold blood in a hot world: remote sensing improves predictions of ectotherm body temperature across the world's major biomes

Adam Algar[1], Kate Morley[1], Doreen Boyd[2]
[1]University of Nottingham
[2]University of Nottingham, United Kingdom

The availability of shade is crucial for ectotherms in hot environments because it reduces incident solar radiation, allowing animals to thermoregulate to cooler body temperatures. However, current models to predict body temperature must assume a fixed shade level. We propose a solution to this problem that uses remotely sensed measures of canopy structure as a proxy for shade availability. We test whether incorporating shade improves predictions of lizard body temperatures across the globe and whether shade's importance varies across the world's major biomes. We find correlations between body temperature and remotely sensed measures of canopy structure consistent with shade effects in closed forests, but not in more open habitats. While these correlations are suggestive, it is possible that the canopy–body temperature relationship is not actually due to shade effects but rather to an unknown covariate. To test this more rigorously, we used nocturnal species as a natural experiment. If canopy structure affects body temperature via shade, then we should observe no correlation between canopy structure and body temperature for nocturnal species. As predicted, we found no such correlation, suggesting a causal relationship between canopy structure, shade and ectotherm body temperature. These results illustrate the potential of high-resolution remote sensing imagery to improve models of how ectotherms will respond to global change, highlight the thermal danger of canopy loss, and demonstrate a globally detectable effect of shade on ectotherm body temperature in the world's forests.

CS1-3

Predicting extinction risk based on available habitat amount

Ricardo Dobrovolski[1], Di Marco Moreno[2], Rafael Loyola[3], Marcel Cardillo[4], José Alexandre Diniz-Filho[5]
[1]Universidade Federal da Bahia, Salvador, Bahia, Brazil
[2]ARC Centre of Excellence for Environmental Decisions, The University of Queensland, Brisbane, Australia
[3,5]Universidade Federal de Goiás, Brazil
[4]The Australian National University, Canberra, Australia

Habitat destruction is the cause of most threatened species status. The effect of this process of species conservation also depends on species functional traits that determines intrinsic extinction risk. Here we combined the habitat amount on species geographical range with an estimated intrinsic extinction risk value to predict data deficient and future terrestrial mammal species' extinction risk. Our model had a high performance with AUC = 0.934. Species risk showed a threshold response to habitat destruction. The higher the intrinsic extinction risk, the more habitat amount species need for not being threatened to extinction. Species that are tolerant to anthropic land are more resistant to extinction. We found that 51% of data deficient species are likely to be threatened. In the future, other 21 species are expected to be threatened due to habitat destruction. The effect of habitat destruction on biodiversity is higher than the observed and will remain extirpating biodiversity from Earth considering current trends of habitat destruction.

CS1-4

A new framework for investigating biotic homogenization and exploring future trajectories: oceanic island plant and bird assemblages as a case study

Kyle Rosenblad[5], Dov Sax[1]
[1]Brown University, Providence, RI, United States

Biotic homogenization research has focused primarily on characterizing changes between past and present. In order to understand the future of homogenization, we must contextualize the processes driving these changes. Here, we examine changes in taxonomic similarity among oceanic island plant and bird assemblages. We use these empirical cases to unpack dynamic properties of biotic homogenization, thereby elucidating two important factors that have received little attention: 1) initial similarity and 2) the influence of six classes of introduction and extinction events. We use Jaccard's Index to explore how these factors have driven change in similarity between human settlement and the present. Specifically, we develop formulas for changes in similarity resulting from each type of introduction and extinction, so that the effect of each event is formulated in terms of initial similarity. We then apply these insights to project how similarity levels would change in the future if the present patterns of introductions and extinctions continue. We show that the six event types, along with initial similarity, can exhibit dramatically different behavior in different systems, leading to widely variable influences on similarity. Plant and bird biotas have homogenized only slightly to date, but their trajectories are highly divergent. If current introduction and extinction patterns continue, then plant assemblages would show little additional change, whereas bird assemblages would homogenize much further. Our results suggest that moderate changes in similarity observed to date mask potential for drastic future changes, and that interactions among initial similarity and differential introduction and extinction regimes drive these dynamics.

CS1-5

Toward a Macroecology of Urban Trees

Darrel Jenerette[1], Julie Ripplinger[2], Peter Ibsen[2]
[1,2]University of California Riverside, Riverside, California, United States

The biogeography of cities and plants within cities has been challenging to place within ecological theory as biophysical and human drivers influence urban plant distributions. To address this need, we describe a new urban macroecological hypothesis of climate tolerances and trait choices. Here, strong filtering associated with low winter temperatures restricts urban biodiversity while weak filtering associated with warmer temperatures and irrigation allows dispersal of species from a global source pool, thereby increasing urban biodiversity and potentially ecosystem services. A test of this hypothesis using tree surveys from twenty cities in the United States and Canada show strong winter-temperature correlations with urban tree community composition. In colder cities, the

community is restricted to species from the local biome while in warmer cities the community reflects a globally distributed source pool. Further, the presence of showy flowers, an important aesthetic ecosystem service, is also correlated with the winter temperature gradient. Ongoing work is looking to evaluate how urban tree functional trait distributions vary among cities in response to climate and cultural differences in trees at a continental scale. At a regional scale we are also using the dramatic climate gradient within urbanized southern California to better identify mechanisms that restrict influence trait variability for a subset of species representing a broad spectrum of biomes and biogeographic provinces. Our results look toward a more comprehensive macroecology that considers the role of humans and biology in shaping the plant communities of rapidly expanding urban ecosystems.

CS1-6

Here, there, and (almost) everywhere: identifying traits of wide-ranging species

Meghan Balk[1], Rosemary Elliott-Smith[2], Felisa Smith[3], John Grady[4], Larisa Harding[5], K. Sara Lyons[6], Melissa Pardi[7], Rasmus Pedersen[8], Katlin Schroeder[3], Catalina Tomé[3], Marie Westover[3]
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[4]Department of Biology, Bryn Mawr College
[5]Arizona Fish & Fame Department
[6]Department of Paleobiology, Smithsonian Institution
[7]Department of Natural Resources and the Environment, University of New Hampshire
[8]Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Denmark

Continents are fundamental biogeographic units that constrain the distribution of terrestrial species and their potential for adaptive radiation. For this reason, species occupying multiple continents shed light on the traits necessary to disperse widely and impact new communities. Here, we seek to understand the traits behind multi-continent occupation by quantifying ranges and functional traits in terrestrial mammals. We use data on body mass, trophic level, and habitat for ~3,000 mammalian species at the continental scale. We exclude introduced species, but include species that were extant pre-human arrival (up to 100,000 years before present). We quantify the characteristics of mammalian species that occur on two, three, and four continents. We find that one species, the lion, occurred on four continents, five species (brown bear, red fox, red deer, gray wolf, and least weasel) occur on three continents, and 225 species, primarily bats, occur on two continents. Body size, diet and taxonomic affiliation of species occurring on three or more continents differ significantly from null models. Importantly, this hints that certain qualities facilitate these species to acquire large geographic distributions.

CS1-7

Upslope agricultural expansion caused mammal range contractions in China over the past two millennia

Shuqing Teng[1], Chi Xu[2], Jens Christian Svenning[3]
[1,3]Aarhus University, Denmark
[2]Nanjing University, China

Extinctions of large mammals characterize the Late Quaternary, spanning from the Late Pleistocene to the Anthropocene. As their causes, apart from climate change, researchers have proposed anthropogenic factors with focus on roles of early foraging behaviors (e.g. hunting and using fire) and industrial development in mammal range contractions and final extinctions. However, much less is known about how such events have unfolded in agricultural societies that lie evolutionarily between Paleolithic ones and modern ones. To fill the gap, using spatiotemporal data derived from historical records in ancient China over the past two millennia, we analyzed the patterns of mammal range contractions and their associations with historical climate change and agricultural population dynamics. We found that it was the long-term upslope spread of agricultural population that consistently contracted the mammal distributions in China during the study period, while periodic warming and cooling may have contributed to temporary range fluctuations. Our study provides direct evidence that biotic interactions can overshadow climate in terms of driving species distributions even at large spatiotemporal scales and suggests that humans may have long been reshaping species distributions and the biosphere progressively in times of agriculture. Better understanding of the processes that have led to current species distribution patterns has great implications for future conservation strategies in the Anthropocene.

CS1-8

Landscape genomic analyses reveal rapid adaptation to climate in introduced biocontrol weevils despite multiple founder events

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The distribution of many species are expected to shift markedly under future climate change scenarios, yet the capacity for populations to adapt to new climates is poorly understood. Introduced species offer excellent opportunities to explore the nature and sources of genetic variation that shape the ability of species to persist under new climates. The hairy weevil (*Eustenopus villosus*), a biocontrol insect for invasive yellow starthistle (*Centaurea solstitialis*), was introduced to the western US by a small number of founders from a single origin in its native range. Although populations successfully established, they have failed to control yellow starthistle, potentially because they lack genetic variation for adaptation to new climates. We identified and surveyed several thousand single nucleotide polymorphisms (SNPs) in hairy weevils using restriction site associated sequencing (RADseq). We compared genomic variation between native and introduced populations, and identified candidate loci underlying local adaptation to climate using regression-based models. We explored the putative function of loci associated with climate, and identified whether climatic adaptation in native and introduced populations has occurred at the same sets of marker loci. Our analyses revealed several candidate SNPs associated with precipitation and temperature in introduced weevils. Introduced populations have similar levels of genetic variation as their native origin, which implies a lack of genetic bottlenecks despite serial founder events. The results support rapid adaptation (less than 40 generations) to climate in small founding populations.

Concurrent Session 2: Historical and Paleo-biogeography(CS2)

Session Chair: Michael Andersen
Date: January 10, 2017 1:30 pm – 3:30 pm
Location: Madera room, Marriott Hotel

CS2-1

Historical biogeography of the plant clade Viburnum, and its bearing on diversification and biome shifting during the Cenozoic

Michael Donoghue[1], Wendy Clement[2], Deren Eaton[1], Erika Edwards[3], Brian Park[1], Elizabeth Spriggs[1], Michael Landis[1]
[1]Yale University
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[3]Brown University

We use a comprehensive and well-supported phylogeny of *Viburnum* (Adoxaceae) to infer the movement of this woody plant lineage around the Northern Hemisphere from the Paleocene to the present. The group appears to have diversified originally in the Eocene in eastern Asia, with multiple shifts inferred within Asia between tropical, warm temperate (lucidophyllous), and cold temperate forests. More recently, and at several different times, there have been four disjunctions between temperate Asia and Europe, and six disjunctions between temperate Asia and North America. One of the North American clades subsequently radiated into the mountains of the Neotropics, ultimately through the Andes. We are especially interested in determining the area and environment in which *Viburnum* originated, and in testing the “dying embers” hypothesis that envisions elevated extinction rates in potentially ancestral tropical forests. For such tests we are developing models that integrate both differential diversification rates and evidence on relationships between climate and leaf form. These studies bear directly on our understanding of the assembly of the forest biomes of the Northern Hemisphere and on the development of new methods in historical biogeography.

CS2-2

The asymmetry in the Great American Biotic Interchange in mammals is consistent with differential susceptibility to mammalian predation

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Globalization is driving increased rates of exchanges between formerly isolated biota, but our understanding of the mechanisms and long-term consequences of such exchanges remains poor. The Great American Biotic Interchange (GABI) (starting approximately 3.5 million years ago) acts as an invaluable natural experiment. Importantly, GABI has been asymmetric for mammals, with half of South American non-flying mammals of northern origin, but very few North American mammals of southern origin. The classical explanation has been differential competitive ability due to the island-like nature of South America. This could seem plausible for mammals, but fails to explain the more balanced exchange in other groups. Using PGLS regressions and phylogenetic binomial regressions of the colonization ability of either each family or each subfamily, we show that the pattern is better explained by predation. South America lacked efficient mammalian predators prior to GABI, and southern lineages that colonized North America were generally larger and therefore relatively unsusceptible to mammalian predation than the lineages which failed to colonize North America. The importance of predation is also supported by the pattern in the Late Pleistocene megafauna extinction, where South American immigrants in North America, evolved under limited predation, had a disproportionally higher extinction rate than non-immigrant taxa after the arrival of human hunters to North America. Hereby, our analysis shows that predation can be a powerful driver of long-term dynamics of biotic interchange.

CS2-3

Global signals of extinction and adaptation in a tropical keystone plant family

Renske Onstein[1], Søren Faurby[2], William Baker[3], Thomas Couvreur[4], Jens Christian Svenning[5], Daniel Kissling[6]
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[3]Royal Botanic Gardens Kew, Richmond, Kew, Surrey, United Kingdom
[4]Institut de Recherche pour le Développement, France
[5]Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Denmark
[6]University of Amsterdam, Netherlands

Frugivory (fruit-eating and subsequent seed dispersal by vertebrates) is a key plant-animal interaction in tropical rainforests. However, the consequences of environmental changes such as habitat fragmentation, climate change and sea level rise on this mutualism at large spatial and temporal scales remain largely unexplored. Here, we combine an all-evidence species-level phylogeny for all palms (Arecaceae, ca. 2600 species), global distribution data and a novel fruit size dataset for 70% of the species to study the consequences of seed dispersal by large-bodied frugivores (> 44 kg) on palm diversification. These large-bodied frugivores disperse the largest seeds and contribute disproportionally to long-distance dispersal events. We show that palms (a keystone resource for frugivores) with megafaunal fruits (> 4 cm) have lower speciation rates than smaller-fruited palms, possibly due to frequent long-distance dispersal events that increase gene flow among populations and thereby limit allopatric speciation. Furthermore, a new time-window analysis demonstrates that, since the onset of the Quaternary (2.6 Mya), extinction rates of New World palm lineages have increased and Old World palms show increasing transition rates (evolving smaller fruits from megafaunal fruits). One possibility is that high New World extinction rates were triggered by (local) megafauna extinction due to climate-driven habitat fragmentation, whereas increased Old World transition rates could reflect adaptation to dispersal by smaller-bodied, volant frugivores against a background of sea level fluctuations in the island-dominated environment of Southeast Asia. Our results suggest that past environmental change may have left global signals in present-day distributions of palms and their functional traits.

CS2-4

Tectonic collision and uplift of Wallacea triggered the global songbird radiation

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[2]Louisiana State University
[3]American Museum of Natural History
[4]University of Kansas

Songbirds (oscine passerines) are the most species rich and cosmopolitan bird group, comprising almost half of global avian diversity. Songbirds originated in Australia, but the evolutionary trajectory from a single species in an isolated continent to worldwide proliferation is poorly understood. Here, we combine the first comprehensive genome-scale DNA sequence data set for songbirds, fossil-based time calibrations, and geologically informed biogeographic reconstructions to provide the first well-supported evolutionary hypothesis for the group. We show that songbird diversification began in the Oligocene, but accelerated in the early Miocene, at approximately half the age of most previous estimates. This burst of diversification occurred coincident with extensive island formation in Wallacea, which provided the first dispersal corridor out of Australia, and resulted in independent waves of songbird expansion through Asia to the rest of the globe. One such wave was the >800-species corvidan radiation, comprising such groups as crows and allies, monarch-flycatchers, and birds-of-paradise. We explore species-level diversification patterns of corvidans by combining a backbone phylogeny based on genome-scale data with ~675 species, representing all corvidans with previously published sequence data. Our results reconcile songbird evolution with Earth history and link a major radiation of terrestrial biodiversity to early diversification within an isolated Australian continent.

CS2-5

Biogeography of the high-spired planorbids (Gastropoda: Planorbidae) east of Wallace's Line: a journey out of Australia

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The biodiversity hotspot Wallacea is a geologically complex region resulting of the collision between the Australian and Asian plates. Since Wallace's pioneer work, this archipelago has become a model region for studying historical biogeography. We examined colonization routes from the enclosing areas into Wallacea and tested biogeographical hypotheses for three freshwater genera of high-spired planorbid snails with poor dispersing capabilities. We performed a Bayesian phylogenetic analysis using nuclear and mitochondrial genes based on an extensive sampling across Australia and the Indo-Australian Archipelago. This time-calibrated tree was further used to infer ancestral geographic areas and to determine the spatio-temporal evolution of the group. Given the topology, inferred ancestral areas, estimated ages and the archipelago's tectonic history, the group potentially originated in Australia. We discuss different biogeographical scenarios for this out-of-Australia-into-Wallacea colonization. The results of this study provide new insights into the origin and colonization patterns of the biodiversity in this region.

CS2-6

Potential drivers of anti-tropical distributions across the fish tree of life

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Anti-tropical species are distributed north and south, but not within, the tropics. Several mechanisms have been suggested, but Plio-Pleistocene genetic divergence times for many anti-tropical taxa reduces the potential explanations to two main hypotheses: dispersal across the tropics during cool glacial periods or modern biotic exclusion. These hypotheses predict different patterns of habitat suitability in the tropics: the former predicts modern unsuitable tropical habitat; the latter predicts suitability. We test these hypotheses using ENMs of 32 fish species from across the fish tree of life. Maxent models of northern and southern populations tested for current tropical

suitability. These predictions, and models trained with full species distributions, were projected onto LGM conditions to investigate potential tropical corridors for glacial dispersal. Results support both mechanisms affecting anti-tropical distributions in different species. Phylogenetic clustering was not observed regardless of mechanism, thus neither mechanism may be phylogenetically conserved. Many species show niche divergence between north and south populations; this may reflect post-LGM adaptation and/or insipient speciation. Our study highlights the species-specific nature of biogeographic patterns responding to abiotic and biotic change since the LGM.

CS2-7

Holocene variability of an Amazonian hyperdominant

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The long-term stability of Amazonian plant communities is unknown. The most abundant species, hyperdominants, may have risen to prominence at the Pleistocene-Holocene transition, following subsequent changes in moisture, or as a result of human activity later in the Holocene. Here, we examined the spatio-temporal patterns of one of the most common Amazonian hyperdominant taxa, *Iriartea deltoidea*. *Iriartea* is a monospecific genus with diagnostic pollen; it is also considered a 'useful' plant, and its abundance could have been enriched by human action. The history of *Iriartea* was investigated using fossil pollen data from 13 lakes. *Iriartea* pollen increased in abundance in the last 3000 years, but did not show a consistent relationship with human activity. Instead, the abundance of *Iriartea* pollen was related to increasing precipitation. This member of the hyperdominant category of Amazonian trees has only recently acquired this status. The suggestion that the hyperdominants in modern Amazonian forests are a legacy of pre-Columbian people is unsupported. This finding is consistent with the suggestion that communities in complex systems are ephemeral and that the even the most abundant of hyperdominants can change over a few tens of generations. The relative abundance of tree species, even in relatively stable systems such as those of Amazonian floodplains, changes on ecological not evolutionary timescales.

CS2-8

Megafaunal ecology and extinction in the Andes: the uncertain role of humans

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>50 genera of megafauna went extinct in South America in the Late Pleistocene. Fossil pollen, *Sporormiella* spore, diatom and charcoal data from five sites in the Andes provide insights on megafaunal ecology, their demise, and the arrival of humans. Megafaunal populations inferred from the abundance of the dung fungus, *Sporormiella*, fluctuated wildly during the last interglacial c. 130-115,000 years ago. Megafaunal peak presence aligned with grassland occurrence, but populations were not maintained during phases of woodland expansion or drought. As glacial conditions gripped the high Andes the megafauna left the Altiplano and were forced down onto the steep slopes and much smaller area (at equivalent temperature) on the Andean flank. By the last glacial maximum (26,000-18,000 years ago: not necessarily the coldest time in the high Andes), *Sporormiella* abundance indicated that megafauna were present in low productivity, superpuna grasslands. The population collapse leading to extinction was temporally and spatially heterogeneous, beginning with a marked decline c. 20,000 years ago, followed by a temporary recovery. The first evidence of humans at c. 16,000 years ago (3200 years earlier than known from the archaeological record) coincided with the functional extinction of megafauna at c. 15,800 years ago at Lake Pacucha. But extinctions also occurred at sites where there was no evidence of humans. Functional extinctions occurred later in upper Andean forest settings (c. 12,000 years ago) than in the high grasslands. Final extinction of megafauna at c. 10,000-9000 years ago suggests that people co-existed with some species for at least 6000 years.

Concurrent Session 3: Gradients, range-limits, and beta-diversity (CS3)

Session Chair: Sabine Rumpf
Date: January 10, 2017 1:30 pm – 3:30 pm
Location: Pima room, Marriott Hotel

CS3-1 Disentangling Geometric and Ecological Drivers of Biodiversity Patterns

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Biodiversity patterns are usually supposed to be molded by underlying ecological rules. However, biodiversity patterns are mostly approached by graphs and maps, thus making them subjects to geometric principles. Several cases, where underlying ecological rules were obscured by geometric principles, have been demonstrated. Of these we will report: (i) Fractal species spatial ranges (i.e. ranges aggregated at various scales) have been shown to produce convex log-transformed SARs, which contradicts to the observations. It has been demonstrated that the Finite Area Effect eliminates the effect of aggregation on SAR and modifies the resulting SAR to become concave as observed. (ii) Maximum Entropy predicts that the mean abundance across species determines the SAR, irrespective of focal taxon. Splitting of the taxon contradicts such universality and shows that the theory is taxon specific. (iii) Rescaling was reported to cause SARs to collapse roughly onto a universal curve. The collapse has been questioned by subsequent research. We explain how geometric effects prevent the SAR from collapsing, even when a collapse is expected from the ecological mechanisms considered. The geometric effects cannot be controlled by means of statistics, but rather by mathematical analysis. We suggest that controlling for geometric effects helps our understanding of the ecology behind biodiversity patterns. (Šizling et al. 2016. *Ecography*, doi: 10.1111/ecog.02181; Lazarina et al. 2013. *Ecography*, 36; Storch et al. 2012. *Nature* 488; Šizling et al. 2011. *AmNat*, 175; Harte et al. 2009. *ELLE* 12; Šizling & Storch. 2004. *ELLE*, 7; Lennon et al. 2002. *Oikos*, 97.)

CS3-2

Linking species-area relationships to common beta-diversity indices: When is beta-diversity scale invariant?

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Whether *beta*-diversity is independent of scale, meaning irrespective of the size of the areas surveyed, is often discussed. Here we link the common indices of *beta*-diversity to the species-area relationship (SAR), in order to examine under which conditions *beta*-diversity is scale invariant. Both the species-area relationship (SAR) and *beta*-diversity indices for presence-absence data are tools that simplify the complexity of nature into something interpretable. We found that familiar beta-diversity indices such as the Whittaker-beta, Jaccard index, and Sørensen index are all linked to the SAR, though directly comparable only given certain assumptions. These assumptions also reveal why *beta*- diversity, for example Whittaker-*beta*, is not inherently scale dependent. The power-law SAR can be used as a null model, constituting the circumstances under which beta-diversity may be scale independent. We follow a simple notation for re-expressing the indices, and we apply this also to the z-value of the power SAR ($S=cA^z$) into a common notation. We find that given simple assumptions, the z-value of the power SAR equals $\log_k$ of Whittaker-*beta*, where k is the size area of *beta*-diversity over the size of the area of *beta* ($k=A_?/A_?$). This means that if we assume species diversity in space to cause power SARs, Whittaker-*beta* is scale dependent. We also discuss the assumptions under which the Jaccard index and Sørensen index can be related to Whittaker-*beta* and the power SAR.

CS3-3

Dispersal Limitation, demographic performance, and predicting geographic range limits in the perennial forb, Astragalus utahensis

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An overarching goal of biogeography and ecology is to understand the determinants of species' distributions and develop the ability to predict where distributional boundaries will occur with environmental change. Hypotheses postulate that range boundaries result from either an inability to disperse into suitable habitat beyond the current boundary or a deterioration of environmental suitability at and beyond the range edge. Few studies have simultaneously tested performance across a species' distribution and beyond its boundary in order to assess these hypotheses. Using the forb *Astragalus utahensis,* we quantified aspects of abundance and demographic performance in extant populations across the distribution and beyond the northern range edge using transplant populations. We assessed the ability of an ecological niche model (ENM) to predict variation in abundance and demographic performance among populations. Plant density decreased from the center of the distribution to both latitudinal range edges, as did survival from the center of the distribution to its northern edge. These declines were significantly correlated to projected suitability from the ENM. Transplants survived and reproduced at levels similar to plants in northern populations, indicating an additional role for dispersal limitation in constraining the distribution. Our study suggests that long-standing hypotheses explaining range edges as either the product of dispersal limitation or declining environmental suitability may represent a false dichotomy and that both likely constrain the distribution of *A. utahensis*. It also suggests that ENM techniques may be predictive of both species presence and performance even if the distribution is fundamentally dispersal limited.

CS3-4

Lower elevational range limits respond more sensitive to climate warming than upper ones

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[2]University of Vienna, Vienna, Austria
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Recent publications report rapid distribution shifts of species along elevational and latitudinal gradients as a major response to climate change. However, analyses of elevational shifts have so far mainly focused on upper range limits or on species' elevational optima, while empirical evidence of lower range limit changes still remains scarce although they co-determine species' extinction risk. We present a global multi-species comparison of elevational range dynamics at both upper and lower range limits during the last century. Our results show that lower limits have moved uphill almost twice as fast as upper limits. Moreover, dynamics of species at their lower limits were not only closer correlated to climate warming but also followed these changes with less delay. The intensity of land use change, as an alternative explanation of range limit shifts, was not correlated to the dynamics at either of the elevational limits. We conclude that, contrary to common expectations, lower range limits have been more responsive to climatic trends than upper ones. This asymmetry of range limit shifts might accelerate population decline and eventual extinction of mountain biota in the future.

CS3-5 Global drivers of terrestrial Beta-diversity

Marc Macias Fauria[2], Alistair Seddon[1], David Benz[2], Peter Long[3], Kathy Willis[2]
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We present a global terrestrial *ß-diversity* map at high resolution for 5 large taxonomic groups (taxa): plants, mammals, amphibians, reptiles, and birds. Environmental covariates (climate & substrate-related) are used to predict species dissimilarity across space using the Generalised Dissimilarity Modelling approach. Species occurrences were obtained from the Global Biodiversity Information Facility (GBIF). The relative role of each environmental driver is presented for each taxon. We discuss the shapes of the curves that relate species dissimilarity along

environmental gradients for the different taxa and biogeographic regions, with emphasis on potential mechanisms behind the observed patterns. We further split GBIF and environmental covariate data into recent past (pre-2000CE) and present (post-2000CE) periods and discuss changes in *ß-diversity* and its drivers. Special attention is given to the effect of human land use on Earth's biodiversity using a spatially explicit human footprint index. Finally, the observed relationships are used to discuss potential future *ß-diversity* trajectories under different scenarios for the late 21st century.

CS3-6

New insights into pathogeography: revealing regions of infectious disease using cluster analysis

Sonia Tiedt[1], Kris Murray[1]
[1]Imperial College London

Infectious diseases remain a major public health priority. They threaten individual well-being and global health, stifle development, endanger biodiversity, and, over the last century, increasingly appear in places far removed from their origins. Understanding what factors drive emergence and shape the global distribution of infectious diseases has thus become of central importance to the global health community. However, our understanding of the spatial and temporal patterns of pathogens, and how they might respond to environmental change, is still rudimentary; the distributions of the vast majority of infectious diseases remain poorly characterized. Yet, it is these poorly understood and unknown agents that are likely to underlie many future disease risks. In light of this, gaining a better understanding of the broad-scale co-occurrence patterns of human infectious diseases and their underlying drivers could offer important prior insights for disease management. Here, we utilize a hierarchical clustering approach and a set of statistical tests to show that human infectious diseases – particularly vector-borne, zoonotic and parasitic diseases – exhibit distinct spatial groupings at a global scale reminiscent of Wallacean zoogeographic patterns. We also assess how different factors contribute to give rise to such groupings. Lastly, we discuss how we could leverage our findings to optimize disease surveillance, guide pathogen discovery or predict what impact global change scenarios might have on future disease assemblage patterns.

CS3-7

The latitudinal variation of mammal and bird distribution range shapes

Adrián Castro-Insua[1], Carola Gómez-Rodríguez[1], Jens Christian Svenning[2], Andrés Baselga[2]
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Many studies have addressed geographical variation in species range sizes but there are relatively few studies assessing species ranges shapes (notably Brown and Maurer 1989, Rosenfield 2002, Pigot et al. 2010, Baselga et al. 2012). We quantified the range shape of the breeding distribution ranges of 10057 species of birds and 5284 species of terrestrial mammals worldwide to assess (1) whether species at higher latitudes or with larger ranges have ranges more elongated in an east–west direction (indicating that higher latitude and widespread species are more determined by climatic variation), and (2) whether the poleward limits of the distribution ranges are shorter (indicating that they are more determined by the climatic variation) compared to equatorward limits, where biotic interactions, dispersal and other stochastic processes might be more relevant processes. Most mammal (83.4%) and bird species (88.7%) have distribution ranges with mean latitude below 30° latitude and do not show a systematic deviation towards east-west elongated distribution ranges. In turn, those species able to live at higher latitudes and/or with larger ranges tend to have ranges that are elongated in an east–west direction. This suggests that distributions are more influenced by climatic conditions at high latitudes and in widespread species. Furthermore, we found that equatorward ranges' semiperimeters are longer than the poleward ones, suggesting that low-latitude limits of distribution ranges are more stochastic than high-latitude ones.

CS3-8

Niche conservatism among disjunct woody-plant genera: an intercontinental comparison along a temperature gradient

Ole Vetaas[1], John-Arvid Grytnes[2], Brad Hawkins[3]
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Phylogenetic niche conservatism predicts that closely related species will have a similar distribution along principal environmental gradients. We test this prediction by comparing the central tendency with respect to temperature for common woody genera in Peru (Andes) and Nepal (Himalayas), which do not share species but have common ancestors. Elevation and temperature range data were compiled for all species belonging to eight disjunct woody plant genera with a common ancestor. Central tendency of congeneric species along the temperature gradient were established by weighted average temperature (weighted by number of species), and reciprocal averaging. Most genera have a bell-shaped or curvilinear pattern with the maximum number of congeneric species in the centre of the temperature range of the genus. The order of central tendency along the temperature gradient in each region is highly correlated ($r>0.88$), i.e. the order in Nepal can predict the order in Peru ($p<0.05$ permutation test). This consistency along the temperature gradient in different continents and hemispheres must be related to phylogenetically conserved temperature tolerances over time and space.

Concurrent Session 4: Functional Biogeography (CS4)

Session Chair: Trevor Fristoe
Date: January 10, 2017 1:30 pm – 3:30 pm
Location: Sabino room, Marriott Hotel

CS4-1

Spatial and evolutionary parallelism between shade and drought tolerance explains the distributions of conifers in the conterminous United States

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Gymnosperms do not follow a latitudinal diversity gradient across the Northern Hemisphere but are influenced by geography at continental scales. Tolerance to physiological aridity is thought to be the main driver of this distribution, yet through evolutionary time conifers have faced frost, shade and fire conditions. We tested four predictions to evaluate how environmental stressors and evolutionary patterns of traits influence conifer distributions: (1) aridity-related variables are most important in explaining geographical patterns of traits; (2) traits responsible for survival in stressful conditions have evolved under niche conservatism; (3) phylogenetic correlations among traits are widespread; (4) there are parallelisms between spatial trait associations and correlated trait evolution. We combined conifer occurrences with 10 traits related to drought, freezing, shade and fire. The spatial distribution of traits was mapped and the relationship between environmental and geographical patterns of traits explored. Niche conservatism was assessed comparing patterns of trait evolution. We computed geographical and phylogenetic correlations among traits to determine the correspondence between spatial and evolutionary trade-offs. Maximum temperature and precipitation best described the geographical distributions of traits. Most traits contained a phylogenetic signal consistent with niche conservatism: major exceptions being fire-related traits and frost tolerance. Drought and shade tolerances showed one of the strongest negative phylogenetic correlations, which was mirrored at the biogeographical scale. Unlike angiosperms, cold does not seem to have been a major driver in the evolutionary history of temperate conifers. A strong shade-drought tolerance trade-off is the simplest explanation for understanding the distribution of conifers in North America.

CS4-2
Scale-dependence of temporal changes in different biodiversity facets

Marta Jarzyna[1], Walter Jetz[1]
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Biodiversity patterns and the mechanisms driving these patterns are inherently scale-dependent. Most research explores scaling patterns in a spatial context, even though the examination of scale-dependence concurrently in space and time has the potential to resolve inconsistencies in biodiversity patterns, identify the scales relevant to different ecological processes, and identify the environmental drivers of biodiversity that are missed with a singular spatial or temporal approach. Employing a novel framework for addressing detectability, we investigated the scale-dependence of a near half century of changes in taxonomic (TD) and functional (FD) diversity of avian communities across the continental US. Changes in TD and FD were assessed using a suite of metrics, including absolute and relative change, dissimilarity, turnover, and nestedness. For both TD and FD, absolute change increased, while dissimilarity and turnover declined with spatial resolution; relative change and nestedness showed a humped relationship and peaked at medium spatial grains. Contribution of turnover and nestedness to dissimilarity showed opposite scale-dependence patterns. Together, these results suggest that processes contributing to changes in biodiversity also show strong scale-dependence, with environmental nestedness dominating at coarser- and environmental sorting dominating at finer spatial grains. Our findings highlight the potential of combining temporal data with novel statistical models to enable a more integrative monitoring of change in the multiple facets of biodiversity and across a range of spatial scales.

CS4-3
The biogeography of novelty: Plant traits link pattern and processes over 21,000 years of global change

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Novel communities emerge as a result of individualistic shifts in species' ranges and abundances in response to changing climates, biotic interactions, disturbance regimes, or anthropogenic activity. Such assemblages pose a challenge in part because it is unclear to what extent novel associations will maintain ecosystem function relative to a baseline of interest. The nature of such communities makes predictions difficult when relying on contemporary observations alone, but the well-documented no-analog plant associations in North American paleorecords provide a promising model system. These late-assemblages were geographically widespread, persisted for several millennia, and were composed of associations of boreal and temperate taxa which are likely to coexist in the future. We reconstructed vegetation dissimilarity, climate dissimilarity, and community trait dissimilarity from present throughout the last 21,000 years, to test whether late-glacial no-analog plant associations occupied novel trait space from present communities. Results show the overall pattern of ecosystem function across space and time as a function of changes in vegetation and climate, and allow us to ask: were novel were novel communities also novel ecosystems? The spatiotemporal pattern of plant trait means and dissimilarity from present also shed light on the mechanisms of vegetation response to climate change, megafaunal extinction, and human activity since deglaciation.

CS4-4
Big brains stabilize populations and facilitate colonization of variable climates in birds

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[3]Washington University, St Louis

Environmental variability is thought to be a major driver in the evolution of cognition because enhanced behavioral flexibility facilitates dealing with the unexpected. Although comparative evidence supports different aspects of this hypothesis, a direct connection between cognition and the ability to survive in highly variable environments has yet to be demonstrated. Furthermore, it is unclear whether this potential mechanism has been a primary driver in brain size evolution. Here, we address these fundamental questions by exploring links between encephalization, population dynamics and environmental variability in 147 North American birds, and by evaluating support for alternative scenarios for the evolution of cognition and climactic niche in a globally distributed sample of 1288 avian species. We show that increased encephalization is indeed associated with more stable population dynamics in variable environments, supporting the idea that cognition confers survival benefits in these conditions. However, we find support for scenarios in which the evolution of increased encephalization often predated and subsequently facilitated colonization of variable habitats. We conclude that although environmental variability has the potential to drive the evolution of cognition, this mechanism is unlikely to explain major changes in brain size among birds. Besides shedding light in the longstanding debate over the benefits and consequences of cognition, these results improve our understanding of how ecological and evolutionary responses to climactic variability shape species distributions.

CS4-5

Ecophysiological basis of the body size gradients in amphibians

Sidney Gouveia[1], Isadora Correia[1]
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An explanation to broad-scale gradients of body size (BS) among ectotherms is still pending. Taking the particular case of amphibians, we propose a reformulation of the water conservation hypothesis, by building upon the species' allometry of water economy and the joint nature of osmoregulatory and thermoregulatory functions in this group. We test this model in different clades of different regions, preferred habitat types and evolutionary scales, including two species, *Dendropsophus minutus* and *Physalaemus cuvieri* with available physiological data, two genera, *Hypsiboas* and *Plethodon*, one subfamily, Phylomedusinae, and one family, Centrolenidae. We propose that, intraspecifically, the existence of a BS gradient will depend on the shape of the relationship between evaporative water loss and BS. Interspecifically, the existence of the pattern will depend on the evaporative capacity of the environment (i.e., the Potential Evapotranspiration – PET) where the clade evolved, so that only specific climatic settings will impose selective pressure on BS. As a result, only clades living in regions with dehydrating conditions and at non-aquatic habitats (ground or trees) may be prone to exhibit a BS cline with PET. Our results, from phylogenetic and non-phylogenetic regression analyses, were as predicted. Arboreal species and clades living at higher evaporative conditions exhibited a positive relationship with PET, whereas one semi-aquatic species (*P. cuvieri*) and one clade from wet regions (Centrolenidae) did not. Our reasoning provide the more comprehensive account to explain body size gradients in amphibians to date, and it also shed light on the limited scope of the phenomenon.

CS4-6

The geography of ecological niche evolution in mammals

Florent Mazel[1], Rafael O. Wüest[2], Maya Gueguen[3], Julien Renaud[4], Francesco Ficetola[3], Sebastien Lavergne[3], Wilfried Thuiller[3]
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Convergent adaptive evolution of species' ecological niches —i.e. the appearance of similar niches in independent lineages—is the result of natural selection and contrasts with neutral drift. Despite the fundamental importance of this topic, we still know little about the role of evolutionary convergence in shaping the niche structure of global biotas. Here, we map convergent evolution of ecological niches for mammal assemblages at a global scale. Using current data on geographic distributions, ecological niches and phylogenetic relationships of species and by comparing observed patterns of ecological niche beta-diversity ('functional beta diversity') to evolutionary neutral expectations, we show that convergence of ecological niches is not restricted to particular lineages but scales up to entire assemblages (i.e. whole species communities). We find region-wide biota convergence in ecological niches between regions with similar climate, and in particular between Australia and other continents. Pairs of assemblages that show ecological niche divergence often imply arctic regions where rapid evolutionary changes occurred in response to extreme climatic constrains. By integrating both macro-ecological and macro-evolutionary approaches in a single framework, our study quantifies the crucial role of evolutionary processes such as natural selection in the spatial distribution and structure of large-scale species assemblages.

CS4-7

History supplements current environment in driving functional diversity patterns

Jens Christian Svenning[1], Marco Girardello[2], Bastian Göldel[2], Daniel Kissling[3], Alejandro Ordonez[4]
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Functional diversity is a key aspect of biodiversity, determining environmental responses and ecological impact. While it is evident that species diversity is co-determined by contemporary drivers and historical dynamics, the importance of the latter for functional diversity remains little explored. Here, we synthesize new work on the relative importance of historical and contemporary drivers for functional diversity, covering continental to global scales, plants and mammals, and a range of historical drivers. We find that Quaternary-scale climate influences broad-scale patterns in assemblage trait means and that high variability and distance to stable areas is associated with reduced functional diversity, with links also to deeper-time climate. Illustrating the importance of historical trophic interactions, we find a stronger link between palm fruit size and frugivore body size when also considering late-Quaternary extinct and extirpated frugivores, consistent with traits sometimes reflecting anachronistic adaptations. Further, we often find strong non-climatic regional effects, consistent with a strong role of regional historical idiosyncrasies. Our findings show that functional diversity patterns cannot be fully understood from contemporary drivers, but also reflect long-term dynamics, with important implications for responses to anthropogenic global change.

CS4-8

Predicting Bird Community Disassembly Using a Functional and Phylogenetic Theory of Island Biogeography

Xingfeng Si[1], Marc Cadotte[1], Di Zeng[1], Andrés Baselga[1], Yuhao Zhao[1], Jiaqi Li[1], Yiru Wu[1], Siyu Wang[1], Ping Ding[1]
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Biodiversity loss in anthropogenically created habitats is often nonrandom, yet the nature and importance of the different mechanisms driving disassembly is unclear. Here, we extend the classic Theory of Island Biogeography to account for deterministic disassembly processes using nonrandom changes in species traits and phylogenetic relationships. Two possible mechanisms can create non-random community patterns on fragment islands. First, small and isolated islands consist of similar or closely related species because they are environmentally homogeneous or select for certain shared traits, such as dispersal ability. Alternatively, communities on small islands will contain more dissimilar or distantly related species than on large islands because limited space and resource availability result in greater competitive exclusion among species with high niche overlap. We tested these mechanisms using bird communities on subtropical land-bridge islands, and found that bird communities indeed became more functionally and phylogenetically clustered on smaller and more isolated islands, a result consistent with environmental filtering. These results highlight the importance of understanding the mechanisms driving community disassembly and further reveal that island biogeography theory can be extended to community measures that incorporate species similarity.

Concurrent Session 5: Biogeography Patterns and Maintenance (CS5)

Session Chair: Elizabeth Miller
Date: January 12, 2017 8:30 am – 10:00 am
Location: Canyon ABC room, Marriott Hotel

CS5-1

Drivers of phylogenetic endemism and the conservation of centres of endemism in the Coastal Forests of Eastern Africa

Christopher Barratt[1], Beryl Bwong[2], Renske Onstein[3], Dan Rosauer[4], Nike Doggart[5], Peter Nagel[6], Daniel Kissling[7], Simon Loader[8]
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[7]University of Amsterdam, Netherlands
[8]University of Roehampton

The Coastal Forests of Eastern Africa are a global biodiversity hotspot with high conservation priority, and amongst the most threatened forest types on the continent. Species distribution data for plants and vertebrates imply several centres of endemism in this region, but a comprehensive assessment with phylogenetic data across large geographic scales is lacking. We use 16 widespread amphibian species and species complexes with high intraspecific diversity and phylogeographic structuring to calculate phylogenetic endemism (PE), a measure of the spatial distribution of evolutionary history. We focus on a part of the coastal forest belt across Tanzania and Kenya, which is thoroughly sampled for amphibians, and encompasses parts of the adjacent Eastern Afromontane biodiversity hotspot. By supplementing PE with species distribution models we show that previous centres of endemism are underestimated in extent and identify four additional evolutionary refugia that were previously undetected. We further test which current and historical environmental factors determine endemism patterns in this region. The results demonstrate the importance of Quaternary climate and forest stability for the persistence of amphibian evolutionary history. Since the distribution of PE in the coastal forest region often falls outside protected areas, there is an urgent need to re-evaluate the prioritization of conservation efforts in this global biodiversity hotspot.

CS5-2

Modelling native and alien vascular plant species richness: at which scales is geodiversity most relevant?

Joseph Bailey[1], Doreen Boyd[2], Jan Hjort[3], Chris Lavers[2], Richard Field[2]
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We aimed to explore the scale-dependency of relationships between novel geodiversity measures and species richness. We calculated native and alien vascular plant species richness (6,932 species in total) across the island of Great Britain at grain sizes of 1x1 km (N = 219,964) and 10x10 km (N = 2,121) and regional extents varying between 25 and 250 km in diameter, centred around each 10x10 km grid cell. We compiled geodiversity data on landforms, hydrology, geology and soils using existing national datasets, and used a recently developed geomorphometric method to automatically extract landform coverage data (e.g. hollows, ridges, valleys, peaks). We used these as predictors of species richness, alongside climate, commonly used topographic metrics, land cover variety and human population. Geodiversity significantly improved models beyond widely used topographic metrics, particularly at smaller extents and the finer grain size, and slightly more so for native species richness. For each increase in extent, the contribution of climatic variables increased and that of geodiversity decreased. All geodiversity variables were noteworthy, but the automatically extracted landform data added the most explanatory power. Geodiversity therefore improves our understanding of, and ability to model, the relationship between species richness and abiotic heterogeneity at multiple spatial scales by allowing us to get closer to the real-world physical processes that affect patterns of life.

CS5-3

Topography and climate explain bias of plant diversity in the genera disjunctly distributed in eastern Asia and eastern North America

Xue Yin
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Disjunct distributions of the same plant clades (e.g. genera) in different continents are common on a global scale. The disjunct plant genera between eastern Asia and eastern North America (EAS-ENA) has puzzled generations of botanists. Although it has been argued that differences in physiography and climate between the two regions are the primary causes of bias in species diversity in these disjunct genera, this hypothesis has not been directly tested. We compiled data of topography, contemporary climate and paleoclimate to quantitatively assess contributions of these

factors to the Asian bias of EAS-ENA disjunct plant diversity, using negative binomial regression. We showed that contemporary climate explained 36% of the spatial variation in diversity of the EAS-ENA disjunct genera, two times more than the variation explained by topography. In contrast, on the species level, topography explained 22% of the variation in species richness while climate only 9%. Historical climate (Last Glacial Maximum climate) was highly correlated with current climate and showed no significant effects on diversity at both genus and species levels. We further found that topography accounted for about 30% of the variation in species richness in topographically more heterogeneous EAS but only 5% of that in ENA. We concluded the diversity patterns of EAS-ENA disjunct genera, to a large extent, could be a product of topographic heterogeneity and contemporary climate, although the importance of each

CS5-4

Geographic shifts and niche dynamics in South American lizards: bringing together macroclimate, microclimate, and thermophysiology

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Species may respond to novel environments in multiple ways. When lineages experience biome shifts, for example, they may 1) maintain their realized and fundamental niches by seeking out buffered microclimates; 2) experiment a different realized climate but maintain the same fundamental niche due to broad physiological tolerances, or 3) undergo evolution of the fundamental niche. To explore how species' climatic niches respond to biome shifts, we focus on a phylogeny of 40 lizard species in South America and characterize historical transitions across biomes and environmental regimes, considering both macroclimate (ambient conditions) and microclimate (substrate conditions). We evaluate thermophysiological traits from a subset of the species to compare changes in the thermal dimension of the fundamental niche with changes in the realized niche. Our results suggest that many species use behavioral buffering to reach similar microclimatic conditions across biomes, while others undergo evolution of their fundamental thermal tolerances.

CS5-5

Understanding diversification in the Asian tropical forests: case study of swallowtail butterflies

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Understanding speciation, diversification and systematics of polytypic taxa in biogeographically complex areas has been a challenge. Here, we examined diversification among swallowtail butterflies in a mainland-island matrix of the geologically and biogeographically complex Indo-Australian Region. We sampled this diverse group across the biogeographic range covering 97% species (over 60% subspecies). We generated a well-supported molecular phylogeny, with which we first reorganized *Menelaides* as a monophyletic group. We then applied multiple recently developed Bayesian and coalescent species delimitation methods to define species and recovered 56 putative species and showed that species diversity to be 20% greater than previously known. Then, we examined the underlying biogeographic processes shaping reproductive isolation and speciation. Biogeographic analyses showed that *Menelaides* has speciated largely in allopatry due to repeated dispersals and back-dispersals across key biogeographic barriers. In addition, we showed species diversified within each subregion at different time periods, which was influenced by multiple geo-climatic processes. *Menelaides* butterflies also exhibited large morphological variation in their wing patterns and participated in mimicry, which is thought to be an ecological adaptation. However, there was no significant effect of mimicry evolution on the diversification rates within this radiation. These results bring critical insights into the speciation process in this morphologically diverse model group, which will be crucial in future studies on systematics, biogeography, speciation, and morphological diversification.

CS5-6
Extinction and time help drive the marine-terrestrial biodiversity gradient: Is the ocean a deathtrap?

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The marine-terrestrial richness gradient is among Earth's most dramatic biodiversity patterns, but its causes remain poorly understood. We use detailed phylogenies of amniote clades, paleontological data, and simulations to reveal the mechanisms underlying low marine richness, emphasizing speciation, extinction, and colonization. We show that differences in diversification rates (speciation minus extinction) between habitats are often weak and inconsistent with observed richness patterns. Instead, the richness gradient is explained by limited time for speciation in marine habitats, since all extant marine clades are relatively young. Paleontological data show that older marine invasions have consistently ended in extinction. Simulations show that marine extinctions help drive the pattern of young, depauperate marine clades. This role for extinction is not discernible from extant taxa alone, and not predicted by most previously hypothesized explanations for this gradient. Our results have major implications for the marine-terrestrial biodiversity gradient, and studies of biodiversity gradients in general.

Concurrent Session 6: Conservation Biogeography (CS6)

Session Chair: Sandra Nogué
Date: January 10, 2017 8:30 am – 10:00 am
Location: Madera room, Marriott Hotel

CS6-1
U.S. protected areas do not adequately conserve forest tree species rarity

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Because forest tree species face threats such as climate change and insect and disease epidemics, prioritizing species and forests for conservation is an important management goal. Key criteria for such efforts should include species' rarity of occurrence (because of increased risk of its loss) and evolutionary distinctiveness (because distinct species may possess rare or unique traits and ecosystem functions). I generated maps of U.S. forest conservation value based on the rarity and evolutionary distinctiveness (ED) of 369 forest tree species. Rarity was determined based on how often each species occurred on ~130,000 Forest Inventory and Analysis (FIA) plots across the country. ED is the degree to which a species is related to the other North American tree species. Species rarity and ED scores were combined with tree importance values from each FIA plot to generate plot-level measures of forest conservation value, which were then interpolated nationally. Mapped forest-level forest tree rarity was the highest in California, the Great Basin, and Florida. Mapped forest evolutionary distinctiveness was highest along the coast of the Pacific Northwest and northern California. Protected areas across the United States do a good job of adequately conserving evolutionarily distinct species, but not rare ones. In fact, forest species rarity was lowest in areas with the highest protection, and highest in areas with no protection. This assessment approach should be valuable for scientists and managers attempting to determine which forests to target for monitoring efforts and for pro-active management activities.

CS6-2
Endemism and conservation in lizards of Northern Australia – intense structure on modest topography

Dan Rosauer
Australian National University, Acton, Australian Capital Territory, Australia

Lizards of Australia's monsoonal tropics (MT) contain much unrecognised by current taxonomy. Our recent work has revealed novel diversity hotspots and biogeographic patterns. This talk presents historical barriers and areas of endemic diversity, based on a large-scale analysis of comparative phylogeography of ten genera of lizards across the tropical savannahs of northern Australia. Using phylogeographic data from over 5000 individuals, we identified

over 320 independently evolving lineages, and used a new method to model the distribution of each lineage. This approach – which supports a seamless analysis of diversity above and below species level independent of current taxonomy – allowed us to map phylogenetic endemism and phylogenetic ? diversity and quantify the location of refugia and the relative strength of biogeographic breaks. Our results highlight areas of endemism in the Kimberley and Top End regions that might represent evolutionary refugia, and confirm a spatial pattern across many species, of deep divergences within species. Coastal islands show surprising concentrations of endemism given their recent connections to the mainland. This information is being used to inform conservation priorities, and to quantify the amount and locations of endemic diversity, even in cases where taxonomy is uncertain or incomplete. These methods are readily applicable to other biomes with high diversity and potential Linnean shortfall.

CS6-3

Using species distribution models in conservation management: more barriers than opportunities?

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Climate change is posing new challenges to conservation management, where a moving target is replacing the goal of returning ecosystems to baseline conditions. Although species distribution models (SDMs) have been widely suggested as a tool to promote climate adaptation in management, most conservation initiatives still do not use them in their planning. In this talk, we review four classes of challenges faced when using SDMs in practice: 1) methodological issues of modelling, 2) uncertainties extrinsic to SDMs (such as socioeconomic pathways), 3) conceptual challenges of linking SDM results to management (e.g. linking broad scales to local, defining relevant time scales), and 4) communication challenges between researchers and managers when interpreting models and translating them to solutions on the ground. Based on case studies from California, we discuss what kinds of management decisions SDMs are able to inform, and how uncertainties can be narrowed down – a key to applying conservation biogeography to address global change issues.

CS6-4

ECOPOTENTIAL – Protected Areas in a Continental Perspective

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Protected areas (PAs) play a crucial role for the protection of biota and ecosystems. Climate change, pollution, tourism, land use change, invasive species are creating pressures to PAs. No longer, local case studies can satisfy the research needs in order to improve and adapt management strategies. The ECOPOTENTIAL project within the HORIZON 2020 research initiative is focused on PAs of international importance. Across Europe, including non-EU member states, outstanding national parks, biosphere reserves, and world heritage sites are investigated with emphasis on vulnerable regions such as mountains, coasts and drylands. ECOPOTENTIAL includes 47 partner institutions from 18 countries. The project is blending in-situ earth and remote sensing earth observations, data analysis and modelling of future ecosystem conditions. Here, we analyze how the selected sites represent European biodiversity and ecosystems, climate, and biogeographical regions. We evaluate the adaptation capacity of PAs in face of climate change and possible threats and losses of benefits. Finally, priority PAs are identified and suggestions are made how European PAs should be developed in the future.

CS6-5

Island biology needs palaeoecology

Sandra Nogué[1], Lea de Nascimento[2], Cindy Froyd[3], Janet Wilmshurst[4], Erik de Boer[5], Emily Coffey[6], Robert Whittaker[7], José María Fernández Palacios[8], Kathy Willis[9]
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Island ecosystems worldwide have been transformed since their first colonization by humans. The small and isolated populations of many island taxa mean that they are particularly vulnerable to human activities. Consequently, even the most degraded islands are a focus for restoration, eradication, and monitoring programmes as centers of endemism and/or of relict distributions. The same characteristics that make island ecosystems unique also make them challenging to manage. Palaeoecology has potential to provide relevant data to inform and improve the management of island ecosystems. For example, time series of fossil pollen grains, spores, and charcoal report on the status of native and non-native species across island ecosystems, the presence of vertebrate herbivore populations and their effects on the native ecosystems, and long-term fire regimes. Here, we aim to build a framework to include the degree of change from multiple baselines to better inform strategies for management of island ecosystems and landscapes.

CS6-6 Integrating biogeography, threat and evolutionary data to explore extinction crisis in the taxonomic group of cycads

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Will the ongoing extinction crisis cause a severe loss of evolutionary information accumulated over millions of years on the tree of life? This question has been largely explored, particularly for vertebrate and angiosperms. However, no equivalent effort has been devoted to gymnosperm. Here we address this question focusing on cycads, the gymnosperm group exhibiting the highest proportion of threatened species in the plant kingdom. We assembled the first complete phylogeny of cycads, and assessed how species loss under two scenarios (i- all threatened species are lost, and ii- top 50% of Evolutionarily Distinct species are lost) would impact the cycad tree of life. We also analyzed the biogeographical pattern of cycad diversity hotspots and tested for gaps in the current global conservation network. First, we showed that threatened species are not significantly clustered on the cycad tree of life. Second, we showed that neither extreme scenario leads to severe loss to the cycad tree of life. These two findings contrast with existing knowledge reported for most vertebrate and angiosperm, and could most likely be linked to the differences in the evolutionary models of species diversification between most taxonomic groups vs. gymnosperm. To inform conservation decisions, we defined five hotpots of diversity, and depending on the diversity metric used, these hotspots are located in Southern Africa, Australia, Indo-Pacific and Mexico and all are found within Protected Areas. We conclude that the cycad tree of life would likely survive the current extinction crisis, and a biogeographical perspective in global prioritization effort would further contribute to safeguarding the evolutionary diversity of the group.

Concurrent Session 7: The geography of species associations (CS7)

Session Chair: Jean-Philippe Lessard
Date: January 12, 2017 8:30 am – 10:00 am
Location: Pima room, Marriott Hotel

CS7-1

Process-based species pools reveal the hidden signature of biotic interactions

Jean-Philippe Lessard[1], Ben Wenstein[2], Michael Borregaard[2], Katharine Marske[3], Danny Rojas[4], Juan Parra[5], Jimmy McGuire[6], Carsten Rahbek[7], Catherine Graham[2]
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A persistent challenge in ecology is to tease apart the influence of multiple processes acting simultaneously and interacting in complex ways to shape community structure. We implement a heuristic null model approach that relies on explicitly defining species pools and which permits assessing the relative influence of the main processes thought to shape community structure: environmental filtering, dispersal limitations and biotic interactions. We illustrate our approach using data on the community composition, global distributions, phylogeny and morphological traits of hummingbirds.

CS7-2

Lightning-fast computation of phylogenetic diversity indices (and when not to trust them)

Brody Sandel[1], Constantinos Tsirogiannis[2]
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Phylogenetic indices such as the Net Relatedness Index (NRI), Nearest Taxon Index (NTI) and Phylogenetic Diversity Index (PDI) describe the composition of a particular assemblage of species with respect to a phylogenetic tree. All of these indices are standardized against species richness such that deviation from a value of zero indicates non-random phylogenetic structure. This standardization is typically achieved by a Monte Carlo process that is both slow and inexact. We outline a set of algorithms that enable highly efficient and exact computation of these phylogenetic indices, even for very large trees. We also briefly introduce their equivalents for phylogenetic beta diversity, and a new measure of phylogenetic structure, the Core Ancestor Cost (CAC). These breakthroughs in computational efficiency allow new approaches to both empirical and simulation studies. For example, it is now possible to repeat analyses over large sets of trees, thereby providing estimates of error due to phylogenetic uncertainty. We illustrate these advantages with a case study on environmental filtering and phylogenetic diversity patterns in California's grasses. Finally, through a set of simulation studies, we show that phylogenetic indices are dependent on species richness in the presence of environmental filtering. This dependence greatly complicates the interpretation of phylogenetic diversity patterns along gradients. Fortunately, it appears that a simple modification of the indices can remove this richness-dependence.

CS7-3

Latitudinal-diversity gradients may be driven by biotic processes: New insights from an individual-based simulation and a large-scale zooplankton dataset

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The processes involved in shaping latitudinal-diversity gradients (LDG) have been a longstanding source of debate. Much attention has been given to climatic, historical and evolutionary factors while biotic processes such as competition and Allee-effects are generally overlooked. We developed an individual-based model of species ranges eco-evolutionary dynamics and simulated multiple competing species (sexual or asexual) expanding across an environmental gradient to show how these two overlooked factors may modulate LDGs. Mate-finding Allee effects increased local extinctions in sexual species, resulting in smaller geographic range sizes (GRS) compared to asexual species as well as a smoother LDG due to lower diversity at the southern end of the gradient. Interspecific competition had a strong effect on both groups: without competition the LDG disappeared because all species were able to expand their ranges, under intermediary competition LDG slopes were smooth whereas they became steep under high competition because strong priority effects resulted in a landscape dominated mostly by one species. Further, the analysis of macroecological patterns in zooplankton corroborated most of the model's prediction. Sexual copepods exhibited, on average, a GRS 70% smaller than cyclic parthenogenetic cladocerans. We found a steep LDG for cladocerans but none for copepods. Cladoceran macroecological patterns were mainly explained by climatic factors and a potential role of priority effects. Copepods were more influenced by dispersal limitation and the influence of a northern glacial refuge. Our results suggest that the role of local-scale biotic processes in shaping well-known macroecological patterns could be more important than it is currently appreciated.

CS7-4

Drought stress structures evolutionary diversity in tropical woody plant communities

Danilo Neves[1], Kyle Dexter[2], R. Toby Pennington[3], Ary Oliveira-Filho[4], Tim Baker[5], Fernanda Souza[6]
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The evolutionary diversity of plant communities may affect ecosystem function and their resilience to climate change, and is therefore of significant conservation interest. However, we have limited understanding of the distribution of evolutionary diversity among different types of tropical forests, the most diverse terrestrial plant communities. In order to examine patterns of evolutionary diversity in neotropical tree communities, we bring together the largest database assembled to date on the composition of woody plant communities across all biomes in lowland tropical South America (>3,000 inventories) with a new DNA sequence-based phylogenetic hypothesis for c.1,000 woody genera. Communities under intermediate water-stress show more lineage diversity than expected given their taxonomic diversity, especially when compared to dry extremes. Dry areas not only have few species, but those species are unevenly distributed across angiosperm phylogeny, being concentrated in a few clades. This finding suggests that phylogenetic niche conservatism for wet environments plays a major role in shaping macroscale patterns of plant biodiversity.

CS7-5

Character release in the absence of a congeneric competitor

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Feeding niches are defined by available resources, but resource availability may depend on competition for those resources. Competition for resources is most intense in closely-related species, which are likely to share similar niches. If a competitor disappears from an ecosystem, the remaining species may experience niche release. This, in turn, may lead to character release. In bird species bill length is a strong indicator of feeding niche, as birds' bills are adapted to handle food efficiently. Here we demonstrate a case of character release in a passerine bird in South-east Sulawesi, Indonesia in the absence of a congeneric competitor. The Lemon-bellied White-eye (*Zosterops chloris*) and Pale-bellied White-eye (*Zosterops consobrinorum*) are closely related species which compete for similar resources. When these species were found in sympatry there was evidence of strict niche partitioning, with no overlap in bill lengths between the two species. However at sites where only the Lemon-bellied White-eye was present its bill length showed increased trait diversity, covering the full range of bill lengths shown by both *Zosterops* species when living in sympatry. This is clear evidence of character release, with the Lemon-bellied White-eye expanding to fill the entire niche space split between the species in sympatry. Phylogenetic analysis of mitochondrial genes indicate that there's no taxonomic separation between the morphologically different populations of Lemon-bellied White-eyes. These results demonstrate the potential for character release in populations which experience a lessening of competition pressure. The phylogenetic results also show the phenotypic plasticity which can exist within taxonomically continuous populations.

CS7-6

Dissecting a biodiversity hotspot: the importance of environmentally marginal habitats in the Atlantic Forest Domain of South America

Ary Oliveira-Filho[1], Danilo Neves[2], Kyle Dexter[3], R. Toby Pennington[4], Arthur Valente[5], Marcelo Bueno[1], Pedro Eisenlohr[6], Marco Aurelio Fontes[7], Pedro Miranda[3], Vanessa Rezende[1], Suzana Moreira[1], Felipe Saiter[8]
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Biodiversity hotspots are a widely used concept in conservation, but often represent a complex mix of different habitat types. We aimed to assess the contribution of marginal, non-rain forest habitats to overall species diversity in the *Mata Atlântica* (Atlantic Forest) biodiversity hotspot and to determine which environmental factors drive their occurrence and distribution. We compiled a dataset containing 366,875 occurrence records of 4,431 tree species from 1,753 site-checklists, which were a priori classified into ten main vegetation types. We then performed ordination analyses of the species-by-site matrix to assess the floristic consistency of this classification. In order to assess the relative contribution of environmental predictors to community turnover, we produced models using climate and substrate-related variables as environmental predictors. Ordination diagrams supported the floristic segregation of vegetation types, with those considered as marginal habitats placed at the extremes of the axes. These habitats are associated with the harshest extremes of five factors: temperature seasonality (high elevation habitats), flammability (rock outcrop dwarf-forests), soil salinity (coastal white-sand woodlands), water deficit (seasonally dry forests) and soil waterlogging (riverine forests). Importantly, 45% of all species endemic to the *Mata Atlântica* are restricted to marginal habitats. Our results showed the key role of the poorly protected marginal habitats in contributing to the high species richness of the *Mata Atlântica*. Our findings also stressed the importance of fire, a previously neglected environmental factor.

Concurrent Session 8: Historical and Paleo-biogeography (CS8)

Session Chair: Bruno Vilela
Date: January 12, 2017 8:30 am – 10:00 am
Location: Sabino room, Marriott Hotel

CS8-1

The 'Flickering Connective System': Why the Pleistocene has been so important for contemporary mountain biodiversity

Suzette Flantua[1], Henry Hooghiemstra[1]
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Current montane biodiversity can be seen as just a snapshot after millions of years of change influencing species richness. The Pleistocene climatic cycles forced species rhythmically along the mountain slopes, opening temporary dispersal pathways to new regions or dividing populations into isolated remnants. We introduce the 'Flickering Connective System' supported by a palaeotopographic reconstruction of alpine biome distributions in the northern Andes to exemplify the temporal and spatial dynamics that forced rapid and recent radiations to occur. We describe species richness and endemism as a consequence of this Flickering Connective System, where the link is laid between oceanic islands and the 'alpine islands' in mountains.

CS8-2

Biogeography and diversification of modern marsupials: Arrival or departure of Australasia?

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It is well established that the South American ancient lineage Microbiotheria is more related to Australasian marsupials than to the American taxa, though the geographic origin of the Australasian marsupials remains unclear. There are different hypotheses regarding the unsolved biogeographical patterns of marsupials. These involve either dispersal or vicariance to Australasia or to the Americas through Antarctica, and from Australia to Papua New Guinea. We constructed and updated a dated phylogeny using mitochondrial and nuclear sequences for 282 marsupial species, adding 18 calibration points and reconstructed the ancestral area of marsupials and their diversification patterns through time. The ancestral area range estimation indicated that Australidelphia originated in South America and dispersed to Australia through Antarctica during the Late Cretaceous-Palaeocene giving rise to the Australasian marsupials. Vicariance, also, had an important role when Australia separated from Antarctica-South America. We recovered two main dispersal and vicariance events to explain how marsupials entered Papua New Guinea during the Miocene and the Pliocene and a possible third dispersal event during the Eocene to explain the current distribution of marsupials. The time calibration analysis suggests that the diversification of the group in the Americas and Australasia coincides with periods of aridification during the Late Oligocene and Miocene. We conclude that the combination of vicariance and dispersal shaped the extant marsupial distribution, furthermore an improved marsupial fossil record of Australidelphian taxa in Antarctica and Australia is needed from the Palaeocene and Eocene for future taxonomic and evolutionary studies to decide between the remaining hypotheses.

CS8-3 The relative role of history and ecology on the spread of farming

Bruno Vilela[1], Trevor Fristoe[2], Ty Tuff[3], Michael Gavin[4], Patrick Kavanagh[4], Hannah Haynie[4], Russell Gray[5], Carlos Botero[1]
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Acquiring the knowledge and technology necessary for species domestication was a key event in human history, opening the door for societies to transition from foraging to farming. The modern prevalence of farming societies suggest that these groups had clear evolutionary advantages compared to foragers, allowing them to spread across the globe. However, this simplistic scenario does not account for the fact that some societies never or only partially adopted farming, and in some cases even reverted back into foragers. These details suggest that ecological factors have interacted with history to dictate the spread of farming. Yet, there is currently a lack of scientific consensus as to the relative importance of ecology vs history. Insufficient quantitative support for either perspective has been compounded by the difficulty in disentangling correlations among cultural, geographic, and environmental variables. We used a global dataset on 1253 human societies to develop a single framework that reveals how historical processes have unfolded within ecological constraints resulting in the cultural and geographic spread of farming. Uniquely, we characterize ecology from the perspective of domesticated species - employing ecological niche reconstruction and current anthropological evidence for the geographic origins of domestication to measure the climactic suitability of species historically available to each society. Overall, our model explains 82.5% of the variation in societal reliance on farming and provides evidence for an intuitive mechanism of cultural spread: while farming was primarily inherited through decent and learned from neighbors, ecological boundaries limited its persistence in climates unsuitable for growing available species.

CS8-4

Natural vs. Human-caused Faunal Change in the West Indies since the late Pleistocene

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The most dramatic late Quaternary biotic phenomenon on American continents was the extinction of large mammals during the Pleistocene–Holocene transition (PHT; 15–9 ka). Because this is also when people first arrived, the causes of continental megafaunal collapse are debated (humans vs. climate). On the other hand, West Indian megafauna, such as tortoises, crocodiles, sloths, monkeys and large rodents, survived until the mid-Holocene or later, a time corresponding to first human arrival in the islands but characterized by much less change in climate, sea level, and land area than during the PHT. Using vertebrate fossils from Bahamian islands and Hispaniola, we establish a chronology for late Quaternary faunal change on low versus high islands. Among 83 vertebrate taxa from late Pleistocene deposits on Abaco (Bahamas), 40 no longer occur there, with 17 being lost during the PHT. Lying on shallow carbonate banks, Bahamian islands were much larger in the Pleistocene when sea levels were lower. Several species of birds recorded as Pleistocene fossils are associated today with cooler climates and more open habitats than exist now in the Bahamas, where a diverse set of 23 species of reptiles (lizards, tortoises, crocodiles), birds (hawks, falcons, owls, pigeons, many others), and mammals (bats, rodents) survived the PHT but not the past millennium of human presence. In contrast, on the large, high island of Hispaniola, many birds and other vertebrates persisted through the Middle Holocene arrival of Amerindians on the island, but were lost after 1492 CE.

CS8-5
Detecting diversification processes in relation to tectonic history from an incomplete fossil record

Tara Smiley
Oregon State University, Oregon, United States

For mammals today, mountains are among the most diverse ecosystems globally, yet the strong relationship between species richness and topographic complexity is not a persistent feature of the fossil record. Based on fossil-occurrence data, diversity and diversification rates in the intermontane west varied through time, increasing significantly during the middle Miocene interval of global warming and regional intensification of tectonic activity. However, variation in the temporal and geographic distribution of the rock record could potentially limit our ability to interpret this diversification history and thus the origins of montane diversity hotspots. To investigate the influence of variable preservation history through the Neogene on estimates of diversification rates, I simulated fossil records under four alternative diversification hypotheses and five different preservation scenarios. Diversification scenarios included tectonically-controlled speciation pulses, while preservation scenarios were based on common trends (e.g., increasing rock record towards the present) or derived from fossil occurrences and rock area. For each scenario, I estimated origination, extinction, and diversification rates and evaluated the ability of the degraded fossil records to accurately recover the underlying diversification scenarios. Despite variable and low preservation probabilities, the simulated fossil record retained the signal of diversification dynamics in most scenarios. These results indicate that preservation alone is unlikely to produce the middle Miocene peak in mammalian diversity. Despite challenges in reading the fossil record, input from the past is necessary in order to evaluate the mechanisms underlying speciation and extinction dynamics.

CS8-6
Ecology of diversification across islands and continents

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Ecological mechanisms of diversification remain elusive and somewhat controversial. Here, we evaluate four classes of prominent mechanisms involving (1) climate (2) geography (3) functional traits and (4) biotic interactions. We use corvoid passerines (800spp) across continents (32 biomes) and Indo-Pacific islands (1000+ islands) as our model system. Integrating diversification analyses with climatic, geographic, and trait data, we find support for each of the studied mechanisms. Diversification on islands whose faunas are phylogenetically overdispersed and therefore likely limited by competition, is largely suppressed. Islands hosting less species than expected, given their geographic area, show increased diversification, presumably because they afford unfilled niches and opportunities for further diversification. These results suggest that island diversification is largely equilibrial and governed by biotic interactions. Diversification across continents, however, follows dramatically different dynamics. We find that species richness across continental biomes increases gradually over time. Consequently, biome richness appears non-equilibrial and governed by the time for speciation. Together, these findings uncover the interplay between several classes of diversification mechanisms across islands and continents. They illuminate that similar mechanisms operate in both geographic settings. However, the relative effects of these mechanisms differ profoundly and produce dramatically divergent diversity dynamics on islands and continents.

Concurrent Session 9: Biodiversity Patterns and Maintenance (CS9)

Session Chair: Eric Treml
Date: January 12, 2017 10:30 am – 12:00 pm
Location: Canyon ABC room, Marriott Hotel

CS9-1

Local and regional drivers linked to diversity of a symbiotic fungal group

Meelis Pärtel[1], Maarja Öpik[1], Mari Moora[1], Robert Szava-Kovats[2], Martin Zobel[1]
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A challenge for biodiversity research is to explore cryptic taxonomic groups, which are important for ecosystem function. Current advances in DNA-based methods have resulted in accumulation of global data on biodiversity of arbuscular mycorrhizal (AM) fungi – root symbionts associated with 80% of land plants. We present global biodiversity patterns of AM fungi and distinguish between the effects of local and regional processes by examining patterns of local diversity and site-specific species pools – the set of potentially suitable species. We also estimated dark diversity – the absent fraction of the species pool – for each site. These diversity measures portray non-random global patterns. The largest species pools of AM fungi are located in areas near tropical grassy biomes of the Last Glacial Maximum. Local diversity exhibits a similar pattern, but is dependent also on current biomes and climate. Dark diversity is related not to historic factors, but to current local vegetation type. Thus, the species pool concept allows distinction of the relative roles of biogeographic history and local processes that underlie global biodiversity patterns of a cryptic taxonomic group.

CS9-2

Quantifying the emergent geography of dispersal barriers and the biogeographic implications across the Indo-West Pacific seascape

Eric Treml
University of Melbourne, University of Melbourne, Parkville, VIC, Australia

Although barriers to dispersal are known to contribute to the distinctiveness of communities, species and populations, the importance of the biophysical processes associated with permeable barriers is not well understood. In this study, we predict the geographic location and strength of multispecies dispersal barriers across the Indo-West Pacific Ocean. Specifically, we ask three questions: (1) What biological and physical attributes are important in influencing the location and strength of dispersal barriers? (2) What is the geographic configuration of multispecies dispersal barriers? (3) How do these predictions compare with previously described barriers across the seascape?
A biophysical dispersal model was used to quantify over 800,000 dispersal kernels simulating 99 model taxa to map the emergent patterns of potential multispecies population connectivity and predict geographic locations and strength of concordant dispersal barriers. Although individual taxa varied in their predicted fine-scale population connectivity, there was broad-scale consistency in the location of dispersal barriers. Across all trait combinations, reproductive output (fecundity and density of reproductive adults), reproductive strategy (spawning phenology) and the length of the larval dispersal phase determined the strength of barriers across the seascape. More than 80% of the previously described marine boundaries in the region were predicted to restrict the dispersal of at least 10% of the simulated taxa. This approach may contribute to the development of an accurate bioregionalisation and robust conservation prioritization across the Indo-West Pacific, and fill gaps in our understanding of the biogeography.

CS9-3

Historical colonization and dispersal limitation shapes African biodiversity

Daniel Kissling[1], Anne Blach-Overgaard[2], Roelof E. Zwaan[3], Philipp Wagner[4]

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To what extent deep-time dispersal limitation shapes present-day biodiversity at broad spatial scales remains elusive. Here, we test to what extent the continental distribution of biodiversity in African lizards (reptile subfamily Agaminae) can be explained by historical colonization and dispersal limitation (i.e. accessibility from areas of geographic origin) relative to current climate, topography, and climate change since the late Miocene (~10 mya), the Pliocene (~3 mya), and the Last Glacial Maximum (LGM, 0.021 mya). Spatial and non-spatial multi-predictor regression models revealed that time-limited dispersal via arid corridors is a key predictor to explain macro-scale patterns of species richness. In addition, current precipitation seasonality, current temperature of the warmest month, paleo-temperature changes since the LGM and late Miocene, and topographic relief emerged as important drivers. These results suggest that deep-time dispersal constraints — in addition to climate and mountain building — strongly shape current species richness of Africa's arid-adapted taxa. Such historical dispersal limitation might indicate that natural movement rates of species are too slow to respond to rates of ongoing and projected future climate and land use change.

CS9-4

Biotic immigration events, speciation, and the accumulation of biodiversity in geologic time

Alycia Stigall
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Biodiversity accumulates separately at the local and global levels via processes that are mediated by geographic connectivity, isolation, and regional differentiation. Biotic immigration events (BIMEs), the large-scale dispersal of taxa from one biogeographic area to another, significantly impact geographic connectivity and regional differentiation. This is formalized via a conceptual model for biodiversity accumulation that links BIMEs and geographic isolation with regional (?) diversity, global (?) diversity, and regional (?) diversity metrics. This conceptual model is tested using seven case studies from the paleontological record: the Great Ordovician Biodiversification Event (GOBE), the regional Richmondian Invasion, the Hirnantian Migration Event, the Great Devonian Interchange, Neogene mollusk migrations, the Great American Biotic Interchange, and Beringian dispersals. Although each case study presents certain idiosyncrasies, major patterns recur. First, intervals of active immigration are characterized by minimal to no successful speciation events, increased species richness within regions, reduced differentiation among areas, and limited impact on global species richness. Once dispersal pathways disconnect and areas become isolated, speciation within basins increases, which results in greater ?-, ?-, and ?-diversity. The diversity partitions (?, ?, ?) are semi-independent, but they are linked through biogeographic processes. Migration events alone are insufficient to produce biodiversity accumulation. However, BIMEs are important facilitators of geographic range expansion and establish the the foundation on which speciation processes can operate during the next interval of regional isolation. Oscillation of area connectivity and isolation can generate a robust and effective mechanism for substantial accumulation of new biodiversity and persistence of existing species.

CS9-5

Phylogenesis on an evolving landscape: Toward a Theory of Continental Biogeography

James Albert
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Five broad regularities of biogeography and biodiversity are observed in many taxa with continental distributions: 1, power function-like species-area relationships; 2, log-normal distribution of species geographic range sizes, 3, mid-domain effects with more species towards the geographic center, and more early-branching, species-poor clades (i.e. living fossils) towards the geographic periphery; 4, exponential diversification with log-linear accumulation of lineages through geological time; and 5, power function-like relationships between species-richness and cladal-diversity, where most clades are species-poor and few clades are species-rich. However, current theory does not provide a robust mechanistic framework to connect these seemingly disparate patterns. Here we present SEAMLESS (Spatially-Explicit Area Model of Landscape Evolution by SimulationS) that generates clade diversification by moving geographic barriers on a continuous, neutral landscape. SEAMLESS differs from other biogeographic methods by studying the evolution of trees on a continuous landscape, rather than treating species geographic ranges as traits changing along branches of a phylogeny. SEAMLESS contributes to a theory of continental biogeography by modeling the effects of barrier-displacement on all three terms of macroevolutionary diversification: dispersal, speciation, and extinction. Barrier-displacement events merge adjacent areas allowing dispersal and larger geographic ranges, separate adjacent areas resulting in vicariant speciation and smaller geographic ranges, and subdivide areas below a minimum threshold for species persistence resulting in extinction. SEAMLESS shows how dispersal is required to maintain species richness and avoid clade-wide extinction, demonstrates that ancestral range size does not predict species richness, and provides a unified explanation for the five biogeographic and phylogenetic patterns described above.

CS9-6

Scale-dependent dissections of geographic diversity gradients

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Biodiversity of the same taxa can vary by many orders of magnitude from place to place as a result of variation in environmental factors, such as climate, and historical biogeographic factors, such as variation in rates of diversification. Unfortunately, most analyses of global gradients in biodiversity focus on species richness, a notoriously scale-dependent variable made up of a number of varying components (including the total and relative abundances of individuals, and their spatial aggregations). Here we dissect two well-known species richness patterns to show that similar decreases in marine fish richness from the central Indo-Pacific biodiversity hotspot are associated with very different component changes along latitudinal and longitudinal gradients. Latitudinal richness is underpinned by complementary scale-independent patterns of total abundance and evenness, suggesting ecological constraints scale up to determine absolute and relative abundance within communities. In contrast, the longitudinal gradient was not detected at small scales, meaning local fish communities in the biodiversity hotspot and species poor islands are remarkably similar in terms of total and relative abundances, and species richness. Longitudinal richness only emerges at the largest scale, and a similar scale-dependent pattern of evenness indicates that species aggregation promotes regional coexistence, but that this does not trickle down to influence local-scale patterns. Dissecting species richness into components provides vital new insights into biodiversity patterns and the processes that shape them.

Concurrent Session 10: Biogeography of Southwestern North America (CS10)

Session Chair: John Wiens
Date: January 12, 2017 10:30 am – 12:00 pm
Location: Madera room, Marriott Hotel

CS10-1

Value in developing focal geographic systems for phylogeography and biogeography: a view from the North American deserts.

Brett Riddle
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Phylogeography has emerged as a major approach within modern biogeography by addressing questions at the nexus of evolution, ecology, and conservation biogeography. With emerging capacities to sample large numbers of co-distributed lineages (i.e., comparative phylogeography), and large numbers of unlinked loci, as well as ongoing development of new analytical approaches, phylogeography will continue to grow in the breadth and robustness of questions addressed. Yet, coordinated efforts among investigators to develop multi-faceted and integrated biogeographic-scale geographies into integrated research arenas that parallel a number of smaller geographic-scale efforts in ecology are relatively rare. What would be the added value of identifying an array of regions as 'model' geographic systems based fundamentally on highly replicated phylogeographic sampling? Here, I explore the value gained when studies are replicated within a focal geographic area and well delineated set of biomes to a degree that provides a foundation upon which next generation studies build upon the canonical phylogeographic and biogeographic architecture. I review the global distributions and locations of such systems in a biogeographic regions context. I then use the phylogeographically relatively well-characterized North American deserts to illustrate how such 'focal geographic systems' can provide a rich template for developing studies that integrate geology,

climatology, and ecology; testing hypotheses of spatially explicit biogeographic and evolutionary history; and producing maps of evolutionary hotspots that are useful in biodiversity planning.

CS10-2
Genome-based phylogeography of the saguaro cactus (Carnegiea gigantea) in the Sonoran Desert of North America

Michelle McMahon[1], Dario Copetti[2], Alberto Búrquez[3], Enriquena Bustamante[4], Joseph Charboneau[2], Noah Whiteman[5], Rod Wing[2], Martin Wojciechowski[6], Michael Sanderson[2]
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[6]Arizona State University, United States

The giant saguaro cactus is the northern-most representative of a clade of large columnar cacti distributed mainly in Mexico and the southwestern US, the Pachycereeae. We assembled a high coverage reference genome for one individual plant from Tumamoc Hill in Tucson using next generation sequencing, and obtained SNPs from 15 other individuals in 8 populations across the geographic range in Sonora, Mexico and Arizona, US. STRUCTURE analysis using 68832 SNPs indicated relatively little population structure with an admixture of two ancestral populations common to all populations. The highest fraction of all populations' genomes were represented from population 1, with low diversity and low Ne. The second population has higher diversity and Ne and was enriched in the most southern Masiaca and Guasimas populations. There is evidence of a weak cline from north to south, with the low diversity ancestral population more dominant in the north than in the south. A population tree was constructed from pairwise Fst estimates obtained in GENEPOP, which also indicated a split between the two southernmost populations and those to the north. This was also seen in a consensus network analysis of gene trees obtained from individual scaffolds in the assembly. Finally, a PSMC demographic reconstruction of the high coverage Tumamoc sample implies low Ne in the present day population with much higher values prior to the last glacial maximum. We compare these results to recent work on the phylogeography of another Pachycereeae, the organ pipe cactus, which is sympatric over much of saguaro's range.

CS10-3
Range shifts, niche shifts, and genetic consequences of species responses to climate change in the southwestern deserts

Tereza Jezkova
University of Arizona, University of Arizona, United States

During climate change, species can shift their geographic distributions in order to track environmental conditions – niches – to which they are adapted. This happens through local extinction of populations that no longer occupy suitable niches and through geographic expansions of peripheral populations that track suitable conditions, usually along latitudinal or altitudinal gradients. Alternatively, populations can shift their niches as the climate changes, which allows them to persist in place despite climate fluctuations. Range and niche shifts are predicted to have a pronounced impact on population genetic structure. For example, populations in which niche shifts are facilitated by evolutionary adaptations can experience selective sweeps, whereas expanding populations may experience loss of genetic diversity due to repeated bottlenecks. We assessed responses to Pleistocene climate oscillations in several iconic animal species occupying the southwestern region of North America. Our results suggest that both range and niche shifts represent a common species response during climate change. We documented large scale range expansions in response to the warming climate after the last glacial maximum (LGM). Many populations also experienced niche shifts towards warmer temperatures at the end of the LGM that allowed them to persist in place. These populations often occur in valley bottoms, possibly indicating that reduced competition (i.e. new species are less likely to expand into valley bottoms during warmings) may facilitate niche shifts. We also found evidence that population expansion is accompanied by considerable reduction in genetic diversity which may in turn affect population viability and evolutionary potential.

CS10-4

Exploring the drivers of fungal endophyte diversity in the arid West

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Plants host numerous fungi that live asymptomatically within their tissues. These fungal endophytes have attracted a great deal of interest because of their putative ecological importance, however biogeographic patterns in endophyte diversity remain understudied. To investigate how host plant genetic structure, population proximity, and habitat variation together structure endophyte communities, we assayed endophyte communities occurring in spotted locoweed (*Astragalus lentiginosus*) across the arid West. Spotted locoweed is a tremendously phenotypically variable plant, with approximately forty nominal varieties that occur in a wide variety of habitat types. Additionally, spotted locoweed hosts a seed-borne, and thus heritable, fungal endophyte that synthesizes a bioactive alkaloid which causes millions of dollars in damages to livestock annually. We took a genotyping-by-sequencing approach to characterize the population genetic structure of spotted locoweed that allowed us to investigate the link between host plant genetic variation and associated fungal endophyte communities. We observed that differences between endophyte communities, and overall endophyte diversity, were shaped by host genetics, population proximity, and variation in abiotic habitat. However, the strongest influence on endophyte community structure was the relative abundance of the heritable fungal endophyte of spotted locoweed. Interestingly, the prevalence, or even occurrence, of this fungal endophyte varied across the West, as did the concentration of the bioactive alkaloid it synthesized. These results bring up important questions about the ecological and evolutionary consequences of geographically variable interactions between plants and their endophytes.

CS10-5

Climate change and biogeography of a montane lizard in Arizona's Sky Islands

John Wiens[1], Agus Camacho[2], Tereza Jezkova[1], Matthew Kaplan[1], Shea Lambert[1], Elizabeth Miller[3], Jeffrey Streicher[4], Ramona Walls[1]
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Around the world, many species and clades are confined to "Sky Islands", with different populations or species occurring in isolated patches of higher-elevation habitat. How does this biogeographic pattern arise? One possible scenario is that these montane species were widespread in lowlands when climates were cooler, and were subsequently isolated by local extinction caused by warming conditions. If true, this scenario implies that many montane species may be unable to shift their climatic niches quickly enough to avoid extinction (locally or globally) from projected anthropogenic warming. Here, we test this scenario in a montane lizard (*Sceloporus jarrovii*) in southeastern Arizona. We surveyed 30 mountain ranges and found it present only in 17 higher ranges (even though many lower ranges currently contain suitable climatic conditions), suggesting that past warming drove populations in lower ranges to extinction. We obtained genomic data (RADseq) from all 17 ranges, and found a pattern of splitting among populations consistent with a low-elevation ancestral population restricted to montane refugia by warming climate and local extinction. We obtained physiological data for lower-elevation populations from 10 ranges and found little divergence among them (from elevations ranging from ~1220–1830 meters asl), consistent with limited physiological adaptation to different climatic conditions. We also analyzed rates of climatic niche divergence among low-elevation populations, and compared these to rates of past and future climatic change. Overall, the results are consistent with the idea that geographic isolation of montane species and populations is caused by local extinction in response to past climate change.

CS10-6

Mammal diversification tracks landscape history in the Great Basin of western North America

Catherine Badgley[1], Tara Smiley[2], William Holt[3], Alireza Bahadori[3], E. Rasbury[3]
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Regions of high topographic complexity are hotspots of diversity, reflecting geological influences on biogeographic processes. We integrated geohistorical and biogeographic data for the Great Basin of western North America to evaluate the influence of landscape history on mammal diversification. The Great Basin formed by tectonic extension and volcanism over the last 30 My, with a gain of 80,000 km^2 between 20 and 15 Ma. Over this interval, the diversity of mammals peaked between 15 and 17 Ma. From geological data, we quantified estimates of the rate of area increase during Great Basin extension. The highest rate of area increase occurred between 17 and 14 Ma, as an ancient highland was pulled apart into parallel mountain ranges separated by intervening basins. The fossil record and molecular phylogenies for rodent clades with high diversity in western North America show branching events that coincide with the middle Miocene interval of rapid extension in the Great Basin. Regional mammalian faunas show low similarity during this interval, implying the presence of strong barriers to dispersal. Since that time, rodent diversity has become a greater proportion of total mammal diversity, and rodent faunas have become more homogeneous across the Great Basin. The middle Miocene peak in diversity involved increased origination rates within resident lineages and immigration into expanding areas.

Concurrent Session 11: Global Change Biogeography (CS11)

Session Chair: Anna Csergo
Date: January 12, 2017 10:30 am – 12:00 pm
Location: Pima room, Marriott Hotel

CS11-1

Extinction rate's complex relationship with area

Petr Keil[1], Juliano Cabral[2], Jonathan Chase[3], Ines Martins[4], Felix May[4], Henrique Pereira[4], Marten Winter[4]
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Biodiversity loss, measured as absolute count of global extinction events, appears to be happening at an accelerated rate during the Anthropocene. While it is often assumed that global extinctions are somehow linked to local and regional extirpations, there has been little theoretical or empirical exploration of the scale-dependence of species extinctions. We provide such link by introducing the *relationship between area and per-species probability of extinction* (PxAR) and between *area and count of realized extinction events in that area* (NxAR). Using five empirical datasets collected at different spatial scales, we show a negative PxAR, but NxAR that follows a variety of functional forms, including nonlinear unimodal, multimodal and U-shaped relationships, depending on region and taxonomic group. Using a range of theoretical frameworks based on theory of island biogeography, neutral models, and species-area relationships, we show that the complex scaling of extinction rates is in fact readily expected. The uncovered wealth of forms of NxAR can help to explain why biodiversity change (i.e., the balance of losses and gains) also appears to be highly scale-dependent. Furthermore, the scale dependence of PxAR and NxAR will pose a challenge in efforts to upscale or downscale extinction rates to scales for which we have poor data, and it underscores the need to treat the extinction crisis as a scale-dependent problem.

CS11-2

Demographic strategies are more constrained in less suitable climates

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Broad-scale predictions of species' geographic redistributions have largely relied on correlative species distribution models (SDMs) that predict habitat suitability from species presences and usually current or future climate. When projecting species redistributions, SDMs assume that current linkages between climate suitability and occurrence will hold in the future, which assumes several, often untested, functional links between climate and demography. Spatially replicated demographic datasets enable direct tests of linkages between modeled climate suitability and demography. We used demographic data from the COMPADRE Plant Matrix Database and presence-based SDMs to test whether integrated measures of population performance and/or underlying demographic processes can be predicted from macroclimate suitability for 93 populations of 34 plant species worldwide. Most populations had positive population growth rates and were resistant to extinction across a wide range of climate suitability values. Macroclimate suitability did not correlate with mean asymptotic population growth rate or time to quasi-extinction. Populations in climates predicted highly suitable showed a wide range of demographic behaviors, including a greater potential for high magnitude and long lasting population size changes in response to transient perturbations. Populations in climates predicted less suitable were subject to increased retrogression (shrinkage) and temporal variability in fecundity and progression. The ability to retrogress buffered populations against extinction, while high temporal variation of progression lowered resistance to extinction. We conclude that low suitability climates constrain plant population performance and persistence, but more studies in relatively unfavourable climates are needed to understand the negative impacts of climatic stress on overall population performance and persistence.

CS11-3

Relative and synergistic effects of climate and land-cover change on species range shifts

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Climate and land-cover change are widespread and known to affect species diversity, abundance, and distribution. Changes in climatic and land-cover are therefore likely an important determinant of observed species occurrence changes. However, species can show differential responses to these global change drivers, which may be explained by species' ecological and life-history. We examined whether observed occurrence changes of 171 Ontario, Canada breeding birds between 1980-85 and 2000-05 were correlated with changes in climatic conditions and land-cover characteristics and whether interspecific response variability is explained by species' traits including habitat preferences, mean body masses and migratory strategies. We hypothesized that small-bodied non-migratory forest species will experience more severe range lost than large-bodied migrant grassland species. All species showed changes in the area of occupancy; 106 and 137 species gained or lost more than half of occupied area over 25 years, respectively. 19%, 13% and 61% of changes in species' occurrence were best predicted by changes in climate conditions, land-cover, or both, respectively. Partial migrant and large-bodied grassland species gained area occupied, while large-bodied forest species lost area occupied between sampling periods. We provide one of the few empirical tests of the relative and combined effects of climate and land-cover changes on species range dynamics and show clear effects of both stressors on bird community dynamics in Ontario. Species traits were

important predictors of interspecific variation in responses to climate and land-cover changes suggesting that a trait-based approach may hold promise for forecasting future biodiversity.

CS11-4

The relative role of vegetation-herbivores interactions, land-use, fire and climate in explaining vegetation dynamics across Europe through the Holocene

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Ecosystems have responded to past environmental changes, but sometimes at insufficient rates to maintain equilibrium with the environment. Notably, there is accumulating evidence that historical legacies play an important role in shaping current biodiversity and ecosystem patterns. This calls for caution regarding the frequent modeling assumption that species distributions are at equilibrium with their environment. It also means that understanding long-term ecosystem dynamics is crucial to improve our ability to predict future ecosystem response to environmental changes. Paleoecology offers a unique possibility to explore the long-term dynamics of ecosystems. Our study for the first time in Europe combines pollen data, charcoal data, mammal fossils, climate reconstructions and estimation of land-use in a coherent statistical modeling framework allowing the joint assessment of the importance of three external drivers, climate, fire and humans as drivers of changes in vegetation and mammal distributions, also estimating the interaction between the latter. By directly modeling the changes in spatial distributions, our study does not rely on any assumption regarding the equilibrium of species distributions with the environment. In addition, our methodological approach allows us to jointly analyze the changes in the ranges of vegetation types and large herbivore species, whilst accounting for their interdependence.
Our results highlight the importance of trophic interactions, here between large herbivores and vegetation, to understand long-term changes in broad-scale vegetation distribution. We further show that climate, fire, land-use and herbivores affect different aspects of vegetation dynamics.

CS11-5

Climatic niches in space and time: seasonal dynamics in migratory birds

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Quantification of the climatic niche is an increasingly important tool for studying species’ relationship to their abiotic environment, for example to predict how species will respond to climate change. However, because both climatic conditions and species distributions change on a variety of temporal and spatial scales climatic niches are dynamic in time and space. The almost one-fifth of birds (~2000 species) that migrate seasonally between breeding and wintering grounds, possibly to escape seasonal changes in temperate climates, pose a particular challenge to niche quantification. Using breeding and wintering range maps, we characterise the seasonal climatic niches of more than 500 closely related migratory and sedentary species of birds from across 8 monophyletic clades. Ordination methods are used to quantify seasonal niche overlap and similarity in order to understand the seasonal dynamics in climatic niches of birds. If migratory birds are moving to track seasonal climatic conditions we would expect them to have higher seasonal niche overlap than that of closely related resident species. Alternatively migratory birds might have different requirements throughout the year and “switch” climatic conditions between seasons. If this is the case we would expect migratory birds to have very different climatic niches in each season. Our results have implications for understanding the drivers of seasonal movements as well as the evolution of both climatic niches and migration.

CS11-6

Stoichiometric distribution models: Ecological stoichiometry at the landscape scale

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Human activities are altering the fundamental geography of biogeochemicals. Yet we currently lack an understanding of how the spatial patterns in organismal stoichiometry affect biogeochemical processes and the tools to predict the impacts of global changes on biogeochemical processes. In this contribution we develop stoichiometric distribution models (StDMs), which allow us to evaluate and map spatial structure in resource and consumer elemental composition across a landscape. We parameterize StDMs for a consumer-resource (moose-white birch) system and demonstrate that we can develop predictive models of resource stoichiometry across a landscape and that such models could improve our predictions of consumer space use. With results from our study system application, we argue that explicit consideration of the spatial patterns in organismal elemental composition may uncover emergent individual, population, community, and ecosystem properties that are not revealed at the local extents routinely used in ecological stoichiometry. We discuss perspectives for further developments and application of StDMs to advance four emerging frameworks for spatial ecosystem ecology in an era of global change, meta-ecosystem theory, macroecological stoichiometry, remotely sensed biogeochemistry, and individual-based spatial nutritional ecology.

Concurrent Session 12: Biological Invasion (CS12)

Session Chair: Hannah Marx
Date: January 12, 2017 10:30 am – 12:00 pm
Location: Sabino room, Marriott Hotel

CS12-1

Phylogenetic patterns of alien invasion across island archipelagos

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Species introductions provide a unique opportunity to address diversity dynamics in nature, particularly within insular island systems. As alien species continue to accumulate across the globe, it is increasingly important to predict their future spread and impact. Darwin hypothesized that the success of alien species would depend on their phenotypic similarity in the context of the native community they invade. On the one hand, he predicted alien species with novel traits would fill niche space and escape competition. However he also posited that in order to pass environmental filters in the new niche space, aliens would be phenotypically similar to the natives. Closely related species are more likely to share similar traits due to descent from a common ancestor, so phylogenetic distance is a useful proxy for assessing phenotypic similarity, especially at macro-scales. There is mounting evidence across diverse systems to support the predictive power of phylogenetic relatedness for invasion dynamics, depending on spatial scale. To address the relationship between invasion dynamics and spatial scale more systematically, we compared the evolutionary similarity of alien plants relative to the native community within 71 islands that belong to 8 tropical archipelagos using a detailed global dataset of island floras and a species-level phylogeny. We also assess potential biogeographic and climatic drivers of phylogenetic diversity patterns. This comparative phylogenetic approach has the potential to lay the foundation for a framework to predict future alien introductions across spatial scales given biogeographic parameters and evolutionary distance in the context of the native community.

CS12-2

Impact of cat predation on continental biodiversity worldwide

Corey Bradshaw[1], Delphine Ducros[2], Elsa Bonnaud[2], Timothy Doherty[3], Irene Castañeda[4], Chris Dickman[1], Franck Courchamp[5]
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The strongly negative ecological impacts of the common cat (*Felis catus*) on naïve island biota are uncontroversial. Despite consuming billions of individuals of native species on continents, its actual impacts in non-island systems remain unquantified. Previous works have focused on number of prey killed, but this doesn't equate to impact until prey population size and dynamics are taken into account. We constructed the largest global database of mainly vertebrate prey of *F. catus*, removing island-only species and unconfirmed predations, to calculate the proportion of threatened and declining prey species worldwide. Globally, and in most regions, < 12% of all confirmed prey species were threatened (Australia was the exception with around 13% of mammal prey considered threatened). Most prey species also had stable or increasing populations. Median population sizes among birds and mammals prey were in the tens of millions (except for Australian mammals at a median population size of 20,000 individuals). Population dynamics models performed for 10 major prey species in the USA show that the most predated upon are not the most at-risk from predation, and that most prey species were in fact little affected by predation. Overall, the impact of cat predation appears to be much lower on continents than on islands, and much lower than suggested by previous studies focusing on individual kills only. However, a minority of prey species are obviously sensitive to cat predation, especially in Australia where they lacked the benefit of co-evolution with native Felidae. Therefore, *Felis catus* remain a worrisome introduced predator.

CS12-3

Mycorrhizal status interacting with morphological traits help explain invasion success of alien plant species

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It is still debated whether alien plants benefit from being mycorrhizal, or if engaging in the mycorrhizal symbiosis constrains their establishment and spread in new regions. We analyzed the association between mycorrhizal status (obligate, facultative or non-mycorrhizal) of alien plant species in Germany and their invasion success. We used generalised linear models to explain the occupied geographical range in Germany, incorporating interactions of mycorrhizal status with additional plant functional traits related to morphology, reproduction, and life-history. Mycorrhizal status significantly explained the occupied geographical range of alien plant species; with facultative mycorrhizal species occupying a larger range than non-mycorrhizal aliens, and obligate mycorrhizal plant species taking an intermediate position. Additionally, aliens with storage organs, shoot metamorphoses or specialized structures promoting vegetative dispersal on the expense of high carbon demand, occupied a larger range if being facultative mycorrhizal. We conclude that being mycorrhizal is important for the establishment and persistence of aliens in Central Europe and constitutes an advantage compared to non-mycorrhizal plants. Being facultative mycorrhizal seems to be especially advantageous for successful spread, as the flexibility of this mycorrhizal status potentially leads to a broader set of ecological strategies, benefiting from trade-offs with other traits related to high carbon cost. The occupied geographical range of native plant species can be explained by mycorrhizal status similarly, but the detected trade-offs are almost absent from natives. This indicates that natives and aliens benefit differently from the symbiosis and the benefits received by natives may be independent of carbon allocation.

CS12-4
Global species invasions across time, space and taxa

Marten Winter[1], Hanno Seebens[2], Franz Essl[3], Mark van Kleunen[4], Petr Pyšek[5], Jan Pergl[6], Kreft Holger[7], Patrick Weigelt[7], Wayne Dawson[8], Tim Blackburn[8], Cesar Capinha[9], Phill Cassey[10], Ellie Dyer[11], Evan P. Economo[12], Emili García-Berthou[13], Benoit Guénard[14], Dietmar Moser[15], Wolfgang Nentwig[16], First Record Data Team
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[12]Institute of Zoology, Zoological Society of London, UK
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[15]School of Biological Sciences, University of Hong Kong
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Human-mediated transport beyond biogeographic barriers has led to the introduction of alien species in new regions worldwide. However, we lack a global picture of established alien species richness for multiple taxa as well as a comprehensive overview how alien taxa have spread over time around the globe. Here I present results of different global synthesis efforts of global alien species (1) richness patterns and reasons for them across different taxa and (2) accumulation dynamics across time. We found that hotspots based on absolute alien richness across taxa are in North America, Europe, Australasia and the Pacific Islands, while hotspots correcting for area and sampling effort are predominantly island regions. Ants and reptiles, birds and mammals, and plants and spiders form pairs of taxonomic groups with the highest spatial congruence. However, spatial congruence in alien richness among groups is lower than often observed for native species richness. Using a novel database of 45,813 first records of 16,926 alien species, we show that the annual rate of first records worldwide has increased during the last 200 years, with 37% of all first records reported most recently (1970-2014). Variation can be largely attributed to the diaspora of European settlers in the 19th century and accelerated trade in the 20th century. For all taxonomic groups, the increase in numbers of alien species did not show any sign of saturation, showing often still increases in the rate of first records over time.

CS12-5
Invasive grasses increase fire frequency and size across a range of US ecosystems

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In the US, invasive grasses are believed to alter fire regimes by increasing fuel load and continuity. In the US alone, there are 189 grass species listed as invasive or noxious, with more than 20% of these species believed to alter fire regimes based on local studies or expert knowledge. However, at regional scales, the impacts of invasive grass on fire regimes are known for only a single species, *Bromus tectorum*. Here, we quantify changes in fire size and frequency in invaded and native landcover types for nine grass species across the conterminous US. We leverage agency records of fire occurrence and size in conjunction with abundance records of invasive grass species and compare the proportion of invaded points that burned to the proportion of uninvaded points that burned, in addition to their mean respective sizes to estimate the effect of the invasive grass on regional fire regimes. Of the nine invasive grass species tested, seven are linked to significantly higher fire frequency, and seven are associated with larger fire size, suggesting that the ability of invasive grasses to alter fire regimes is pervasive across species and ecoregions. Fire frequency as much as tripled and fire size as much as doubled in areas associated with high invasive grass abundance. While many authors have highlighted the potential for an invasive grass-fire cycle, this is the first

study to quantitatively demonstrate the widespread impact of invasive grasses on fire size and frequency across a range of US ecosystems.

CS12-6

Hierarchical climatic filtering: towards a mechanistic concept of plant invasion on islands

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A mechanistic understanding of plant invasion, especially in relation to how climatic conditions control these processes, is still missing. We develop and test a theoretical framework called hierarchical climatic filtering that captures the principles of changing hierarchies of abiotic factors in driving plant invasion. We expect a *gateway filter* to drive alien establishment by selecting species with climatic requirements overlapping the gateway region. Then a *system imminent filter* acts along climatic gradients structuring alien niche widths within an island. Both filters select for alien generalists by favoring large niche widths due to the increased likelihood of generalists to overcome the gateway filter. Once established alien generalists are able to spread into other climatic conditions within the island, while this is not the case for alien specialists adapted to the gateway conditions. We test these assumptions by using thirteen elevational transects on windward and leeward sides of six high elevation islands. Understanding the basic mechanisms of plant invasions might help predict future invasions on islands, which are particularly vulnerable to human-induced alterations.

Concurrent Session 13: Biodiversity Patterns and Maintenance (CS13)

Session Chair: Deborah Boro
Date: January 12, 2017 1:30 pm – 3:30 pm
Location: Canyon ABC room, Marriott Hotel

CS13-1

No effect of patch area and isolation on plot-scale species richness after controlling for habitat amount

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The habitat amount hypothesis predicts that the effects of both patch area and isolation on species richness at a plot can be replaced by the effect of a single variable, habitat amount in the local landscape surrounding that plot. We tested the habitat amount hypothesis using forest understory herbaceous plant data from Ontario, Canada. Data were species occurrences and forest cover from 189 forest plots. If the habitat amount hypothesis is correct, the effect of forest amount in the local landscape surrounding a sample plot encapsulates both the effects of local patch area and

isolation on species richness. We tested six predictions from the hypothesis: forest amount in the local landscape should have a positive effect on plant species richness at a sample plot when the local patch area (prediction A) or local nearest neighbor patch distance (prediction B) are controlled. Conversely, local patch area (prediction C) and nearest neighbor distance (prediction D) should have no effect on plant species richness at a plot when the effect of forest amount in the local landscape is controlled. In addition, plant species richness at a plot should increase with increasing forest amount in the local landscape even if the local patch area decreases (prediction E) or nearest neighbor distance increases (prediction F). Our results supported all predictions, except E. We conclude that patch area and isolation effects are simply components of the habitat amount effect. For predicting plot-scale species richness, patch area and patch isolation can be replaced by habitat amount.

CS13-2 Investigating the resource breadth hypothesis as a mechanism for the abundance-occupancy relationship

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The abundance-occupancy relationship (AOR) is a nearly-ubiquitous observation in biogeography, in which species with expansive distributions are locally common while species with restricted distributions are rare. Although AORs have been observed in a wide variety of taxa and spatial scales, the mechanism(s) that drive this relationship are not well understood. We tested one such mechanism—dietary generalism—and predicted that species that use a wide variety of C_3 and C_4 resources (dietary generalists) would occupy more sites and be more abundant given occupancy than dietary specialists. Using mark-recapture analysis we found a positive abundance-occupancy relationship among 8 small mammal species across a large rainfall gradient in Laikipia, Kenya. Within this AOR, we used hair carbon and nitrogen isotope values to quantify population-level diet breadth, which we compared to available forage biomass to assess if a species was a dietary generalist or specialist. While the most abundant and widespread species (*Gerbilliscus robustus*) was a dietary generalist and the two rarest species (*Grammomys dolichurus* and *Graphiurus microtis*) were C_3 dietary specialists, there was no clear pattern between abundance-occupancy and foraging strategy for the other 5 species. Our results provide mixed support for Brown's resource-breadth hypothesis, which posits that differences in niche width underlie the AOR.

CS13-3

Variation in interaction networks across local to regional scales

Daniel Carstensen
Center for Macroecology, Evolution and Climate, Copenhagen, Denmark

Interactions constitute an integral part of biodiversity, forming complex networks that vary across space and time. Even without spatial or temporal constraints the identity of pairwise interactions may vary across space, but this variability is not well understood. Here, we study the spatial variation in network structure and in the identity of pairwise interactions across local and regional scales. Specifically, we investigate whether the beta diversity of species and interactions follow a similar trend across space, and attempt to explain the turnover of pairwise interactions. We find that the turnover of species and interactions is positively correlated with geographical distance at both local and regional scales. Replacement of species is a major driver of interaction turnover but interactions between repeatedly co-occurring species also vary, or rewire, to an extent which is also positively correlated with distance between communities. Furthermore, at the species level, the number of interaction partners and the identity of these vary increasingly with distance. Local abundance and trait complementarity are both important for the local realization of interactions and thus for network turnover. Increasing our knowledge on the variability of interactions is important for understanding the importance of interactions in forming species distribution patterns, understanding ecosystem function and stability, and the prospects of eventually inferring interaction networks from proxies.

CS13-4

Does the colonization of new biogeographic regions influence the diversification and accumulation of clade richness among the Corvides (Aves: Passeriformes)?

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Regional variation in clade richness can be vast, reflecting differences in the dynamics of historical dispersal and diversification among lineages. Although it has been proposed that dispersal into new biogeographic regions may facilitate diversification, to date there has been limited assessment of the importance of this process in the generation, and maintenance, of broad-scale biodiversity gradients. To address this issue, we analytically derive biogeographic regions for a global radiation of passerine birds (the Corvides, c. 790 species) that are highly variable in the geographic and taxonomic distribution of species. Subsequently, we determine rates of historical dispersal between regions, the dynamics of diversification following regional colonization, and spatial variation in the distribution of species that differ in their rates of lineage diversification. The results of these analyses reveal spatiotemporal differences in the build-up of lineages across regions. The number of regions occupied and the rate of transition between regions both predict family richness well, indicating that the accumulation of high clade richness is associated with repeated expansion into new geographic areas. However, only the largest family (the Corvidae) had significantly heightened rates of both speciation and regional transition, implying that repeated regional colonization is not a general mechanism promoting lineage diversification among the Corvides.

CS13-5

Stability and distribution of predator–prey systems: local and regional mechanisms and patterns

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Explaining the coexistence and distribution of species in time and space remains a fundamental challenge. While species coexistence depends on both local and regional mechanisms, it is sometimes unclear which role each mechanism takes in a given ecosystem. Consequently, it is very hard to predict the response of the ecosystem to environmental changes. I will present a recent model we developed to study spatial patterns of coexistence, focusing on predator–prey and host–parasite populations (Ecol. Lett., 19(3):279-288 (2016)). I will show, both theoretically and empirically, that these systems may exhibit both local and regional patterns and mechanisms of coexistence. Changes in environmental parameters, such as spatial connectivity, may lead to a transition from regional to local coexistence or it may lead directly to extinction, depending on demographic parameters. This demonstrates the importance of simultaneously analysing interacting mechanisms that act at different spatial scales to understand the response of ecosystems to environmental changes.

CS13-6

Uncovering the extraordinary pace of hybridization on wild species: a crocodiles' story

Ella Vázquez-Domínguez[1], Gualberto Pacheco-Sierra[1], Jéssica Pérez-Alquicira[1], Marco Suárez-Atilano[1], Zachariah Gompert[4]
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Hybrid zones represent natural laboratories to study gene flow, divergence and the nature of species boundaries between closely related taxa, whole also are hotspots of biodiversity. We evaluated the level and extent of hybridization between *Crocodylus moreletii* and *C. acutus* using morphological, genetic and genomic data (400 crocodiles from 76 localities), including the entire historic range and sympatric zone of the two species. Contrary to expectations, Bayesian admixture proportions and maximum likelihood estimates of hybrid indexes revealed that most sampled crocodiles were admixed and that the hybrid zone is geographically extensive, extending well beyond their historical region of sympatry. Our results suggest that hybridization has been going on for several to many generations. We identified a few geographically isolated, non-admixed populations of both parental species. Also,

non-admixed individuals from the two species were distinguishable based on morphological characters, whereas hybrids had a complex mosaic of morphological characters that hinders identification in the wild. Importantly, very few non-admixed *C. acutus* and *C. moreletii* populations exist in the wild; in consequence, the last non-admixed *C. moreletii* populations have become critically endangered. Indeed, both the parental species and the naturally occurring hybrids should be considered for their potential conservation value.

CS13-7

Patterns of Amphibian trait diversity of the New World

Leticia Ochoa-Ochoa[1], Nancy Mejía-Domínguez[1], Katharine Marske[2], Carsten Rahbek[3]
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We examine the distribution of diversity of life history traits for American Amphibians and explore potential environmental conditions which might underlie these patterns. Also we explored the relationship between species and trait diversity. As measure of functional diversity we estimated a multi-trait index of functional diversity based on nine traits (including size, habitat use, and reproductive aspects) and calculated trait diversity and evenness using Hill numbers, Shannon and Gini-Simpson indices. To characterize the relationship between trait diversity and climate we performed autoregressive models (SAR) including different regional additional weights to account for the influence of the source pool defined as: dispersion field, biomes, terrestrial and freshwater ecoregions. With the positive upper quartile and negative lower quartile of the species ~ trait diversity residuals, we performed SAR with the same variables. We obtained 212 different traits for 2776 species. The regions with highest diversity of traits were mountainous (e.g. Appalachians, Andes, Guyana's Shield, southeast coast of Brazil). The best fitting SAR models did not include additional regional weights for all diversity indices except Shannon. Evenness of trait structure of amphibian assemblages varies depending on the region, but in general is high. Overall trait diversity is positively correlated with humid and warm environments with low precipitation seasonality. However, areas with more traits than expected, given the species diversity, are associated to water availability as precipitation and low precipitation seasonality regardless of temperature.

CS13-8

When the species-time-area relationship meets island biogeography: Diversity patterns in avian communities over time and space on a subtropical archipelago

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The species-area relationship and the species-time relationship are of vital importance in community ecology. Previous studies have suggested that a unified, general species-time-area relationship (STAR) may hold, with comparable but non-independent scalings of richness across space and time. Most studies to date considered relatively homogeneous habitats, with sampling curves for SARs and STRs. Here, we aim to (1) test the generality of STAR relationship in an island system (2) and assess which factors, other than area, influence species richness, species accumulation, and turnover through time. We surveyed bird communities on 36 islands using line transects, and calculated annual species richness of breeding birds from 2007 to 2015, in Thousand Island Lake, China. We built STAR models at both island and transect levels. We employed partial correlations and multiple regressions to examine potential influence of island attributes other than area (i.e. isolation, edge effect, habitat richness and elevation) on the slopes of STRs. The STAR models explained 89.6% and 83.2% of the total variance, respectively, and both models have a significant negative space-time interaction. The STAR pattern indeed generalised to an island system, indicating an interdependency of time and space in determining species richness. Islands attributes other than area could influence patterns of species accumulation and turnover through time. There is an intriguingly high degree of temporal turnover in the bird community, which we suggest may be related to the edge habitat on an island. Overall, we recommend ecologists should consider the role of both space and time, along with their interdependency, when characterising patterns in species richness.

Concurrent Session 14: Island Biogeography (CS14)

Session Chair: Robert Anderson
Date: January 12, 2017 1:30 pm – 3:30 pm
Location: Madera room, Marriott Hotel

CS14-1

Are we close to understanding island diversity?

Michael Borregaard[3], Robert Whittaker[1], Jonathan Price[2]
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Island biogeography focuses on understanding the processes that underlie a set of well-described patterns on islands, but lacks a unified theoretical framework for integrating these processes. The recently proposed General Dynamic Model (GDM) of oceanic island biogeography promises a step towards this goal. We used computer simulations to extend the GDM to include subduction-based island arcs and continental fragment islands, revealing how the geological dynamics of these distinct island types are predicted to lead to markedly different evolutionary dynamics. However, many of the key processes within the GDM operate at the scale of archipelagos, rather than islands. By quantifying the processes of colonization and speciation at the archipelagic scale, it appears to be possible to disentangle the effect of the important processes underlying island diversity.

CS14-2

A generalization of the taxon cycle

Manuel Steinbauer
Ecoinformatics & Biodiversity, Department of Bioscience, Department of Bioscience, Aarhus University

Analyzing species-specific dispersal characteristics and systematic within-island differences in isolation I will show how environmental pre-adaptation, dispersal traits as well as directional dispersal vectors (wind current systems, bird migration routs etc.) cause colonization rates to differ between species resulting in distinct, observable spatial patterns of isolation within islands that may vary with time. These findings, together with mounting evidence for species-specific evolutionary pathways gained from phylogenetic studies, urge us to integrate species characteristics and interactions in the environmental context within islands for novel developments of island biogeographical theory. A generalization of Wilson`s taxon cycle related dynamics for differing species groups and the complexity of entire island systems would allow to acknowledge that species interact within local communities and will help bridge analyses of short-term species interactions (ecology) and long-term evolution.

CS14-3

Island Species–Area Relationships: Form and Application

Robert Whittaker[1], Tom Matthews[1], Kostas Triantis[1], Francois Guilhaumon[1], Michael Borregaard[1]
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The island species–area relationship (ISAR) has broad applicability in ecology and conservation. However, the precise form of the relationship in different island types, and the biological mechanisms underpinning the observed form of the relationship, is still debated. To this end, we undertook the largest comparative study to date of the form of the island species–area relationship (ISAR) using 207 habitat island datasets and 601 true island datasets. We used an information theoretic approach to compare the fit of 20 ISAR models to these different island datasets. We analysed how the z- and c-values of the power (log–log) model varied between different island types, and which ecological and geographical factors influenced z and c values. We also examined the relationship between beta-diversity and z values. Our multimodel comparisons demonstrated the nonlinear implementation of the power model to be the best overall model, and thus to be a sensible choice for general use. Average z values were significantly lower for habitat island datasets than for true islands. There was a significant positive relationship between z values and beta-diversity for true islands, but not for habitat islands. As the z value of the log–log power model varied in relation to ecological and geographical properties of the study systems, and as both z and c values show much variation within island types and taxa, we conclude that caution should be employed when using canonical values for applied purposes, such as forecasting extinction debts.

CS14-4

Disentangling the drivers of species richness in island floras

Jonathan Price[1], Michael Borregaard[1], Robert Whittaker[2], Holger Kreft[3], Patrick Weigelt[4], Luis Valente[5]

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The floras of oceanic islands are formed by an equilibrium among three processes: immigration, speciation and extinction. The diversity dynamics of island plants are best characterized at the archipelago scale, at which colonizing species form endemic radiations that are increasingly documented by phylogenetic studies. Here, we present a global analysis of the relative contribution of the main processes of immigration and speciation to island plant diversity for 24 archipelagos, representing a majority of the world's oceanic archipelagos within the subtropical and tropical climate zones. We estimate the number of colonization events based on the phylogenetic relationships among species on 11 archipelagos that have numerous, well-resolved phylogenies. For an additional 13 archipelagos, we develop a heuristic sampling tool that generates a probability distribution for the estimated number of colonization events, based on the taxonomic status of endemic species and genera in published checklists. The heuristic is parameterized using checklists and phylogenies for the 11 well-resolved archipelagos. The number of speciation events is then determined as the total number of species minus the number of colonization events. The results reveal that the well-known species-area relationship for archipelagos is driven most strongly by differences in within-archipelago rates of speciation. The modest slope of the Colonization Area Relationship ($z = 0.19$) may relate to the highly dispersable nature of island floras. The steep slope of the Phylogenesis Area Relationship ($z = 0.87$) is consistent with similar relationships in both island and continental systems.

CS14-5

Great theories of species diversity in space: Who thought of them first?

Even Tjørve[1], Kathleen Tjørve[2], Arnost Sizling[3], Eva Sizlingova[3]
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Each epoch has given rise to groundbreaking theories, though sometimes we stumble over literature revealing somebody else has already proposed them much earlier. The early age of theoretical and geographical ecology was pioneered chiefly by Europeans, but with the rise of systems ecology and theoretical ecology in the 1960s and 70s, the Americans took the lead. New theories in ecology and biogeography were linked to the species-area relationship (SAR), as Darlington's rule, Preston's canonical hypothesis, MacArthur and Wilson's equilibrium theory, Diamond's rules of reserve design, and Coleman's random-placement theory. In 1989 Brown and Lomolino reported Munroe's "independent discovery of the equilibrium theory of island biogeography", fifteen years before MacArthur and Wilson. Going back to the 1920s and the "Uppsala School" of community ecologists, we discovered they had already accomplished much of what Darlington, Preston, Coleman, and others did only half a century later – and they had proposed the same theories. These early Scandinavian botanists worked with sample areas as well as island systems, examining spatial patterns and even attempting to build species-area models from natural laws. We examined their publications (which are usually in Swedish) and recalculated their results from their original data, and compared these to the later rediscoveries of their theories.

CS14-6

First test of the trait-based model of dynamic island biogeography: small mammals on Venezuelan sky islands

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Major challenges exist for considering the roles of historical and regional processes in determining local communities. We provide the first test of the trait-based model of dynamic island biogeography, which helps fill this gap in theory (Burger et al., this conference). The model uses organismal traits and environmental conditions to predict species composition for islands or habitat patches that are dynamic through time (due to directional or cyclical environmental changes). It does so via: 1) colonization probability, which reflects a species' ability to cross the matrix; and 2) extinction probability, which depends on spatial requirements for population maintenance. We apply the model to small non-volant mammals from two montane "sky islands" in northern Venezuela: the Serranía de San Luis and the tiny, peripheral Cerro Santa Ana. We tested hypotheses of: 1) differential immigration from San Luis to Santa Ana, via mesic fidelity; and 2) differential extinction on Santa Ana, using body size/home-range scaling. We detected only weak insinuation of lesser immigration by species with higher mesic fidelity, yet found a strong pattern of higher extinction of species with greater home-range needs. This result matches the trajectory for this fauna inhabiting mesic areas currently constricted during an interglacial. Using this model, trait data should hold general utility in biogeography.

CS14-7

Parallel Ecological-Evolutionary Processes in: Microbes–Macrobes, Alleles–Taxa, the Past and Present?

Michael Dawson[1], J Beman[2], Jessica Blois[3], Julian Sachs[4], Herwig Stibor[5], Stephan Behl[5], Matthew Meyerhof[2], Tessa McGee[6], Philippe Pondaven[7], Lauren Schiebelhut[2], Holly Swift[2], Jesse Wilson[2]
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Marine lakes present hundreds of independent evolutionary ecological 'natural experiments'. These systems can reveal the extents to which deterministic and stochastic processes (e.g. drift, selection) influence taxonomic, genetic, and functional diversity in parallel culminating in shared and unique attributes of modern communities. Each lake has a high-resolution sedimentary record for its ~6000-15000 year history so we can comprehensively describe modern patterns of biodiversity of microbes and macrobiota, and how these communities assembled and changed through time. We surveyed a total of ~15000 geolocated datapoints and collected ~1500 samples of modern marine microbes, invertebrates, fishes, and algae in 15 lakes for comparative species- and genetic-level analyses. We recovered sediment cores up to 15 m deep and >10,000 years old from 5 lakes. Experiments with microbial communities explored how functional diversity is shaped by, and shapes, environmental variation, with potential knock-on effects for macrobiota. Our preliminary analyses indicate the following. (1) Macrobiota and microbiota show somewhat similar patterns of diversity in relationship to area and distance; those predominantly deterministic patters are overlayed by some non-equilibrium dynamics. (2) Alleles may predominantly drift, while species may be filtered; in part physical properties and microbes shape—and are shaped by—the environment, which in turn influences communities of macrobiota. (3) Environmental variation within a lake through time can exceed current variation among lakes; changes may be driven in general by climate, but internal dynamics also need to be explained.

CS14-8

Environmental filtering not dispersal limitation shapes the Galápagos archipelago flora

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Remote locations typically harbor relatively few species, some of which go on to generate endemic radiations. Colonizing species tend to be a non-random subset from source communities, which is thought to reflect dispersal limitation. For instance, colonizers of remote oceanic islands should be the continental species with high dispersal ability. However, environmental characteristics of the islands could also impose a strong filter to species, whereby only a few continental species arriving to those islands are able to establish. We integrate information on species evolutionary relationships, dispersal strategies, and distributions to infer the relative importance of dispersal versus environmental filtering in structuring Galápagos native flora. Using a comprehensive regional phylogeny for ~39,000 species, we found that the native flora of the archipelago is a phylogenetically non-random subset of the continental pool of potential colonizers. In addition, we found evidence that suggest environmental filtering is more important than dispersal in determining species composition of the archipelago. First, the match between species' continental climate niche and the climate of the Galápagos was a better predictor of colonization success than species' dispersal strategy. Second, the phylogenetic structure of native species inhabiting individual islands within the archipelago was better explained by island area and climate, rather than island isolation. Our results can help to explain why adaptive radiation is common on oceanic islands as they suggest that some colonizing species can be relatively poor dispersers with specific niche requirements, facilitating reproductive isolation and niche differentiation.

Concurrent Session 15: Climate Change Biogeography (CS15)

Session Chair: Caroline Greiser
Date: January 12, 2017 1:30 pm – 3:30 pm
Location: Pima room, Marriott Hotel

CS15-1

Projected changes in prevailing winds for transatlantic migratory birds under global warming

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A number of terrestrial bird species that breed in North America cross the Atlantic Ocean during autumn migration when travelling to their non-breeding grounds in the Caribbean or South America. When conducting oceanic crossings, migratory birds tend to associate with mild or supportive winds, whose speed and direction may change under global warming. The implications of these changes for transoceanic migratory bird populations have not been addressed. We used eBird occurrence information to estimate the geographic location and timing of transatlantic migration. We estimated how prevailing winds are projected to change within the transatlantic flyway using daily wind speed anomalies (1996-2005 and 2091-2100) from 29 Atmosphere-Ocean General Circulation Models implemented under CMIP5. Autumn transatlantic migrants have the potential to encounter strong westerly crosswinds early in their transatlantic journey at intermediate and especially high migration altitudes, strong headwinds at low and intermediate migration altitudes within the Caribbean that increase in strength as the season progresses, and weak tailwinds at intermediate and high migration altitudes east of the Caribbean. Thus, as global warming progresses, the need for species to compensate or drift under the influence of strong westerly crosswinds during the initial phase of their autumn transatlantic journey may be diminished. Existing strategies that promote headwind avoidance and tailwind assistance will likely remain valid. Thus, climate change may reduce time and energy requirements and the chance of mortality or vagrancy during a specific but likely critical portion of these species' autumn migration journey.

CS15-2
Spatial and temporal patterns of global environmental predictability

Andreas Schweiger
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Global climate change has been shown in numerous studies to affect the functioning of ecosystems. The ecological consequences of gradual shifts in temperature and precipitation are thereby well recognized and extensively studied for all biomes of the world ranging from tropical rain forests to high latitude tundra systems. In contrast, knowledge about changes in environmental predictability and its ecological consequences is largely missing so far. However, the predictability (stochasticity) of environmental conditions is of major evolutionary but also ecological importance as several empirical and theoretical studies show. Thus, studying the temporal changes in environmental predictability seems to be of major importance in basic as well as applied ecological and biogeographic research. Here we provide a global map of the predictability, variability and periodicity of air temperature and precipitation based on climatic data with high spatial and temporal resolution (monthly values of temperature and precipitation with 0.5 degree spatial resolution). We furthermore provide spatial information about the temporal changes of all three measures over the last century and demarcate differences in environmental predictability, variability and periodicity and their temporal changes for all major biomes of the world. By providing this kind of information with a global extent we hope to stimulate research on a very important but still understudied topic.

CS15-3
Ectomycorrhizal symbioses facilitated rapid post-glacial expansion of North American tree distributions

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Between 16 and 7 thousand years before present, the distributions of North American tree genera shifted dramatically, corresponding to rapid changes in temperature and widespread retreat of continental ice sheets. The rate and direction of these shifts varied widely across taxa for reasons that remain unclear. Trait-based explanations have yet to satisfactorily explain this variation, while explanations focused on biotic interactions are often invoked as alternatives, but are difficult to test. Symbioses between trees and mycorrhizal fungi can profoundly influence host establishment and resilience, but their roles in biogeographic processes remain poorly understood.
Using a multi-model inference approach, we explored climate velocity, shade tolerance, seed mass, cold tolerance, maximum height, and mycorrhizal type (ectomycorrhizal or “EM” versus arbuscular mycorrhizal) as potential predictors of rates of post-glacial distribution expansion (at leading boundaries) and contraction (trailing boundaries) among 23 dominant North American tree genera. We also explored promiscuity (number of compatible mycorrhizal fungi) as a predictor among the 13 EM tree genera. Climate velocity, cold sensitivity, and mycorrhizal type were strong predictors of the rate of distribution contraction, together accounting for 33% of the variation, while distribution expansion rates were poorly explained overall. However, among the 13 EM genera, promiscuity and seed mass accounted for a remarkable 62% of the variation in distribution expansion rate, with the former variable accounting for 44% of the variation on its own. Our results reinforce calls to include biotic interactions alongside trait- and climate-related variables when evaluating and modeling the drivers of geographical range shifts.

CS15-4

Modelling forest understory climate to detect microrefugia and stepping stones

Caroline Greiser[1], Eric Meineri[2], Miska Luoto[3], Johan Ehrlén[2], Kristoffer Hylander[2]
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[3]University of Helsinki, Finland

Microclimate models improve spatial predictions of species range shifts, the spread of invaders, the survival in climate refugia and establishment in stepping stone habitats. The majority of models have been done in montane landscapes, accounting for local topography. Only few have taken up the challenge to model near-ground temperatures in lowland forests, which may be much more moderated by vegetation. We want to quantify the relative influence of forest features (density, composition) and topography on understory temperatures in managed forest of the southern boreal zone. A grid of 208 loggers in an area of ~ 24 000 km^2 recorded temperature and humidity over one year. Remote sensed and field-based data of topography and forest structure, together with weather station data of cloudiness, were used to model daily minimum and maximum temperatures and their monthly averages. We combined multiple regression with spatial interpolation to produce temperature maps with a 50-m-resolution. The first daily models of summer 2015 show that canopy cover had the largest influence on minimum and maximum temperatures, and that topography plays only a secondary role. The models for maximum temperature had a lower performance than for minimum temperature, but could be improved by including air humidity. We could better model maximum temperature on cloudy days, due to extreme heterogeneity of light and temperature on the forest floor during sunny days. Our results highlight that vegetation dominates over topographic drivers of local temperature in forested lowlands, which opens up the opportunity of managing climate with wisely managing our forests.

CS15-5

Predictability in community dynamics

Benjamin Blonder[1], Derek Moulton[1], Jessica Blois[2], Brian Enquist[3], Bente Graae[3], Marc Macias Fauria[3], Brian McGill[4], Sandra Nogue[4], Alejandro Ordonez[5], Brody Sandel[5], Jens Christian Svenning[6]
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The coupling between community composition and climate change can be conceptualized as a gradient from perfect tracking to lags. The no-lag hypothesis is the foundation of correlative species distribution modeling and many climate reconstruction approaches based on analysis of paleoecological data. Simple lag hypotheses have become prominent in disequilibrium ecology, proposing that communities track climate change following a fixed function or with a time delay. However more complex dynamics are possible and may lead to memory effects and alternate unstable states. We develop graphical methods for assessing these scenarios and show that these dynamics can appear in even simple models. The overall implications are that 1) memory effects and alternate unstable stable states are common, and 2) detailed knowledge of past climate change and community states will often be necessary yet sometimes insufficient to make accurate predictions of a community's future state.

CS15-6

Adaptation corridors: integrating genetic information into the mapping of past and future climate corridors

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Genetic adaptation can play an important role in driving species distributions, yet this sort of information is rarely integrated into models of species responses to climate change. Here, we present a new method to model shifts in species distributions in response to climate change while taking into account population-level adaptive genetic differentiation. We illustrate this method using balsam poplar (*Populus balsamifera* L.), a northern broad leaf tree species. Using generalized dissimilarity modeling, for each population we identified a series of locations through time, since the last glacial maximum, that minimized the genetic distance with respect to current climate. We call these series of locations an 'adaptation corridor,' which we used to estimate the velocity at which populations would need to migrate in order to track climatic change while minimizing the amount of adaptive evolution required. We repeated this process for future climate scenarios and compared the predicted future and past velocities. We found that predicted future migration velocities along adaptation corridors far outpace predictions of past migration velocities. Furthermore, in comparison with a method that ignored adaptation and just minimized climatic distance, we found that the genetic-based distance predicted faster migration velocities required for populations to keep pace with climate change. These finding suggests that, not only may the rate of future migration need to be faster to keep pace with future climate change compared to past climate change, but that methods based solely on climate may underestimate the velocity required for populations to successfully track future climates.

CS15-7

Predicting persistence of marine invertebrates: flow patterns influence poleward dispersal and tolerance phenotypes

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Species persistence in future climates depends on redistribution and adaptation potential, both of which depend on dispersal ability. Dispersal may be limited for marine species where currents flow opposite the direction of climate shifts. We determined the relationship between flow dynamics, population growth, and thermal tolerance for mussels on the US west coast. We paired intensive time-series observations of recruitment and thermal tolerances of mussel cohorts with simulated dispersal using ocean circulation models. Modeling results were used to predict the proportion of individuals in each recruiting cohort that originated from sources south or north of our study site. We found that recruitment of both total individuals and those of southern origin increased during periods of poleward flow. However, thermal tolerance of mussel recruits was higher during periods of lower recruitment and equatorward flow. Thus, conditions likely to promote persistence under climate change – including increases in poleward dispersal and population tolerances – are decoupled. Persistence will depend on trade-offs between distributions of population sizes and tolerance phenotypes.

CS15-8

Biogeography of tropical montane epiphytes: considering Rapoport's rule, climatic tolerance and elevational shifts

Emily Hollenbeck[1], Dov Sax[1]
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Tropical montane forests are staggeringly biodiverse, and may be at high risk due to climate change. However, very little is currently known about the biogeography and climatic niches of tropical species, making risk assessments elusive. This study provides a first estimate of distribution patterns and climatic sensitivity for 557 species from two genera of tropical epiphytic plants. We analyzed over 30,000 GBIF occurrence records to characterize the geographic and elevational ranges of each species, and also tested whether species with large latitudinal ranges occupy different elevations in different latitudes. We found a positive relationship between elevational and latitudinal range size (R^2=0.15 and 0.20 for the two genera, both with $p<0.01$). Rapoport's rule, the validity of which has been debated for tropical systems, was tested on both latitudinal and elevational gradients using several methods. In all cases, the Stevens method supported Rapoport's rule, with larger average range sizes represented in higher latitudinal and elevational bands. In contrast, the midpoint method yielded the opposite pattern, with peaks in range size at the equator and mid-elevations, due to the mid-domain effect. Finally, among wide-ranging species, only 65% occupy a wide elevational range across latitudes, while 25% of the species appear to track temperature:

they are found at high elevations near the equator and descend in elevation at higher latitudes. Despite having wide geographic and elevational ranges, these species may be occupying a narrower climatic niche than estimated based on overall range extent, and should be of elevated conservation concern due to climate change.

CS16 Models and drivers of biogeographic patterns

Concurrent Session 16: Models and drivers of biogeographic patterns (CS16)

Session Chair: Cynthia Wallace
Date: January 12, 2017 1:30 pm – 3:30 pm
Location: Sabino room, Marriott Hotel

CS16-1

Mapping Presence and Predicting Phenological Status of Invasive Buffelgrass in Southern Arizona Using MODIS, Climate and Citizen Science Observation Data

Cynthia Wallace
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The USGS has developed a new and innovative suite of landscape metrics (i.e., “Climate-Landscape Response” or CLaRe metrics) that have proven effective for mapping when and where invasive buffelgrass (*Cenchrus ciliaris*) is green in Saguaro National Park (SNP) near Tucson, Arizona (see: doi:10.3390/rs8070524). Buffelgrass fills the interstices between widely-spaced desert plants, forming a continuous mat of fine fuels that can carry fire widely across the non-fire adapted Sonoran Desert landscape. The introduction of frequent, intense fire has the potential to transform the iconic, species-rich, ecosystem into a monotypic grassland. CLaRe phenometrics capture the strength of the landscape greenness response to climate and expose buffelgrass due to its rapid and strong response to recent precipitation. Buffelgrass remains dormant much of the year, but has short windows when it is photosynthetically active and vulnerable to herbicide. By knowing when and where buffelgrass is green, land managers can optimize their treatment activities. In addition, current results suggest that it is possible to detect nascent populations of buffelgrass comprising less than 5 percent of the landscape by monitoring CLaRe phenometric trends. This is the first technique that can map the location and phenological status of buffelgrass, including newly established populations, on a regional scale. This method may be transferable to many other invasives that display similarly rapid and strong response to precipitation, including Lehman’s lovegrass (*Eragrostis lehmanniana*) and cheatgrass (Bromus tectorum).

CS16-2

Mechanistic modeling of environmental controls on of woolly mammoth carrying capacity and extinction on St. Paul Island, Alaska

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The late Quaternary megafaunal extinctions are a natural system for studying the patterns and mechanisms of species extinction. On St. Paul Island, a small (110km^2) isolated remnant of the Bering Land Bridge, a late-surviving population of woolly mammoth (*Mammuthus primigenius*) persisted until 5,600 +/-100 yr BP, at a time with no known human presence. Proposed drivers include temperature changes, food resource loss and freshwater shortage. Here we estimate the carrying capacity for mammoths on St. Paul Island and tested these three hypothesized extinction drivers, using a physiological model (Niche Mapper) to estimate mammoth metabolic rate, dietary requirements, and freshwater requirements. Niche Mapper simulations were driven by alternate climate driver datasets from the Community Climate System Model version 3 (CCSM3) SynTrace simulations and alkenone temperature reconstructions, vegetation simulations from the LPJ-GUESS dynamic vegetation model, and newly tabulated trait data for woolly mammoths. Results indicate island vegetation primary productivity and freshwater availability tightly constrained the carrying capacity of St. Paul for mammoth populations, with less than 20 individuals set by forage availability in the middle Holocene, due to island area loss by sea level rise. The Niche

Mapper simulations also suggest the mammoth populations could not have been sustained by inland maar lakes, and so were highly vulnerable to the loss of coastal lagoon freshwater sources by hydrological variability or saltwater intrusion. The Niche Mapper simulations are consistent with the available proxy data, help resolve the drivers of extinction, and reinforce the high vulnerability to extinction for a small island megaherbivore population.

CS16-3

Modeling seasonal distributions of migratory birds

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Billions of small birds migrate regularly between continents as an adaptation to predictable seasonal changes of resources. Such movements have great impact on biodiversity but understanding migrants ecological niches and how populations and individuals fit their annual schedules to seasonal resource availability remain poorly understood. Technological developments have only recently allowed detailed spatiotemporal mapping of the seasonal distributions of small, long-distance migrants. Many species show much more complex movement patterns than just commuting between breeding and wintering grounds posing great challenges for modelling their distributions. We model the seasonally changing distribution of the common cuckoo in a single species distribution model covering the annual cycle using spatiotemporally explicit environmental data. Based on maximum monthly temperature, mean precipitation of the previous month, mean monthly NDVI and the difference between the month's NDVI and that of the previous month, our model predict seasonal changes well with apparent generality at the species-level. Most migratory bird species are declining and our model holds great promise for guiding effective conservation measures as well as a basis for evaluating effects of climate change. Forecasts of migrants' distributions need to be based on projected seasonal vegetation changes as within-year changes, i.e. how seasons are affected, are most important with potential mismatching between resources and birds' occurrence in the future.

CS16-4

Modeling the pathogenic niche of Ebolavirus for a more reliable transmission risk assessment

Erica Johnson[1], Carlos Zambrana-Torrelio[2]
[1,2]EcoHealth Alliance, New York, United States

The ability to map the distribution of diseases, predict their potential dispersal and determine high risk areas of transmission is of great interest to epidemiologists, public health and policy makers. Nonetheless, the complex ecological and evolutionary processes underlying pathogen distributions have been widely ignored until the fairly recent establishment of disease ecology. Ecological Niche Models (ENM) have been frequently used to assess risk of transmission by modeling suitable habitat for host species. This however, misrepresents potential disease distribution since pathogen presence is dependent on host presence, but the opposite is not true. For this reason, the nature of host-pathogen relationships must be considered when applying ENMs to predict pathogen habitat suitability. More importantly, risk can only be defined relative to a target population (e.g. humans, cattle) and its interactions with hosts or pathogens. We present an improved framework for transmission risk assessment, using Ebolavirus as an example that 1) models habitat suitability using pathogen occurrence data including host presence as a predictor variable and 2) includes target population data.

CS16-5

News from the roof of Africa: Which factors structure plant-pollinator networks along elevational gradients on Mount Kilimanjaro?

Alice Classen[1], Marcell Peters[2], Ingolf Steffan-Dewenter[1]
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The degree of specialization in species and mutualistic networks is widely assumed to decline from the tropics to the poles, but empirical evidence is rare. Here we used the unique environmental amplitude of Mt. Kilimanjaro to study plant-pollinator interactions in different climates, spanning an elevational gradient of 3.4 km. Based on 83 observed networks, we calculated local specialization of plants and pollinators on species and network levels and found that specialization decreased with increasing elevation. Mean annual temperature was the best predictor of specialization, while species richness and pollination-relevant traits (e.g. tongue length) could not be linked to levels of specialization. The impact of temperature on species and network specialization decreased with increasing proportions of syrphid flies in pollinator communities. Using thermo-block experiments, we show that syrphid flies tolerate lower temperatures than e.g. bees. We conclude that temperature shapes species and network specialization patterns along climatic gradients, but the extent of this effect depends on the cold-sensitivity of the involved taxonomic groups.

CS16-6

Productivity and snow persistence drive multiple vegetation properties in low-energy systems

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Climatic and edaphic conditions are considered to be the main drivers of high-latitude ecosystems. Still, vegetation modelling studies struggle to find the most influential predictors with robust biophysical bases and ecophysiological relevance. We used all available Landsat clear-sky images from 1984 to 2015 to construct four biophysically based predictors to model multiple vegetation properties in low-energy ecosystems. Normalized difference vegetation index (NDVI) is used as a proxy of productivity. Snow persistence represents both the winter conditions and growing season length, thermal images reflect the summer temperature, and tasseled cap wetness the soil moisture conditions. We used an extensive data set of 1200 study sites comprising 464 vascular plant, moss and lichens taxa. The study area encompasses a complex mountain system in northern Norway. We tested whether we can predict the species composition, richness, and occurrence of individual species using information from satellite images only and assessed the relative importance of the predictors. The main drivers were uniform through the community and taxonomic levels although the response shapes and directions varied between the species groups. Species richness of vascular plants and mosses were highest at the most productive sites with intermediate snow melt date. Lichens showed the opposite trend: species richness of lichens peaked at the sites characterized by early snow melt and intermediate productivity. Productivity and snow persistence were the two most influential predictors for every studied taxa, irrespective of the community level. We conclude that remotely sensed predictors are capable of representing the main ecophysiological drivers of high-latitude vegetation patterns.

CS16-7

Using hierarchical occupancy models to identify characteristic scales of species-environment associations

Katherine Mertes[1], Marta Jarzyna[2], Walter Jetz[2]
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Species-environment relationships are both hierarchically structured and scale-dependent; thus, a key challenge in biogeography is to identify appropriate spatial scales at which to estimate niche properties and species' spatial distributions. We identify two characteristic spatial grains at which species respond to their environment: (i) *selection grain*, the spatial unit at which a species selects (by actively seeking, or more passively persisting in) and uses environmental resoures, and (ii) *occupancy grain*, equivalent to the size of a typical home range. We used a scale optimization procedure to estimate selection grain, measured occupancy grain from telemetry data, and used hierarchical occupancy models with use (finer) and occupancy (coarser) levels to evaluate species-environment relationships at these biologically relevant grains. For an example study species - the Von der Decken's hornbill (*Tockus deckeni*) in a heterogeneous East African landscape - we identified a selection grain of 10m *a priori,* based on 5 years of field observations, and measured an occupancy grain of 1000m. However, optimization of the use level of the model across 30 grains between 10 and 500m revealed the optimal selection grain to be 60m. In addition, models constructed at *a priori* and optimal selection grains different dramatically: model parameters varied in magnitude, significance level, and in one case switched sign. These results strongly indicate that the appropriate spatial units for research and conservation are optimal selection and occupancy grains. In addition, our results demonstrate that employing a spatial grain without verifying its biological relevance risks mis-characterizing species-environment associations, and extrapolating these errors into mis-specififications of niche relationships and inaccurate distribution predictions.

CS16-8

Integrating occurrence data and expert maps to refine species range predictions

Cory Merow[1], Adam Wilson[1], Walter Jetz[1]
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Knowledge of species' geographic distributions is critical for many ecological and evolutionary questions and underpins effective conservation decision-making, yet usually remains limited in spatial resolution or unreliable. Over large spatial extent, range predictions are typically derived from expert knowledge or, increasingly, species distribution models based on presence records. Expert maps are useful at coarse resolution where they are suitable for delineating unoccupied regions. In contrast, point records typically provide finer-scale occurrence information that can be characterized for its environmental association, but often suffers from observer biases and does not address the geographic or environmental range occupied by a species representatively or fully. We develop new modeling methodology to combine the complementary informative attributes of both data types to enable improved fine-scale, large extent predictions. Specifically, we use expert delineations to constrain predictions of a species distribution model parameterized with incidental point records. We introduce a maximum entropy approach for combining the two data types and generalize it to Poisson point process models. We illustrate critical decision making during model construction using a detailed case study and illustrate features more generally with applications to species with vastly different range/data attributes. We highlight an application in which ~10,000 expert maps for plant species in South Africa are updated with presence data to reflect novel spatial patterns of diversity.

MINI-TALK SESSIONS

Mini-Talk Session 1: Climate Change Biogeography (MT1)

Session Chair: Helen Sofaer
Date: January 10, 2017 4:00 pm – 5:30 pm
Location: Canyon ABC room, Marriott Hotel

MT1-1

Non-stationary control over the range limits of species inferred from spatially-distributed ecological niche models

Adam Smith[1], Erik Beever[2], Mimi Kessler[1], Aaron Johnston[2]
[1]Missouri Botanical Garden, Saint Louis, MO, United States
[2]US Geological Survey, Bozeman, Montana, United States

A long-standing proposition in biogeography posits that multiple factors act to shape most species' ranges, with different factors having different effects in different parts of a range. Despite the venerability of this claim, we have few methods and opportunities for testing this hypothesis. Here we leverage an unprecedented data set comprising >13,000 records of *Ochotona princeps* (American pika). We apply a novel modeling technique using spatially-distributed ecological niche models (SD-ENMs), a machine learning tool that captures local species-environment relationships. We use SD-ENMs to identify the most important variable(s) affecting distribution and how they change across geographic space. We find that 1) climatic predictors vary in their importance both within and among genetic clades, and that 2) the importance of these factors is corroborated by numerous site-specific field studies. The results contrast markedly with a "generic" ENM that assumes a stationary response of the species to the environment across its range. Our results demonstrate the importance of considering context-specific responses of species to the environment in light of global change.

MT1-2

Mapping climatic mechanisms likely to favour the emergence of novel communities

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Climatic conditions are changing at different rates and in different directions, potentially causing the emergence of novel species assemblages3. Here we identify areas where recent (1901–2013) changes in temperature and precipitation are likely to be producing novel species assemblages through three distinct mechanisms: emergence of novel climatic combinations, rapid displacement of climatic isoclines and local divergences between temperature and precipitation vectors. Novel climates appear in the tropics, while displacement is faster at higher latitudes and divergence is high in the subtropics and mountainous regions. Globally, novel climate combinations so far are rare (3.4% of evaluated cells), mean displacement is 3.7 km decade?1 and divergence is high (>60°) for 67% of evaluated cells. Via at least one of the proposed mechanisms, novel species assemblages are likely to be forming in the North American Great Plains and temperate forests, Amazon, South American grasslands, Australia, boreal Asia and Africa. In these areas, temperature- and moisture-sensitive species may be affected by new climates emerging, differential biotic lags to rapidly changing climates or by being pulled in opposite directions along local spatial gradients. These results provide spatially explicit hypotheses about where and why novel communities are likely to emerge due to recent climate change.

MT1-3

Scaling up phenological mismatch, it's trajectory, drivers, and demographic consequences for passerine birds across North America

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Consistent with climate warming, birds are shifting the timing of their migrations. We test if their migration phenology has kept pace with the changing environment, because increasing asynchrony between birds' arrival and availability of their food resources could result in negative fitness consequences. We combined satellite, field, and citizen science data in a multi-scaled, high resolution, continental extent analysis to estimate the rate of change in the interval between spring green-up and arrival for 48 breeding bird species across North America. We found that both arrival and green-up changed over time, usually in the same direction (earlier or later). Although birds adjusted their arrival dates, they did not keep pace with rapidly changing green-up. Further, phenological mismatch accelerated over time. We conducted an ecoregional analysis and show that as green-up became earlier in the east, arrival of eastern breeding species increasingly lagged behind green-up, whereas in the west—where green-up typically became later—birds arrived increasingly earlier relative to green-up. Species with increasing mismatch tended to exhibit declining populations, but were not well predicted from phenotypic traits. Our results highlight that organisms at different trophic levels adjust their phenologies at different rates, and that this mismatch in rates can result in growing differences between phenologies across trophic levels, leading to demographic impacts.

MT1-4

Climate change vulnerability rankings based on species distribution models are unreliable

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Climate change poses ongoing and increasing threats to biodiversity. Understanding the relative vulnerability of different organisms would allow managers to target monitoring and management towards the most susceptible species. Species distribution modeling is a prominent tool used in multi-species climate change vulnerability and risk assessments. Previous work has validated the performance and transferability of distribution models using simulations and projections to new locations and time periods. However, studies have not focused on whether distribution models can reliably predict the relative climate change vulnerability of a large set of species. We validate methods used in multi-species vulnerability assessments using data for North American breeding birds. We estimated ensembles of distribution models for 190 passerine species using Breeding Bird Survey data for the conterminous U.S. from the late 1970s. We then predicted occurrence under climatic conditions from recent years, and validated model ensembles by comparing predictions to recent observations. Our results provide a striking demonstration of how distribution models can fail to reliably predict relative vulnerability, even when models show good performance during the validation period. Indeed, vulnerability rankings based on projected range loss can bear little resemblance to observed vulnerability rankings. We highlight how performance was worst in locations with range shifts, and consider implications for climate change vulnerability assessments and the allocation of scarce conservation resources.

MT1-5

Using a process-based model to explain the global bird migration system and predict its past

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Nearly twenty percent of bird species are migratory, their seasonal movements causing a redistribution of bird diversity that radically changes avian community composition worldwide. Being highly mobile organisms, birds exhibit an impressive migration system composed of hundreds of migrating species, some travelling short distances while others undertake extraordinary journeys across continents. And yet, despite its ecological importance and global extent, bird migration has been largely ignored in previous studies of avian biodiversity. In this study, we mapped global macroecological patterns associated with bird migration for the first time. We found that, despite the great biological and ecological diversity in migratory birds, strong spatial patterns emerge when all species are pooled together, suggesting common underlying ecological drivers to which migratory birds respond. We then developed a spatially-explicit, process-based model of bird migration at the global scale. It was built from first principles, converting key ecological processes (i.e. thermoregulation, migration cost, competition and reproduction) into a common currency of energy, and was based on simple rules to relate these processes to climate and the energy supply in the environment. This model successfully explains the global patterns previously described and, in contrast to correlative approaches, can be a great tool for prediction. In particular, we used it to investigate the impact of past global changes on bird migration, retracing the evolution of this phenomenon since the Last Glacial Maximum.

MT1-6

Lags in the climatic response of community shifts on European mountain summits

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Climate is warming and species shift their ranges to track their climatic niche. This has resulted in increased species richness on mountain summits all over Europe. However, many species may encounter difficulties while shifting their ranges, including dispersal limitation, biotic interactions and (especially in the case of mountain vegetation) soil development, resulting in lags in the relationship between species composition and temperature. A long-term monitoring dataset of 231 mountain summits (usually the uppermost 10 m) from 9 mountain regions in Europe was collated. The data consists of historical (originating from 1880 to 1972) and recent (2008 to 2014) presence-absence species lists from mountain summits. For each summit mean summer temperatures (June-August) for the 5 years prior to sampling were derived based on a combination of statistical downscaling and temporal trend analyses. A relationship between summer temperatures and species compositions was established using the historical data in a weighted average approach. This relationship was then used as a transfer function to estimate floristically inferred temperatures on the summits based on the floristic composition of today. If the species are able to track the changes in temperature without lag the floristically inferred temperatures should equal the observed temperatures on the same summits. However, we generally found that the observed temperatures were 1-2 degrees C higher than the floristically inferred temperatures indicating that the species are lagging behind the climatic warming. This is especially pronounced in the Alps and less pronounced in the Scandes.

MT1-7

Beyond taxonomic diversity: Impacts of climate change on multiple facets of amphibian biodiversity

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With the rapidly increasing threats from climate change to biodiversity we need to expand our thinking and conservation planning efforts beyond taxonomic diversity, to include other biodiversity descriptors such as phylogenetic diversity (PD). PD in a region reflects both species richness and the evolutionary relatedness among species, consequently, assessing the effects of climate change on PD identifies whether different segments of the evolutionary tree will require more urgent attention. Here, we predict how ? and ? components of taxonomic and phylogenetic dimensions of amphibian diversity might be influenced by projected climate change. Speci?cally, using current and projected future distributions of amphibians (~2800 species) in Neotropics, we assess the potential erosion of ? diversity and the change in ? diversity by 2070. We also examine how climate change may alter patterns of diversity along altitudinal and latitudinal gradients. Consequences of future climate change on species richness, phylogenetic relatedness, and assemblage composition of species will be fairly severe, resulting in an average loss of 60% of species ? diversity per grid cell. Additionally, climate change will tend to disassemble the phylogenetic structure of Neotropical assemblages beyond the effect of simple reductions in ? diversity. For instance, by 2070 climate change is expected to increase the phylogenetic clustering of assemblages in the northern Andes, most part of Central America and the Caribbean islands. Finally, an important reduction in ? diversity (i.e. homogenization of amphibian assemblages) is also predicted in mountainous areas of South America, Central America and Mexico, and the Caribbean islands.

MT1-8

Phylogeny and co-occurrence improve species distribution model forecasts

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Predicting future species' distributions as a response to climate change is a major challenge for ecology and biogeography. Species distribution models (SDMs) are the main tool to achieve such predictions but most often ignore the evolutionary relationships among species. While novel frameworks show that phylogenetic relatedness can aid improving the explanatory power of species distribution models, its usefulness to enhance future distributions remains untested. Here, we combine phylogenetic relationships and co-occurrences to forecast distributions of birds and butterflies under climate change. We first calibrate the models with data prior to 1980 (e.g. pre-climate change) and project the distributions to contemporary climate. We evaluate the extent to which phylogenetic SDMs improve environmental SDMs by comparing forecasted and observed distributions. In addition, we test model improvement due to factors such as range size, range shifts and evolutionary distinctiveness. Finally, we forecast species distributions under climate change and identify the species that are likely to undergo the most dramatic shifts in their distributions. Our results suggest that phylogenetic relationships not only improve current species distributions but also future ones, in a majority of species and, particularly, when they have narrow distributions, tend to decrease their ranges and are not evolutionarily distinct. All in all, the co-distributions of relatives weighted by their phylogenetic relationships species can unveil species responses to climate that are not fully captured by commonly used climatic variables. Our approach can be a promising venue to reach more accurate predictions of future species distributions under climate change.

MT1-9

Impacts of methodological choices in multi-species distribution modeling under climate change

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Species distribution models are commonly used to predict species distributions in space and time to assess species invasions or climate change vulnerability. Implementing these analyses requires many decisions by the practitioner that can impact predictions. The consequences of these decisions to model validation has received limited investigation. We developed models for 190 bird species using 1970's Breeding Bird Survey data and then applied these models to current environmental conditions, comparing predictions to recent (2012-2014) bird observations.

A common recommendation in generating species distribution models to guard against inflated performance metrics is to limit the geographic extent from which absence points are drawn. We used both geographically restricted and geographically extensive absence locations from the lower 48 US states to estimate models, and examined impacts of this decision on prediction success of current distribution. Our results highlight trade-offs in the spatial extent of calibration data, with the geographically restricted data set more poorly capturing observed range change. We discuss the implications of these methodological decisions to the validity of model predictions, including climate change vulnerability assessments.

MT1-10 Tracking the Desert's Edge with a Pleistocene Relict

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The southern extent of Pleistocene woodlands and location of desert refugia in North America remain unknown. A series of 900–1200 m desert peaks surrounded by arid lowlands occur throughout the southwestern U.S. and northwestern Mexico where temperate affiliated species occur at highest elevations. The presence of disjunct long-lived plant taxa on under-explored summits, especially Isla Tiburón at 29º latitude in the Gulf of California, suggests a more southerly extent of Ice Age woodlands than previously understood. The phylogeography of the desert edge species Canotia holacantha (Celastraceae) was investigated to test the hypothesis that insular desert peak populations represent remnants of Pleistocene woodlands rather than recent dispersal events. Sequences of four chloroplast DNA regions totaling 2,778 bp were amplified from 59 individuals of 14 populations across the entire range of C. holacantha as well as the other two species in its clade. Five haplotypes were recovered; three in C. holacantha (Arizona populations, disjunct Sonora populations, and Isla Tiburón) and one for each outgroup. Greater genetic variation in Sonora and no variation in Arizona indicate a broader distribution in southern reaches of mainland Sonora during the Pleistocene and post-glacial expansion from south to north. The Chihuahuan Desert microendemic C. wendtii is shown to be sister to the Tiburón population, with this clade basal to all other Canotia populations. These results suggest that the occurrence of Canotia in Sonora is not due to recent long distance dispersal. Instead, it seems Canotia has been present in Sonora since at least the last glacial maximum.

MT1-11

What to expect from ecological niche models? A comprehensive evaluation of transferability of 10 algorithms

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Ecological niche modeling (ENM) is widely used in biogeography studies. ENM applications frequently involve transferring the model through space and time, but the transferability of ENM algorithms is rarely evaluated. We evaluated the transferability of 10 frequently used algorithms in a virtual species framework. To simulate the incomplete knowledge of the fundamental niche, a reality of most ENM applications, we divided the study area into six regions and alternatively used one region to train models. Additionally, to simulate a gradient of completeness of the knowledge of fundamental niche, we used combinations of two to five regions to train models. We argue that model transferability should be distinguished as interpolation and extrapolation, thus we separated the model testing data into three categories based on environmental novelty compared with the training dataset. All models were evaluated separately for each category. We found that none of the algorithms adequately estimated the fundamental niche given incomplete knowledge of the fundamental niche and that most algorithms produced estimations in between the fundamental and realized niches. Model evaluation metrics decreased as the environmental novelty of the testing data increased. Therefore, we recommend that ENM applications clarify the similarity between the training and projecting environments, thus providing an avenue for inferring uncertainty. We also found that ENM algorithms have different sensitivity to completeness of the knowledge of fundamental niche. Thus we suggest a possible algorithm selection strategy: choosing a conservative algorithm when the fundamental niche is well known, but choosing a liberal algorithm when little is known.

MT1-12

Origin from Gondwana and Disjunction in Northern Hemisphere--The biogeographic history of Paliurus (Rhamnaceae)

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Paliurus is a small genus of Rhamnaceae with 5 species and currently disjunct between East Asia and the Mediterranean. Fossil evidence indicated it once had a broad distribution area in the world (India,Asia, North America, Europe) during the Mesozoic and Cenozoic. To trace the biogeographic history of the Paliurus in Northern Hemisphere, phylogenetic and biogeographical reconstructions were performed based on ITS, trnL-F, and rbcL sequences. The results showed that Paliurus is a monophyletic genus. Biogeographical inference integrated with fossil information indicated that the origin and dispersal pattern of the genus coincide with the “out-of-India” hypothesis. This genus may originated in India or other parts of Gondwana first and then dispersed to East Asia after the collision of the Indian plate with Eurasia, and through Bering Strait to North America. Paliurus reached the Mediterranean region in the Miocene following the closure of Turgai strait. The uplift of Qinghai-Tibet Plateau and the climates change in Miocene might bring about the present-day disjunct pattern. Species of Paliurus in different region either became extinct or adapted to the local ecological conditions accompanying the global climatic through geological time.

MT1-13

Anthropocene impacts on the distribution of gymnosperm tree species in China

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China is one of the oldest civilizations in the world, with dense human populations in wide areas for more than 4.000 years, exerting large impacts on the environment. Species distributions have changed globally and in China both according to climate changes, but also increasingly due to human influence such as clearing of forest for agriculture and other land uses. Considering the ongoing climate change and human population increase, it is important to understand the relative importance of these two key drivers of species distributions in a country already dominated by human influence. Human presence is potentially forcing species into sub-optimal habitats making it difficult, and important, to define their habitat preference and potential range, to gain instrumental knowledge for planning ecological restoration. Our main focus was therefore to test how anthropogenic and climatic factors influence current distributions of gymnosperm tree species in China, with a focus on gymnosperms due to their extraordinary diversity in China, with many relict lineages, and their enormous ecological, economic, and cultural importance. As a key aspect, we test the role of not just present, but also historical human population density as drivers of species distributions. Our methodology involves analyzing a large database (243 species, ~13.000 occurrences) of extant gymnosperm tree occurrences in China using SDM modelling approaches. We expect historical human population density to be a main driver of current gymnosperm species distributions; moreover, we expect species occurrences to be more strongly related to topographic range in areas of high historical human population density.

MT1-14

The use of new high resolution recent climate change data in biogeography

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Climate change has picked up pace in the last decades, with many of the recent years being warmer then the preceding ones. Tracking the environmental changes that ecosystems worldwide have experienced has, however, been difficult due to the lack of climate data at a high spatial resolution that extends to the years before 2000. With ecosystems often being distributed at a small spatial scale of ~1km, there has also been a spatial gap between ecological and biogeographical data and climatic data. Here, we present the application of a newly developed high resolution climatology (CHELSA) spanning the years 1979-2013 for tracking the impact of changes in the world's ecosystems. Among others, we present data on how the global potential treeline has already been changing; show how to what degree mountain cloud forests, one of the most biodiverse ecosystems worldwide, has been impacted by climate, how strongly and where; and that islands have heated considerably more than mainlands. As the newly available climate data is available on a monthly basis at a resolution of 1 km^2, starting in January 1979, we are now able to track recent climate change in some of the most important ecosystems worldwide, with an unprecedented spatial and temporal resolution. This will not only prove valuable for climate change mitigation, but can also inform us about the underlying ecological dynamics in today's ecosystems.

Mini-Talk Session 2: Biodiversity Patterns and Maintenance (MT2)

Session Chair: Peter Galante
Date: January 10, 2017 4:00 pm – 5:30 pm
Location: Madera room, Marriott Hotel

MT2-1

Geographic distribution of pest and pathogen infection: a tool for phytosanitary risk assessment

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Phytosanitary agencies provide plant biosecurity from early detection of potential ways of introduction of pests and pathogens, to plague control and eradication. However, to carry out these actions it is necessary to get analytical tools based on solid scientific knowledge about plant-pest or pathogen relationships to help evaluating pests that represents risk. Recent empirical evidence that species closely related share greater chance of becoming infected by pests has allowed to identify taxa with different degree of vulnerability. Here we show how phylogenetic or taxonomic relationships can be used to estimate the probability of sharing pests and finally how this can be projected on geographic space as a more complete spatially-explicit tool for risk assessment. We first demonstrate this by explaining the theoretical model and secondly using a case study on a 23 beetle x 298 host matrix. Overall, the predictions first allow us to identify generalist versus specialist pests, which is then translated into what interactions could be a limiting factor on species distributions. Secondly our results can be useful to identify hotspots (or coldspots) of pests and hotspots of vulnerable hosts, and what could be potential consequences of these interactions for disease transmission. We propose this type of approach combining several biodiversity dimensions (e.g. phylogenetic and geographic) can be generalized to multiple biological systems in evolutionary biology and biogeography for the analysis of biotic interactions in a geographical context.

MT2-2

Productivity directly, and not its indirect influence on food resources, is the primary determinant of mammal elevation diversity

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To protect biodiversity, we need improved comprehension of the creating and maintaining mechanisms. Elevational diversity of small mammals on mountains around the world is known to peak at intermediate elevations with a strong link to climate. But whether climate has a direct impact on mammal distributions through physiological responses or indirect impact through food resources was untested. Here we assessed mammal distributions and population sizes, arthropod biomass, vegetation biomass, and climate at eight sites along each of four elevational transects in the Colorado Rocky Mountains. At each site, we conducted standardized mammal live-trapping and visual surveys, and repeatedly sampled 20 vegetation plots and arthropod pitfall trap pairs. Statistical models for mammalian diversity and abundance assessed temperature (annual means and variability), precipitation, NPP, land area, MDE, habitat heterogeneity, standardized arthropod and vegetation biomass, tree size and density, canopy coverage, and various plant coverages. Mammal diversity peaked at intermediate elevations on all four gradients, but peak location varied elevationally among transects. In both multiple regressions and structured equation modeling, only NPP was included in the optimal models. Local productivity, assessed through overall mammal population sizes, was not significantly related mammal diversity. Variation in food resources did not consistently support relationships with either mammal population sizes or mammal diversity. A direct, regional, productivity-diversity relationship predicts stronger links to climate change than would climate influences mediated through local food resources or mammal abundances.

MT2-3

Diversity patterns and geographic affinities of Himalayan plants

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With respect to plants, the Himalayas is one of species rich locations in the world, but regional affiliations and elevational distributions have yet to be comprehensively assessed. We compiled a checklist of 10526 vascular plant species recorded in 41 volumes of regional floras. Past data deficiencies and anomalies include a relative lack of documentation from the large eastern state of Arunachal Pradesh. We recorded the presence of species in the Himalayan surroundings i.e. Tibet on north, Indian plains on south, Myanmar and Yunnan to the east and Pakistan to the west and the global distribution of all species from available online databases. The Himalayan flora represents 254 families and 2349 genera with 7007 (67%) native but non-endemic, 2158 (20%) endemic and 1368 (13%) exotic species. Within the Himalayas, richness peaks at about 1000m. However, species endemic to the region show maximum richness at about 4000m, where species to genus ratio is also highest, implying a higher rate of diversification at higher elevations. The subtropical region in the southeast shows the highest richness which declines threefold towards the temperate northwest Himalaya. 970 species are shared with Africa and 503 species with Australia, and these species shows an approximately linear decline with increasing elevation. Europe shares 789 species, and the number shared peaks at mid-elevations (1500m). These patterns are expected from climatic affinities. Exotic (non-native) species are highest at the foothills and decline with elevation. The maximum number of exotics is from North America followed by South America, Africa, Europe and Australia.

MT2-4

Similar emerging ecological and evolutionary patterns in biodiversity and computer operating systems

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Comparing biodiversity with other complex systems can help exchange theories between disciplines and identify key system processes and constraints. Here, computer operating systems seem promising, due to structural and functional analogies to biological systems, coupled with good data availability. Employing analogies between species and Linux operating systems (distros), we demonstrate quantitative similarities in established macroecological and macroevolutionary patterns: Distro commonness (popularity) shows a lognormal distribution, power law mean-variance scaling of temporal fluctuation, and a significant positive relationship with niche breadth (no. of software packages). Phylogenetic lineage diversity increases linearly through time, with clear per-distro diversification and extinction slowdowns, while functional trait (software package) composition exhibits significant phylogenetic signal. Such similar patterns might emerge from common system-level properties, independent of system identity, offering empirical arguments for non-biological explanations for fundamental biodiversity patterns, as well as suggesting Linux as a potential model system for eco-evolutionary studies.

MT2-5

Joint Bayesian estimation of niche models and niche evolution: comparing algorithms

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Current methods for studying phylogenetic niche conservatism and rates of niche evolution typically work by (1) estimating Ecological Niche Models (ENMs) for each species in a clade independently; (2) simplifying the ENM down to a summary statistic (e.g., mean temperature); (3) treating this summary statistic as if it were a measurement such as body size, and applying a simple evolutionary model such as Brownian motion. While this approach has value, it can be criticized on several grounds. We propose that an improvement would be to jointly estimate ENMs for a group of related species, as well as parameters for the evolution of each niche model axis, using Bayesian MCMC. However, because joint estimation combines the complexities of ENMs and evolutionary models, implementation and computation speed are nontrivial concerns. We perform a feasibility study by comparing implementations of phylogenetic ENM using R and RevBayes in terms of inference accuracy against simulations, and speed. We also assess the prospects for modeling additional processes that are often confounded in ENM, such as dispersal limitation and historical biogeography.

MT2-6

Biodiversity conservation and the Nature Improvement Area Initiative: An investigation of the contribution of the NIAs to the protection of wild nature in England

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Protected designations form an integral part of the global initiative to conserve nature. Such areas are intended to protect all aspects of biodiversity and maintain ecological function indefinitely. These spaces support ecological networks, operating across scales and maintaining a coherent and functional suite of sites for nature. Such areas face increasing pressures and it is important to understand the biodiversity contained within such designations and explore the impacts of new areas on biodiversity conservation, particularly those operating at landscape scales. The Nature Improvement Area (NIA) initiative is intended to enlarge, enhance and connect existing wildlife sites to improve England's ecological network through the establishment of 12 new landscape designations. Little research has been conducted on the biodiversity contained within these areas and their contribution to the existing ecological network. This is particularly relevant for two indicators: priority habitats and priority species. Priority habitats are the 56 habitats identified as being of importance for the conservation of biodiversity in England. Priority species are species of particular conservation concern that require conservation action. This research addresses that gap by quantitatively evaluating what priority habitats and species are contained within the NIAs and then considering their contribution to priority habitat and species in the existing ecological network of both landscape and smaller-scale

designations. The results are then discussed in the context of national and international targets for conservation, including those outlined in the UK Post-2010 Biodiversity Framework and the Department for Environment and Rural Affairs' (Defra) developing 25-Year Environment Plan.

MT2-7

Selecting predictor variables for Maxent models of environmental suitability: what goes in and what gets used?

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The utility of ecological niche models of environmental suitability depends on key implementation practices, such as the selection of environmental variables of those deemed ecologically plausible. Because 1) variables may be highly correlated and 2) overly parameterized models lead to poor transferability, the issue of reducing dimensionality represents a hotly debated topic. Some implementations of the machine-learning algorithm Maxent borrow from the regression-modeling paradigm by removing variables above an arbitrary correlation threshold. However, this may remove relevant environmental information. Here, we use a simulated species where the effects of input variables are known, to address complexity for Maxent models, using sample sizes realistic for rare species. Specifically, we compare four variable-selection schemes. A strategy whereby models were tuned using variables included in a previously tuned Maxent model had 1) the highest success in reconstructing the virtual niche, and 2) showed superior performance in predicting withheld data. These results indicate that removing variables above a correlation threshold may be a detrimental step for Maxent models, regardless of if the aim is prediction or explanation. Simulation experiments using varied niche complexities and number of available occurrence localities will help further elucidate these relationships.

MT2-8

Generality of Ecological Rules at the Holocene Scale

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Recent decades have witnessed an accelerating development of agricultural technologies and climatic change. Such changes raise the question: "Can we project future biodiversity from observed correlations between recent diversity and its predictors?" Only if diversity predictors that are universal across space are also universal across time, we can use them as general laws of ecology. We examined (i) the relationships between species richness and temperature, and (ii) the patterns of distance decay in the Jaccard index and the Simpson beta, which both measure the similarity between two assemblages. In macroecology, the patterns of distance decay in similarity are suspected to affect other important ecological patterns of diversity, like the Species-Area Relationship. We report a substantial variation in the (i) species-richness–temperature relationship and in the (ii) distance–decay relationships between archaeologically known periods, with the most noticeable breaks when arable agriculture was introduced and when the Roman Empire collapsed. (Šizling et al. 2016. *GEB*, DOI: 10.1111/geb.12467; Šizling et al. *In Progress*.)

MT2-9

Phylogeographic syntheses of South Pacific hotspot archipelagos reveal both departures from and confirmations of hotspot diversification models

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Phylogenetic and modeling studies have suggested that the biotas of oceanic hotspot archipelagos (such as the Hawaiian, Canary, and Galápagos islands) diversify in parallel with the formation of the islands on which they live. Here, we synthesize molecular phylogenetic studies of the native terrestrial biota of two South Pacific hotspot archipelagos, the Society Islands (formed < 4.6 Ma), and the Marquesas Islands (formed < 5.5 Ma). These island groups are situated 1400 km apart in French Polynesia and share a similar biota. We review 49 and 33 phylogenetic and phylogeographic studies incorporating terrestrial animal and plant taxa from the Society and Marquesas archipelagos, respectively, and find that emergent patterns across taxa are quite different in these two archipelagos. Polyphyly of Societies-endemic "radiations", limited evidence for among-island differentiation, and divergence time estimates suggest that much of the Societies biota does not appear to have diversified in parallel with the formation of the archipelago. These findings differ markedly from "progression rule" and general dynamic models for the diversification of oceanic archipelago biotas. Rather, many Societies "radiations" may have been assembled via repeated, independent colonizations, which may have entailed extensive macroevolutionary turnover of colonizing lineages. In contrast, the diversification of the Marquesas biota more closely resembles a more limited version of the Hawaiian islands, in that many of the well-sampled radiations are monophyletic and some appear to diversify in parallel with the formation of the archipelago. We conclude by discussing hypotheses that may explain these divergent patterns.

MT2-10

Did demographic changes drive the rise of agriculture? Predicting potential population densities of foraging societies in prehistory.

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Population density has been linked to fundamental changes in societies that have shaped the trajectory of human history, including the origins of agriculture during the late Pleistocene and early Holocene. However, previous examinations of the role of population density in cultural change have relied on narrative arguments, limited sample sizes, and site-specific archeological evidence. Furthermore, recent global estimates of historic population densities lack the spatial and temporal resolution required to enable robust tests of hypotheses invoking population density as a causal mechanism. To overcome these limitations, we used methods from biogeography and macroecology to estimate potential population densities (carrying capacities) for foraging societies from the last glacial maximum until 8,000 YBP at 0.5° latitude x 0.5° longitude resolution across the globe. First, we tested for the determinants of population density among 220 foraging societies using structural equation models and data from a recently released database of human societies, culture, and the environment (d-place.org). We then used the results to estimate potential population densities and examine the degree to which changing demographics may have promoted one of the most important developments in modern human history: the origins of agriculture.

MT2-11

Supermatrix phylogeny and biogeography of the Australasian Meliphagides radiation (Aves: Passeriformes)

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The Meliphagides represents one of the largest and most conspicuous Australasian bird radiations comprising nearly 300 species. Although the group has been the focus of a number of recent phylogenetic studies, a comprehensive species-level phylogenetic hypothesis is still lacking. This has impeded the assessment of broad-scale evolutionary, biogeographic and ecological hypotheses. In this study, we use a supermatrix approach including five mitochondrial and four nuclear markers to infer a time-calibrated phylogeny of the Meliphagides. Our phylogeny, which includes 286 of the 289 (99%) currently recognized species, is largely congruent with previous estimates. However, the addition of 60 newly sequenced species reveals some novel relationships. Our biogeographic analyses suggest an Australian origin for the group in the early Oligocene. In addition, we find that dispersal events out of Australia have been numerous and frequent, particularly to New Guinea, which has also been the source of multiple back-colonizations to the Australian mainland. Furthermore, our study indicate that the honeyeater clade represents a classic adaptive radiation, possibly driven by the evolution of key traits relating to a diet rich in nectar and co-evolution with plants. Interestingly, honeyeaters have apparently radiated in parallel with other meliphagoid lineages, both in time and space, producing mutually independent and geographically congruent gradients of regional diversity. Unlike their relatives, however, honeyeaters sustain much higher richness locally, possibly because of limited competition with other passerines and significant ecological divergence among honeyeater species facilitating their coexistence.

MT2-12

A world of sequences. Can we use georeferenced nucleotide databases for an Automated Phylogeography?

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Automatic retrieval of georeferenced sequence data from nucleotide databases (‘Automated Phylogeography’) can potentially boost comparative phylogeography across a large number of species, allowing to investigate community-level processes at continental and global scales. Here we present a new bioinformatic approach [1] to investigate and improve geographic information available for tetrapod GenBank accessions to assess whether georeferencing of nucleotide databases has increased in frequency through time, and whether accumulated data allow for broad phylogeographic analeyses of automatically retrieved sequence data and their associated geographic information. We found that only a tiny fraction (6.2%) of surveyed GenBank submissions reported geographic coordinates, without any increasing trend in recent years, while our newly developed automatic geocoding increased the proportion of georeferenced accessions to 15.1%. The geographic distribution of georeferenced accessions is patchy, weakly correlated with species richness, and especially sparse in economically underdeveloped areas. Automatically retrievable informative data sets covering most of the range are available for very few species of wide-ranging tetrapods. While geocoding offers a partial solution to the scarcity of direct georeferencing, the amount of data potentially useful for Automated Phylogeography is still limited. Sampling logistics in hardly accessible areas represent one main limitation. Future research agendas should focus on enhancing collaborative efforts to standardized georeferencing of genetic data and sample genetic diversity in biodiversity-rich tropical areas.
Gratton, P., Marta, S., Bocksberger, G., Winter, M., Trucchi, E. & Kühl, H. (2016) A world of sequences: can we use georeferenced nucleotide databases for a robust automated phylogeography? Journal of Biogeography, early online

MT2-13

Demystifying dispersal: migration in marine intertidal invertebrates is predicted by functional life-history trait differences

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Dispersal potential should correlate positively with gene flow, though recent aggregate global analyses suggest pelagic duration is only poorly correlated to Fst. In 2011, a major mortality event coinciding with a harmful algal bloom occurred along 100km of central California coast, providing a unique opportunity to test how dispersal potential relates to patterns of migration. The first year following the die-off, we began studying four species with differing dispersal traits that suffered elevated mortality across the impacted coastline: *Strongylocentrotus purpuratus*, *Leptasterias* sp., *Henricia* sp. (~100% mortality), and *Pisaster ochraceus* (elevated, spatially variable mortality). We [1] quantified the abundance and size-frequency distribution of the target species at sites across the impacted range and unaffected reference sites to the south and north from 2012–2015; additionally, we developed and used RADseq markers to [2] identify the likely sources of new recruits and [3] determine the relatedness among settling individuals that recolonized the impacted range from 2012–2014. Species with higher dispersal potential re-colonized a broader extent of the impacted range, and did so more quickly, than species with lower dispersal potential. High dispersal taxa also showed higher gene flow than low dispersal taxa, and recruits of high dispersal taxa also were more diverse than low dispersal taxa. These results suggest species' attributes (e.g. fecundity, pelagic duration, and population size) can influence realized dispersal.

MT2-14

Biogeographical effects on forest net primary production

Timo Conradi[1], Jens Christian Svenning[2]
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Spatial variation in terrestrial net primary production (NPP) is thought to be driven by gradients in temperature, precipitation and growing season length as well as by stand characteristics such as standing biomass and plant age. We suggest that additional consideration of biogeographical factors can improve our understanding of variation in NPP over large spatial scales. Specifically, we propose two alternative scenarios in which biogeographical factors co-determine the NPP of local forest stands: The first scenario is based on reported positive effects of local tree richness on forest NPP. As local richness is controlled by the size of regional species pools, we hypothesized an indirect effect of Quaternary climate instability on NPP via its negative influence on species pool size. The second scenario assumes that region effects, i.e. evolutionary processes operating over longer time scales, shaped large-scale variation in species' growth rates and stand biomass which in turn influence NPP. We tested these ideas using plot-scale data from across Northern Hemisphere forests and Structural Equation Modeling. We demonstrate that region effects on stand NPP are important and go beyond the influence of climate, but found no support for the species-pool scenario. The most important direct drivers of NPP were stand biomass and age, followed by a region effect and climate parameters. Moreover, region effects strongly influenced stand biomass, thereby exerting strong indirect effects on forest NPP too. Our results show that the integration of biogeographical factors can improve our understanding of large-scale variation in ecosystem functioning.

Mini-Talk Session 3: Conservation Biogeography (MT3)

Session Chair: Sabrina Mazzoni
Date: January 10, 2017 4:00 pm – 5:30 pm
Location: Pima room, Marriott Hotel

MT3-1

Island Species–Area Relationships and Species Accumulation Curves Are Not Equivalent

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While those working with species–area curves have long recognized different forms of curve, the implications of different means of quantitative depiction of the relationship remain contentious. Arguably, the most important distinction is between species accumulation curves (SACs), which present cumulative counts of increased species number with sampling area, and island-type species–area relationships (ISARs), in which the function fitted is based on how many species are found in each sampled area. Using a set of 97 habitat island datasets, we aimed to better understand the empirical differences between SAC and ISAR data structures by (1) establishing the variation in form of the relationship between the two distinct methods applied to the same datasets, (2) exploring the relevance of several key dataset properties for variation in the parameters of these relationships, and (3) assessing the implications for application of the resulting models. We focused on several versions of SACs, giving priority to a randomized form (Ran-SAC). We found that slopes of the ISAR and SAC for the same data set can vary substantially, revealing their non-equivalence. For example, the Ran-SAC was steeper than the ISAR in 77% of datasets. The differences in slopes between the ISAR and SAC were primarily driven by the degree of nestedness. Through these analyses we highlighted the implications for applications of species–area curve parameters in conservation science.

MT3-2

Developing MODIS-based cloud climatologies for biogeographical applications Current procedures and next steps

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Worldclim (Hijmans et al. 2005) has been the de-facto source of basic climatological analyses for most species distribution modeling research and conservation science applications because of its global coverage and high spatial resolution. However, satellite-based cloud (e.g. Wilson and Jetz 2016) and precipitation climatologies have very recently been developed to supplement the original Worldclim quantities. This talk describes aspects of two techniques that have been used to develop Moderate Resolution Imaging Spectroradiometer (MODIS) daytime cloud climatologies. We compare the two procedures and highlight areas of agreement as well as differences. Some important applications of such climatologies will include 1) help in restoring long-degraded cloud-impacted environments 2) improving estimations of the spatial distribution of cloud-impacted species and 3) helping to identify areas for rapid biological assessments. This last application can benefit from even qualitative perusal of the current MODIS climatologies. Finally, we mention some of the next steps that will be needed to make these, and other remotely-sensed products, more useful to the biogeography and conservation communities.

MT3-3
Dark diversity facilitates pseudo-absence selection for species distribution modelling

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Presence only species distribution modelling (SDM) requires *a-priori* the selection of background localities for model parameterization. Referred to as pseudo-absences, the method in which background localities are generated influence model parameterization and subsequently the efficacy of model predictions. Several extant methods are commonly adopted. These range from complete random selection, to environmental- or geographically-weighted exclusion; methods which vary in their ability to place background localities in 'unsuitable' environmental space for a focal species. Here, we introduce a novel pseudo-absence selection technique, one which broadly considers the species pool of cells prior to generating background localities. This is achieved through use of an independently generated co-occurrence matrix adopting methodology employed to estimate dark diversity (i.e. an absent portion of a species pool). For a modelled species, these co-occurrence probabilities facilitate the selection of background localities, excluding cells where a high probability of occurrence is estimated. We illustrate the conceptual framework behind co-occurrence generated pseudo-absence data and assess the performance of predictive models for *ca*.900 plant species across Norway using the novel vs common (i.e. random and geographically-weighted) pseudo-absence selection techniques. Generally, the method improved the predictive accuracy of species distribution models. We discuss our results in the context of presence only SDM and share our views on how the uptake of co-occurrence generated pseudo-absences can compensate for the shortcomings when using large presence-only databases (e.g. www.gbif.org) for modelling species distributions.

MT3-4
Biogeography of aquatic infectious diseases: The case of the Viral Hemorrhagic Septicemia virus in wild fish

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The distributional ecology of diseases of aquatic organisms remains largely neglected. The Viral Hemorrhagic Septicemia virus (VHSV; *Norovirhabdovirus*) is responsible for massive mortality of farmed and wild fish worldwide. Response to VHSV has largely been reactive, not proactive, given the limited understanding of its ecology. To that end, we explored the biogeography of VHSV in freshwater and marine environments. We evaluated the environmental features that shape the spatial distribution of VHSV and plausible niche similarities among VHSV lineages in geographic and environmental dimensions. Analyses were done coupling ENMTools and NicheA with Maxent software, and remote sensing and climate data. VHSV occurrences were obtained from available reports of virus confirmation in laboratory facilities. Our findings suggest that VHSV is not yet at equilibrium and will continue its expansion in fresh-waters and marine environments and lineages have niche conservatism when explored at coarse scale allowing prediction of environmental suitability in areas where this virus does not occur yet. For example, Chile, the second largest salmon producer in the world, is at high risk for VHSV translocation. Fish are a major source of protein for several developing countries that were predicted suitable for VHSV, thus, the role of biogeography to understand pathogens in fish is crucial for better design preventive mitigation strategies.

MT3-5

Phylogeography of Draconid Lizards in the Pacific Ring of Fire

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The "regional endemism paradigm" predicts that island biodiversity is driven via extinction amongst regionally endemic species, rather than allopatric diversification between isolated locations. Biogeographical evidence, both, for and against this hypothesis has been uncovered across the Greater Sunda Region (Sundaland) of Southeast Asia. However, few studies have systematically targeted the montane forest "islands" of Java and Sumatra to investigate the potential for within island diversification in highland species of Sundaland. We analyzed nearly complete mitochondrial genomes and a single nuclear gene for montane forest lizards (subfamily: Draconinae) across twelve Javan and Sumatran forest "islands" and examined genetic divergence between species. We uncovered an overwhelming amount of untapped, cryptic species diversity, distributed allopatrically across montane forest "islands". Deep genetic divergence between species suggests subaerial refugia were more widely distributed than was previously hypothesized during periods of high sea levels during the late Miocene and Early Pliocene Epochs. Furthermore, we hypothesize that contemporary distribution of point endemics and lack of sympatry between species, provides biological evidence for the elevational lower limit of montane forests during cold periods of glacial maxima of the Pleistocene Epoch. Our results suggest that extinction amongst regional endemics did not drive montane draconid lizard diversification in Java or Sumatra and many areas yet to be inventoried, likely hold other undiscovered endemic species.

MT3-6 Areas of endemism in the Iranian plateau identified based on the hyperdiverse plant family Asteraceae

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Areas of endemism are fundamental entities of analysis in evolutionary biogeography and many basic questions of historical biogeography concern areas of endemism and their interrelationships. The Iranian plateau is one of the most diverse regions of Southwest Asia with respect to both organismal as well as landscape diversity, but little is known about factors responsible for this high diversity. Here we investigate and describe patterns of endemic richness across this region as well as identify areas of endemism and their ecological and/or historical correlates. To this end, we have chosen the hyperdiverse plant family Asteraceae, which includes 634 endemic and subendemic taxa from 5984 localities. Applying Endemicity Analysis, we identified five areas of endemism. These are limited to the major mountain ranges of the region. The areas of endemism are positively correlated with topographic heterogeneity and elevational range, suggesting that geographic isolation and high habitat diversity, due to high heterogeneity and extensive altitudinal gradients, played an important role in the evolution of Iranian endemics.

MT3-7

MIAmaxent: functional unwRapping of the MIAToolbox for MaxEnt modelling.

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Combining a descriptive ecological and informatics narrative, the aim is to present MIAmaxent, a jointly developed R package for training, selecting, and evaluating MaxEnt models. MIAmaxent's main functionalities will be described using a language accessible to ecologists and biogeographers with diverse or limited computational expertise. Whilst retaining most of the functionalities of the MIA Toolbox, the modular set of R-scripts implementing the strict maximum likelihood interpretation of maximum entropy, the core components have been once again decoupled and turned into individual R-functions, giving users more flexibility in how they are applied. The major advantage in this alternative methodology is greater user control -- in variable transformations, in variable selection, and in model output. Comparisons also suggest that this methodology results in simpler models with equally good predictive ability, and reduces the risk of overfitting. Furthermore, we provide additional context on how ecologists with little or no R-specific programming skills, but a shared passion for disentangling complexity, developed these tools, hoping to inspire further developments by others.

MT3-8

Implementing species distribution models for exotic springtail species in Antarctica: an unexplored tool to assess invasion risk

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Invasive species are one of the most important threats to Antarctic terrestrial biodiversity. At least four exotic species of springtails (Collembola) have been found in this continent, but their spatial distributions, potential geographical expansion and effects on native species remains largely unknown. While Species Distribution Models (SDMs) are a useful tool to assess the suitability of non-occupied areas to invasive species, they have been rarely applied in Antarctica. Perhaps one of the major challenges to produce SDMs in this continent is the paucity (or lack) of environmental layers to parameterize the models. We have overcome this limitation by generating a set of 19 bioclimatic variables from global temperature and specific humidity MERRA-based satellite data at different spatial resolutions (30 seconds, 2.5 minutes, 5 minutes and 10 minutes). Using global occurrence data for those springtail species that have been recorded as exotic in Antarctica, we implemented nine presence-only (and pseudo-absence) modelling algorithms to better understand their geographic distributions and range dynamics in this continent. Our results show that only small areas of maritime Antarctica offer similar climatic conditions to those found in other parts of the world where these invasive springtails occur. Despite minor differences between algorithms, SDMs provide spatially congruent responses on the location of areas that show the highest risk for the establishment and geographical spread of these invasive species.

MT3-9

Invasive species distribution models: validation with independent data shows good accuracy

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[3]Museum National d'Histoire Naturelle, France
[4]MNHM
[5]Université Paris Sud, CNRS, France

Biological invasions are one of the biggest threat that biodiversity has to face, a threat also involving important economic costs to human societies. To help and better prioritize management strategies, species distribution models (SDMs) are often used to predict the potential invasive range of introduced species. However, validation studies – with independent data – are lacking to assess the predictive accuracy of SDMs in general and for invasion biology in particular. Yes invasions are a good opportunity to do so as invasive alien species are quickly spreading into their potential climatic niche, a temporal process for which data are available on occasion. Here, we used temporal occurrence data for 16 invasive species (selected from a wide range of taxa, including terrestrial and freshwater species and with invasion ranges on different continents), to investigate this issue. Specifically, for each species, we compared occurrence data from the last stage of invasion to the predictions from SDMs calibrated with data from the early stage of invasion. As current SDM evaluation techniques are not satisfying for the special case of invasive species, we further provide a new method to assess the predictive accuracy of SDM for the case of predicting ongoing invasions. For 15 out of the 16 species, SDM predictions showed a good accuracy in predicting the ongoing expansion of these invasive species in their invaded ranges. As a first case of validation with independent data, our findings are very encouraging for the use of SDMs in invasion biology.

MT3-10

Predicting the spatiotemporal distributions of marine fish species utilizing earth system data in a maximum entropy modeling framework

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Understanding how ocean conditions influence fish distributions is critical for elucidating the role of climate in ecosystem change and forecasting how fish may be distributed in the future. Traditional species distribution models are often applied to scientific-survey data, which include species presence and absence information, to predict distributions. Maximum entropy (MaxEnt) models are promising tools as they can be applied to presence-only data, such as those collected from fishermen targeting a specific species or citizen-science programs. We used MaxEnt to relate fish occurrence records (Atlantic herring, Atlantic mackerel, and butterfish) based on commercial fisheries landings to environmental conditions. Environmental variables included sea surface temperature (SST) and chlorophyll-a from NASA satellite observations, bathymetry, and climate indices. We developed habitat suitability maps for these species in US Northeast Shelf area, and assessed the relative influence of environmental factors on their distributions. Across months, their suitable habitat areas varied and were closely related to known inshore-offshore and north-south movements in response to changing environmental conditions. Environmental variables that had the greatest influence on distributions varied across months. Overall, SST and chlorophyll-a had the greatest influence on their distributions, with bathymetry having moderate influence and climate indices having little influence. We utilized a modeling framework that integrates presence-only data and high-resolution environmental data from satellite to describe fish's spatiotemporal distributions. These MaxEnt models have the potential to provide hindcasts of where species might have been in the past in relation to historical environmental conditions, nowcasts in relation to current conditions, or forecasts of future distributions.

MT3-11

Evaluating suture zones and refugia through comparative phylogeography of amphibians in the Southeastern Coastal Plain

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The Southeastern U.S. provided the foundation for ideas in comparative phylogeography, but few direct comparisons across widely distributed anurans exist for this region. We investigate the influence of historical processes and species-level characteristics on phylogeographic structure within four anuran species, evaluate previously described suture zones, and test hypotheses of expansion from putative glacial refugia. We sampled four anuran species from the same 36 localities and assembled mitochondrial genomes from Illumina sequence data. Phylogenetic relationships and divergence times were estimated within each species. We used spatial diffusion phylogeographic analyses and ecological niche models (ENMs) to test predictions about suture zones and glacial refugia and estimate species-specific parameters including dispersal, migration direction, and center of origin. ENMs for four time periods were compared within species to assess niche stability. Species differ in spatial and temporal patterns of mitochondrial divergence, with only one species displaying a pattern consistent with previously described suture zones. Few predictions for hypotheses of expansion were met. ENMs suggest species have responded differently to historical climate changes, possibly contributing to discordant genetic patterns. Two species with deep mitochondrial divergences (>2.5 Ma) had low niche stability and potentially isolated regions of suitable habitat, while two species with relatively stable, continuous niches exhibit less genetic structure. These Coastal Plain anurans appear to have been affected by historical climate change, but were not necessarily isolated in glacial refugia. Different natural history characteristics have likely produced discordant patterns, with more generalist, ephemeral breeders exhibiting greater niche stability and lower phylogeographic structure.

MT3-12

Putting process on the map: modeling intraspecific variation for multi-taxa conservation prioritization.

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Natural populations face rapid and large-scale alterations of their habitat. Because habitat fragmentation increasingly limits their potential to shift their ranges, they need to adapt *in situ*. To maximize the adaptive potential of species, it is crucial to protect the available standing environmentally associated variation (EAV). We have developed a modeling framework to incorporate EAV with traditional measures of biodiversity and tested its applicability in four areas across the globe, differing in size, the available environmental gradients, and level of human disturbance. We used spatially explicit ecological modeling approaches in conjunction with environmental variables to model species distributions and patterns of genetic and morphological variation. We then used reserve selection software to prioritize areas for conservation based on EAV or species distributions (species richness). Reserves selected using species richness data showed little overlap with those based on EAV. In addition, results suggested that the spatial patterns of EAV are comparable between species, regardless of the environmental gradient or level of human disturbance, but only at regional scales. Our results imply that in order to maximize the chances of natural populations for long-term persistence, EAV can and should be explicitly included in conservation prioritization.

MT3-13

Boldness and aggression in Merriam's kangaroo rat: an urban tolerant species?

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Urban development can fragment and degrade habitat, and such habitat alterations can have profound impacts on wildlife behavior. In urban areas, individuals may occur closer to each other and experience high levels of disturbance, which may favor increased boldness and aggression in urban-dwelling wildlife. We investigated the influence of urbanization on boldness and aggression and the correlation between these traits in Merriam's kangaroo rat (*Dipodomys merriami*). We predicted that Merriam's kangaroo rats living in urban areas would be more bold and more aggressive than Merriam's kangaroo rats in wildland areas, that the two traits would be positively correlated, and that the correlation would be stronger in urban areas. We live trapped Merriam's kangaroo rats at 4 urban and 4 wildland sites in and around Las Cruces, NM, USA, and assessed aggression using a mirror image stimulation test and boldness using a predator scent exposure test. We found no difference between urban and wildland Merriam's kangaroo rats in either aggression or boldness. We found a positive correlation between aggression and boldness, but there was no difference in the strength of the correlation between urban and wildland areas. These results indicate that Merriam's kangaroo rats may be tolerant of urbanization, if habitat patches within urban areas are similar to wildland habitats.

MT3-14

Phytogeography of endemic species richness in the Guinean Forests of West Africa

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[3]University Félix Houphouet-Boigny, Abidjan, Côte d'Ivoire (Ivory Coast)

In 1978, Dr. Brenan conducted a comprehensive study of the phytogeography of tropical Africa, but limited efforts have been made to update this in spite of new taxonomic information in the last four decades. This study was carried out to update endemic flora list in each country within the Guinean forests of West Africa, one of the 34 global biodiversity hotspots. The methodological approach involved screening the Flora of West Tropical Africa (FWTA), online databases of International Union for Conservation of Nature (IUCN) red list of threatened species, African Plant Database (APD), International Plant Names Index (IPNI), JSTOR virtual herbarium, The Plant List, Tropicos, Angiosperm Phylogeny Group (APG) III, Terrestrial Biozones, and Global Biodiversity Information Facility

(GBIF). Also, published FWTA revisions, and checklists of pteridophytes and orchids were evaluated. We documented 879 endemic plant species, excluding endemic taxa considered as “imperfectly-known species”, in contrast to 1001 endemic species previously reported by Dr. Brenan. Furthermore, Cameroon and Sao Tome and Principe had the highest number of endemics per country, while endemic hotspots in each country were also identified. There is paucity of empirical research on most of these documented endemic species; consequently, species-specific conservation measure are lacking for each country. Subsequently, authors seek to use endemism metrics (weighted endemism and corrected weighted endemism) to analyze data for each country; and also identify environmental variables associated with high endemism in each country.

Mini-Talk Session 4: Gradients, range-limits, and beta-diversity (MT4)

Session Chair:
Date: January 10, 2017 4:00 pm – 5:30 pm
Location: Sabino room, Marriott Hotel

MT4-1 Non-stationarity in the co-occurrence patterns of species across environmental gradients

Yoni Belmaker[1], Avi Bar Massada[2]
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Quantifying the role of biotic interactions in driving community assembly often relies on analyzing species co-occurrence patterns, where segregated patterns are taken to indicate antagonistic interactions such as competition. It is unknown, however, if co-occurrence patterns are stationary across environmental gradients, as it is possible that the strength of biotic interactions that drive these patterns also depends on the environment. In this study, we aim to understand how patterns of co-occurrence change when species move from their environmental range center towards their range periphery while isolating the potential signal of biotic interactions from confounding factors. For this, we quantified pairwise co-occurrence patterns for tree species sampled in 9,382 plots distributed across the conterminous US, as well as those that emerge from a simple meta-community model. We found strong non-stationarity in co-occurrences, with patterns shifting from segregated at the environmental range center towards aggregated at range margins for the majority of tree species. Patterns were in full agreement between model simulations and empirical data. This pattern may originate from a tradeoff between the abundance of the focal species pair, which decreases towards the environmental range margin, and the increasing abundance of non-focal species to which the environment is more suitable. The strong dependence of co-occurrence patterns on environmental conditions might limit the predictive ability of joint species distribution models, which couple species co-occurrences and their environmental responses, because co-occurrence patterns and environmental responses are confounded.

MT4-2 Quantifying species aggregation from species accumulation curve-like functions

Robert Szava-Kovats
University of Tartu, University of Tartu, Tartu, Estonia

Beta-diversity is a metric used to quantify species aggregation among communities. However, raw estimates of beta-diversity can be compromised by the effects of scale and sampling effort. For count data, resampling strategies have been proposed to mitigate these effects by which the observed beta-diversity is compared with that of a randomized community. These strategies, however, are suitable only if the estimate of gamma diversity represents the genuine large-scale biodiversity. A new method is introduced based on a species accumulation-like function of the estimated alpha- and gamma-diversity. Like resampling methods, the proposed index quantifies the degree of species aggregation with respect to a null-model, specifically a non-aggregated community. Unlike resampling methods, the index quantifies species aggregation even when gamma-diversity underestimates regional diversity. Moreover, the index is scale invariant for any given degree of aggregation. This method is used to estimate species aggregation of tree species along a latitudinal gradient. The results suggest species aggregation decreases towards the equator, in contrast to standard beta-diversity measures, which increase towards the equator.

MT4-3
Macroecology of grasses: insights from the phylogenetic structure of assemblages worldwide

Anne-Christine Monnet[1], Jens Christian Svenning[2], Brody Sandel[2]
[1]Aarhus University, Aarhus, Denmark
[2]Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Denmark

The family Poaceae, the fifth largest family of Angiosperms, is an ecologically and economically important group, present in all continents and in very diverse habitats. So far, grasses do not occupy a central place in the macroecological studies, as tree species or the major vertebrate groups do. However, they display striking distributional patterns, especially a shallow latitudinal gradient. Richness is concentrated in the warm, wet tropics, but there are also a number of lineages adapted to cold and arid environments, keeping diversity unusually high there. Through analysis of diversification and of the geographic variation in the phylogenetic diversity and structure of grass assemblages, we assessed importance of the evolution of cold tolerance in explaining the unusually shallow latitudinal gradient. Phylogenetic information provided new insights into the evolution of grasses, revealing a strong effect of tropical niche conservatism and more rapid diversification in colder places. For this study, we gathered geographic, functional trait and phylogenetic information for the Poaceae family at the species level, c. 11000 species. However, the limited accuracy of occurrence data is still a substantial problem at such large spatial extents. We will also show how recent downscaling methods of species distribution models could help to estimate fine-grain presence/absence of grass species and to establish the grass family as a model group for macroecological studies.

MT4-4
What is the relative importance of biotic and abiotic determinants of occupancy for avian species distributions in North America?

Sara Snell[1], Allen Hurlbert[1]
[1]University of North Carolina, Chapel Hill, Chapel Hill, NC, United States

Understanding how biotic and abiotic interactions determine species distributions is a fundamental question in ecology with important implications for how distributions are expected to shift with climate change. In this study, we examine the relative importance of biotic and abiotic factors in explaining temporal occupancy for 63 bird species across North America based on a uniform set of criteria. Unlike previous studies which tend to model distributions in terms of presence/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 first characterize the extent to which temporal occupancy varies across the geographic range, and then use variance partitioning and generalized linear models to evaluate the relative importance of biotic variables (the abundance of potential competitors) and abiotic variables (elevation, temperature, precipitation, a vegetation index) for explaining patterns of temporal occupancy. The results of this study can be used improve biodiversity modeling, gain a better understanding of what factors influence species distributions and temporal persistence, and identify species at risk for habitat loss due to climate change.

MT4-5
Small mammal community assembly along elevational gradients: insights from a functional perspective on co-occurrence patterns

Brooks Kohli[1], Eric Rickart[2], Rebecca Rowe[1]
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[2]Natural History Museum of Utah, Salt Lake City, UT, United States

Null model analysis of species co-occurrence has proven to be an informative approach for determining the mechanisms of community assembly operating at a variety of temporal and spatial scales. However, in heterogeneous landscapes and along strong environmental gradients it can be difficult to determine whether species associations are due to environmental filtering (shared abiotic limits and/or habitat requirements) or competition. We integrated a multi-scale sampling scheme with functional group analysis to develop testable hypotheses of co-occurrence patterns and to enable a mechanistic understanding of assembly. We analyzed the associations of non-volant small mammals at sites spanning the elevational gradient of two mountain ranges in the Great Basin of western North America. To differentiate among drivers, we analyzed associations at two spatial resolutions: the site level and among all microhabitats present within sites. Few non-random species pairs were observed, but significant aggregations and segregations were identified. Our results strongly support environmental filtering as the primary mechanism driving small mammal co-occurrence patterns, and functional group analysis was useful for discriminating between competition and habitat filtering at the local scale. Competition was supported for only a very small proportion of pairs. Although the assemblages of these two mountain ranges have many species in common (60%), only one significant pair was shared between them. Despite this variability, the functional relationships characterizing aggregations and segregations were fundamentally similar between the isolated mountains. Thus, a functional approach can provide insight on the generality of assembly mechanisms that would otherwise be masked.

MT4-6

Do postglacial dispersal limitations influence the distribution of North American trees?

Benjamin Seliger[1], Jacquelyn Gill[1]

[1]University of Maine

The degree to which dispersal influences a species' geographic range is not fully understood. Some large fruited trees (e.g. Osage Orange, Honey Locust) are rarely dispersed today, and are proposed to be relics once dispersed by Pleistocene megafauna. Given the paucity of dispersers available to these trees since deglaciation, it has proposed that their modern ranges are reduced relative to their potential ranges. Using bioclimatic envelope models, we calculated potential ranges for over 400 North American trees based on their natural distributions mapped by E.L. Little. We hypothesized that species adapted to megafauna dispersal would occupy a lower proportion of their potential range relative to trees with extant dispersal mechanisms. Surprisingly, dispersal mechanism appears to have little influence on range filling, as species with megafauna dispersal adaptations fill their ranges similarly as to other species. Most trees do not fill the majority of their potential range (average 49% filled), which suggests tree species in North America are not in equilibrium with climate. This may be due to postglacial dispersal lags, as has been proposed for European taxa. Understanding the factors which determine species' ranges is vital for predicting range shifts and the biodiversity consequences of climate change.

MT4-7

The credibility of expert opinion

Kumar Mainali[1], Leslie Ries[2], William Fagan[1]
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[2]Department of Biology, Georgetown University, Washington, DC, United States

Species distribution modeling (SDM) is widely used to estimate species spatial distributions. However this approach suffers important problems related to comprehensiveness of occurrence records, identification of covariates, and appropriateness of statistical models. Whereas SDM cannot be replaced by subjective assessment of distribution, expert-delineated species range can provide a general guideline about species distributions and serve a complement to SDM methods. We obtained ranges of 175 butterfly species from two widely used sources (Scott and Glassberg), developed and peer reviewed by well-known experts on butterfly ecology and distribution. We then (1) compared these two sources and (2) evaluated them against occurrence records of North American Butterfly Association (NABA), Butterflies and Moths of North America (BAMONA), and Global Biodiversity Information Facility (GBIF). The two sets of expert ranges differed in important ways. Across all species, the average area shared was 62%. Scott ranges exceeded Glassberg ranges for 75% of species, and on average were 1.5 times bigger. Agreement between the two expert sources was lowest for species with small ranges, in some cases identifying completely disjunct ranges. Differences between Scott and Glassberg datasets were substantial when compared to occurrences from other sources. Scott and Glassberg ranges enclosed 83% and 82% of NABA occurrences, 86% and 83% of BAMONA occurrences, and 83% and 73% of GBIF occurrences, respectively. These differences can be partly explained by larger Scott ranges. We conclude that expert opinion can help guide spatial analyses but cannot substitute for SDM, especially for questions involving habitat suitability at fine spatial resolutions.

MT4-8

Cenozoic dynamics of shallow-marine biodiversity in the Western Pacific

Moriaki Yasuhara[1], Hokuto Iwatani[2], Gene Hunt[3], Hisayo Okahashi[2], Tomoki Kase[4], Hiroki Hayashi[5], Toshiaki Irizuki[5], Yolanda Aguilar[6], Allan Gil Fernando[7], Willem Renema[8]
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[5]Shimane University, Japan
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[8]Naturalis Biodiversity Center, Netherlands

Cenozoic dynamics of large-scale species diversity patterns remain poorly understood, especially for the Western Pacific, in part because of the paucity of well-dated fossil records from the tropics. Here we show the spatiotemporal dynamics of species diversity in the Western Pacific through the Cenozoic, focusing on the tropical Indo-Australian Archipelago (IAA) biodiversity hotspot. We analyzed well-preserved fossil ostracodes from the tropical Western Pacific and combined their diversity data with other published data from the region to reconstruct Cenozoic dynamics of species diversity in the tropical- and northwestern Pacific Ocean. Low-, mid- and high-latitude regions all show a similar diversity trajectory: diversity is low in the Eocene and Oligocene, increases from the Early Miocene to the Plio-Pleistocene but then declines to the present day. Latitudinal diversity patterns are relatively flat and rarely show the typical decline from tropics to high-latitude. Modern-level high biodiversity in the tropical IAA and the northwestern Pacific Ocean was established during the Pliocene. The modest diversity decline from the Plio-Pleistocene to the present day may be attributable to large amplitude glacial-interglacial climate and sea-level changes. The weak and irregular (i.e., inverse, mid-latitude-peaked, or mid-latitude-depressed) latitudinal species diversity gradients are unexpected, because the northwestern Atlantic Ocean displays a standard tropical-high and temperate-low diversity pattern throughout the Cenozoic. In addition, ostracodes are known to show standard latitudinal diversity gradients in the North Atlantic. These differences suggest an important role for regional factors (e.g., plate tectonics and temporal geomorphological dynamics), in shaping the biodiversity of the Western Pacific.

MT4-9

Mountain building is a prerequisite – not a driver – for alpine plant radiations in hotspots of biodiversity surrounding the Qinghai-Tibet Plateau

Adrien Favre[1], Jana Ebersbach[1], Alexandra N. Muellner-Riehl[1]
[1]Leipzig University, Leipzig, Saxony, Germany

Orogenesis is often considered the main driver for the radiation of alpine plants. Yet, the role of climate oscillations and key opportunities as well as key innovations as contributors to the establishment of high levels of biodiversity around the Qinghai-Tibetan Plateau (QTP) is often overlooked. In order to understand the contribution of orogenesis to the radiation of alpine plants, we investigated the evolutionary history of two predominantly alpine taxa, *Gentiana* and *Saxifraga*. We performed analyses on molecular dating, historical biogeography, diversification rates and climatic niche evolution. Similar to several other studies, we found a tremendous delay between the start of orogenesis and radiations. Rather, our study underlines the complexity of processes and factors underpinning plant radiations in mountain systems. For example, even in closely related lineages occupying the same life zone, radiations are not necessarily governed by the same factors. In conclusion, the underlying causes for alpine plant radiations can be multi-faceted and do not necessarily derive from orogenesis, but rather result from a complex interaction between geological settings (a prerequisite) and/or climatic modifications providing key opportunities, as well as from the evolution of key innovations.

MT4-10
Niche evolution patterns across spatial scales in bats

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Niche evolution is an important evolutionary mechanism that can explain how ecology and contemporary characteristics interact with evolutionary processes to determine biogeographical patterns. Although climatic niche evolution has been continually tested in many organisms, including bats (the only mammal group with real flight capability), yet we still know little about the role of spatial scale in niche evolution. Here we explored the scale-dependence in niche evolution in extant bat assemblages across the globe and in different biogeographical regions. We used bat geographical distributions and environmental variables to estimate their climatic niches at different grain sizes (~1, 2.5, 5, 10, 50, 100, 500, 1000, 2500, 5000 and 10000 km^2) across each biogeographical realm. We employed contemporary phylogenetic comparative methods to test and compare climatic niche evolution rates across different grain sizes and between biogeographical realms. Our results show that patterns of niche evolution change across spatial scales and across biogeographical regions. At larger scales, climatic niche is generally more evolutionary conserved than the climatic niche at local scales. Due to the major differences between Old World and New World bats, patterns of niche evolution in the New World biogeographical regions differ more in relation to Old World regions. Our findings show that ecological and evolutionary processes act at different spatial scales and differ across regions, highlighting that addressing scale-dependence may improve our precision in understanding the scales at which niche evolution acts to shape present day assemblages.

MT4-11
Low phylogenetic beta diversity and geographic neo-endemism in Amazonian white sand forests

Juan Guevara[1], Gabriel Damasco do Vale[2], Chris Baraloto[3], Paul V.A. Fine[2], Maria Cristina Peñuela[4], Carolina Castilho[5], Alberto Vicentini[6]
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[6]Instituto Nacional de Pesquisas da Amazônia-INPA, Coordenação de Pesquisas em Ecologia, Manaos, Amazonas, Brazil

Over the past three decades, many small-scale floristic studies of white-sand forests across the Amazon basin have been published. Nonetheless, a basin-wide description of both taxonomic and phylogenetic alpha and beta diversity at regional scales has never been achieved. We present a complete floristic analysis of white-sand forests across the Amazon basin including both taxonomic and phylogenetic diversity. We found strong regional differences in the signal of phylogenetic community structure with both overall and regional Net Relatedness Index and Nearest Taxon Index values found to be significantly positive leading to a pattern of phylogenetic clustering. Additionally, we found high taxonomic dissimilarity but low phylogenetic dissimilarity in pairwise community comparisons. These results suggest that recent diversification has played an important role in the assembly of white-sand forests causing geographic neo-endemism patterns at the regional scale.

MT4-12
A 120,000-year vegetation and wildfire history from the San Bernardino Mountains, Southern California

Katherine Glover[1], Glen MacDonald[2], April Chaney[2], Sargam Saraf[2]
[1,2]UCLA, San Jose, CA, United States

Vegetation in the San Bernardino Mountains (SBM) today consists largely of coniferous trees, riparian vegetation, and juniper-sage-pinyon woodland in its drier habitats. This study reconstructs paleoclimate, vegetation, and fire regime in Big Bear Valley (elevation 2060 m) over the past ~120,000 years, using core samples from Big Bear and

Baldwin Lakes. We find that long-term changes in lake productivity and regional temperature were largely driven by local summer insolation. The penultimate interglacial (~60,000 – 29,000 years BP) supported a consistently productive, stratified alpine lake, suggesting broadly moist conditions in Southern California. Pollen analysis further highlights past hydroclimatic conditions and extreme events. Low Pinus tended to coincide with high amounts of upland herb pollen, suggesting arid conditions at the onset of each glacial (~70,000 and ~26,000 years BP). Pinus resurgences within 2000-3000 years mark times of forest re-expansion, and the return of moist conditions. Charcoal data show that wildfire was an important agent of landscape change throughout the basin history, except for its suppression throughout the last glacial. This wildfire hiatus, spanning 12,000 years, was likely initiated with dry conditions just prior to the Last Glacial Maximum, and then sustained by the combined effects of low insolation, temperature, and evaporation. Charcoal influx was highest beginning ~2000 years BP, coinciding with evidence for the onset of seasonal human occupation in the SBM. Recent studies in California indicate that due to enhanced warming and sustained drought, its forests may be in the midst of another period of widespread ecological disturbance, and possible community turnover.

MT4-13

Ontogenetic differences in odonate nestedness patterns: Confirmation that baby dragonflies *also* live in nests!

Karen Gaines
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It has often been observed that species in patchy landscapes can occur in non-random, nested subset patterns, but rarely are two life stages with vastly different dispersal abilities and habitat requirements explicitly compared to determine if these patterns are consistent throughout the life cycle, despite the conservation implications and additional insight into community structure that such comparisons can offer. To compare the degrees of nestedness exhibited by the larval vs. adult odonate communities of a desert sinkhole complex and identify idiosyncratic distribution patterns, the 'nestedness temperature calculator' (Atmar & Patterson, 1995) was used with cumulative exuvial (proxy for larval) and adult species richnesses measured over three flight seasons to calculate system temperature (T) values for the two life stages (note: T near 0° suggests highly nested subsets, T approaching 100° indicates maximum disorder). The resulting T values ($T_{adult} = 19.8°$, $T_{exuvia} = 8.6°$) were significantly lower than the respective T values derived for randomized, simulated matrices ($T_{adult} = 66.0°$, $T_{exuvia} = 49.2°$), suggesting that while the adult odonate community does exhibit a degree of nestedness, aquatic larvae live in more highly ordered communities. The euryhaline seaside dragonlet *E. berenice* had an idiosyncratic $T_{exuvia} = 80°$ consistent with its unusually-tolerant larval physiology, which suggests that this widespread species may be uniquely unconstrained by some ecological factors that otherwise dictate the sinkhole system's larval biogeography.

MT4-14

Reconciling the effects of time, area, and energy on geographic gradients of species richness and coexistence

Walter Jetz[2], Alex Pigot[1], Alex Pyron[2], Nathan Upham[3]
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The absolute and relative importance of different causes behind the latitudinal gradient in species richness remain contested. Advances in the completeness and quality of phylogenetic, environmental, and species distribution information, and increased appreciation of the scale-dependence of different processes have led to significant progress. Specifically, empirical and conceptual progress is enabling a more explicitly multi-causal, hierarchical, and macroevolutionary perspective. I will present recent work on terrestrial vertebrates that attempts to take an integrative approach to compare multiple predictors of regional variation in species richness and gage the relative importance of energy availability vs. species functional similarity on broad-scale species coexistence. I will also draw on recent phylogenetic and macroevolutionary findings from the NSF "VertLife" project addressing the global diversification and species richness of terrestrial vertebrates in geographic space.

POSTER SESSIONS

Poster Session 1: Biodiversity Patterns and Maintenance (PS1)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS1-1

We need time, a neglected component, in metacommunity analysis

Francesc Mesquita-Joanes[1], Andreu Castillo-Escrivà[2], Juan Rueda[3]
[12,3]University of Valencia, Burjassot, Spain

The development of metacommunity theory at the beginning of this century boosted empirical tests using field data, mostly focused on the relative importance of spatial *vs*. environmental factors for the explanation of metacommunity structures. Yet few works deal with time *per se* as a component in explaining these patterns, even when repeated samples are analysed. We consider necessary to take time into account explicitly in metacommunity dynamics, as many biological processes (e.g. ontogenetic development, reproduction and population growth, migratory movements…) depend on the amount of time spanned. We review the (uncommon) evaluation of the importance of time in empirical metacommunity analyses using variation partitioning and provide examples from aquatic invertebrate metacommunities where pure temporal effects (i.e. excluding the overlap with environmental and spatial influences) are found to significantly affect their assembly.

PS1-2

Using functional diversity to set conservation priorities: a methodology and a case study of global parrot diversity

Evsey Kosman[1], Kevin Burgio[2], Steven Presley[2], Michael Willig[2], Samuel Scheiner[3]
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Central to conservation planning is prioritizing which areas or species to protect. In addition to species rich areas, maintaining ecosystem function requires conservation of functionally distinct species and communities. We present a new method for calculating functional distinctiveness of species based on a newly published concept for functional diversity, and apply it to data on the global distribution and functional traits of all extant parrots. We calculated the functional distinctiveness of each parrot species and averaged those scores for each 500 x 500 km grid cell across the global distribution of parrots. For each grid cell, we compared average functional distinctiveness to species richness. Functional distinctiveness was greater than expected in Patagonia, Africa, India, Indochina and western Australia; patterns were driven by traits associated with diet and foraging location. Generally, these areas are relatively low in species richness, with parrots being generalists and functionally distinct from those living in more species-rich regions. This new method can provide vital information when constructing regional or global conservation networks.

PS1-3

Disturbance effects on community patterns in savannas of the Marajó region

Ana Luisa Albernaz
Museu Paraense Emilio Goeldi, Museu Paraense Emilio Goeldi, Belem, PA, Brazil

The Marajo region is an extensive area in the mouth of the Amazon River. The region includes the largest river island of the World and surrounding environments, between the Tocantins and Amazon Rivers. A large part of this region is covered by savannas, related mostly to alluvial soils, while the its flora is related to those of Brazilian Cerrados, but considerably less rich regarding its tree composition. Recently the savannas of Marajó are being crossed by power lines, and this study was designed to investigate their possible impacts. A first step was to characterize the savanna tree composition found there. In order to better understand its composition, it was compared with that of another Amazonian savanna, located near the Santarem municipality. Marajo savannas, in an area of approximately the same size, are less rich than those of Santarem, with 1-11 species per sample and a total of 11 species registered, against, 9-16 species per sample and a total of 26. Three species found in Marajó region do not occur in Santarém area. Also, despite its relative poverty in species, tree composition Marajó of samples are more variable, and much more disperse in a multivariate space. While the main disturbance suffered by Santarem savannas are related to fire, Marajo savannas are disturbed by fire, floods, and temporary or permanent presence of cattle. The large difference between samples, related to the intensity and combinations of these disturbances, makes difficult to isolate the possible disturbance effect of the power line.

PS1-4

Mapping biodiversity patterns of coastal fish in Japan

Takayuki Shiono[1], Haruhiko Yasumuro[2], Buntarou Kusumoto[1], Yasuhiro Kubota[1]
[1,2]University of the Ryukyus, Japan

Mapping species geography and biodiversity patterns is fundamental research in macroecology and conservation planning. In marine realm, the region of East Asian Pacific Ocean is known as one of marine biodiversity hotspots; Japanese waters harbor 24.3% species of all marine fish across the globe, and thus it is supposed that a variety of environmental factors including climate and the ocean current flow from tropical to temperate contribute to increasing marine biodiversity. Nonetheless, geographical pattern of marine organisms in this region remain unclear, and also the underlying mechanisms has not been tested. In this study, we focused on coastal fish that inhabits less than 200 meters deep around the East Asian continental islands. We compiled occurrence data (283,846 occurrences for 3068 species) by searching the literature, angler magazine, and databases of specimen and distribution survey. In the analysis, we divided the Japanese coastal area into 742 grid cells of 20 × 20 km, and created the map of species richness. In addition, we compiled environmental variables (sea temperature, nutrients, current speed, distance from Kuroshio Current, and geographical characteristics). Using these datasets, we explored environmental factors that explained coastal fish diversity pattern in East Asian Pacific Ocean.

PS1-5

Diversity without abundance: minimal support for predictions of the productivity hypothesis as a driver of the species richness of North American wintering bird assemblages

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It is well-documented that primary productivity and animal species richness are positively correlated for a variety of taxa across a wide range of spatial scales and extents. The productivity hypothesis had been credited for explaining these correlations by asserting that places with more energy fixed in the system (i.e. high primary productivity) should support more animal individuals, whereby the community accumulates more species. For birds in particular, many observational studies have interpreted the spatial association between richness and productivity as support for the hypothesis. It follows that when vegetation biomass increases or declines temporally, so should bird richness. However, a recent study of North American birds found that when evaluated temporally, the productivity hypothesis failed to explain interannual changes in avian richness. Yet, it is possible that avian richness has stronger dependence on primary productivity in winter months when birds are stressed by colder temperatures and food scarcity. Using community data from the North American Christmas Bird Count from 1982 - 2002, we evaluated if wintering local avian richness tracks changing primary productivity. By regressing avian species richness against winter NDVI (a proxy for primary productivity) at each CBC site through years, we found that species richness weakly responds to interannual changes in NDVI. However, we found no support for the more individuals mechanism predicted by the hypothesis. Thus, the productivity hypothesis apparently explains none of the interannual variation in North American species richness of avian assemblages in summer and only a small fraction of the variation in winter.

PS1-6

Convergent patterns of functional diversity across tropical and temperate mountain forests

Kiri Staiger[1], Andrew Kerkhoff[2]
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Largescale biodiversity gradients are one of ecology's most fundamental patterns, yet unified drivers remain controversial. At the community level, biodiversity is maintained by both the abiotic environment and the biotic interactions between species. Because both of these forces act more directly on communities' functional identity than they do on taxonomic or phylogenetic composition, recent literature has focused on functional trait approaches in identifying the presence and relative importance of biotic and abiotic forces in the assembly of varying communities. Here, we characterize functional diversity for woody plant communities in six elevational forest gradients, spanning 30 degrees of latitude across North and Central America. We investigate the drivers of community assembly along these elevational gradients, and whether or not similar drivers act on elevational communities across the latitudinal span. We find consistent patterns of functional diversity in relation to species richness and elevational shift across the six forest gradients, despite the large shifts in latitude and climate that separate these sites. Species rich sites (more than 30 species) are functionally dispersed, possibly reflecting limiting similarity in community assembly. Functional turnover within gradients was relatively low, suggesting that environmental drivers have a more subtle influence in structuring these communities than expected.

PS1-7

Phylogeny as a window on the evolution of plant hyperdiversity in tropical rain forest

Wolf Eiserhardt[1], Thomas Couvreur[2], William Baker[3]
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Tropical rain forest (TRF) is the most species-rich terrestrial biome on Earth, harbouring just under half of the world's plant species in 7% of the land area. Phylogenetic trees provide important insights into mechanisms underpinning TRF hyperdiversity that are complementary to fossil evidence. Focusing on plants, we searched the literature for studies that capitalized on phylogenetic data to formally test hypotheses on the accumulation of species diversity in this biome. We found surprisingly few studies that fulfilled these criteria, going beyond informal interpretation of phylogenetic patterns. The few studies we found mainly focused on whether TRF is an evolutionary "cradle" or "museum", emphasising speciation and extinction rates. However, other explanations, such as biome age, immigration and ecological limits, must also be considered. To this end, we present an integrative conceptual framework for addressing the drivers of TRF diversity, within which we interpret the results of the reviewed studies. Empirical data point to old age of TRF, low extinction and high speciation rates as credible drivers of TRF hyperdiversity. There is less evidence for immigration and ecological limits, but these cannot be dismissed due to the limited number of available studies. Rapid methodological developments in DNA sequencing, macroevolutionary analysis and the integration of phylogenetics with other disciplines may dramatically improve our grasp of TRF hyperdiversity in the future. However, such advances are critically dependent on fundamental systematic research yielding numerous, additional, well-sampled phylogenies of TRF lineages.

PS1-8

Distinguishing between environmental productivity and predictability in relation to geographic patterns in species traits of South African birds

Mgr. Anna Tószögyová [1,2], Prof. David Storch, Ph.D. [1,2]
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The understanding of trait-environment linkages may help to reveal the general mechanisms affecting biodiversity patterns. Our study was based on a wide variety of traits of 650 bird species in South Africa. The comprehensive data set comprised approximately 50 traits and life-history characteristics divided into four groups; morphological parameters, feeding, breeding and migratory strategies. We identified two main environmental gradients, in productivity and predictability, that were responsible for geographic trends in trait composition. Morphological parameters and feeding characteristics co-varied with species richness along productivity gradient, while breeding characteristics and migratory strategies were associated mainly with environmental predictability. This spatial distribution according to environmental predictability revealed traits with strong phylogenetic clustering. Our results indicated that energy availability and stability influenced different sets of functional traits and thus geographic distribution of differences among species on the basis of their particular life-histories differently influence processes that shape geographic patterns in species diversity.

PS1-9

Ecological divergence or conservatism? Geographical patterns and evolution of the ecological niches in the spadefoot toads (Anura: Pelobatoidea)

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Two mechanisms are generally recognized for speciation by natural selection: mutation-order speciation, and ecological speciation. Ecological speciation occurs when reproductive isolation between populations results as a byproduct of adaptation to divergent environments. In contrast, mutation-order speciation occurs when different adaptive mutations are fixed between populations adapting to similar environments. In this context, progress towards speciation is dependent on the ability of populations to diverge and adapt to new environments (niche divergence), or to occupy the same ecological niche (niche conservatism) accompanied by reproductive isolation. These two mechanisms of speciation affect the functional diversification of evolutionary lineages and the interaction of closely related species. However, the relative importance and prevalence of the two mechanisms in speciation remain largely unknown. Spadefoot toads (Anura: Pelobatoidea) offers a great system to test this question, this relatively diverse family is distributed across the Northern Hemisphere, inhabiting a wide array of climates, from tropical regions of the South-Eastern Asia (Megophryidae) to the steppes and plains of Europe and Central Asia (Pelobatidae, Pelodytidae) and the dry deserts of North America (Scaphiopodidae). Combining ecological niche models (Maxent models) with phylogenetics (Pelobatoidea dated phylogeny) we were able to reconstruct the ecological niche evolution of the group to visualize niche evolution, evaluate the relative influence of the climatic factors in niche evolution and to test for rates of divergence within the spadefoots. Generally, we found a mixed signal of niche conservatism (consistent with mutation-order speciation or neutral processes) and niche divergence (consistent with ecological speciation) within lineages and across Pelobatoidea.

PS1-10

Direct and indirect forces on the elevational pattern of ground arthropod community in Oak forest

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Ant-aphid mutualism is known to play a key role in structuring arthropod community in tree canopy, but knowledge on its possible effects of ground arthropod are scarce. In this work, structure equation modeling was used to evaluate the effects of ant-aphid mutulism in shaping the variation of ground arthropod community along an elevational gradient in a deciduous temperate forest, Beijing, China. The results showed that ants and aphids are positive correlated. The abundance of ground beetles is negitive correlated with ants and aphids. Struture equation models shows that the mutualism of ant-aphid determine the ground beetles variation. These results suggest that aphids located in the tree canopy have indirect negative effects on beetles by enhancing the ant abundance on the forest floor which woud shed lights on trophic cascading effectsof ant-aphid mutualism on the forest floor food web.

PS1-11

The relative influence of local environment and regional enrichment on local woody plant species richness

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Local species richness reflects both regional (extinction, speciation, and dispersal) and local (interspecific interactions) processes. However, their relative influence on local species richness remains poorly understood.

Difficulties in distinguishing regional and local effects are partly due to sampling limitations (in particular, using non independent datasets for regional and local richness, and incomplete species sampling). Here, we use species lists, as well as climate and soil data, for 46 ~0.1-ha tree plots widely distributed across Costa Rica and summarized in Holdridge et al.'s *Forest environments in tropical life zones* (1971). We defined "local" richness as the number of species in each plot and estimated "regional" richness from collections of Costa Rican woody plants (Tropicos.com) within a 100 km^2 circular area surrounding each plot. Generalized linear models showed that variation in local species richness across Costa Rican forests was related primarily to the local environment and secondarily to species richness in the surrounding area, suggesting that local ecological species sorting is stronger than tree dispersal at this spatial scale.

PS1-12

Measuring biodiversity across ecological and geographic variables among diplommatinid land snails of Belau (Republic of Palau, Oceania)

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Three measures of alpha diversity (species richness, Shannon index, Simpson's index), two measures of beta diversity (Sørensen index, ubiquity index), and site use (number of live and dead specimens found) were used to assess land snail diversity across ecological and geographic features in the Belau archipelago (Republic of Palau, Oceania) using Diplommatinidae, the most species-rich land snail family in Belau. Belau land snails occur in three distinct island types (volcanic, Rock Islands, low coralline) and habitat types (leaf litter, emergent vegetation, limestone karst). Island and habitat types were used to measure ecological differences throughout Belau, and geographic differences were measured by political state and island identity, nested within island type. Island type significantly predicts two alpha diversity measures (richness, Shannon index) and Sørensen index (lowest in coralline islands) but does not predict use. Habitat type predicts all biodiversity indices (lowest alpha diversity and use in emergent vegetation, lowest beta diversity and highest use in limestone karst). Political state (presence within specific states of the Republic of Palau) predicts all alpha diversity measures and use, while island identity is not predictive of alpha diversity or use. These results show regional and ecological biodiversity differences within Belau despite limited land area (415 km^2 across 586 islands). Findings can be used to target high-biodiversity areas for land snail conservation.

PS1-13

Standardized biodiversity monitoring of arthropod assemblages in two South China forest plots with contrasting land-use history

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Standardized biodiversity monitoring across large scales provides comparable data for supporting ecological research and conservation management. For this purpose, the Center for Tropical Forest Science (CTFS) established the long term monitoring network of Forest Global Earth Observatory (ForestGEO) plots worldwide, while more recently the Arthropod Initiative has endeavored to monitor arthropod diversity associated with these plots. As part of this effort, starting in 2013 we implemented standardized monitoring protocols in two South China forest plots in Dinghushan (DHS), Guangdong Province, and in Tai Po Kau (TPK), Hong Kong. The two sites share very similar climates and topography, but contrast significantly in their land use histories. DHS is a 400 year old primary forest and TPK is a 70 year old secondary forest, regrown since large scale wood vegetation clearing during WWII. We conducted 429 butterfly transect walks, 160 termite quadrat samplings, 100 Winkler samplings, 80 McPhail weekly-traps and 120 light night-traps to assess arthropod biodiversity in both sites. Our results show that DHS has a generally higher abundance and species diversity relative to TPK. For example, we found 64 species of butterfly and 7 species of termite in DHS while recording only 53 species of butterfly and 2 species of termite in TPK. Interestingly, arthropod diversity and abundance recorded at both sites was generally much lower than diversity found at other CTFS forest plots in Panama, Thailand and Papua New Guinea. The results taken together

demonstrate the importance of global biogeographic and local environmental factors in determining arthropod biodiversity.

PS1-14

Multiple filter effect on species assembly: a driver of latitudinal biodiversity gradient in temperate forest communities

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Species assembly in a local community is the outcome of multiple filters that sample individual species from species pools at the regional scale. Species sorting through environmental filters and/or species interaction related to resource exploitation or survival is associated with a hierarchy in the concept of ecological niche. The conceptual distinction of the hierarchical niche is based on trait evolution and phylogenetic conservatism. Therefore, functional and phylogenetic structure of local communities should provide insights into hierarchical role of filtering in species assembly. Based on the concepts of multiple environmental filters associated with the ? niche and the ? niche, we examined the climatic favorability hypothesis on latitudinal diversity patterns in temperate forests. Specifically, we tested phylogenetic clustering and functional clustering of cold tolerance, leaf traits and wood traits in local communities, and explored the environmental predictors of non-random assembly patterns. Finally, we discussed the relative importance of multiple environmental filtering and dispersal in tree species assembly and how niche assembly contributes to the formation of latitudinal biodiversity gradient in temperate forests.

PS1-15

Climate drives latitudinal and elevational beta diversity gradients across the Americas through elevated tropical speciation rates

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Latitudinal and elevational diversity gradients are some of the oldest and most conspicuous ecological patterns, yet the mechanisms underlying their formation are still intensely debated. A multitude of hypotheses have been put forward to explain diversity gradients, but many focus on how the greater climatic stability of the tropics either promotes increased speciation rates or decreased extinction rates relative to temperate regions. Crucially, speciation and extinction-based hypothesis make differing predictions for how recent and deep divergence events should be distributed across the phylogeny of tropical and temperate regions. Here we use species as well as phylogenetic beta diversity metrics, which differ in sensitivity to recent and deep divergence events, to show that diversity gradients in New World plants are driven by increased tropical speciation rates. To accomplish this we utilized one of the largest botanical datasets yet assembled, encompassing the vascular plants of the Americas with extensive phylogenetic and

geographic coverage. As predicted by the increased speciation hypothesis, species and terminal-weighted phylogenetic beta diversity was higher in the tropics, while basal-weighted phylodiversity was higher in the temperate zone. In addition, we found that species and terminal-weighted beta diversity gradients were steeper in tropical mountain ranges than temperate ones, supporting Janzen's climate-centered mountain passes hypothesis. Taken together, these results implicate climate-influenced speciation rates as a key driver of latitudinal and elevational diversity gradients across the New World flora.

PS1-17
Integrated monography of the genus Saxifraga L. as a window on the evolution of the European Alpine flora

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Mountains can harbour high and unique plant diversity, but in spite of long standing scientific interest the fundamental principles responsible for the diverse mountain biota are not fully understood. This project aims to use the species-rich, predominantly alpine genus *Saxifraga* L. (ca. 440 spp.) as a model to elucidate the eco?evolutionary assembly of mountain floras, with emphasis on the European Alps. We are assembling a high-resolution phylogenetic tree of *Saxifraga* and to this end use next generation sequencing (HybSeq) to obtain genome-wide data to overcome problems due to a lack of genetic variation among recently diverged species. In addition, a global database will be built of *Saxifraga* occurrences, niche models and functional traits. Combined with the phylogeny we will infer historic dispersal events and radiations, and the role of habitat- and trait evolution therein. Furthermore, many *Saxifraga* taxa are narrow endemics in sensitive alpine habitats. Our study also aims to unveil to what extent species diversity and functional diversity are at risk due to global climate change.

PS1-18
The effect of large sample sizes on Ecological Niche Models: analysis using a North American rodent, Peromyscus maniculatus

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Correlative ENMs aim to approximate the abiotically suitable areas for a species. Recently, there have been several studies to determine the minimum number of occurrence records needed to implement ENMs; however, cosmopolitan species with many occurrence records have their own challenges and the effects of larger sample sizes have yet to be determined. To address this issue, we focused on a New World rodent, *Peromyscus maniculatus*. We downloaded occurrence data from GBIF.org and spatially filtered the localities, obtaining 990 unique records. We then modeled suitable area for the species using Maxent, six uncorrelated climatic variables, and 12 different numbers of occurrence records (and 50 replicates each): 25, 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, and 800. We evaluated the models with k-fold cross-validation, AUC (calculated by two different methods), and an omission rate. Further, we calculated the variability among predictions within and between datasets to indicate variation in geography. As sample size increased, both measures of AUC decreased. Additionally, omission rate decreased as sample size was increased. Lastly, as sample size increased similarities in geography increased within and between datasets. Using large number of occurrence records may not be necessary for ENMs, and in fact larger datasets may hinder model performance.

PS1-19
Completing the Plant and Fungal Trees of Life

William Baker[1], Abigail Barker[2], Steven Dodsworth[2], Wolf Eiserhardt[2], Ester Gaya[2], Jan Kim[2], Olivier Maurin[2], Joe Parker[2], Lisa Pokorny[2], Felix Forest[2]
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Evolutionary trees are powerful tools for prediction, discovery, monitoring and conservation. Through comparative analysis of DNA sequence data, the backbones of the plant and fungal trees of life are relatively well understood, and many subcomponents have been studied in great detail. However, DNA data are still lacking for numerous genera and the vast majority of species of plants and fungi, preventing their accurate placement within this evolutionary framework and hindering downstream science. To better understand how the world's plants and fungi are related to each other and how they have evolved, we have initiated a project at the Royal Botanic Gardens, Kew to complete the Plant and Fungal Trees of Life (PAFTOL). We will utilise our collections and work with our collaborative networks to produce extensive new DNA sequence data for a representative species from each genus of plant and fungus using high-throughput sequencing technologies. This comprehensive investigation of phylogenetic relationships will be a rich resource enabling the discovery and study of evolutionary patterns in the plant and fungal kingdoms, and will provide a unifying framework for comparative research.

Poster Session 2: Conservation Biogeography (PS2)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS2-1

Spatial ecology and summer grazing areas of wild reindeer in Hardangervidda National Park, Norway

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The protection of the largest population of wild reindeer in Europe was one of the main reasons to designate Hardangervidda National Park (HNP). To understand the spatial ecology and distribution patterns of this population is therefore a central part of the park's management. GPS collars have enabled the visualization of reindeer movements since 2001, and while the animals do not predictably use the same areas as winter grazing pastures, there is high site fidelity for the summer grazing pastures. We compare the primary summer grazing area of the last 15 years with other suitable summer grazing pastures, to determine if the present grazing area is indeed more suitable in terms of its vegetation cover and topography. The area primarily used for summer grazing is not the only one that is suitable in terms of available herbaceous biomass, and it is possible that the animals return here because it is the most isolated from human disturbance. However, it is also possible that the more mountainous terrain here provides a more suitable summer habitat as the animals can escape warm temperatures that encourage the presence of insects (average temperature difference between the highest peaks is ~0.4ºC). If reindeer are indeed limited by temperature, this will have important consequences in the face of climate change, particularly as HNP is already at the southern end of their distribution.

PS2-2

Nature reserves may play key roles in protecting endemic seed plants on Tibetan Plateau under climate change

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Evidences show that many species have already shifted their distributions as a response to climate change, which may greatly impact the function of local or even global ecosystems. As a place sensitive to climate change and unique for its rich biodiversity, the Tibetan Plateau has undergone a rapid warming process along with changes in precipitation during last decades. Here, we assessed the impacts of future climate change on the diversity and distribution of 1473 seed plants endemic to the Tibetan Plateau using an ensemble species distribution modeling framework and evaluated the conservation effects of current nature reserves. We projected range shifts of these species to year 2050 and 2070 under two RCP scenarios and further evaluated the threatened status for these species based on the IUCN Red List criteria considering different dispersal scenarios. It was predicted that the range of about 17.3% to 33% species would decrease by year 2070 even in a full dispersal scenario. Severe species loss may happen in the marginal area of southeastern plateau, especially in the deep valleys of Hengduan mountains. The average protection rate of current nature reserve system for endemic seed plants is 19.5% and may increase in the future. Our study stressed the negative impact of climate change on this area and indicated the importance of nature reserves under climate change.

PS2-3

Modeling the environmental tolerances of Lontra canadensis

Danaan DeNeve Weeks[1], Jessica Blois[2]
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Identifying species responses to environmental changes is necessary to preserve biodiversity in a changing world. Climate and habitat are important drivers of species' geographic distributions, and likely also of persistence. As many species are strongly impacted by humans, anthropogenic factors may also be important drivers of distributions and persistence. The North American river otter is a freshwater carnivore that occupies much of North America. While it is frequently used as an indicator species, little is known about its environmental tolerances. In this study, we use species distribution models (SDMs) to examine the climatic, habitat, and anthropogenic variables that explain otter distribution across its range. We paired occurrence data from GBIF and other sources of occurrence data with present-day climate variables from WorldClim, and habitat and anthropogenic variables from NASA's SEDAC program. We ran Generalized Linear Models, Generalized Boosted Models, and Maximum Entropy models using the R package “BIOMOD2” on each variable type alone to determine their individual effects, and then on a de-autocorrelated set of the most explanatory variables from each individual model. Preliminary results indicate that climate is not a strong predictor of otter presence. Overall, this study informs our understanding of otter habitat requirements and the conditions under which we should and should not expect persistence, which can be used to inform conservation and resource management decisions that are made for river otters.

PS2-4

Reconsidering EU biogeographical regions - a network approach

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Natura 2000 is a network of protected sites in the European Union (EU) for species and habitats listed in the (EU) Directive on the conservation of natural habitats and of wild fauna and flora (Habitats Directive) and the Directive on the conservation of wild birds (Birds Directive). The network cover 28 EU Member States, and is the world's largest ecological network united under a unified regulatory framework, and protect over 194 birds species, 897 taxa (other than birds), and 231 habitats. The evaluation of network effectiveness is made by European Commission and Member States at the biogeographical region level. These biogeographical regions include areas with similar natural conditions across countries, irrespective of political and administrative boundaries. Using network analysis we evaluated the similarities between EU biogeographical regions and highlight the shortcoming of the current approach. For this, we applied a community detection approach using Natura 2000 sites, species, and habitats as network data. Our results show that the actual system including 9 biogeographical regions (Alpine, Atlantic, Black Sea, Boreal, Continental, Macaronesian, Mediterranean, Pannonian, and Steppic) must be revised in order to better reflect the biological diversity of European Union.

PS2-5

Modelling the distribution of Turtle doves Streptopelia turtur in East Spain.

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Since 1970, Turtle Doves *Streptopelia turtur* in Spain have declined in number by 50% and in breeding range by at least 30%. We present a re-analysis of the results of a study undertaken during the breeding seasons of 2001–2004 as a part of the Atlas of breeding birds in the province of Alicante (SE Spain). We analyze the principal factors related to its occurrence in this province using Hierarchical Partitioning analysis. Several studies show that Turtle doves in the Iberian Peninsula are more common in forest environments of the supra- and meso-Mediterranean layers, with the least abundant populations in the thermo-Mediterranean layer. Our results show an opposite trend, since in Alicante higher densities are estimated in environments with higher temperatures (thermo- and meso-Mediterranean layers), with the denser populations in pine forests and wooded farmland. One of the problems for the population decline of the turtle dove is forest fires, that are recurrent in the Mediterranean region, and changes in agricultural types and methods. Given our results, we expect that restoration strategies that contribute to increase the resilience of burned pinewoods would benefit the recovery of turtle dove populations.

PS2-6 Environmental and biodiversity representativeness of global protected area network

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Protected areas have long been the leading conservation instrument in response to continuing biodiversity loss worldwide. However, lack of good understanding of the representativeness of a protected area with respect to its surrounding region limits our ability to maximize conservation outcomes. To address this, we developed a remote sensing-based representativeness index and assessed and mapped the environmental and biodiversity representativeness of global protected areas. We measured the environmental dissimilarity between a protected area and its surrounding region and used generalized dissimilarity modeling to make the dissimilarity measure also reflect the dissimilarity of species composition. We generated a quasi-binominal generalized linear model to evaluate the effectiveness of this approach in estimating biodiversity representativeness of 415 protected areas where comprehensive inventory data on bird species are available. The approach was then used to assess and map the environmental and biodiversity representativeness of individual protected areas and protected area networks around the world. The generalized linear model explained about 50% of the variation in biodiversity representativeness among the protected areas, and the maps of the environmental and biodiversity representativeness provide information that cannot be obtained by assessing the coverage of protected areas. This study provides essential information to evaluate the performance of existing protected areas and to guide the expansion of the current network. Going beyond reserve evaluation and selection, the approach could also be used to fill the knowledge gap on fine-grain local species richness, and thus used as an essential biodiversity variable for biodiversity monitoring.

PS2-7

Freshwater megafauna: Global hotspots, threats and conservation status

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Freshwater megafauna is a diverse group of animals including fish, reptiles, mammals and amphibians that spend an essential part of their life in freshwater or brackish ecosystems and could gain a body mass of 30 kg or more. Following this definition, we listed 208 species, e.g. sturgeons, river dolphins and turtles. Despite their iconic character, these large bodied animals remain underrepresented in both scientific research and conservation efforts. Thus, our objective is to give an overview on the global distribution of freshwater megafauna but also on their main threats. Highest species richness can be found in Amazon, Congo, Mekong and Ganges River basins. We show that since the early 1990s, human pressure increased in 63% of the freshwater megafauna distribution range. In addition, 54% of freshwater megafauna species are already listed as threatened according to the International Union for Conservation of Nature (IUCN) Red List of Threatened Species, while 25% of them are listed as Data Deficient or Not Evaluated. We thus also discuss the potential of freshwater megafauna species as both flagship and umbrella species and likely benefits for a wider range of species.

PS2-8

Deconstructing the Grinnellian niche of the White Stork (Ciconia ciconia)

Ben Carlson[1], Martin Wikelski[2], Walter Jetz[2]
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Studies of individual ecology show that intraspecific variation exists within variables such as diet items or prey size (Eltonian variables), and that intraspecific variation can influence the outcomes of demographic rates, competition, and predator-prey interactions. Species distribution models (SDM) assume niches constructed using Grinnellian variables—such as precipitation or temperature—are conserved among individuals and across space and time. This assumption supports the use of occurrence data from opportunistic sampling procedures (such as citizen science or museum specimen data) to model species distributions by projecting an estimated niche onto geographic spaces and into time periods in which no samples exist. While intraspecific variation among Eltonian niches has been established, it cannot be concluded that this variation is reflected in Grinnellian niches, because resources such as prey items and size can vary within the same environmental conditions. Here, using a dataset of 440 European White Stork (*Ciconia ciconia*) movement tracks from 23 populations across the species' range, we deconstruct the species-level niche by describing fine-grained environmental associations of individuals. We show that individual niches constructed using Grinellian variables do not represent samples from an overall species niche, but rather vary strongly among individuals, falsifying a central assumption of SDM of no intraspecific variation in niches. Our results imply that individual variation in environmental associations may play an important role in the structure and dynamics of species' geographic ranges.

PS2-9

Toward a macroecology of roadkill

Nathaniel Smith[1], Molly Grace[1], Kim Arnaldi[2], Christina Bunner[2], Kevin Guilfoyle[2], Mimi Klein[2], Katie Mercier[2], Johnathan Napier[2], Danae Perry[2], Katrina Phillips[2], Rhett Rautsaw[2], Gustavo Stahelin[2], Dan Volk[2], David Jenkins[1]
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Vast numbers of wildlife are killed annually by road traffic, an evolutionary novelty. Most analyses examine local spatial patterns and habitat factors. Instead, we asked whether roadkill mortality could be predicted across ~5° latitude using variables such as taxon, body size, and trophic level. We amassed >4,200 data from 2006-2014 collected near ~30 state and national parks across the Florida peninsula. We hypothesized quadratic effects of size and trophic level. Roadkill was modeled as a function of adult mass or length and trophic level, while accounting for random effects of sampling effort (months surveyed), location (latitude, longitude, area), and traffic and road conditions that varied among parks. Analyses were conducted separately for mammals, birds, and squamates (snakes, lizards). Most plausible models (AICc) included effort and: significant effect of quadratic body size (length) for squamates; nonsignificant effect of size for mammals; a marginal quadratic effect of log(body size) for birds. Trophic level models were weak, perhaps related to narrow range of values. Predictive macroecological models for roadkill are possible (especially for squamates?) and may help steer efforts to mitigate wildlife mortality due to roadkill. But quadratic patterns may also represent "veiled" patterns, where smaller animals are also hit but scavenged, degraded, or simply missed during driving surveys. Global roadkill data should be organized (akin to GBIF) to better understand patterns for this major source of wildlife mortality.

PS2-10

The art of modelling biodiversity with small sample size

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Many studies used models to make inferences about different aspects of biodiversity patterns and their environmental drivers, often applying the conclusions to conservation, management, and risk assessment. Appeals to have robust models, inspired by a number of challenges with available data and methods, led to raising demands for improved models to deal with such challenges. One of these challenges relate to small sample size that is common for many situations, either as a consequence of poorly known area where biogeographical data are scarce, or due to having incomplete records. This issue causes problems not only for developing a model, but make the evaluation of a such model difficult and imprecise. A few studies showed that the quality of models (i.e., performance) is influenced by the number of records used to fit the models, but solutions to deal with the issue have been rarely discussed. In this study, we first investigated how and to what extent different modelling algorithms are affected by the issue of the small sample size, and how the current state-of-the art methods for evaluation perform. We then introduced a novel approach based on a bootstrapping procedure to develop the models and showed that how our approach can effectively improve the performance of both modelling algorithms and evaluation methods. We

focused on species distribution models (SDMs) that have been used enormously in the last decade not only for biodiversity modelling but for many other applications.

PS2-11

How species assembly processes are captured in conservation priority areas: a multi-taxon comparison in the East Asian islands

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Spatial prioritization is an essential step to design reserve networks for efficient and effective biodiversity conservation. From the view point of conservation biogeography, priority areas (optimal arrangement of protected areas) aim to capture evolutionary and ecological processes for a long-term persistence of biodiversity. However, the existing methods are mainly devised mathematically based on static patterns of individual species, and not explicitly accounts for species assembly processes underpinning biodiversity patterns. Therefore, how the prioritization methods capture key biodiversity processes should be examined from evolutionary and ecological viewpoints. Geographical biodiversity patterns differ among taxonomic groups, suggesting taxon-specific biogeographical processes. In this study, we focused on consistent representation scheme among eight taxa of terrestrial and marine organisms in the East Asian islands. Specifically we asked how eco-evolutionary processes are captured by prioritization analysis. We identified taxon-specific priority areas using the existing software. Then, we compared various biodiversity metrics, which surrogate macroecological processes, between the priority areas and the whole region. Finally, we explored implications for better emulating the mechanisms of biodiversity persistence across multiple taxa.

PS2-12

Conservation assessment for an endemic Malagasy rodent (Gymnuromys roberti) and recommendation of new niche modeling software to facilitate such studies

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Highland tropical biodiversity, already threatened by deforestation, is particularly vulnerable to future climate change. Thus, creating conservation assessments for endemic species in these regions remains vital to their protection. Performing these assessments may be complicated and time-consuming for management/conservation personnel, which highlights the need for tools that can streamline and simplify the process. Here we provide an example of a conservation assessment for the endemic highland, humid forest-dwelling Malagasy rodent, *Gymnuromys roberti*. Currently, this species is considered "Least Concern" by the IUCN, but this may change in the future. To reevaluate the species' conservation status, we build ecological niche models (ENMs) while exhaustively addressing issues of both sampling bias and model complexity. We projected ENMs to future climatic conditions, restricting the predictions to only those areas with sufficient forest cover. This revealed significant future contractions and possible fragmentation in the southern and northern parts of the species' range, which should change the IUCN prognosis. Because conservation assessments based on niche modeling approaches can be laborious and time-consuming, we make further recommendations for use of user-friendly niche modeling software, *Wallace,* to aid in the formation of current conservation assessments.

PS2-13

Current situation of the nature preservation in private properties in the state of Parana, Brazil: first notes

Gustavo Schacht[1], Yuri Rocha[1]
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Nature conservation in private properties is a fundamental measure in biodiversity conservation. In Brazil, this conservation is recognized by law. Even with conservation incentives, these areas suffer problems in their management. This article presents results of 106 RPPN (Private Reserve of the Natural Patrimony) visited in Parana,

Brazil until September of 2016. Out of this total, 86,8% belong to the natural person and are localized in the Semideciduous Forest (49,1% of the properties). The RPPN that protect bigger area than the 20% required by law, are 56,6% and only 9,4% do not form ecological corridors. Regarding to the motivation of the creation, 52,8% of the proprietors understand and support the protection of species and ecosystems, 34,9% meet their personal satisfaction and 57,1% meet public entities requests. Only 9,4% have a management plan. Regarding the receiving of technical support, 74,5% claim they have not been receiving public or private support. The main pressures on RPPN are the hunting and the burning. Are 61,1% of the proprietors qualify themselves as satisfied or very satisfied. Based on these partial results, it's possible to determine the abscence of the public authorities related to the support of the RPPN area's management in Parana. The RPPN are without management plans and without protection. Thanks to: São Paulo Research Foundation (FAPESP), grant n. 14/01871-8.

PS2-14

Using a novel model approach to assess the distribution and conservation status of the endangered Baird's tapir

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We test a new species distribution modeling (SDM) framework, while comparing results to more common distribution modeling techniques (e.g., Maxent). This new framework allows for the combination of presence-only (PO) and presence-absence (PA) data, accounts for imperfect detection, and provides a means to account for spatial bias in presence data. The new framework tested here is based on a Poisson point process model, which allows for predictions of population size. We compare these estimates to those provided by experts on the species. A hotspot analysis (Gi*) was used to identify habitat cores from the predicted probability of occupancy. Significant variables to model the distribution of Baird's tapir included total annual precipitation, percent forest cover, human population density, and slope. Also, accounting for spatial bias in the presence data affected which variables were significant in the model. Though the PA occupancy model generally had higher accuracy than the Combined model, spatial predictions from the PA framework did not match well with expert opinions, while the Combined model did. Total population as predicted by the model was higher than expert opinion on the species, but local density estimates from our model were similar to available independent assessments. We suggest that these results warrant further validation and testing through collection of independent test data, development of more precise predictor layers, and improvements to the model framework.

PS2-15

The context of creation and the main motivations on nature conservation in private properties in the State of Parana (Brazil) and in Catalonia (Spain)

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The nature conservation in private areas stands out all over the world in the 20th century. In Brazil, after 1990, with the law that creates a Private Reserve of the Natural Patrimony (RPPN). In Catalonia, the Territory Custody attains prominence after the Declaration of Montesquieu in 2000. This article presents the characteristics of the protected private areas in Parana and Catalonia. In Parana, 106 RPPN have been visited a total of 253 and nine properties, a total of 844 in Catalonia. In Parana, 13,2% belong to the companies; in Catalonia, they are 55,6%. The ecosystems conservation is reason to the creation of RPPN to 52,8% and 77,8% (Catalonia). Out of the RPPN, 58,5% have received incentives for creation; in Catalonia, 66,7% haven't received incentives. Of all the RPPN, 90,6% don't

have a Management Plan; in Catalonia they are 66,7%. In Catalonia, 55,6% have leisure activity; in Parana, only 16%. The management support doesn't exist in 74,5% of the RPPN; in Catalonia only 33,3%. Regarding the satisfaction with the reserve creation, 61,1% (Parana) and 88,8% (Catalonia) are very satisfied or satisfied. It is noticed that the context and the measures in Catalonia, even without a legal recognition, incentive and value the proprietor. The motivations are similar, and there are differences in the technical support.

Thanks to: São Paulo Research Foundation (FAPESP), grants n. 14/01871-8 and 15/25460-0

PS2-16

Estimating Wallacean shortfall of plant richness (Fabales: Fabaceae) in the Brazilian semiarid: a geostatistical approach.

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Knowledge gaps in species distribution (Wallacean shortfall) afflict research on biodiversity patterns at broad spatial scales. In Brazil, the semiarid Caatinga, is a highly neglected biome regarding its biodiversity. We proposed an analytical approach to predict the diversity and the existing knowledge gap for Fabaceae plants in the biome. Based on 220,781 records from online databases, we mapped local (0.5 resolution) species richness and used model selection to find the best predictors subset from 15 climatic, topographic and soil variables. We drew the better-known localities (the upper richness quartile) and estimated the spatial pattern of species richness through a co-kriging analysis, involving these localities and the best set of predictors. Best model ($R2 = 0.845$) had sampling effort, altitudinal range and nitrogen as best predictors. The predicted richness varied from 92 to 283 species, in contrast to the current knowledge of 0 to 289 , rendering richness deficits of up to 192 species. Further them evidencing expressive gaps in the Brazilian semiarid region, with critical implication for its conservation, our approach proved promising to challenge Wallacean shortfallsKnowledge gaps in species distribution (Wallacean shortfall) afflict research on biodiversity patterns at broad spatial scales. In Brazil, the semiarid Caatinga, is a highly neglected biome regarding its biodiversity. We proposed an analytical approach to predict the diversity and the existing knowledge gap for Fabaceae plants in the biome. Based on 220,781 records from online databases, we mapped local (0.5 resolution) species richness and used model selection to find the best predictors subset from.

PS2-17

WhatFrog: Anuran classification by voice recognition

Courtney Shadik[1], Mark Bush[2], Ronaldo Menezes[1], Eraldo Ribeiro[1]
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The WhatFrog app for the i-phone uses voice recognition to identify a calling frog or toad. Of the 100 amphibians in the USA, the commonest 48 are included in the app. Designed primarily for use by schoolchildren and citizen scientists, the app provides images, range maps, and vocalizations of frogs and toads. When a recording is made the user sees a screen that provides a sonogram, and a probability for the five most similar calls. The probabilities are optimized for the geographic location of the user, which is captured from the smartphone's GPS information. Recordings are automatically uploaded to a central server where the data can be verified and added to the pool of recordings available for each species. The recognition method was tested on a dataset of 736 calls from 48 species recorded across the USA. This dataset is much larger and diverse than those of previous works on automatic anuran classification. The method's average classification accuracy is 86%. The app also provides a social network environment that enables users to exchange ideas and connect based on their interests.

PS2-18

Are Gelada monkeys keystone species? A broad-scale analysis of the population status of Ethiopia's herbivorous primate and consequences for ecosystem processes

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The Gelada monkey (*Theropithecus gelada*) is the only primate that is primarily gramnivorous and a genuine grazer. As this descendant of a once widespread primate genus represents the majority of the native large herbivore biomass throughout the Ethiopian Highlands, an investigation into their impact on ecosystem processes is needed. Understanding landscape-scale responses of vegetation to changing mammalian populations requires a synthesis of existing large-scale animal census data, and high-resolution habitat characterization. Ethiopia, experiencing rapid human population expansion, provides an opportunity to investigate the relative importance of natural and anthropogenic drivers of ecosystem processes. We conducted the first broad-scale census of *T. gelada* at sites throughout their central range, to evaluate their potential role as keystone species in the Afroalpine ecosystem. Large herbivore assemblage surveys, rapid botanical assessments, and unmanned aerial vehicle (UAV) surveys were carried out from March-July 2015 and January-July 2016 at 89 sites in the Oromia, Amhara, and Tigray regions. Sites were chosen that had been previously aerially censused in 1972 (Watson et al, 1973). We report patterns of large herbivore species abundance, and plant community spatial heterogeneity as defined by the mean dissimilarity of species composition among plots within the sample sites. A two-way ANOVA revealed that large herbivore assemblage and plant diversity both significantly affect plant community heterogeneity, with a significant interaction. These results point to a need for an updated conservation status assessment of *T. gelada*. Ethiopia should manage mammalian populations considering their ability to greatly alter ecological processes in this increasingly degraded highland ecosystem.

PS2-19

Habitat loss and species extinction: a global analysis on the terrestrial ecoregions

Daniel Souza[1], Ricardo Dobrovolski[2]
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A biodiversity crisis is happening due to human activities – mainly habitat destruction. Here, we predict species extinction in the world terrestrial ecoregions based on the destruction of natural habitats. We quantified the proportion remaining natural habitats and fitted an endemic species area relationship in global ecoregions to predict the number of threatened terrestrial vertebrates. Moreover, we used a projection model of 2040 land use to quantify the number of species that are likely to be threatened in the future. We found that 327 vertebrates are threatened due current habitat loss and this number can increase to 414 in the future. Our prediction was consistent with the IUCN Red List of threatened species. However, on the Pacific Islands our model overestimated threatened species number, as many species were listed as data deficient or not evaluated. There was a tendency of underestimation on smaller ecoregions, suggesting that results are scale dependent. Our study shows the effect of habitat destruction on species survival worldwide and forecasts that the ongoing trend in habitat decrease could lead to further biodiversity loss.

PS2-20 Historical and contemporary factors generate unique butterfly communities on islands

Raluca Voda[1], Leonardo Dapporto[2], Vlad Dinca[2], Tim G. Shreeve[3], Mourad Khaldi[4], Ghania Barech[4], Khellaf Rebbas[4], Paul Sammut[5], Stefano Scalercio[6], Paul D.N. Hebert[7], Roger Vila[2]
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The mechanisms that shape island biotas are still not entirely understood, mostly because of a lack of studies comparing eco-evolutionary fingerprints over entire taxonomic groups. In this study we linked community structure (richness, frequency and nestedness) and genetic differentiation (based on mitochondrial DNA) in order to compare insular butterfly communities occurring over a key intercontinental area in the western Mediterranean (Italy-Sicily-Maghreb). We found that community characteristics and genetic structure were influenced by a combination of contemporary and historical factors, and among the latter, connection during the Pleistocene had an important impact. We showed that species can be divided into two groups with radically different properties: widespread taxa had high dispersal capacity, a nested pattern of occurrence, and displayed little genetic structure, while rare species were mainly characterized by low dispersal, high turnover and genetically differentiated populations. These results offer an unprecedented view of the distinctive butterfly communities and of the main processes determining them on each studied island and highlight the importance of assessing the phylogeographic value of populations for conservation.

Poster Session 3: Phylogeography (PS3)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS3-1

Phylogeographic and molecular analyses reveal a dynamic and complex biogeographic history in the widespread North American meadow vole (Microtus pennsylvanicus)

Donavan Jackson[1], Jason Malaney[2], Joseph Cook[1]
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Climatic and environmental fluctuations of the Quaternary played an integral role in geographic distribution and genetic structure within many organisms today. Understanding how these historical biogeographic events may have partitioned genetic variation throughout the landscape is critical to forecasting the implications of modern climate change and how animals will respond to projected climate shifts. Through geographic and taxonomically comprehensive sampling, we used multi-locus and species delimitation analyses along with niche modeling methods to investigate the evolutionary and biogeographic history of the meadow vole, *Microtus pennsylvanicus*. The meadow vole occupies a vast latitudinal and longitudinal range, making it the widest-ranging vole in North America. Using multilocus DNA analyses, we found that the biogeographic history of *M. pennsylvanicus* is characterized by isolation and subsequent expansion from multiple distinct refugia and Bayes Factor species Delimitation analyses decisively supported the presence of multiple independent species. Moreover, the findings of this study highlight the vulnerability and importance of distinctive peripheral populations that will require special conservation strategies. The dynamic evolutionary and geographic history of the meadow vole furthers our understanding of the important role Quaternary climatic oscillations played in the diversification and geographic distribution of North American organisms.

PS3-2

Novel approaches to studying the evolution of species niches and geographic distributions using the ENMTools R package

Dan Warren
Macquarie University, Australia

The ENMTools software package is one of the most widely-used pieces of software for performing measurements and hypothesis tests using niche and distribution models. Although this software is still quite popular, it suffers from a number of drawbacks: it is only useful for making comparisons based on geographic projections of models, is designed to interact primarily with Maxent, and is a standalone application that requires the installation of specific Perl distributions. In order to remedy these limitations and to develop a more accessible, community-extensible framework for implementing new methods in the study of niche evolution, I am now developing a new ENMTools package for the R statistical programming environment. This package implements all of the most widely used functionality of the standalone ENMTools application, along with many new features, including:

- Ability to use different modeling algorithms (currently Maxent, GLM, GAM, Bioclim, and Domain)
- Ability to measure model overlap, breadth, and discrimination accuracy in an n-dimensional environment space
- New functions for visualizing models and data in geographic space
- Automated figure and report generation for species distribution models and hypothesis tests
- An extensible framework for developing new tests and metrics

In addition, a number of new methods are currently being developed within this framework, with the specific goal of incorporating evolutionary history into the SDM/ENM construction process.

PS3-3

Genetic characterization of the North American wolverine (Gulo gulo luscus): microsatellite and mitochondrial DNA variation in wolverines of Alaska and western Canada

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[4]University of New Mexico, United States

We explored population and geographic structure within the North American wolverine (*Gulo gulo luscus* Linnaeus, 1758) in the complex landscapes of mainland Alaska, Southeast Alaska, and western Canada. The impact of dynamic glacial history, peninsular effects, and separation-by-distance were examined using nuclear microsatellite and mtDNA loci. Mitochondrial data reflected stable populations in Northwest Alaska and Southeast Alaska, indicating the possibility that these regions were unglaciated and harbored wolverine populations since at least the last glacial maximum. The Kenai Peninsula populations showed mixed signals of stability dependent on marker type—matrilineal mtDNA showed a signal of stability, but nuclear data showed low variation with no unique genotypes consistent with Holocene colonization. A break between mainland Alaska and western Canada was detected and mirrors breaks identified in ermine and brown bear. The region supports complex populations and differences in mitochondrial and nuclear genomic histories, eliciting a need for proper understanding and management of unique populations in this region.

PS3-5

Comparative phylogeography of four pika species in Central Asia

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[2]National Museum of Natural History, United States

Evolutionary relationships, species limits, and geographic distributions of species of pika (genus *Ochotona*) in Central Asia are poorly known due to inadequate geographic sampling and few studies of geographic variation within species. Species delimitation and phylogeographic history of pikas in Central Asia has been especially problematic, so we focus on four species that occur in Mongolia, *O. pallasi, O. hyperborea, O. alpina,* and *O. dauurica*. All four partially overlap in their ranges, but have distinctive behavior and habitat preferences. Using a phylogeographic comparative approach, we address questions regarding structure and demography of current and historic populations of pikas across the climatically and topographically diverse landscape of central Asia. We ask: 1) How does the current distribution of each species reflect geologic and demographic history? 2) How have differences in ecology between species influenced current phylogenetic relationships and distributions at both interspecific and intraspecific levels? and 3) How does the history of Mongolian pikas fit within the broader context of the genus as a whole? Our study reveals that *O. pallasi* reflects a largely panmictic population across its range resulting from probable long-term persistence across this region of Central Asia. This history does not appear to be shared by the three other species of pika in Mongolia, which show geographically structured populations consistent with patterns of isolation and subsequent expansion despite current range overlap. These distinctive biogeographic histories highlight differential response of close relatives to changing environmental conditions.

PS3-6

Phylogeographic history of the desiccation tolerant “resurrection plant” Myrothamnus flabellifolius

Joanne Bentley
University of Cape Town, South Africa

Myrothamnus flabellifolius Welw. (Myrothamnaceae: Gunnerales) is a member of a group of plants named “resurrection plants” that are unique in their ability to survive dehydration to an air-dried state. Its closest known relative (and only other member of Myrothamnaceae) is the rare *M. moschatus,* endemic to Madagascar. *M. flabellifolius* is a slow-growing, woody shrub distributed throughout southern Africa, from the summer rainfall regions of South Africa, Namibia, Zimbabwe, Angola, Zambia, Mozambique, Malawi, Kenya and the Democratic Republic of Congo (DRC), where it inhabits shallow, well-drained crevices on isolated sandstone and granite outcrops (inselbergs) and platforms. Not only are the rocky platforms isolated across the landscape and separated by a mosaic of different habitats, but the south-western (Namibian) populations are isolated geographically from the rest of the populations by the expansive Kalahari Desert. Populations may remain in a quiescent state on the rocky outcrops for a year or more, rehydrating only after summer rainfall when they commence growth and photosynthesis. The annual mean precipitation decreases south-westwards and populations in Namibia may be required to survive multiple consecutive drought seasons. There are also morphological differences in leaf shape observed along this rainfall axis. Historical changes in climate and geology are able to shape the genetic patterns of a species. Here, two non-coding chloroplast regions are used to characterise the spatial genetic distribution of *M. flabellifolius*. Morphology and habitat differentiation are used in combination with the genetic signature to provide insights into the evolutionary history of this unusual plant.

PS3-7

Heterogeneous effects of climate and geography on spatial patterns of genetic diversity in Mabuya skinks

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Understanding how geography and climate impact individual movement and population genetic structure is crucial to disentangle local drivers of adaptation and diversification. While tests of Isolation by Distance are widely used, other metrics like Isolation by Resistance and Isolation by Environment are increasingly found to have an impact on genetic diversity and structure of widespread species. Focusing on two widely-distributed *Mabuya* skink complexes which occur through eastern South America, we test for genetic structure, the effect of environmental barriers on gene flow, and ask how climate and geography influence genetic divergence. In both groups, we find mitochondrial lineages to be spatially structured along the coastal forests and the savannas of Brazil. However, the signal emerging from nuclear data is different from that of the mitochondrial markers. The geographic location of major genetic breaks is consistent with those of other taxa, suggesting common responses to former landscape change in eastern South America, particularly along geological faults. Levels of genetic differentiation are correlated to environmental turnover and geographic separation in one, but not in the other, group of skinks. Compared to other studies of similarly widely distributed organisms, the link between spatial environmental gradients and genetic differentiation is not as strong or consistent, suggesting the need for other metrics to describe current phylogeographic patterns. In agreement with the literature, the genetic data indicate the existence of yet undescribed diversity in these lizards, and the need of a detailed taxonomic evaluation of both species.

PS3-8
Effects of climatic oscillations on phylogeography of moustache toads (Anura: Megophryidae: Leptobrachium) in southern China

Jun Li[1], Zhenhua Luo[2], Mian Zhao[2], Hua Wu[2]
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Deciphering spatial distribution of population genetic structure and interpreting the underlying historical processes are major tasks of phylogeography. Southern China which is characterized by complex paleoclimate and topography is still less understood. Herein, we chose three moustache toad species (*Leptobrachium boringii, L. liui and L. leishanensis*) to elucidate the effects of climatic oscillations and/or geological processes on phylogeographical patterns in southern China because of their long evolutionary history, low vagility as well as their sensibility to climate changes. Molecular results based on mitochondrial DNA sequences and microsatellites suggested deep genetic variations within species. Matrilines genetic divergence within *L. boringii* and *L. liui* were estimated to occur during the Pliocene. Such simultaneous divergences within different species highlight the primary roles of general climate oscillations (Pliocene warming period and subsequent Northern hemisphere glaciations), instead of regionally geographical events. Furthermore, mismatch distribution analyses revealed interglacial expansions in *L. boringii* and *L. leishanensis*. Bayesian skyline plot and species distribution models (SDMs) indicated that species in higher mountain regions survived in several refugia (the Yunnan-Guizhou Plateau and Nanling mountains), whereas matrilines in lower mountain regions displayed diverse demographics during the last glacial maximum, which might be associated with regionally climatic characteristics. These findings highlight the important roles of Pliocene climate shifts on phylogeographic pattern in southern China, which was less valued before. It also contributes to the general understanding on phylogeography in this biodiversity hotspot region.

PS3-9
The Carpathian Mountains as a potential Pleistocene refugium for common toads (Bufo bufo).

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Where in Europe did cold-blooded animals survive the dramatic climate fluctuations of the Quaternary period, in particular the ice-ages? And what effect did these changes have on the genetic make-up of these species? These questions are still unanswered for many species, including the most common European amphibian, the common toad (*Bufo bufo*). The *Bufo bufo*-complex has undergone intense research over the past years, resulting in recognition of several separate species. These studies have shown that the origin of the Central-European common toads is most likely in Southeastern Europe, but it remains unclear where exactly. There is accumulating evidence that the Carpathian Mountains provided a refugium for several different amphibian species during the last glacial maximum ~ 19,000 years ago. We investigated whether this may also have been the case for common toads, using microsatellites and mitochondrial DNA sequences of populations from Bulgaria, Romania, and a few Central-European countries. We found that common toads from Northern Bulgaria and Romania are genetically more closely related than to those from Southern Bulgaria. Central-European common toads are most closely related to these northern populations, suggesting that the source population of the recolonization of Europe after the last glacial maximum stems from that region. Using generalized dissimilarity modeling the expected transition areas of the genetic clades in Romania and Bulgaria could be modeled. The Carpathian populations also show the highest microsatellite variation, suggesting they constitute refugial populations.

PS3-10

Preliminary phylogeography of Synuchus dubius (Coleoptera: Carabidae) in Arizona's Madrean Sky Island Archipelago

Alan Yanahan[1], Wendy Moore[1]
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The Madrean Sky Island Archipelago is a natural laboratory within which to study the relation between landscape structure and genetic variation across time. This region is located within the southwestern United States and northwestern Mexico and is composed of over 60 isolated mountain ranges located between the Rocky Mountains and the Sierra Madre Occidental. While the pine forests that many of these mountains support are currently isolated from one another, paleoecological data (e.g., fossil packrat middens) suggest that pine woodland corridors were present between Sky Islands during the Last Glacial Maximum at the end of the Pleistocene (~10,000–20,000 years ago). Within Arizona, two geographically distinct north-south corridors provided opportunities for gene flow between Sky Islands. To infer the patterns of historical gene flow for this region, we produced a preliminary maximum likelihood phylogeny using COI data for *Synuchus dubius* (Coleoptera: Carabidae), a flightless ground beetle species restricted to the isolated, high-elevation pine woodland forests of this region. While we expected populations of *S. dubius* to be more closely related to populations from the same habitat corridor, the phylogeny instead recovered instances where populations from the two separate corridors were more closely related. However, paleoecological data indicate that there were no east-west habitat corridors along which genes could flow. Rather, a large source population that is present at the northern boundary of the Sky Island region has repeatedly provided dispersing individuals during the Pleistocene glacial cycles, and that each east-west relation represents the southern-most extent of independent colonization wave fronts.

PS3-12

Integrating spatial distributions, reconstructed landscapes, and phylogenetics to elucidate Quaternary drivers of Amazonian biodiversity

Robert Guralnick[1], Stephen Mayor[1]
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Amazonia is among the most intact, largest, and biodiverse forest regions on Earth, but the paleobiogeographic drivers of this biodiversity are still not well understood. We investigated the drivers of diversification and endemism throughout Amazonia with targeted (well known) narrowly endemic plant genera of the Melastomataceae family, with the aim of scaling up our protocols to selected taxa of mammals, birds, and butterflies. We tested three hypothetical drivers: Wallacean river barriers, Pleistocene climatic forest refugia, and edaphic heterogeneity. We i) georeferenced and assembled a comprehensive data collection from herbaria and online databases on species point location distributions; ii) generated and evaluated species ranges by spatial, expert assessment, and niche-based methods; iii) estimated areas of endemism; iv) assembled novel Quaternary river, refugia, and edaphic heterogeneity spatial distributions through multiple time steps; and v) tested relationships of spatial properties of distributions, ranges, and areas of endemism to Quaternary rivers, forest refugia, and edaphic conditions. We report results elucidating the influence of these hypothetical drivers and offer next steps in our methodology: reconstructing ranges of ancestral taxa to investigate phylogeographical predictions, testing the scale dependence of estimation of ranges and areas of endemism on results, and evaluating the influence of dispersal related traits on support for each hypothesis. Our findings may be relevant to predictions of future Amazonian biodiversity under climatic and land use scenarios which anticipate increasingly isolated refugial forest patches.

PS3-14

Assessing marine population connectivity in a biogeographic transition zone using a morphogenetic approach

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The owl limpet, *Lottia gigantea*, is a conspicuous marine gastropod which ecological function is strongly affected by body size. Its southernmost distribution range is limited by the temperate-subtropical transition zone in the Northeastern Pacific, where Cedros island (Mexico) is located. Morphometric and genetic differentiation were tested between four populations of *L. gigantea* as a response of oceanographic variability on Cedros island. The electrophoretic analysis considered seven morphometric parameters. Correlation tables were obtained to perform an empirical orthogonal function analysis, and a principal components analysis was applied. Six enzyme systems were analyzed and 14 loci were resolved by polyacrylamide gel electrophoresis, and main genotypic estimators were obtained. Morphological analysis shows low differentiation between organisms across sites, but larger sizes were present in the northern site. The genetic analysis (Wright's F test) showed high gene flow, heterozygote deficiency and low values for Nei's genetic distance, indicating high population connectivity. There is not enough evidence of morphometric or genetic differentiation between populations of *L. gigantea* exposed to different conditions in a marine biogeographic transition zone.

Poster Session 4: Paleoecology and Paleobiogeography (PS4)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS4-1

Coastal refuge: a biogeographic framework for early hominin evolution in Africa

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Paleoanthropological studies often focus on the influence of climate and tectonic change on hominin evolution. However, the significance of the spatial distribution of hominin fossils remains underexplored: phylogenetic relationships between fossils are evaluated predominantly on the basis of morphological affinities. Moreover, the currently known hominin fossil sites in Africa likely represent only a part of the total hominin occupation area. This hampers our understanding of hominin dispersal and speciation. To remedy this, we postulate a biogeographic framework for hominin evolution in Africa, based on patterns in forest dynamics, recent faunal distribution and molecular phylogeny. The conceptual model holds that between ~5 and 2.8 Ma the humid Indian Ocean coastal forest strip provided for hominins a refugium (core area) conducive to evolution, during recurrent (every ~ 400 kyr) dry episodes. From this refugium, evolved hominin species could disperse inland to rift basins (marginal areas) via riverine corridors, whenever onset of wet episodes allowed expansion from the coastal enclave. We hypothesize that from 2.8 Ma onwards, the Northern Hemisphere Glaciation caused contraction and fragmentation of the Indian Ocean coastal forest, geographically isolating hominin populations then present in the coastal forest strip. This dramatic climatic and environmental change likely led to speciation within the *Homo* and *Paranthropus* lineages.

PS4-2 The role of small-scale slash-and-burn farming in a deforested Amazonian lowland forest: interactions among vegetation, fire, and land cover dynamics

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Deforestation is one of the main threats to rainforests in modern time. In recent decades the losses of forest in the Amazon basin has increased dramatically, where the second major cause of deforestation is small-scale slash-and-burn farming. In this study, we examine local-scale spatial and temporal relationships between vegetation, fire, and land cover dynamics over a period of 30 years in a lowland tropical forest. Aerial photographs (1983 and 2014), 25 soil cores, and lake sediment cores from two lakes, Lake Kumpak^a and Lake Ayauch^i, in southeastern Ecuador are analyzed and compared. A 10-cm diameter AMS soil sampling hand auger was used to collect the soil cores while lake sediment cores were collected using a Colinvaux-Vohnout sampler and a gravity corer. Subsamples of 0.5 cm^3 were analyzed for pollen and charcoal and were compared with phytolith and vegetational survey data. Total percentage forest cover and percentage forest cover within a 100-m radius of each soil sampling point were calculated for 1983 and 2014, respectively. Preliminary results show that pollen and phytolith data from soil provide accurate classification of modern land cover. A strong signal of landscape disturbance began in the 1960s at Lake Kumpak^a, where Lake Ayauch^i has had a much longer history of occupancy. The photographic record suggest that after the initial clearance the open area has remained relatively constant for the last 30 years, occupying approximately 20% of the landscape. The stability in land use is reflected in less input of charcoal to the system.

PS4-3

Paleoclimatic analysis of areas of endemism in the Mexican Transition Zone: searching for patterns in mammals and beetles

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The Mexican Transition Zone (MTZ) is the area of overlap between the Nearctic and Neotropical regions. It is exceptionally rich in species and endemism. Our aim was to describe and analyze potential changes in the configuration and geographic location of areas of endemism (AE) of beetles and mammals belonging to the MTZ during the Last Glacial Maximum, the Middle Holocene, and the Last Interglacial periods. We constructed ecological niche models of 245 Mexican mammal (121) and beetle (124) species and transferred these to past scenarios. We performed parsimony analysis of endemicity (PAE) of each period based on the models obtained, comparing areas between the present and the past using three matrices: mammals, beetles, and the union of these two. Of the 24 cladograms, we only obtained AE in 16, which were classified into altered (geographically and/or in species composition), persistent, and primitive (exclusive of the past). Primitive areas and those altered in composition were formed mainly by mammals, while areas altered geographically were formed by beetles, suggesting that some current areas of endemism could be the result of changes in climate over time. Therefore, the MTZ may have changed in its composition and geographical location during the last 130,000 years. The climatic analysis of AE suggests that climate plays an important role in the formation of AEs implying that the species making up these areas do not have a common biogeographical history.

PS4-4

Extrapolating species richness across spatiotemporal scales in an East African large mammal community to predict fossil community richness

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Comparing ecological pattern and process between modern and fossil communities is challenging because both exist on spatial and temporal scales that vary by many orders of magnitude which only partially overlap. This presents an obstacle for the exchange of theory and methods between the two fields and the ability for researchers to

successfully integrate both types of data in order to study ecology across the full spectrum of scales. I use the species-time-area relationship (STAR) to scale large mammal species richness in the modern Amboseli National Park community to the spatiotemporal scales observed in the 2-1.5 million-year-old Koobi Fora Formation paleocommunity, both of which occur in Kenya. I then compare richness predictions using the STAR to observed fossil richness and investigate whether there are any systematic differences that shed light on which ecological processes are dominant at small and large scales. I find that agreement between predicted and observed fossil species richness changes as a function of increasing spatiotemporal scale. The STAR model has shortcomings for extrapolating modern species richness to larger fossil spatiotemporal scales. I conclude this is primarily because speciation events (even on short geological time scales of 10^4-10^5 years) change the composition of the species pool, which fundamentally alters how species accumulate with increasing spatial and temporal scale. These results highlight the limitations of extrapolating modern ecological patterns to larger scales and emphasize the need to study the fossil record in order to understand large-scale ecological processes.

PS4-5

A phylogenetic perspective on the phytogeography of Western Ghats, India

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The Western Ghats is an escarpment stretching along the west coast of India. It is a biodiversity hotspot harboring more than 5000 plant species with over 30% endemics. The western slopes constitute the wet zone (with evergreen forests) and the eastern plateau constitutes the dry zone (with deciduous forests). The evergreen forests have existed since 65 million years, whereas the deciduous forests are fairly recent, being established 10-8 million years ago during the aridification of the Peninsula. Within the wet zone, there is a gradient of seasonality from south to north that affects the species composition, with the south being a “refuge”. In this study, we analyze the phylogenetic diversity (PD) of tree species of Western Ghats to assess the imprints of this evolutionary history. Our premise is that older forests will have species with longer phylogenetic branch lengths, thus have high PD, and newer forests will have recently evolved species with shorter branch lengths and thus low PD. Our results show that the deciduous forests indeed have much lower PD compared to the evergreen forests. Within the wet zone, we found a decreasing pattern of PD from south to north, which also corroborates the southern refuge hypothesis. Additionally, we analyzed the phylogenetic turnover between these forests in comparison to species turnover. We found interesting patterns of decoupling between phylogenetic turnover and species turnover.

PS4-6

Climate disequilibrium in North American pollen assemblages since the Last Glacial Maximum

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Individual plant species’ response to climate change has lagged since the Last Glacial Maximum. However, these individual responses may combine non-additively, such that the prevalence and drivers of community-scale disequilibrium (mismatch) are less well established and have not been fully described in predictions of future community states. We ask what factors have driven spatiotemporal patterns of disequilibrium over time. Using the *community climate framework*, we analyze how North American fossil pollen assemblages (n=531, 106 taxa) responded to temperature and precipitation change since 21,000 BP. The framework allows measurement of local climate mismatch of an assemblage relative to an expectation for the dynamics of the regional species pool. We tested hypotheses for how spatial gradients, life-forms and pollen-dispersal mechanisms affect variation in mismatch and filtering in assemblages over time. Our findings show that climate mismatch was strong during periods of rapid climate change following the Bølling-Allerød and in the mid-latitudinal bands. Strong mismatch was measured

where there were increased presences of herbs and trees, as well as along the paleo-precipitation niche axis. Weak climate mismatch was observed at the assemblage level through time and at very northern or southern latitudes, while evidence for matching was found with paleo-temperature, increased presences of shrubs, and insect pollination. These results suggest that incorporating dispersal limitations and complex species interactions tied to climate forcing interactions will be necessary to accurately predict future community states. Models that account for temporal variations in mismatch will help inform what changes will occur in response to future climate change.

PS4-7

Time-calibrated molecular phylogeny of killifishes (Cyprinodontiformes): evolutionary and biogeographical implications

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The teleostean order Cyprinodontiformes comprises over 1200 species of mainly fresh and brackish water fishes, commonly known as killifishes, and are globally distributed with the exceptions of Oceania and Antarctica. The intercontinental distribution of killifishes is of particular interest, considering that only few derived species can live in a marine coastal environment. Consequently, continental drift, especially fragmentation of the southern supercontinent Gondwana, features prominently in biogeographical scenarios for the clade. Here we present the first detailed time scale for the evolution of killifishes, based on a fossil-calibrated molecular phylogeny for Cyprinodontiformes reconstructed using five nuclear markers. We sampled 10% of all known species, representing 60% of the valid genera and encompassing all major phylogenetic lineages within Cyprinodontiformes. Twelve external paleontological calibrations were used to date the tree. Additionally, ancestral areas for all internal nodes were inferred under various biogeographic models. The reconstructed phylogeny suggests a closer correspondence between evolutionary and biogeographic history than previously thought. Specifically, all Mediterranean and Afrotropical taxa within the major lineage Cyprinodontoidei (currently classified in three different "families") appear to form a monophyletic "Old World" clade. Strikingly, the results show that the order Cyprinodontiformes probably originated in the Late Cretaceous, after the major breakups of Gondwana, and diversified in the Paleogene, hinting at a fundamental role of long-distance dispersal in the biogeographic history of this clade.

PS4-8

EcoRe3: Resistance, Recovery and Resilience in Long-term Ecological Systems.

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EcoRe3 is a new PAGES working group aiming to devise a set of standardised approaches for comparing components of resilience from the palaeo-record. Resilience is a key attribute needed to ensure the persistence of Earth's ecosystems in the face of increasing anthropogenic stressors and climate change, but definitions of resilience, and the methods used to measure it, can differ markedly between studies due to the variety of components that can be identified. These disagreements make it difficult to compare and identify systems with more or less resilience and to plan future mitigation strategies, and to understand the underlying biotic and abiotic controls of resilience along ecological and climatological gradients. In a recent preliminary workshop, members of EcoRe3 have outlined the theoretical basis of two alternative approaches for deriving components of ecological resilience in sediment data. One approach is based on measuring resistance (the amount of change following a disturbance) and recovery rates (the speed to return to equilibrium following a disturbance) in individual proxy records. A second combines statistical modelling, present day and past information on vegetation distributions to infer probabilities of biome transitions for a given set of climate conditions. Here we present preliminary results of the first attempt at applying these concepts to empirical datasets from the palaeorecord and outline future research strategies for the working group over the next three years.

PS4-9

Holarctic views of hydroclimatic changes in Pliocene through Holocene time using non-marine ostracode biogeographic databases

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Biogeographic databases of non-marine ostracodes (common microscopic crustaceans) are now available for large scale studies of environmental conditions through open access community databases such as Neotoma (www.neotomadb.org) and Biofresh (www.biofresh.org). Here, circumpolar and Holarctic distributions of key species are mapped, with the result that biogeographic time slices can be used to understand major changes in past hydroclimatology. Taxonomic harmonization continues, but it is now possible to map selected species with paleoclimatic and paleobiogeographic significance for Pliocene through Holocene time. *Cytherissa lacustris* occurs today in permanent, cold freshwater lakes of mid to high latitudes of the Northern Hemisphere. Its fossil distribution identifies permanent, cold, freshwater habitats in Plio-Pleistocene and Holocene time slices in North America and Europe, showing its southernmost extent during the MIS2 glacial and retreating northwards during the Late Glacial and early Holocene. *Cytherissa lacustris, Candona caudata* and *Limnocythere friabilis* have co-occurred since the Pliocene and today are found in permanent, freshwater lakes in North America and Europe (an example of Clementsian style distribution). In contrast, *Limnocythere ceriotuberosa* and *L. bradburyi*, species that prefer elevated salinities of bicarbonate-enriched water, co-occurred in the North American Pleistocene but dispersed into different climatic zones in the Holocene (an example of Gleasonian-style distribution). Ongoing taxonomic harmonization shows that whereas some species became extinct during the Pleistocene in Europe, they are extant in North America. This understanding provides an opportunity to expand the use of several taxa as modern analogs for Pleistocene assemblages.

PS4-10

Spatial variation in Pliocene Paleohabitats: Implications for large-mammal community assembly

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Ecological theory connects environmental variation to mammalian community assembly at landscape scales through mechanisms such as interspecific competition and species' environmental tolerance. Using this conceptual framework to connect large mammal paleo-niche space to climate and vegetation variation in the past, this study analyzed the regional-scale vegetation patterns within East Turkana, Kenya using extant ecosystems as a baseline. Extant vegetation was measured within 16 ecologically-diverse parks in Kenya using global land cover maps (USGS website). Climate data were derived from WorldClim Global Climate Data. Fossil vegetation was derived from 192 pedogenic carbon isotope values, which are a proxy for vegetation cover and were collected from contemporaneous paleosols in four sites across northern Kenya, as well as two time replicates above and below a tuff dated to 3.42Ma. A principal components analysis of eight climate variables, showed that the coefficient of variation of precipitation and mean precipitation were the main drivers of climatic variation in modern Kenya; a multiple regression showed that these variables had a positive relationship with habitat cover type and variability (R^2=0.49, p<0.001 and R^2=0.29, p<0.02, respectively). In the fossil record, habitat variability varies across sites and is different across time periods (F= 4.02, p<0.001), suggesting that climatic variables, such as precipitation extremes that drive vegetation variation in extant record, may have changed through time. Indeed, the younger sites, which have lower habitat diversity than the older sites, are associated with a shift in the global climatic regime toward cooler and drier temperatures and have lower species richness.

PS4-11

Mass extinctions and speciations during geomagnetic reversals

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Current evidence suggests that mass extinctions events are not correlated with the magnetic reversals of the earth. However, new available data allows analysis with long temporal-scale including more taxonomic groups. Here, an analysis with the 16 major taxonomic groups used as stratigraphic biomarkers, with data ranging from the Permian-Triassic (236-273 million years ago) to the present day is presented. Statistical tests (Spearman and Kendall) showed low correlation for 14 taxonomic groups, being the ammonites and belemnites those with a significant correlation between speciation events and the geomagnetic reversals ($p= 0.0083$; $p= 0.041$, respectively). Furthermore, ammonites showed a significant correlation with extinction events and the geomagnetic reversals ($p= 0.0514$). This results may suggest that extinction events were more common in those species with geographic distributions, conformed by scarce populations, and therefore low adaptation capacity to climate changes associated with the increase of solar radiation as a result of geomagnetic reversals. This study highlights the need for comprehensive analysis that include the global climatic changes resulted of geomagnetic reversals, to understand their influence in mass extinctions and the evolutionary dynamics of species.

PS4-12

The southern coastal Beringian land bridge: cryptic refugium or pseudo refugium for woody plants during the Last Glacial Maximum?

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The Bering Land Bridge (BLB) connected Asia and North America during glacial periods, supported a diverse ecosystem of now-vanished megafauna, and is a proposed glacial refugium. This study tests whether southern coastal Beringia was a refugium for woody taxa (*Picea, Betula, Alnus,* and *Salix*) during the last glacial maximum (LGM) and the hypotheses about habitats available on the BLB for late-Pleistocene megafaunal and human populations, by multiple paleoecological indicators (sedimentary ancient DNA [sedaDNA], macrobotanical fossils, and pollen) from Lake Hill sediment. Results indicate that St. Paul has been continuously occupied by prostrate shrub-graminoid tundra since 18,000 years before present (yr BP). Fossil pollen of *Picea, Pinus, Betula,* and *Alnus* are present in the Lake Hill sediments at low abundance, with moderate *Salix* abundances. Macrobotanical fossils and sedaDNA analyses do not support *Picea, Betula,* and *Alnus* presence. Stratigraphically constrained cluster analysis indicates no major change in vegetation composition after woolly mammoth extinction at 5,600 yr BP, although more forb taxa occur and Poaceae, Cyperaceae and *Equisetum* abundances increase. This study strongly indicates that St. Paul and southern coastal Beringia were not refugia for woody taxa during the LGM. The persistence of prostrate shrub-graminoid tundra is consistent with the interpretation that herbaceous tundra prevailed on Beringia during the LGM, while not ruling out the possibility of mesic shrub tundra in the central lowlands. This tundra supported an island refugium for woolly mammoth for 8,000 years, showing no major vegetation composition changes after extinction.

PS4-13

Cultural transmission shape phylogenetic trees

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Cultural traits are known to spread through human societies using a number of different social, environmental, and evolutionary transmission mechanisms, however, no methods currently exist to link specific mechanisms to the spread of specific traits across broad spatial scales or deep historical time. To overcome this limitation, we developed a method for disentangling the relative contribution of two specific mechanisms of cultural information transfer, horizontal and vertical transmission. Ideas and technologies that are horizontally transmitted are shared between societies, while ideas that are vertically transmitted are inherited from parents passing them to their offspring and only expand when populations displace neighboring societies. We describe the relative contributions each of these mechanisms make to the spread of ideas using both spatial and linguistic phylogeny data and competing those data against a series of simulations describing the possible outcomes under each transmission mode. When applied to the trait of agriculture, our results show a dominance of horizontal transmission with little contribution from the alternative. These results indicate that the idea of domesticating plants and animals was spread primarily through sharing between neighbors rather than the expansion of societies that became powerful through the development of agriculture.

PS4-14

Determining patterns of community assembly over the last 18,000 years using species distribution models and Late Quaternary fossil assemblages

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The importance of neutral (i.e. ecological drift) and non-neutral (i.e. climate filtering and biotic interactions) processes on the composition of communities is often debated. The relative importance of different processes can vary depending on the scale of the study, species pool size, and the nature of climate or habitat change experienced by a community. However, it is difficult to predict which processes are important under specific scenarios, making it difficult to determine how species will assemble into communities as they respond to future climate change. In this study we assess the relative importance of climate in facilitating the assembly of small mammals at Samwell Cave over the previous 17,500 years. We build species distribution models to generate climate-based predictions of community composition at fourteen different past time periods. The predicted communities were compared to the fossil communities in each of the time periods; matches and mismatches were attributed to climate, interactions, or other processes. Preliminary results suggest that the presence of some species in the community can be attributed to climate but mismatches for other species suggest that climate is not the only factor determining the composition of small mammal communities.

PS4-16

Trait space dynamics in a mammal community

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Quantifying functional diversity – the role or influence organisms have within ecosystems – can provide important insights into the structure and resilience of ecological systems. Yet, at least within modern ecology, this aspect of biodiversity is understudied. Here, we examine functional diversity of a mammal community over the past 22 ka and ask if community composition in trait space changes over time and if there is a difference pre- and post- the end-Pleistocene extinction. Our site, Halls Cave in west-central Texas, contains an unparalleled record of the mammalian fauna across 16 time slices averaging 44 species per time interval (22-73 species), with 92 species in total. We employ a non-parametric hypervolume approach to characterize the trait-space over time. We use mean trait values for each species for body size, diet and mode of life to estimate the community hypervolume for each time-period. Our preliminary results show that the volume of trait space is not constant through time, nor is its position in space. Further, we see that the evenness of how densely the space is packed varies considerably through time. This gives us important insight into how functional traits of communities change through time. Further, we learn how and if this has changed due to human impact.

Poster Session 5: Climate Change Biogeography (PS5)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS5-1

Demographic responses to climate and relation to historic range shifts

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In response to climate change, species are predicted to shift their distributions in order to track optimal environmental conditions. Generally speaking, this means a poleward or upward (in elevation) shift. However, range shifts are nuanced and evidence highlights non-responsive species, range expansions and range contractions, even downhill shifts have been documented where plants track their optimal water balance. Currently, the most common method for prediction only uses presence/absence data, but the nuances of documented range shifts imply that predictions could improve from identifying the crucial environmental axes. Quantifying how fitness changes across environmental gradients can identify these key environmental drivers of distribution shifts. I explored the relationship between documented range shifts and sensitivity of vital rates to climate variables, specifically climatic water deficit (CWD) and temperature with a California subset of the Forest Inventory and Analysis database (FIA). Preliminary data analysis suggests that temperature and CWD are important drivers of tree growth (fitness). Current work is exploring the relationship between climate sensitivity and historic range shifts.

PS5-3

Projected climate changes affect isolation and connectivity among montane forests in the sky islands archipelago of southwestern North America.

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The sky islands of southwestern North America represent an archipelago of distinct mountain ranges that link the Sierra Madre of northern Mexico and the Rocky Mountains of the western United States. For some species the islands represent refugia from gradual warming since the last glacial period ca. 20,000 to 100,000 years ago, while for other species they serve as avenues of short- and long-term connectivity over ~8 degrees of latitude. A common characteristic shared by the sky islands, and their larger northern and southern counterparts, is a set of montane coniferous tree species. Here, we evaluate the effects of six projected climate change models over 3 time steps on measures of isolation and connectivity among 11 montane coniferous species. Models indicate an ~25% decline in the number of forest patches, while forest area is projected to decrease by ~40% by 2100. Cohesion, a measure of connectivity, also decreases by ~15%. These changes are likely to affect the ability for some species to maintain viable populations as habitat shrinks. Species constrained within refugia may be increasingly isolated, while those that use the sky islands for migratory purposes may be constrained as well.

PS5-4

Vulnerable plant communities across the Southwest: A view through two CCSM4 scenarios

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Public land managers are keenly interested in how plant communities will respond to climate change. Species-specific habitat suitability models provide one perspective, but their use is limited. A composite view of how plant communities might respond to climate change has been missing. We characterized the vulnerability of major plant communities of the U.S. Southwest under current and two future climate scenarios based on WorldClim temperature and precipitation data. The future scenarios, Community Climate System Model version 4.0 (CCSM4) scenarios 4.5 and 8.5, represent lower and higher end projections of future conditions. We spatially modeled the likelihood of occurrence of 71 plant species under each of these scenarios. These plants characterized 30 major plant communities, as mapped by the National Gap land cover, within six Southwest ecoregions. Predicted change (delta) in likelihood of occurrence of each plant between current climate conditions and each future scenario was calculated and categorized into four suitability categories – increasing, stable, less, and declining. We combined the plant suitability rasters for each community to characterize their vulnerability (high, medium, or low) under the future climate scenarios. Lastly, we combined all community vulnerability rasters to assess vulnerability across the landscape. We found for the CCSM4 4.5 and 8.5 scenarios, 10% and 7% of the 735,335 km2 study area was predicted to have low vulnerability to climate respectively, and 34% and 41% of the area was predicted to have high vulnerability. Results from this characterization can inform public land management decision-making toward the complex challenges climate change poses.

PS5-5

Piñon and juniper distribution forecast under 21st Century climate change.

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Populations of piñons and junipers across the interior west of the United States have been highly dynamic over the last two centuries, undergoing an overall expansion but punctuated with regional mortality. Accumulating demographic studies across the interior west indicate the drivers of expansion and contraction of populations have an underlying climatic component. The key implication is that piñon and juniper distributions respond to climatic variation across scales by expansion from, and contraction to, areas of long term persistence relative to their centurial (piñons) and millennial (junipers) life spans. Individualistic climatic tolerances among piñon and juniper species lead to temporally dynamic assemblages in the landscape which vary regionally. We develop climate-based distribution models for the species of piñons and junipers in the interior west and project their distributions into 21st century climate change scenarios. For each species, the projected distributions are classified into zones of expansion, persistence, and contraction. Taken together, the species distributions identify areas of assemblage shift.

PS5-7

Studies on the Betula platyphylla Suk. Forest dieback phenomenon in Hustai National Park, Mongolia based on remotely sensed data

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This study we approached the dieback phenomenon of the *Betula platyphylla* Suk. forest in Hustai National Park in Mongolian using remotely sensed data. Recently the significant growth reduction in semi-arid pine forest, why?
Our approaches including such as a rapider warming in dryer region; more evaporation; less available soil water; growth reduction and more frequent drought or long drought are major driving forces. But in our study region, we

have chronic forest dieback, likely because in winter the temperature is < 0 ^{0}C and water storage in winter benefits tree growth. Early spring warming could exhaust this water storage. It is therefore hypothesized that early spring temperature is most crucial for tree growth. Rising temperature in spring overly evaporates winter water storage and leads to more frequent drought events in early spring. Frequency of spring drought in 1990s is 2.6 times of the average for the last century as a whole, explaining the most recent forest dieback. Remaining of this trend in the future will lead to more serious forest dieback and even vanishing of the semi-arid forests. Soil moisture is higher in deciduous broadleaved forest than in coniferous forest; Water consuming is more in deciduous broadleaved forest than in coniferous forest during the growing season.

PS5-8

Phylogeography of forest birds of the Himalayas

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The Last Glacial Maxima (LGM) was associated with the contraction of species' ranges in response to glaciation and species were largely limited to warmer and wetter regions (glacial refugia). When the glaciers retreated, new habitats became available and organisms from refugia colonized these areas. The study is aimed at investigating two competing hypothesis: i) During LGM, Eastern Himalayas acted as a glacial refugia followed by westward colonization in the Himalayas when the glaciers retreated. ii) There were multiple local refugia in the lower altitude regions in the entire Himalayan belt during LGM followed by upward colonization of organisms when the glaciers retreated. Himalayas are known for their complex topography and environmental heterogeneity. Despite their extraordinary dispersal abilities, birds are limited by complex topography and heterogeneous environments. Birds have diversified across varying conditions of topography, climate, resource distribution, and competition. Regional variation in the phenotype and genotype of bird populations of the same species in different locations across the Himalayas may reflect local adaptation or geographic barriers. I compare the genetic variation in multiple populations of forest bird species of Himalayas which have different dispersal abilities in order to determine their genetic structure. I am also investigating the potential biogeographic barriers (for Himalayan forest birds) present in the Himalayas of the Indian subcontinent. Preliminary results from race analysis indicate that the Central and Eastern Himalayan populations are more closely related to each other than to Western Himalayas, indicating that a major biogeographic divide might exist between Western Himalayas and Central Himalayas.

PS5-9

Assessing impacts of climate change on phenology using a common garden study

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Many species have been shown to shift their phenology as a response to climate change, but the mechanisms by which these shifts occur are relatively understudied. Since phenology has generally been studied at either a local scale using site- and species-specific temporal shifts or at a regional scale using remote sensing, patterns of within-species phenology in relation to genetic heritability and environmental factors across the species' range have not largely been studied. By linking phenology to genetic and environmental factors, we are able to better understand the drivers behind shifts in phenology. Here, we observed phenology at a common garden of 32 seed sources of northern red oak (*Quercus rubra*) in West Lafayette, Indiana, from 2013 through 2016. We assessed how seed source (genetic heritability) can explain variability among populations, and how local environmental conditions can drive annual shifts in phenology. In general, we found that the timing of spring phenology events is closely linked to local environmental factors. Accumulated growing degree days account for most of the variability in spring phenology (R-squared = 62-91%), whereas the timing of bud burst is only weakly explained by seed source climate (such as mean annual precipitation, R-squared = 6-25%). However, the timing of leaf senescence is strongly linked to seed source climate (such as mean annual temperature, R-squared = 59-72%). In general, northern populations

begin their growing season slightly earlier but are more limited at the end of season, leading to an overall shorter growing season compared to southern populations.

PS5-10

High Andean plant communities' thermal niche traits and sensitivity of their species to climate warming

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Although alpine plant communities are mainly influenced by extreme temperature gradients in their habitats, thermal niche traits (TNT) are hardly known for a large number of alpine species. Climate change is projected to have strong impacts on alpine communities. Therefore understanding the patterns of these traits is particularly important. Here we test 1) The effect of seasonality and elevation on TNT of tropical alpine plant species and communities and 2) The sensitivity of these plant species and communities to climate change based on their TNT. We surveyed 50 plant communities located in summits along the Tropical Andes in 2 high elevational grassland biomes: Puna (seasonal) and Páramo (non-seasonal). We found that species endemic to Páramo have a narrower thermal niche breadth and thus could be more sensitive to climate change than species endemic to Puna. However, while communities located in Puna summits have a clear dominance of Puna endemics, Páramo summits are less dominated by Páramo endemics. When TNT were aggregated at the community level we found that community minimum temperatures were influenced by both elevation and seasonality (biome) while the thermal optimum was only influenced by elevation and the thermal niche breadth by none of them. This suggests that seasonal Puna communities are not necessarily less sensitive to climate change than non-seasonal Páramo communities because their niche breadths are similar. Our results confirm the importance of low temperatures in structuring tropical alpine communities.

PS5-11

IberianPonds: Measuring responses to climate change across macroecological gradients

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Climate change ranks amongst the greatest threats to biodiversity across the Earth's biomes.
Following changes in the climate, communities disassemble and reassemble in seemingly unpredictable ways. Still, the question of whether species respond to environmental changes individualistically or whether there is synchrony at higher levels of organization (e.g., functional groups) remains unresolved. The IberianPonds project is addressing this gap in knowledge by integrating different disciplines (i.e. Macroecology, Biogeography, Community and Molecular Ecology) by combining different sources of information, such as species occurrences, functional traits and phylogenies to improve predictions of changes in food web structure under simulated climate change. Ongoing work includes large-scale biodiversity assessments and small-scale mesocosm experiments using the IberianPonds experimental facility that consists of 192 artificial ponds distributed across six locations in the Iberian Peninsula and spanning a representative environmental gradient within Iberia (sites in Arid, Mediterranean, Temperate and Alpine environments). This poster will provide a first look at preliminary data from the mesocosms experiments.

Keywords: global change, biogeography, macroecology, experiments, biodiversity

PS5-12

Vegetation change in Europe: effects of environment, socio-economics and conservation status

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The Natura-2000 network of protected areas includes 23,115 terrestrial reserves that cover >17% of the EU. The large extent poses practical challenges in assessing the efficacy of Natura-2000, but biogeographic, environmental and socio-economic gradients also generate divergent conservation goals. Here we pursue a unified approach in which vegetation structure serves as an indicator of ecosystem functioning, while recognising that changes in vegetation structure need to be interpreted in a biogeographic context (vegetation type, environment, potential community turnover rates). We use the leaf area index (LAI) derived from Earth observation satellites to quantify vegetation change between 2000 and 2015 and compare Natura-2000 with analogous unprotected areas. LAI increased strongly throughout Europe's (semi-)natural vegetation. LAI change in most vegetation types was strongly related to climate, with smaller changes in harsh environments (seasonally cold or dry) and larger changes in mild environments. While the magnitude of LAI increases was indistinguishable between Natura-2000 and analogous unprotected areas, the shape of the change trajectories differed. The results suggest that, in absolute terms, vegetation responds more vigorously to environmental change in mild environments than in harsher environments. Taxonomically or environmentally driven differences in leaf-phenological plasticity may explain these patterns, but differences in potential community turnover rates (e.g. because of species pools or niche volume) may also play a role. The distinct spatial pattern of vegetation change further highlights the importance of large-scale socio-economic dynamics, such as farmland abandonment in Eastern Europe and southern Europe and high herbivore pressure on marginal land in the UK.

PS5-13

Can Bumblebee (Bombus) Species' Geographic Responses to Climate Change Be Predicted by their Realized Thermal Niches?

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As climate continues to warm precipitously, bumblebee species across North America and Europe are experiencing range contractions at their southern range margins while failing to expand beyond their northern range boundaries (Kerr et al. 2015). The processes governing climate change-induced range dynamics are likely to differ at species' leading and trailing range margins. I examined whether bumblebee species' with wider thermal ranges were more likely to expand beyond their leading edge and whether species' with higher warm thermal limits were less vulnerable to range contractions at their trailing range margins. I used observations from 65 different bumblebee species across North America and Europe to determine their thermal limits, thermal range, and their geographic displacement between a baseline time period (1901-1974) preceding the major impacts of climate change and a latter time period (1999-2010). I performed ordinary least squares and subsequent phylogenetic least squares analyses to determine if components of species thermal niche could predict differences in their geographic responses to climate change. Overall thermal range and upper thermal limits were poor predictors of shifts at species range margins, however patterns were often inconsistent between North America and Europe. My results suggest that, the underlying mechanisms governing climate change related range shifts should be assessed at smaller spatial scales despite geographic trends being consistent in a much larger geographic context.

PS5-14

Caterpillars Count! -- Building a Biogeographic dataBase of Bird Food

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Caterpillars Count! is a citizen science project that aims to characterize variation in time and space in the resource availability to the foliage gleaning bird community to address questions about biogeographic variation in avian community structure and phenology. Surveys carried out by citizen scientists record the size and density of foliage arthropods identified to taxonomic Order. Here I present a preliminary analysis assessing (1) the efficacy of citizen scientist-contributed data relative to data collected by trained scientists, (2) differences in tree species with respect to resource availability, (3) a comparison of avian breeding phenology with avian resource phenology. I find that foliage arthropod phenology can reliably be estimated at a site by sampling ~20 branches every 10-14 days. I highlight potential linkages between Caterpillars Count!, iNaturalist, eBird, and various butterfly and moth monitoring networks for achieving a detailed picture of avian resource macroecology across North America.

PS5-15

Climate change may threaten size and connectivity of seasonal ranges in migratory birds

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Long-distance migratory birds travel thousands of kilometers annually between summer and winter ranges. They are thus affected by climatic conditions in different parts of the world. Unfavorable 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, climate impact analyses primarily focus on breeding ranges. Here, we examine potential climate change impacts on migratory birds taking into account different stages connected to breeding, overwintering and the migratory journey. We concentrate on long-distance migratory birds of the Holarctic and estimate potential climate change risks from summer range contraction, winter range contraction, and from increased migratory distance between seasonal ranges. Further, we evaluate whether these risks are similar in magnitude between migrants breeding in Palearctic and Nearctic, and whether these are randomly distributed across the functional and phylogenetic tree. Our projections suggested stronger changes in species richness patterns during summer than during winter. Even when dispersal was accounted for, the majority of migratory species were projected to experience range contractions with more severe contractions in Palearctic breeders. By contrast, migration distances were projected to increase mainly in Nearctic breeders. We found significant phylogenetic signals in all sensitivity measures considered suggesting that losses in seasonal range size and connectivity are not random across the phylogeny. Furthermore, although functional relationships were weak overall, our results indicate that functional losses may be underestimated when ignoring potential climate change risks for wintering ranges.

PS5-17

Towards Critical Biogeography in Montology: Andean páramo revisited

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More than most other landform, tropical mountains have been at the vanguard of geographical inquiry. Whether promontories, cultural works on slopes, or even metaphorical/spiritual heights, biogeographical research inform current narratives of global environmental change. We review how Montology shifts geographic paradigms via the novel approach of critical biogeography in the Andes. We use it to bridge nature and society through indigenous heritage, local biodiversity conservation narratives, and vernacular nature-culture hybrids of biocultural landscapes (BCL), focusing on how the socio-ecological systems (SES) enlighten scientific query in the Andes. In our Andean study cases, integrated critical frameworks guide the understanding of BCLs as the product of long-term human-environment interactions. With situated exemplars from place naming, wild edible plants, medicinal plants, sacred trees, foodstuffs, ritualistic plants, floral and faunal causation, we convey the need for cognition of mountains as BCLs in the Anthropocene. We conclude that applied Montology allows for a multi-method approach with the four 'C's of critical biogeography, a model that engages forward-looking geographers and interdisciplinary Andeanists in assessments for the distribution of biota in the fragile BCLs in the Andes.

PS5-19 Climate Change, Range Shifts, and 'Horticultural Rescue': a case study with Magnolia tripetala

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As climate changes, species that face strong barriers to dispersal could experience range collapse and have an increased risk of extinction. Species in horticulture poleward of their native range could circumvent dispersal barriers, if individuals are able to 'escape' and establish populations in the wild. Here we provide the first empirical case study of such 'horticultural rescue'. The historic range of *Magnolia tripetala* is collapsing. Independent field work and analysis of FIA plots show frequent adult mortality events and a lack of juvenile recruitment in the southern portion of the range. In contrast, populations at the northern edge of the historic range are robust, but in spite of climate warming they have not been able to expand northwards through an agricultural landscape. Individuals have been planted in horticulture north of the native range in New York and New England for more than 150 years. Prior to recent warming, no individuals in these regions escaped into the wild, but over the past 70 years, populations have begun to escape from horticulture into natural habitats in a non-random, sequential pattern of increasingly northern sites over time. Consequently, while the historic range is collapsing, the range as a whole is shifting northwards, due to mortality in the south and escape from horticulture in the north. This bodes well for species persistence in the context of climate change, at least for those species currently planted in horticulture and so long as local conservation agencies don't invest resources in actively eradicating these newly established populations.

PS5-21

Optimizing Computing Platforms for Climate-Driven Ecological Forecasting Models

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Species distribution models are widely used, climate-driven ecological forecasting tools that use machine-learning techniques to predict species range shifts and ecological responses to 21st century climate change. As high-resolution climate and biodiversity data becomes increasingly available and statistical learning methods become more computationally intensive, choosing the correct computing configuration on which to run these models becomes more important. With a variety of low-cost cloud and desktop computing options available, users of forecasting models must balance performance gains achieved by provisioning more powerful hardware with the cost of using these resources. We present a framework for estimating the optimal computing solution for a given modeling activity. We argue that this framework is capable of identifying the optimal computing solution – the one that maximizes model accuracy while minimizing resource cost and computing time. Our framework is built on constituent models of algorithm execution time, predictive skill, and computing cost. We demonstrate the results of the framework using four leading species distribution models: multivariate adaptive regression splines, generalized additive models, support vector machines, and boosted regression trees. Each constituent model is shown to have high predictive accuracy, and can be used independently to estimate the effects of using larger input datasets, such as those that incorporate data from the fossil record. When used together, our framework shows highly significant predictive ability, and is designed to be used by researchers to inform future computing provisioning strategies.

Poster Session 6: Island Biogeography (PS6)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS6-1

Are climate-richness relationships repeatable and predictable? A natural experiment using replicated evolutionary radiations on islands

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Climate is a strong correlate of species richness along global and elevational gradients. However, macroecological patterns cannot be easily manipulated and thus the causal nature of these relationships, and their utility for predicting biodiversity change, has proven difficult to establish. Here, we take advantage of a set of replicated evolutionary radiations to test whether climate–richness relationships are repeatable and predictable. *Anolis* lizards have independently radiated on the four islands of the Greater Antilles, producing, via convergent evolution, ecologically similar, but independent faunas. However, whether they show convergence in macroecological patterns through space is unknown. We produce the first maps of how anole species richness varies spatially within individual islands. We then test whether climate-richness regression models fitted on one island can predict the richness gradients on the other three, thus taking advantage of a naturally replicated ecological experiment to test the predictability of species richness gradients.

PS6-2

A trait-based model of dynamic island biogeography

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How trait-environment interactions mediate the population-level processes that shape communities is poorly understood. We present a model of dynamic island biogeography (DIB) that predicts candidate species for community assembly on islands that undergo directional and cyclical environmental change. Using information from organismal traits, the DIB model predicts that as islands cycle between increasing and decreasing size and connectivity to a source, the dominant process driving species presence or absence and thus availability for community assembly *switches* between colonization and extinction. Colonization probability is determined by species' tolerance to the intervening matrix between source and island. Extinction probability is determined by the minimum resource requirements to sustain an isolated population of a given body size, trophic level, and specialization. Because different suites of traits mediate colonization and extinction, the DIB model reveals how similar environmental states — combinations of island connectivity and size — can result in *different* candidate species despite similar richness. Hence, it highlights the critical role of historical contingency in the form of *hysteresis*, where not only the current environmental states, but also trajectory in the cycle can influence community composition. The DIB model is general and likely applies to all organisms and to islands that cycle on timescales from years to millennia.

PS6-3

Seasonal changes in the spatial structure of bird communities

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While it is recognized that many communities undergo large seasonal changes, the consequences for spatial structure of communities are poorly known. We used beta diversity partitioning, nestedness and null communities to test for differences in landbird communities among seasons and between resident vs. seasonal assemblages. Winter resident beta diversity was high and mainly driven by richness differences, whereas that of summer residents was low and dominated by species turnover. Winter visitors showed similar nestedness patterns compared with randomly-drawn assemblages, and were less clearly related to island characteristics than winter or summer resident species. The results suggest a selective-extinction process for winter residents, probably due to winter food shortage. Conversely, summer residents appeared more dependent on turnover in local island factors, such as habitat conditions, which mediate competition. Winter visitors appeared randomly distributed across islands. We conclude that residents maintain strong spatial structure seasonally, whereas winter visitors show considerably less structure.

PS6-4

Morphometrics and species distribution modeling elucidates cryptic biodiversity in the Coprosma foliosa Complex (Rubiaceae) of the Hawaiian Islands

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The biodiversity of the *Coprosma foliosa* Complex includes many morphologically similar plant taxa in similar seeming habitats across the main Hawaiian Islands. Here, we investigate two novel taxa that are in need of segregation from *Coprosma foliosa* from the islands of Moloka‘i and Kaua‘i. *Coprosma* ‘sp. Moloka‘i’ occurs in mesic to wet forests of Moloka‘i and is the tallest taxon of the complex. It is a single stemmed tree reaching heights of over 7.5 m, often with two differently sized seeds per fruit and a persistent fruit calyx of 3.4-7.1 mm. *Coprosma* ‘sp. Kaua‘i’ occurs in mesic forests of Kaua‘i and is a many stemmed scrambling liana, with leaves that are moderately pilose. The pedicels of *C.* ‘sp. Kaua‘i’ are the longest of any taxon of the complex ranging from 13-30 mm. SDM analyses suggest the two novel taxa are distinct in their suitable niche with minimal overlap, from each other and from other taxa of the complex. Conservation status of the two taxa is likely to be Vulnerable for *C.* ‘sp. Moloka‘i’ and Endangered for *C.* ‘sp. Kaua‘i’.

PS6-5

Land snail diversity patterns in Palau: community assembly in a 14,000 year-old tropical forest fragmentation experiment

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The Republic of Palau comprises approximately 500 islands, but during the last glacial maximum, all but eleven of these were part of a single "Paleopalau" landmass. The most diverse *in situ* radiation so far described is a clade of approximately 100 species of land snails in the family Diplommatinidae (Caenogastropoda). In this study I describe patterns of species richness in the contemporary archipelago for the Palau endemic diplommatinid genus *Hungerfordia*, using a dataset of 51 species with distribution data from 37 islands with areas ranging across five orders of magnitude (~300km^2 to ~0.03km^2). I explore landscape metrics that correlate to species richness and species density, and demonstrate which parts of the archipelago have higher levels of beta-diversity. Because all of the islands that have not been surveyed for land snails are smaller than 1km^2, I perform a CART analysis of those landscape factors that seem most predictive of species richness and endemicity (e.g., location, area, distance to an island larger than 4km^2, maximum dimension, etc.). Finally, I discuss the spatial distribution of *Hungerfordia* species richness in the context of the Single Large or Several Small problem in conservation biology, and highlight situations in which the inclusion of several small islands could maximize the number of species included, even when the total land area of the several small islands is <20% the area of the single large island. These findings illustrate the complicated ways that species richness, species turnover, and patterns of nestedness can interact to create unusual biogeographic patterns that can persist for thousands of years following the fragmentation of lowland tropical rainforest by changing sea levels.

PS6-6

Community assembly of island mammal metacommunities: The role of the regional species pool

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One of community ecology's main goals is to understand community assembly, which involves teasing apart the ecological, evolutionary, and biogeographic processes that structure communities. Essentially, local communities are a subset of potential colonizers from a regional species pool that successfully pass through abiotic and biotic filters, and ultimately coexist within their environment. When these local communities are linked together by dispersal, they form a metacommunity. However, the role of the regional pool's composition and the relative role of these filters remain unclear, and are rarely investigated beyond the scope of a single metacommunity.
According to the species-sorting perspective of metacommunities, species are filtered from the regional pool based on their functional traits, which dictate their ability to disperse and occupy local environmental niches. Here, we determine which mechanisms are driving the community assembly of terrestrial mammals in multiple island metacommunities across the globe (including South-East Asia, Japan, the Sea of Cortez, the Mediterranean, the West Indies, the British Isles, and the Alexander Archipelago). More specifically, we will quantify how much compositional variation between local communities is explained by environmental features and dispersal dynamics, both separately and interactively. We will also explore whether the regional pool's functional diversity influences the species-sorting process, by supplying communities with potential colonizers whose range of functional traits match local niches to different degrees. Investigating these relationships across several regions will provide greater insight into the generality of community assembly mechanisms, and how environmental changes might impact communities at local and regional scales.

PS6-7

Dispersal modality determines the relative partitioning of beta diversity in spider assemblages on subtropical land-bridge islands

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Beta diversity describes the extent of change in community composition in relation to complex gradients of environmental variation. However, the widely used broad-sense measures of compositional dissimilarity (e.g. the Sørensen or Jaccard index) are not able, in their own right, to reveal the processes and underlying mechanisms that drive community assembly. To identify geographical drivers determining the relative partitioning of species replacement and richness difference or nestedness-resultant components of beta diversity in spider groups with differing dispersal modality, we collected occupancy data of spiders on 31 subtropical land-bridge islands in the Thousand Island Lake, China and separated beta diversity (B_{jac}) of each group into either species replacement (B_{-3}) and richness difference (B_{rich}) components, or turnover (B_{jtu}) and nestedness-resultant (B_{jne}) components. The dominant process of extinction resulted in high contribution of turnover to beta diversity in island spiders. Specifically, frequent ballooners contributed less species replacement to overall dissimilarity than occasional ballooners and non-ballooners. The rational is that frequent ballooners might potentially colonise all islands. However, occasional and non-ballooners were constrained by water barriers and were unable to occupy most islands. Contrasting dissimilarities among dispersal groups of spiders demonstrated the importance of beta diversity partitioning, and the mechanistic insight gained on trait-dependence in community assembly.

PS6-8

Historical Biogeography of Bananaquits in Puerto Rico

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We use contemporary genetic diversity to characterize the within-island population structure and historical demography of bananaquits (Coerebinae, *Coereba flaveola*) in Puerto Rico. We investigate the relationship between periods of invasiveness across the Lesser Antilles and the genetic architecture of the source population, and describe the relationships among differentiated populations within Puerto Rico. We further test for signatures of demographic expansion and compare metrics of genetic diversity. Contemporary populations of bananaquits diverged within Puerto Rico beginning 430 to 320 thousand years ago (ka), coincident with the latter half of a period of invasiveness originating in Puerto Rico and extending through the Lesser Antilles. We find signatures of renewed demographic expansion beginning in the eastern portion of the island approximately 180,000 years ago and in the western portion approximately 40,000 years ago, the latter period being coincident with expansion by the same species in the Northern Lesser Antilles and in Jamaica.

PS6-9

Raised atoll and high volcanic island influence spatial pattern of native plant species richness on the atolls of Eastern Polynesia (Pacific Ocean)

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We selected forty-nine remote atolls of Eastern Polynesia with complete botanical surveys to test the relative influence of eight abiotic factors on native plant species richness (i.e. indigenous and endemic species). Abiotic factors used as potential predictors included atoll area (km²), shoreline length (km), atoll elevation (m), and index of isolation (UNEP), but also the coastal index of the atoll (I_c), the distance to the nearest similar atoll (km), the distance to the nearest large volcanic island >1,000 km² (here, the island of Tahiti) and the distance to the nearest raised atoll >15 m a.s.l. (here, the atoll of Makatea or Henderson as a potential refugium during sea-level highstands). No relationship was found between the species richness and the index of isolation or the distance to the nearest similar atoll. Atoll area and distance to the nearest raised atoll of Makatea explained 47.1% and 40%, respectively, of the native species richness variation observed on the remote atolls while 36.9% of the variation was explained by the distance to the volcanic island of Tahiti. Native species richness on the atolls surveyed increased with the increasing atoll area, elevation and shoreline length but decreased with the increasing distance to the nearest raised atoll of Makatea and the large volcanic island of Tahiti. Our results show that raised atoll may be viewed as a refugium during sea-level highstands while the large volcanic island played the role of stepping-stone island in Eastern Polynesia.

PS6-10

Evolutionary assembly, dispersal and climatic niche evolution in the Hawaiian flora

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Understanding the interplay of climatic niche evolution and dispersal underlying the geographical distribution of species remains a central goal in island biogeography. Due to the strong physical barriers conferred by an insular setting, the evolutionary biogeography of island clades will be determined, in part, by the interaction between the relative geographic accessibility and availability of habitats (both within and between islands) and the degree to which climatic niches are conserved within clades. For example, clades with a high propensity for niche differentiation might be expected to diversify into different habitats, the degree to which may depend on the habitat's relative availability. In contrast, clades that exhibit high niche conservatism may have their dispersal and diversification restricted to the availability of one or a few habitats. Here, we evaluate the role of habitat availability on the relative contribution of niche differentiation and conservatism in shaping the assembly of island biotas. We focus on the endemic flora of Hawaii, elements of which have diversified to occupy a wide range of different habitats. To do this, we first compiled natural history collection locality data and published phylogenies for multiple endemic Hawaiian plant clades. We then estimated rates of habitat transitions in the flora using phylogenetic models of trait evolution, and explore whether the relative isolation and area of different habitats may be influencing the relative rates of habitat shifts in the evolutionary history of these clades.

PS6-12

Testing the General Dynamic Model of Island Biogeography in Brazilian Continental-Shelf

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The General Dynamic Model of island biogeography [Whittaker et al, 2008, J Biogeogr, 35:977] was proposed to explain patterns of species richness in oceanic islands by incorporating geological processes. Here, we tested the ability of GDM to explain these patterns in continental-shelf islands. Specifically, we tested area, geographic isolation and age of islands as predictors of species richness of amphibians, reptiles and birds in 139 Brazilian continental islands. The best model had area as a single predictor (AIC_c=53.8; $wAIC_c$=0.443 – for all taxa). Area was positively related to species richness for amphibians (slope, z=0.51; $F_{1,28}$=31.39; R^2=0.529; p<0.001), reptiles (z=0.35; $F_{1,30}$=62.67; R^2=0.666; p<0.001) and birds (z=0.29; $F_{1,116}$=57.37; R^2=0.33; p<0.001). Although island biogeography models proposed that age and isolation are important predictors of species richness, continental-shelf islands do not respond to them, likely due to homogeneity in their time of formation and isolation. The effect of area varied according to the dispersal ability of the taxonomic groups. An extension of the GDM to include continental-shelf islands still needs to be developed.

Poster Session 7: Biodiversity Hotspots (PS7)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS7-1

Distribution and hotspots of higher plants in China

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Identifying biodiversity hotspots has become a core issue for setting up priority protection areas, while financial resources used for biological diversity conservation are limited. Our aim was to describe the geographical patterns of species richness, endemism, and endangerment of high plants and to analyze the congruence between these three measures. In particular, we sought to test the accuracy of hotspots used in identifying conservation priorities with regard to higher plants. We used China's Higher Plants Red List (CHPRL) as the data source and analyzed the diversity, endemism, and endangered status of higher plants based on three aspects of richness information: species richness (SR), endemic species richness (ER), and threatened species richness (TR). We then tested the congruence of the three aspects of biodiversity and made a comparison of the similarities and differences between the hotspots described in this paper and the hotspots described in previous studies. We found that the core region of species distribution is located at latitudes of 21°- 35° and longitudes of 95°-111°, in which 89.1% of species, 93.4% of endemic species, and over 90% of threatened species in China are concentrated. In addition, there is a high spatial congruence among the three measures but a low congruence between two different sets of hotspots. Our results demonstrate that the three aspects of biodiversity have a high congruence between each other when the taxa are confined to higher plants. And with the expansion of the criteria used to define hotspots, this congruence generally increases. In addition, our results

PS7-2
Geographic range responses to past climate change in an endemic sigmodontine rodent from central Chile

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We evaluated the geographic range response to climate change of an endemic rodent from a biodiversity hotspot in central Chile, using current and Last Glacial Maximum (LGM) bioclimatic data. The studied species was the sigmodontine rodent *Phyllotis darwini* distributed between 27 to 36? S and from coastal areas up to 2000 m. We characterized the intraspecific diversity using phylogeography, and considered the lineages as relevant units to build distribution models for present and past climatic conditions. We interpreted differences in distribution for current and LGM conditions as distributional responses to past climate change. We also tested the hypothesis that during LGM populations of *P. darwini* experienced altitudinal descents from the Andes to the lowlands and to the coastal cordillera, and range retractions during interglacial that may have left remnants of populations on the mountaintops in central Chile. We evaluated the occurrence of intraspecific lineages for the species to construct distribution models at LGM and at present. Our results suggest that Quaternary glaciations may have triggered the descending of populations to the lowlands and to the coastal Cordillera in central Chile. Backward movements of populations after glacial retreats may have left isolates on mountaintops of the coastal Cordillera, suggesting that current species distribution would be the outcome of climate change and habitat reconfiguration after LGM. In addition, current distribution of lineages inside *P. darwini* would be consequence of a cryptic distributional response to climate change after LGM: postglacial northward colonization, with altitudinal segregation of both phylogroups.

Acknowledgments FONDECYT 1140929.

PS7-3
Estimating regional species richness: the case of China's vascular plant species

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Estimating regional species richness has been a major challenge in ecology but is crucial for setting up conservation priorities. Discovery curves are a principal tool for estimating regional richness but are very sensitive to historical fluctuation of species discovery. We proposed a new discovery model considering historical influences. We applied this model to estimate the number of vascular plant species in China, a country of mega-biodiversity and also suffered endless wars and social turmoil in modern history. We compiled the discovery time for each vascular species *Flora of China* over the period between 1753 and 2000, leading to 31000 valid species names. Our model estimated 44238 (lower=42138, upper=46338) vascular plant species in China, i.e., ~10000 species remained to be discovered and it would take about 100 years to discover all the species should the current discovery rate of 100 species per year persist.

PS7-5
Patterns of distribution in Carpathian endemic subterranean species: diversity or uniformity?

Oana Moldovan[1], Ruxandra Nastase-Bucur[1], Marius Kenesz[1], Ionut Mirea[1], Silviu Constantin[1]
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Eastern Europe is one of the richest regions in the world in subterranean (caves and associated habitats) endemic species, with a declared hotspot represented by the Dinaric mountain range. Although considered as one of the main refuge area for several groups of surface fauna during the climate changes of the Pleistocene and the Holocene, the Carpathian Mountains subterranean fauna importance is underestimated especially due to dispersed information on its diversity and the scarcity of molecular studies in the area. Here, we present a first general view of the cave fauna hotspot represented by the Carpathians and the geological and historical processes that shaped the patterns of

subterranean distribution and diversity at regional scale. Phylogeography and environmental parameters are adding to the general view at small-scale and offer additional explanation for this exceptional subterranean diversification in a non-Mediterranean region. The Carpathians are an amalgam of various geological units with different paleogeographical evolution that is reflected in completely different species assemblages dominated by unit specific fauna groups. We discuss the significance of these differences and the relationship with the present day surface fauna groups within the same mountain units.

Poster Session 8: Biological Invasion (PS8)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS8-1

An ecosystem engineer invading the New World: Ecological Niche Modeling of Wild Boar in the Neotropic

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Biological invasions are considered one of the main drivers of extinction of native species and changes in ecosystem processes. Such effects are more severe when species act as ecosystem engineers. Our aim was to determine current and future potential distribution of *Sus scrofa* (wild boar). We performed ecological niche modeling by using ensemble forecasting combining 12 algorithms in order to produce a consensus model of wild boar distribution. We found a potential distribution of about 742400.5 km^2, including Chile, Bolivia, Argentina, Paraguay, Uruguay and Brazil. The future potential distribution presented a reduction of 18.45% of the total area in relation to the current range and a southward shift. Also, we found that there was no niche shift between the original distribution in Palearctic and the invaded area in Neotropics. The disturbance caused by the wild boar can affect ecosystem processes and cause economic losses. Forecasting the potential distribution of this species is a necessary step for planning actions to manage this invasion process.

PS8-2

Recent range expansions by Japanese stiltgrass (Microstegium vimineum (Trin.) A. Campus) in the forestlands of Tennessee

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The impact from non-native plant invasions on forests is far reaching and responsible for ecological and economic losses. Within the southeastern USA invasive grasses in particular have led to drastic changes in forest understory structure and composition. Japanese stiltgrass (*Microstegium vimineum* (Trin.) A. Camus) is one of the most successful grass invaders in Tennessee. Being a prolific seeder and tolerant of low-light environments has aided in its persistence in natural areas and displaces most native understory plants. Herewe aim to quantify the range expansion of Japanese stiltgrass within forestlands of Tennessee. We analyzed an extensive dataset collected as part of the Forest Inventory and Analysis Program of the United States Department of Agriculture (USDA) Forest Service to quantify the range expansion of Japanese stiltgrass in the forestlands of Tennessee from 2002 to 2012. Japanese stiltgrass generally expanded its range, with the number of sample plots in which Japanese stiltgrass was detected increasing 50%. The mean percent coverage of Japanese stiltgrass in sample plots increasing significantly ($t = -2.8322$, $P < 0.05$) during this period. Our empirical results indicate the trend of expansion, and hence, likely paths of invasion, forest managers can develop long term monitoring and control strategies for effectively slowing range expansion and mitigating its effects.

PS8-3

Using time series of remotely sensed imagery to quantify pine invasion

Caroline Curtis[1], Bethany Bradley[2]
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In the southern hemisphere, invasive pine species are prominent invaders and constitute a major ecological threat. The spatial extent and high detectability of invasive pines in Chile provide a unique opportunity to apply remotely sensed data to quantify current land cover and measure land cover change through time across the landscape. Invasive pine species (especially *Pinus contorta* and *P*. radiata) were established in plantations and have since escaped and spread into the surrounding ecosystem, altering the ecosystem and threatening native species. Despite the potential risk from invasive populations, the extent of plantations and invasion in Chile is currently unknown. Pine percent cover has been projected for small areas only and studies of dispersal have focused on local patterns and short time scales. I selected eight Landsat scenes from throughout Chile and obtained a time series of Landsat images from 1984 – current for each scene with at least one image per five year period. For each scene, I created landcover training data based on historical aerial photos concomitant with one Landsat image. Random forest was used to classify images into five categories: water, bare ground, invasive pine, native forest, and other vegetation. By creating landcover maps for each step in the time series, I am able to quantify the amount and types of native habitat that have been converted to pine plantations. This method allows us to quantify the spread of invasive pines across a landscape and, therefore, gain a better understanding of how environmental factors impact invasion.

PS8-4

Global variation in the elevational distributions of nonnative vs. native species

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Much is now known about the elevational patterns and mechanisms of native species, how widespread of such patterns for nonnative species needs to be determined. Moreover, given the ever-increasing human population pressures, how nonnative species might further impact native species is of growing conservation concern. Using published data compiled from 65 case studies on elevational patterns of nonnative plants from around the world, we examine the elevational pattern of nonnative species and compare resulting patterns to those observed for native species. We found that, relative to native species, the distributions of nonnative species in relation to elevation were less unimodal (39%), and more negative (49%). Although other patterns than negative (51%) also emerged for nonnatives, the degree of invasion always decreased with elevation. The richness of nonnative species was highest at lower elevations, whereas that of native species peaked at mid-elevations. In cases where species richness for both nonnative and native species on the same mountains showed unimodal patterns in relation to elevation, peak values in species richness occurred at lower elevations for nonnative species. The general decline of nonnative species with increasing elevation and the reduced differences in elevational extents and upper limits between native and nonnative species were clearly associated with the concentration of human populations. As the nonnative species typically show strong associations with human activities, future changes in human population (e.g., growth and migration) and land use may promote upward spread of nonnative invasive species and may thus increase risks of impact on native species.

PS8-5

Drivers of invasive species richness in wildlands of western United States

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We examined how invasive plant species richness in wildands of the western United States is affected by climate (temperature, precipitation), geography (latitude, elevation), disturbance, and nutrient deposition. We specifically asked three questions: 1) What is the optimum spatial scale for detecting region-wide invasive plant species richness? 2) Are disturbance and nutrient deposition important predictors of plant species richness at the regional scale in the Southwest? 3) What climatic and geographic factors drive species richness of invasive plants in the Southwest? We used invasive species survey data from the Southwestern Exotic Plant Mapping Program (SWEMP), which includes > 60,000 occurrences of target noxious weeds from wildlands of California, Nevada, Arizona, Utah, Colorado, and New Mexico. In a preliminary analysis, climate, geography, and nutrient deposition were not significant predictors. On the other hand, we observed that human disturbance has a strong, positive linear relationship with invasive species richness in our study area. This result contradicted our expectation that invasive plants will exhibit highest richness in areas of intermediate disturbance. For the results presented in our poster, we used structural equation modeling to determine significant predictors, spatially-corrected regression to further examine trends, and GIS modelling to visualize spatial patterns.

PS8-6

A View From Above: using an Unmanned Aerial Vehicle (UAV) to investigate scale and patterns of liana infestation in tropical forest in Malaysia.

Catherine Waite[1], Richard Field[2], Doreen Boyd[2], Geertje van der Heijden[1]
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Tropical forests are a major global carbon sink, storing ~30% of terrestrial carbon. However, recent increases in liana abundance are pervasively altering forest structure; reducing carbon accumulation and long-term storage by enhancing tree mortality and reducing growth by up to 84%. Relying on trees for support, lianas allocate a higher proportion of biomass to foliage production over carbon-dense stems, reducing net above-ground carbon uptake by as much as 76%/year. Despite this, lianas are chronically understudied. Ground-based censuses are extremely time-consuming and, while mapping and monitoring studies utilising satellite and airborne images have occurred, they are limited by relatively coarse spatial and temporal resolutions, cloud obscuration, and high costs. UAV imaging may provide an affordable and accessible tool to overcome these limitations. Combining UAV and ground-based canopy censuses in two areas of Malaysian forest, this research will investigate whether canopy cover of lianas can be accurately distinguished using UAS imagery. It aims to assess the viability of UAVs for mapping and monitoring lianas in tropical forests while providing information on the extent and spatial patterning of liana infestation. This is crucial for analysing and quantifying lianas' effect on forest function, while helping uncover mechanisms behind their proliferation, as a continued increase may further reduce tropical forest carbon storage and sequestration, thus endangering the future of the tropical carbon sink. Preliminary results (r values = 0.68 to 0.83, n = 20, p values = <0.001) indicate a strong, positive correlation between UAV-derived and ground-derived %liana canopy cover on an individual tree level.

PS8-7

Detecting consistent morphological shifts across biogeographic boundaries in the fossil record

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Long-term morphological trends within a clade are frequently attributed to shifts in the physical environment. The intensity and direction of this relationship, however, can be difficult to assess at broad spatial and taxonomic scales. Here, we introduce a comparative framework for exploring the role of the environment in driving long-term morphological shifts. Specifically, we focus on the biota in and around the Cretaceous Western Interior Seaway (WIS) during its formative stages to test whether taxa undergoing similar environmental shifts – moving into a deepening seaway – also occupy similar positions in morphospace relative to their non-seaway counterparts. We compiled a database of Albian and Cenomanian fossil occurrences for ammonites, a diverse marine group whose shell shapes are often associated with distinct modes of life. We identified genera that include both species found within the WIS and species that appear excluded from it and digitized shell aperture shape from images representing each species. A morphospace generated from an elliptical fourier analysis of those shapes captures the high variation in shell compression and whorl overlap found in ammonites as well as the morphological distinctiveness of individual genera. We then compared morphospace positions of congeneric species using mixed models and found

evidence for a common directional shift towards increased whorl overlap for species present in the WIS compared to those that were not. This approach facilitates future work in assessing how frequently consistent, subtle changes in morphology occur across environments in other taxa and the ecological and evolutionary drivers of these changes.

PS8-8

Ecological implications of living on a host: the 'environmental stability' hypothesis and scale-effects on population patterns of an ectocommensal hypersymbiont.

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In order to test the 'environmental stability' hypothesis, so as the replication of population patterns at various scales in a symbiont, we analysed SW European populations of the hypersymbiont ciliate *Lagenophrys discoidea* living on the ectosymbiotic ostracod *Ankylocythere sinuosa*, hosted by the crayfish *Procambarus clarkii*. The relative role of host *vs*. off-host environment on hypersymbiont prevalence and abundance was assessed through model selection and variance partitioning, controlling for spatial effects. We also quantifyed scale-effects (i.e. 2nd order host *vs*. off-host locality) on the mean-variance of abundance and the occupancy-abundance patterns. The results showed a predominant role of off-host environment, suggesting that the 'environmental stability' has reduced impact in freshwater ectocommensals hosted by small crustaceans, due to: i) a weak dependence on the host, ii) a host with poor homeostatic abilities, and iii) living in a highly unstable environment. Furthermore, the mean-variance pattern was replicated at both scales but we found a scale dependence of the occupancy-abundance pattern, perhaps arising from differential rescue effects on this last pattern.

PS8-9

Expansion of invasive plants over the past two centuries in the Eastern United States

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Expansion of nonnative invasive plants have been a major challenge for various ecosystems worldwide. Despite the importance of understanding of invader expansion patterns to manage those species, the spatio-temporal progression of invaders is not well understood. Using herbarium specimen records, we reconstructed invasion networks of 29 nonnative invasive species over the past two centuries across the eastern USA and examined how socioeconomic factors and invader traits affect the expansion patterns. We found that invaders had a long-distance structured dispersal during the initial lag phase and a short-distance infilling during the later expansion phase. Human associated factors (e.g. human population, road density) had more significant impacts on the invader dispersal during the lag phase than during the expansion phase, while plant traits and introduction purpose of the invaders had no clear impacts on the invader expansion patterns. Our results suggest that socioeconomic factors play a significant role in the expansion of nonnative invasive species in the Eastern USA and that controlling potential invaders during the initial spreading stage is important for the overall success of invasion prevention and mitigation.

PS8-10

Investigating the drivers of invasive raccoon spread with dynamic occupancy models in Kanagawa, Japan

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Since the 1960's, the invasive North American raccoon (*Procyon lotor*) has spread across most of Japan, and is responsible for damage to crops and cultural buildings, disease transmission, and predation on endangered species.

To inform invasive species management, we built a multi-season occupancy model for Kanagawa (the most recent introduction) to determine variables related with raccoon expansion. These models estimate occupancy probability as a function of probabilities for site colonization and extinction. We used data from a 6-year raccoon trapping effort by local stakeholders that resulted in bycatch of other carnivores. Our results indicate that 1) occupancy probability had negative relationships with distance to introduction site and building density, and a positive relationship with stream length, whereas colonization probability had relatively weak negative relationships with all three that became more pronounced with time, 2) average colonization probability more than doubled region-wide, 3) population-level average occupancy has a weak downward trend. We also report on ongoing work that shows temporal correlation between raccoon non-detection and detection of other carnivores. Raccoons in their native range occupy higher elevations than those sampled here, and future field work should help clarify whether raccoons will colonize more mountainous regions in Kanagawa.

PS8-11

What drives plant invasion? The relative importance of phylogenetic space and environmental factors in the East Asian continental islands

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The mechanism of invasion success is mainly composed of species invasiveness related to species traits, habitat invasibility, and stochastic factors such as propagule pressure or residence time. Although the relative importance of these factors is expected to change according to the extent of spatial scale, limiting similarity between natives and non-natives is a key factor related to both invasiveness and invasibility. While native and non-native species that have specific traits to adapt environments in recipient communities may be filtered or sorted in concert, non-natives that share similar traits with natives may fail to invade into a local community because of limiting similarity and competitions with natives. In this context, phylogenetic relatedness between natives and non-natives surrogates the degree of niche overlap that determines invasion success or failure. Therefore, we explored drivers of plant species invasion from a view point of phylogenetic limiting similarity. We collected occurrence information of non-native plant species in Japan and created their distribution map, as well as geography of native plant species. Then we applied community phylogenetic field analysis for individual non-native species and evaluated the role of phylogenetic niche in range expansion after invasion, in addition to the influence of the residence time.

PS8-12

A dynamic modeling approach for estimating the potential distribution of the invasive Asian ambrosia beetle Xyleborus glabratus Eichhoff in North America

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Since its introduction to the east coast of the United States in 2002, the fungus *Raffaelea lauricola* T.C. Harr., Fraedrich & Aghayeva, which is transmitted by the ambrosia beetle *Xyleborus glabratus* Eichhoff (Coleoptera: Curculionidae: Scolytinae), has caused major mortalities to species of trees in the Lauraceae family. Here we present the predictions of the invasion dynamics of *X. glabratus* 25 years after its introduction using a spatially explicit dynamic modeling approach based on a logistic growth model that incorporates dispersal. Results show how the distribution of the species is shaped by a heterogeneous set of favorable conditions (belonging to the abiotic ecological niche) and resource availability (distribution Lauraceae tree species) and could replicate the known distributional pattern that we know for this beetle from 2002 to 2016. Results also indicate that this modeling approach has several advantages over correlative approximations to detect and predict species' distributions. The incorporation of population processes associated to the intrinsic population growth rate and dispersal in process-based modeling represents an advantage when modeling species geographic distributions because these allow us estimating the relevance of parameters related to the movement and colonization of the species in contrast to solely the abiotic ecological niche, thus providing a better means of assessing the potential distribution of a given species through time.

PS8-13

Distinguishing invasive from indigenous species in terrestrial arthropod communities on Moorea, French Polynesia, though metabarcoding signatures

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New genetic diagnostic approaches are facilitating the documentation of biodiversity, particularly for organismal groups for which morphological identification is difficult or incomplete. Species identification through DNA requires that a previous DNA fragment be associated with a named species, typically in a database, such as the Barcode of Life (BOLD) or GenBank. However, many taxa, particularly invertebrates, have not been sequenced, entered in an accessible database, or formally identified. Here, we describe an approach to distinguish invasive from indigenous species based on DNA signatures and test the approach with groups of Lepidoptera, Diptera, spiders, and other arthropods from the all taxon BioCode inventory of Moorea, French Polynesia. The Moorea BioCode project (http://www.mooreabiocode.org) was the first comprehensive inventory of all non-microbial life in a complex tropical ecosystem. Collections of all taxa were accompanied by voucher specimens and mitochondrial DNA barcodes. We constructed sequence alignments and distance trees for each arthropod order and assigned individuals to "species groups" using Automatic Barcode Gap Discovery (ABDG). Where possible, species groups were then updated with species names from GenBank, other web-based resources, or morphological identification. Predictor variables included branch length and average percent similarity. The analysis was able to identify previously unidentified specimens that were likely invasive as well as those that were unknown and likely indigenous, and thus in need of further taxonomic work. This approach provides a mechanism for rapidly assessing the extent of community invasion in metabarcode samples or other large samples of DNA from unknown specimens.

PS8-14

Out of range; short term effects of grazing by exotic large ungulates in a Mediterranean shrubland

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The introduction of some individuals of the European bison (*Bison bonasus*) in a wildlife reserve, Valdeserrillas (330 ha, 600 masl), located in a Mediterranean shrubland (Valencia province, eastern Spain), was an opportunity to learn about the potential effects of grazing by these large ungulates in a Mesomediterranean forest, out of their natural distribution range. With this aim we studied two fenced plots next to each other: one (7 ha) inhabited for a year by between 4 and 6 large ungulate individuals (first only bison, later bison and Asian water Buffalo, *Bubalus bubalis*) and another (25 ha) without such mammals. In order to characterize and compare the features of both areas we studied the vegetation composition and diversity, using interception transects and also measured several environmental variables (vegetation cover, slope, soil depth…). The results showed that grazing by large ungulates in the short term, reduced significantly the coverage of the herbaceous and bushes layer, also reducing the richness and diversity of the forest shrub. Grazing had a selective influence on some species of bushes, affecting negatively *Erica multiflora, Pistacia lentiscus* and *Quercus coccifera*, but also young individuals of *Pinus halepensis*, *Juniperus oxycedrus* and *Juniperus phoenicea*. The selective reduction in vegetation cover and diversity, along with more compacted soil by trampling, were the main effects observed, at least in the short term, on this ecosystem

PS8-15

A novel method to characterize the abiotic niche of the Invasive Asian Hornet

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The Asian Hornet (*Vespa velutina nigrithorax*) has invaded a large part of France since its arrival in 2004, and is now spreading over the rest of Europe at an exceptionally high speed. As a major predator of bees, it represents an emerging and rapidly growing risk for the already threatened pollination services. Many factors are responsible for this successful invasion; from suitable climatic conditions to the presence of nesting and foraging resources, but the relative importance of these factors in explaining its current distribution are unknown. Yet, this is critical to anticipate future invaded areas and mitigate the hornet's impacts. We identify the climatic drivers that best explain the distribution of the hornet, show the correlation between *V. velutina* nests and high human influence, and we provide a score for each land use class according to its attractiveness for the hornet. Climate and habitat are then combined, at their scale of effect, to identify hotspots of potential invasion. Since each variable type affects invasibility at a different spatial scale, we use a hierarchical procedure, applying variables successively at the scale at which they are the most influential. We obtain local and high resolution risk map of invasibility and provide a framework that can be applied elsewhere to target areas where action is needed in priority, measure the vulnerability of the area and take action to prevent or mitigate the invasion.

Poster Session 9: Biogeography of the Anthropocene (PS9)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS9-1

Fine-scale temporal mapping of fences reveals an accelerating human-wildlife conflict in the Greater Mara ecosystem

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Humans have affected and shaped terrestrial ecosystems for thousands of years. Over the past few hundred years human impacts have driven a shift from half of the terrestrial biosphere being in a wild state (dominated by non-anthropogenic processes) to a situation where 25% or less can be considered wild. Moreover, many of the remaining natural ecosystems are under pressure. The Greater Mara ecosystem illustrates this situation. It constitutes the northern part of the large Serengeti-Mara plain, famous for the largest and most species diverse migrations of large mammals in the world, including 1.3 million wildebeests, 200,000 zebras and hundreds of thousands of Thomson's gazelles. The Greater Mara ecosystem is also home for the Maasai tribes, with a traditional semi-nomadic pastoralist way of life that has been relatively compatible with the area's wildlife. Now, however, this situation is changing due to introduction of private land ownership, sedentarization, and a strong human population increase. Importantly, this har created a high risk that fencing of private land parcels will hinder the wildlife migrations that are key to the functioning of the greater Serengeti-Mara ecosystem as well as traditional pastoralist nomadism. We provide here a fine-scale mapping of fences based on Landsat satellite imagery from 1985-2016. Eight images were analyzed spanning this period and all fences within the Greater Mara region were identified and digitized. The spatio-temporal resolution of the mapping makes it possible to measure the speed and acceleration with which the fencing is evolving and thus to identify critical hot-spots where this

PS9-2
Exploring the dietary variation of pikas (Ochotona princeps) across a latitudinal gradient and a century of climate change

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Climate change is driving shifts in the range boundaries of taxa globally, but in addition to shifting distributions, climate change may also alter the life history traits or ecology of many animals. The American pika *(Ochotona princeps)*, an alpine mammal is considered an indicator species for animal responses to climate change, as climatic factors predict patterns of decline in parts of their range. However, recent work has implicated shifts in forage availability and quality, rather than temperature, as the primary driver influencing *O. princeps* abundance, persistence, and body size evolution. Here, we utilize carbon (?^{13}C) and nitrogen (?^{15}N) stable isotope analysis to characterize the dietary niche of *O. princeps* across six Rocky Mountain populations spanning a latitudinal gradient. The questions we address are 1) How much do individual *O. princeps* and population dietary niches vary across their range in the Rocky Mountains? 2) Have *O. princeps* altered their diet over the past century of climate change? We utilized museum specimens and wild caught specimens spanning a century of climate change. We sampled winter molt, summer molt and bone collagen from each individual to assess temporal variation among individuals and populations. We find that pika diets tend to exhibit geographical, seasonal and temporal variation with historical diets being more restricted. Given that *O. princeps* are considered bell-weather species for other alpine mammals and are of conservation concern, understanding how diet may link climate with ecology is vitally important.

PS9-3 Species distribution modeling for everyone: Undergraduates predict species responses to climate change

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Predicting the responses of biodiversity and ecosystem function to anthropogenic climate change is arguably the key scientific challenge in ecology and biogeography, yet traditional undergraduate curricula do little to equip young scientists with the ecoinformatic tools essential to studying climate change. Here, we describe a multiweek laboratory project that allows undergraduate ecology students to pursue original climate change research using online biodiversity and climate data resources and near state-of-the-art species distribution modeling approaches. Each student selects a single species of interest, with a focus on plants and animals native to the local region. After researching the natural history of their study species, each student uses distributional data from the Global Biodiversity Information Facility (GBIF) as well as climate norms and future projections from Worldclim, to construct, analyze, and visualize, Maxent species distribution models in R. In the process, student researchers become familiar with the basics of database queries, data management and quality assurance, and the construction, validation, and visualization of complex models. A public poster session with faculty and student peers then allows students to practice scientific communication about climate change in an informal but intellectually challenging context. In addition to providing students with a basic introduction to data intensive, replicable, ecoinformatic approaches, the project allows students to engage in discussions of both species-specific natural history and the insights, uncertainties, and limitations associated with species distribution modeling and climate change prediction.

PS9-4
Predator-prey theory indicates the "population bomb" is still ticking

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Human demographic models do not explicitly recognize resource limits, but predict will smoothly approach 11.2B people by 2100. But how smooth will that ride be? Classic predator-prey theory may inform population projections. If so, two curves are needed: prey growth (here plant NPP) should scale quadratically with biomass (B), and human appropriation of NPP (HANPP) should follow a satiation curve (type I, II, or III) with B. NPP scaling has been shown to be quadratic or sigmoidal, but general HANPP ~ B has not been modeled. I use spatially explicit, global data for terrestrial NPP, HANPP, and B from year 2000 (~1.5M data points) to estimate a predator-prey model. The theory applies well: logNPP scales quadratically with logB (AICc weight=1.0), and logHANPP follows a type III consumption curve with logB (AICc weight=1). But data are also quite variable. Latitude and longitude represent ~ 4.5% of variance. Vitousek et al. (1986) and Pimm (2001) estimated HANPP ~40% NPP. Analyses here use data from Haberl et al. (2007) and match their 24% in year 2000. Projecting simply to 2100, total HANPP will increase 83% to consume 45% of NPP. Whereas maximal local HANPP was 95% of local NPP in 2000; by 2100, 12% of terrestrial HANPP will exceed NPP (100-173%). Classic predator-prey theory can inform demographic human population projections and indicates the population bomb has a long fuse and is still ticking. Fundamental resources will be increasingly limiting for many more people this century, and natural ecosystems will be even more pressured.

PS9-5 Biogeography and Citizen Science: A Study of Ants

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Ants are ubiquitous and easily recognized, yet we still know relatively little about their diversity and distribution. Although often regarded as a nuisance, ants perform many important processes, such as controlling pests in agricultural fields and dispersing seeds. A new Citizen Science project aims to map the distribution and investigate the resource preferences of ants across three continents. This facilitates us to answer key questions about the relative effects of climate change and human activities on resource necessities and availability. Furthermore, we hope to study local adaptation of potential cryptic species and hybrids to measure the consequences of climate change on genetic diversity gain and loss.

PS9-6

A SIGNATURE OF HUMAN PRESSURE AMID ECOLOGICAL CONSTRAINTS ON THE DISTRIBUTION OF BODY MASS IN TETRAPODS

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Body size is arguably the single most important trait of animals, underlying most of their physiological, ecological and evolutionary processes. Examining geographical patterns in body size is thus crucial for understanding how animal communities are assembled and maintained. Traditionally, explanations for variation in assemblage-level body size have focused on broad-scale ecological constraints such as temperature and moisture. Yet, increasing evidence suggests that millennial-scale human pressures have influenced contemporary biodiversity patterns and may be partially responsible for the taxonomic and spatial heterogeneity we observe in present-day body size distributions. In this study, we used a tetrapod-level dataset (13,360 species mapped on a 110 x 110 km grid) for the Western Hemisphere to test whether a signal of millennial-scale human pressure could be detected on contemporary body mass distributions, once known ecological constraints had been taken into account. Our results show that a small set of ecological constraints is sufficient to explain much of the biogeography of body mass across tetrapods. Tetrapod classes are subject to different ecological controls, with body mass variation in endotherms being primarily explained by temperature and that among ectotherms primarily explained by moisture. Nevertheless, once these ecological constraints are accounted for, we can detect a signal of ~12,000 years of human impact. Both across and within tetrapod classes, assemblages have a smaller median body mass than expected given ecological constraints in areas with a longer history of human presence and human-induced land conversion . The signal of human pressure on tetrapod body mass is likely to increase with ongoing anthropogenic impacts.

PS9-7
Blight-resistant American chestnut: Reintroduction of a Novel Organism

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Over the past several decades, emerging molecular technologies have allowed conservation biologists to use insight into the genetic diversity of plant and animal populations to delineate, evaluate, and sustain them. New advances in genomics and genetic engineering are now expanding the capacity for human intervention in natural systems for conservation purposes, making possible the de-extinction of lost species and the re-wilding of domesticated landscapes. Unlike many other de-extinction proposals, efforts to reintroduce American chestnut (*Casta nea dentata* (Marsh.) Borkh.), which was rendered functionally extinct by chestnut blight (*Cryphonec tria parasitica*) in the early 1900s, are well underway. Both hybrid and transgenic trees have been developed for the large-scale reintroduction of the species, and over 12,000 trees produced through backcross breeding have been planted in national forests to date. This and other reintroduction projects aim to create self-sustaining, evolving populations of a lost species, often throughout its historical range. But while the promise is great, so are the philosophical, ecological, political, and practical concerns. Central among them is the potential for resurrected organisms to be maladapted to their historical environments due to land use, biotic, or climatic changes that have occurred in their absence. Here, we use maximum-entropy species distribution modeling (Maxent) to illustrate shifts in the distribution of suitable habitat for American chestnut both since its decline and over the next century. We then consider some of the implications of "reintroducing" novel organisms -- versions of extirpated or extinct species produced through hybridization and genetic engineering -- into no-analog ecosystems.

PS9-8 Biogeography and Critical Zone Science in the Anthropocene

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Critical Zone Science (CZS) represents a powerful confluence of research agendas, tools, and techniques for examining the complex interactions between biotic and abiotic factors located at the interface of the Earth's surface and shallow subsurface. The Critical Zone is a global phenomenon, and its interacting subsystems drive macroecological patterns and processes at a variety of spatial scales. Despite the analytical power of CZS to understand and characterize complicated rate-dependent processes, CZS has not historically captured the effects of ecological disturbance and anthropogenic influences on Critical Zone processes. Methodological approaches from biogeography and ecology show promise for providing Critical Zone researchers with tools for incorporating the effects of ecological and anthropogenic disturbance into fine-grained studies of important Earth processes. Similarly, mechanistic insights from CZS can inform biogeographical and ecological interpretations of pattern and process that operate over extensive spatial and temporal scales. In this paper, we illustrate the potential for productive nexus opportunities between CZS, biogeography, and ecology through use of an integrated model of energy and mass flow through various subsystems of the Earth's Critical Zone. As human-induced effects on biotic and abiotic components of global ecosystems accelerate in the Anthropocene, we argue that the long temporal and broad spatial scales traditionally studied in biogeography can be constructively combined with the quantifiable processes of energy and mass transfer through the Critical Zone to answer pressing questions about future trajectories of land cover change, post-disturbance recovery, climate change impacts, and urban and peri-urban hydrology and ecology.

Poster Session 10: Biogeography of the Anthropocene (PS10)

Odd numbered posters present: Jan 10; Even numbered posters present Jan 11
Location: Combined Canyon/Madera/Pima/Sabino rooms, Marriott Hotel

PS10-1

Potential microcrustacean dispersal by endozoochory and ectozoochory in a temporary lake from central Spain

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Dispersal is a key process for the maintenance and evolution of metapopulations /metacommunities. In Mediterranean temporary water bodies, which suffer a dessication period during the warm season, the formation of resting forms is an important strategy of microcrustaceans in order to survive unfavorable seasons but also for dispersal, allowing crossing the terrestrial areas among lakes. They do so by means of vectors capable of moving on their own from one lake to another. In this context; endozoochory, the dispersal inside the body of such vectors (for instance inside digestive systems) and ectozoochory, the dispersal outside their body (for instance on animal legs, bird feathers, mammal furs, but also on boots or other items related to human activities) are two important mechanisms. In Manjavacas lake, a brackish, shallow, temporary lake (100 ha) in central Spain, we wanted to compare the potential of both mechanisms. We obtained sediment from waders used during sampling campaigns (ectozoochory) and waterfowl faeces (endozoochory) and, in order to estimate the species pool, sediment from different areas of the lake, so as microcrustacean samples from the active community. By mean of hatching experiments done on waders' mud and faecal samples we obtained information on the diversity and amount of microcrustacean propagules which can be transported by birds and on the boots, a different dispersing community compared to the lake's species pool

PS10-2

Incorporating biotic interactions improves the prediction of mountain ecosystem plant species abundance and distribution

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Understanding the relative importance of biotic and abiotic controls of the distribution and abundance of species can improve forecasts on the ecological consequences of climate change. Here, we constructed statistical ecological niche models that incorporate a large suite of biotic interactions as well as traditional abiotic environmental data to ask: What is the relative importance of biotic interactions versus the abiotic environment in predicting the local abundance and distribution of a species? We assessed the presence/absence and abundance of three focal plant species (*Poa alpina*, *Festuca brachyphylla*, and *Elymus scribneri*) over 6 mountains and 67 sites in the Upper Gunnison Basin, Colorado, USA. At each site, variables relating to geography (e.g. elevation, aspect), the abiotic environment (e.g. soil depth, nutrients), and biotic interactions (e.g. herbivory, mammal disturbance) were used to predict focal species presence/absence and abundance using maximum likelihood and AICc model selection statistical methods. *Poa alpina* is less likely to be found in the presence of livestock, followed by decreased abundance with herbivore damage and increased abundance with declining temperature. Abundance of *F. brachyphylla* increased with decreasing temperatures at high elevation and decreased at sites with high levels of mammalian disturbance and herbivory. Low temperatures and high conspecific cover predicted the greatest abundance of *E. scribneri*. In all cases, a combination of abiotic and biotic were needed to predict abundance, suggesting that models lacking information on biotic interactions could fail. Experiments aimed at understanding how biotic interactions may change with climate are required to establish causality behind model findings.

PS10-3
Roles of plant clonality in shaping species-specific niche properties and community assemblages across East Asian continental islands.

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Plant clonality is a ubiquitous trait that prevails in various types of vegetation across tropical and arctic biomes. Despite the fact that plentiful investigations regarding the ecological and/or physiological properties of clonality, macroecological aspect of how clonal growth contributes to species assembly processes remain largely unknown. In this study, we focused on evolutionary processes of clonal growth for vascular plants (fern, herb, tree) and geographical pattern of clonality prevalence across the East Asian continental islands including subtropical to boreal forests. We compiled the information of clonal growth types and their presence-absence for individual species, as well as the data of species geographical distributions and phylogeny. In order to clarify alpha- and beta-niche properties that may be related to clonal growth, we investigated the correlations of species clonality with environmental and phylogenetic factors. In the analysis, we hypothesized that clonal plants perform better (and/or worse) in (1) harsh climate conditions, (2) disturbance regimes, (3) isolated or insular habitat, and (4) high species diversity with severe inter-specific competitions, and in addition that (5) clonality is a derivative trait in evolutions of vascular plants. Based on these predictions, we explored specie-specific pattern of clonality and environmental drivers of clonality prevalence in species assemblages. Finally, we address the evolutionary mechanisms of plant clonality and its role in environmental filtering and species sorting relative to community assembly.

PS10-4
Patterns in elevational range size are not explained by climate stability along a tropical elevational gradient

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[5]University of Missouri, St. Louis, United States
[6,7]Missouri Botanical Garden, United States

The degree of temporal variability in environment conditions changes dramatically across the globe, and this can have important implications for the evolution and distribution of species. Climate seasonality, for example, increases with latitude. This means that temperate species experience a wider range of environmental conditions than their tropical counterparts. In turn, these differences in seasonality have been hypothesized to select for broader niches in temperate species, which result also in wider geographic distributions. Most tests of this hypothesis have focused on latitudinal comparisons. However, in mountainous regions of the Tropics, daily climatic variation is often much larger at high elevations than in the lowlands. If temporal variation in climate influences niche breath and species distributions, then species near mountain tops should have more extensive distributions than species in the lowlands. In this study, we tested this idea using distribution records of ~2,000 tree species across a network of 490 forest plots. We related the size of elevational distributions to the temporal variability that each species experiences. Then, we compared observed patterns with null model expectations. Contrary to what is predicted by the hypothesis, we found that the size of distributions becomes smaller as elevation increases. Even though species near mountain tops are exposed to higher levels of temporal variability, climatic tolerances needed to survive in these conditions do not translate into broader geographic distributions. These results have important implications for understanding how large-scale environmental changes might influence patterns in the distribution of forest ecosystems across the Andes.

PS10-5

Quantifying species tolerances and functional diversity using n-dimensional hypervolumes: a comparison of methods

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Multidimensional hypervolumes enable ecologists to visualize the functional trait space occupied by an ecological community. Previously, hypervolumes have been measured using a minimum convex hull, but convex hulls are exclusively determined by extreme points and they cannot account for possible holes in the trait space. A multivariate kernel density estimation method with hyperbox kernels was proposed to deal with high-dimensional or holey datasets, but this method produces unrealistically blocky hypervolumes. We examined two alternatives: a Gaussian kernel density estimation method and a support vector machine method. We tested these two new methods and the hyperbox method by creating hypervolumes for three New World biomes using trait and bioclimatic data from plants and mammals. We varied the parameters for each method in order to determine sensitivity to parameter variation. The resulting hypervolumes were compared with respect to their total volume, shape, and overlap. The hyperbox hypervolumes consistently had the largest volume of the three methods. The Gaussian method proved least sensitive to variation in bandwidth, while the support vector machine is the most customizable in terms of its two parameters, but may be susceptible to overfitting.

PS10-6

Divergent influences of local-scale processes on lizard and velvet ant turnover along a Neotropical forest-savanna ecotone

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Understanding the role of spatial and environmental processes in species turnover is essential to explain community assembly, biogeography, and to deal with conservation planning in changing environments. The South American Cerrado is a diverse tropical savanna with remarkable heterogeneous landscape, often separated by abrupt transitions from neighbor regions. We modeled Cerrado lizard and velvet ant turnover as a function of differences in habitat parameters and spatial distances across a riparian forest - woodland savanna - grassland savanna gradient in central Brazil. By comparing two phylogenetically distant groups, we seek for generalities in factors regulating the assembly of Neotropical communities. We sampled animals along a transect with 57 pitfall trap arrays, recording parameters descriptive of the variation in habitat structure. A NMDS of environmental dissimilarity depicted a gradient of increasing soil exposure/nearest tree distance and decreasing number of logs/tree basal area. Abundance was highest in the woodland, intermediate in grassland, and lowest in forest. GDM indicated turnover was much higher in velvet ants, related to increased soil exposure, nearest tree distance, and leaf litter weight. Lizards showed a steady turnover with increasing termite nests, canopy openness, tree height, and number of burrows; and little turnover at low soil relative humidity, shrub density, and tree diameter, but turnover increased rapidly above this threshold. Discordant patterns may arise from differences in body size, trophic position, dispersal ability and physiological tolerance to environmental change. Our results highlight the differential responses of organisms to environmental transitions, underscoring their importance in maintaining local and regional biodiversity.

PS10-7

Wood anatomical correlates of the geographic ranges of Arctic shrub species in Greenland

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Anatomical features of wood are determined by the overall ecological strategy of the plant to maintain hydraulic conductivity and mechanical support under the environmental conditions prevailing in the distribution area. Arctic shrubs depend on a safe and efficient water transporting system to cope with the short window for growth that is available to them. Here we investigate the links between wood anatomical traits of Arctic shrub species and their distribution in Greenland. Wood anatomical information on 33 Arctic shrub species occurring in Greenland was retrieved from various data bases and supplemented with our own findings. This information will be compared with the distributional ranges of the individual species and climate data obtained for Greenland on a 10' grid resolution. First we will map the overall functional diversity of the shrub species and relate it to environmental variation. We expect that this will reveal how the species have adapted their water transporting system to the extreme growth conditions in the Arctic. Secondly, we will try to model the relationship between wood anatomical traits and environmental conditions at the shrubs' range limits to understand if the distribution of Arctic shrubs in Greenland is limited by physiological factors related to the water transporting system. We expect species to experience physiological constraints at their northern range limits where the climatic conditions are severest whereas the species might be limited by other factors such as competition at their southern range limits.

PS10-8

ENVIREM: An expanded set of bioclimatic and topographic variables increases flexibility and improves performance of ecological niche modeling

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Species distribution modeling is a valuable tool with many applications across ecology and evolutionary biology. The selection of biologically meaningful environmental variables that determine relative habitat suitability is a crucial aspect of the modeling pipeline. The 19 bioclimatic variables from WorldClim are frequently employed, primarily because they are easily accessible and available globally for past, present and future climate scenarios. Yet, the availability of relatively few other comparable environmental datasets potentially limits our ability to select appropriate variables that will most successfully characterize a species' distribution. We identified a set of 16 climatic and two topographic variables in the literature, which we call the envirem dataset, many of which are likely to have direct relevance to ecological or physiological processes determining species distributions. We generated these variables for the present, mid-Holocene, and Last Glacial Maximum (LGM). For 20 vertebrate species, we then assessed whether including the envirem variables led to improved species distribution models compared to models using only the existing WorldClim variables. We found that including the envirem dataset in the pool of variables to select from led to substantial improvements in niche modeling performance in 17 out of 20 species. We also show that, when comparing models constructed with different environmental variables, differences in projected distributions were often greater in the LGM than in the present. These variables are worth consideration in species distribution modeling applications, especially as many of the variables have direct links to processes important for species ecology.

PS10-9

Linking trait variation to the environment: critical issues with community-weighted mean correlation resolved by the fourth-corner approach

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Establishing trait-environment relationships has become routine in community ecology. Here, we demonstrate that the Community Weighted Means correlation (CWM) and its parallel approach in linking trait variation to the

environment, the Species Niche Centroid correlation (SNC), have important shortcomings, arguing against their continuing application. Using mathematical derivations and simulations, we show that the two major issues are inconsistent parameter estimation and unacceptable significance rates when only the environment or only traits are structuring species distributions, but they themselves are not linked. We show how both CWM and SNC are related to the fourth-corner correlation and propose to replace all by the Chessel fourth-corner correlation, which is the fourth-corner correlation divided by its maximum attainable value. We propose an appropriate hypothesis testing procedure that is not only an unbiased but also has much greater statistical power in detecting trait-environmental relationships. We derive an additive framework in which trait variation is partitioned among and within communities, which can be then modeled against the environment.

PS10-11

Linking species interactions with phylogenetic and functional distance in European bird assemblages at broad spatial scales

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Coevolution among species via species interactions is one of the major driving forces of biodiversity. Yet, interactions are usually assumed to be important only at local scale. We examined whether local interactions reflect to geographical scale by examining signals of positive, neutral and negative pairwise bird species associations in geographical abundance patterns as a function of functional and phylogenetic proximity. We used French and Finnish breeding bird surveys. We calculated pairwise correlations between residual variation of each species pair in the community, which we assumed to reflect species interactions and compared the observed values to a null model. Our results show the prevalence of negative species associations but also provide evidence for positive interactions. Functionally similar and/or closely-related species were more likely to show strong associations, both negative and positive, than more distant species. We emphasize the importance of functional and phylogenetic proximity in generating negative, but also positive, species associations, which can reflect to geographical scales. In addition to compensatory dynamics versus environmental forcing, future studies testing assembly theories should also consider the possibility of positive species interactions.

PS10-12

The contribution of phylogenetic lineages to the functional and species diversity in tree assemblages worldwide

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Phylogenetic and functional diversity are routinely quantified in community ecology to understand species co-occurrence. Such analyses typically also quantify phylogenetic signal in trait data for the species in the assemblage. While this work is interesting, the integration of phylogenetic information with trait data in the context of species assemblages will be most informative on larger spatial scales with denser taxonomic sampling. In other words, it is nearly impossible to make robust inferences about the evolution of traits as it relates to community assembly using local scale community inventories. This has slowed progress towards an interesting synthesis of community ecology and evolutionary history and the phylogenetic and functional dimensions of biodiversity. Here we scale out the community phylogenetics research program to trace trait evolution on large molecular phylogenies containing the species from local assemblages around the world while placing this information back into the context of local scale assemblages. The work uses a large molecular phylogeny and detailed trait information for the species found in 14 Center for Tropical Forest Science forest plots located in temperate and tropical forests in Asia and the Americas. We first identify nodes that are hot spots and cold spots of functional diversity within the large phylogeny. Next, we quantify whether these nodes contain species that are typically over-represented individual forest plots indicating that a locally dominate lineage is spectacularly functionally diverse or poor. Finally, we quantify whether these lineages tend to have species that co-occur on very fine scales.

PS10-13

Community structure in environmental transitions: the Cerrado-Amazon ecotone is a sink for lizard species

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Ecological gradients have a crucial role in the flow of species, genes and nutrients between adjacent areas. Limits do not simply separate, but also connect areas, acting as filters of varying permeability. Community structure varies with proximity to the ecotone, and species richness in the ecotone can be higher than, lower than, or similar to adjacent areas. Here, we investigate how the ecotone isolates two Neotropical biomes, the Amazon and the Cerrado, acting as a filter on the lizard fauna exchange between them. Based on field and literature data, we performed correlation analyses between diversity indices and the distance of each sampling point to the ecotone and to the biomes centroids. To investigate the processes responsible for the observed patterns along the gradient, we conducted a canonical correspondence analysis (CCA) relating species incidences in sampled communities and environmental variables. Our results demonstrate that proximity to the Amazon-Cerrado ecotone negatively affects the diversity of lizard communities. The ordination by the CCA clearly distinguished two groups of species (from open and from forest habitats), associated with potential vegetation, soil moisture and mean diurnal range of temperature. Our results reveal that the Amazon-Cerrado ecotone acts as a species sink, probably resulting from environmental conditions unsuitable for both Amazon and Cerrado species. Still, the Amazon-Cerrado ecotone can harbor genetically diverse populations resistant to environmental change and able to persist in unstable environments, an important genetic repository in the face of predicted global climate changes.

PS10-14

Historical biogeography and current productivity explain lemur community structure

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In this study, I aimed to elucidate how broad-scale biogeography in deep time and present-day ecology and habitat loss have shaped patterns of primate diversity across landscapes on Madagascar. I collected data on lemur species co-occurrence from range maps and survey literature for 100 lemur communities in protected areas. I quantified and compared taxonomic, phylogenetic and functional dimensions of alpha and beta diversity and tested environmental and geographic predictors of diversity. I calculated deforestation rates within protected areas between the years 2000 and 2014, and tested if diversity is related to forest cover and loss. Implementing this multidimensional approach with the most comprehensive dataset for the first time in Madagascar, I found the phylogenetic structure of lemur communities could be explained by the river barrier hypothesis, with old lineages separated by rivers. Taxonomic and phylogenetic diversity increased with greater plant productivity, implicating resource-limitation influences community assembly, while functional diversity was not strongly related to environment. Diversity also increased with topographic heterogeneity, indicating that rugged landscapes with abundant microhabitats support greater diversity. Approximately 3,000 km^2 were deforested in protected areas since the year 2000, threatening the most diverse communities (up to 31% deforestation / park). These results underscore the need for focused conservation efforts to staunch the erosion of irreplaceable evolutionary and ecological diversity.

PS10-16

Multi-hierarchical macroecology: comparing the variation of Iberian terrestrial mollusc and leaf beetle assemblages at the species and genetic levels

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Multi-hierarchical macroecology assesses patterns of variation of biological assemblages at multiple-hierarchical levels from haplotypes to species, aiming to discern the major processes controlling species distributions (Baselga, Gómez-Rodríguez & Vogler 2015). The rationale is that the geometry of lineages' distribution ranges at multiple hierarchical levels is fractal only under neutral evolutionary and ecological dynamics, thus providing a testable

unique predictions. This has previously tested in beetles (European water beetles and Iberian leaf beetles). Here we assess macroecological patterns (range size, occupancy, local diversity, assemblage dissimilarity) of Iberian terrestrial molluscs at multiple hierarchical levels, and compare them to those of Iberian leaf beetles.

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A novel measure of species co-occurrence based on joint models offers little advantage over previous approaches

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Species co-occurrence analyses are confounded by species' shared environmental responses. Joint species distribution models (JSDM) were suggested as more robust alternatives, as they separate co-occurrences into components based on shared environmental preferences and their residuals. The latter, Rho, denote co-occurrences that are not confounded by shared environmental responses. It is unknown, however, if Rho is a more robust co-occurrence metric compared to previous measures. We addressed this gap by quantifying tree co-occurrence patterns in 200 US regions, using two standard co-occurrence measures and JSDM. We found that Rho is strongly correlated with both co-occurrence measures. This suggests that either the ability of JSDMs to partition the variation in co-occurrence patterns to environmental and residual correlations is limited, or that species' shared environmental responses play a minor role in driving tree co-occurrences in the US. The latter seems unreasonable given previous results, which revealed strong effects of species niche overlap on co-occurrence patterns in the same data set. This calls for a thorough analysis of JSDMs to ensure that their output of Rho can indeed serve as a useful measure of co-occurrence that is not confounded by species' environmental preferences.

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CS3-1, MT2-8	Kunin	William
CS5-5	Kunte	Krushanmegh

PS10-3, PS8-11, PS2-11, PS1-4, PS1-14	Kusumoto	Buntarou
CS15-1	La Sorte	Frank
PS10-5	Lamanna	Christine
CS10-5	Lambert	Shea
CS13-5	Lampert	Adam
CS2-1	Landis	Michael
PS6-9	Larrue	Sébastien
CS4-6, CS12-1	Lavergne	Sebastien
CS5-2	Lavers	Chris
MT3-14	Lebbie	Aiah
PS10-11	Lehikoinen	Aleksi
PS10-6	Lenza de Oliveira	Eddie
CS11-6, CS11-3	Leroux	Shawn
CS7-1, PS6-6	Lessard	Jean-Philippe
MT3-3	Lewis	Rob
MT1-8	Lewthwaite	Jayme
MT1-3	Leyk	Stefan
CS4-8	Li	Jiaqi
PS3-8	Li	Jun
MT1-12	Li	Zhimin
PS7-1	Li	Jinya
PS6-10	Lim	Jun Ying
MT2-10	Lima-Ribeiro	Matheus
MT1-14	Linder	H. Peter
PS3-5	Liphardt	Schuyler
PS8-12, MT2-1	Lira-Noriega	Andres
MT1-12	Liu	Yusheng
PS5-10	Llambí	Luis
CS5-1	Loader	Simon
MT1-3	Loescher	Henry
CS3-5, S1-1	Long	Peter
MT2-6	Longnecker	Marie
PS2-15	López	Joan Manuel Soriano
PS2-5	López-Iborra	Germán
PS9-1	Løvschal	Mette
CS13-1, CS1-3	Loyola	Rafael
PS10-4, PS1-11	Loza	Isabel
PS7-3	Lu	Muyang
CS2-6	Ludt	William
PS1-13	Luk	Chung-Lim
PS3-8	Luo	Zhenhua
CS15-4, CS16-6	Luoto	Miska
PS10-2	Lynn	Joshua
CS1-6, S1-3, PS4-16	Lyons	K. Sara
MT1-13	Ma	Keping
PS1-10	Ma	Keming
MT3-13	Mabry	Karen
MT2-4	MacDonald	Andrew M
MT4-12	MacDonald	Glen
MT2-6	Mace	Georgina
CS8-6	Machac	Antonin
PS10-4	Macia	Manuel
CS15-5, PS4-6, CS3-5, S1-1	Macias Fauria	Marc
S1-4	Maguire	Kaitlin

MT4-7	Mainali	Kumar
PS10-5	Maitner	Brian
PS3-1	Malaney	Jason
MT1-5	Manica	Andrea
PS9-8	Mann	Sarina
PS2-4	Manolache	Steluta
PS2-15	Mañosa	Albert Pélachs
PS1-15	Marcuse-Kubitza	Aaron
PS10-6	Marimon	Beatriz
PS10-6	Marimon-Junior	Ben Hur
MT2-11	Marki	Petter
CS3-3	Maron	John
CS7-5	Marples	Nicola
PS8-5	Marshall	Diane
PS6-10	Marshall	Charles
CS7-1, CS13-7	Marske	Katharine
MT2-12	Marta	Silvio
PS1-9	Martin	Ryan
PS6-4	Martine	Christopher
CS11-1	Martins	Ines
CS12-1	Marx	Hannah
S2-8, PS5-11	Matias	Miguel
PS8-11	Matsuhashi	Saeko
MT3-1, CS14-3	Matthews	Tom
MT2-5	Matzke	Nicholas
PS1-19	Maurin	Olivier
CS11-1	May	Felix
MT1-3, PS3-12	Mayor	Stephen
CS4-6	Mazel	Florent
MT3-7	Mazzoni	Sabrina
MT2-2	McCain	Christy
PS1-15	McFadden	Ian
CS14-7	McGee	Tessa
CS15-5, CS11-2, S3-3, S2-7, PS1-15	McGill	Brian
CS7-1	McGuire	Jimmy
CS1-1	McGuire	Jenny
S1-2	McLachlan	Jason
CS6-3	McLaughlin	Blair
CS10-2	McMahon	Michelle
CS2-7, PS4-2	McMichael	Crystal
CS8-2	Medina-Romero	Margarita
CS15-4	Meineri	Eric
MT3-2	Mejia	John
CS13-7	Mejía-Domínguez	Nancy
PS2-18	Mekonnen	Addisu
PS2-14	Mendoza	Eduardo
MT1-7	Menéndez-Guerrero	Pablo
PS2-17	Menezes	Ronaldo
CS12-3	Menzel	Andreas
PS2-9	Mercier	Katie
CS16-8	Merow	Cory
CS16-7	Mertes	Katherine
PS10-1, PS1-1, PS8-8	Mesquita-Joanes	Francesc
PS8-8	Mestre	Alexandre

MT3-9	Meunier	Hugo
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PS2-14	Meyer	Ninon
CS14-7	Meyerhof	Matthew
PS10-16	Miller	Kirsten
CS5-6, CS10-5	Miller	Elizabeth
MT1-3	Miller	David
CS16-2	Miller	Paul
PS6-6	Millien	Virginie
PS5-12	Mimet	Anne
PS9-8	Minor	J.
CS7-6	Miranda	Pedro
PS7-5	Mirea	Ionut
S1-2	Mladenoff	David
MT1-14	Mo	Lidong
PS1-17	Moerland	Michelangelo
PS5-5	Moisen	Gretchen
PS7-5	Moldovan	Oana
MT1-10	Molina-Freaner	Francisco
PS10-11	Mönkkönen	Mikko
MT4-3	Monnet	Anne-Christine
PS8-14	Monrós	Juan
MT1-8	Mooers	Arne
CS9-1, CS12-3	Moora	Mari
PS3-10	Moore	Wendy
PS4-2	Mooyman	Serge
MT1-8	Morales-Castilla	Ignacio
CS7-6	Moreira	Suzana
CS1-3	Moreno	Di Marco
CS5-4	Moritz	Craig
CS1-2	Morley	Kate
PS4-8	Morris	Jesse
CS6-3, PS1-15	Morueta-Holme	Naia
CS15-5	Moulton	Derek
CS2-4	Moyle	Robert
MT4-9	Muellner-Riehl	Alexandra N.
PS5-10	Muriel	Priscilla
PS9-8	Murphy	Patrick
CS3-6	Murray	Kris
CS2-6	Myers	Corinne
CS5-1	Nagel	Peter
CS12-5	Nagy	Rachel
PS2-10	Naimi	Babak
PS2-9	Napier	Johnathan
PS7-5	Nastase-Bucur	Ruxandra
PS4-2	Neill	David
CS7-4, CS7-6	Neves	Danilo
PS4-12	Newsom	Lee
CS13-2, S1-3, PS4-16	Newsome	Seth
MT2-11	Nguyen	Jacqueline
PS2-18	Nguyen	Nga
MT1-12	Nie	Ze-long
PS10-7	Nielsen	Sigrid Schøler
S1-4	Nieto-Lugilde	Diego

CS16-6	Niittynen	Pekka
PS2-4	Nita	Andreea
CS15-5, CS6-5	Nogue	Sandra
S1-5	Nogues Bravo	David
PS5-12, PS10-7	Normand	Signe
MT3-6	Noroozi	Jalil
S2-2	Novotny	Vojtech
CS7-5	O'Connell	Darren
PS2-14	O'Farrill	Georgina
PS8-13	Oboyski	Peter
CS14-6	Ochoa-G.	Jose
CS13-7	Ochoa-Ochoa	Leticia
MT4-8	Okahashi	Hisayo
MT3-8	Olalla-Tárraga	Miguel Ángel
PS8-1	Oliveira	Gilherme
CS7-4, CS7-6	Oliveira-Filho	Ary
CS2-4	Oliveros	Carl
CS2-3, CS5-1	Onstein	Renske
CS9-1	Öpik	Maarja
CS15-5, PS4-6, MT1-2, CS4-7, CS15-3, CS4-3	Ordonez	Alejandro
PS1-12	Osborne	Teresa Rose
PS8-12	Osorio-Olvera	Luis
MT1-3	Otegui	Javier
CS12-6	Otto	Rüdiger
PS5-13	Ouimette	Sarah
CS13-6	Pacheco-Sierra	Gualberto
S1-2	Paciorek	Chris
PS7-2	Palma	Eduardo
CS15-7	Pandori	Lauren
MT1-11	Papes	Monica
CS10-4	Parchman	Thomas
CS1-6	Pardi	Melissa
CS2-1	Park	Brian
PS1-19	Parker	Joe
CS7-1	Parra	Juan
CS9-1	Pärtel	Meelis
PS9-8	Pearl	Jessie
MT1-3	Pearse	Ian
S3-6	Pearse	William
CS1-6, PS4-16	Pedersen	Rasmus
PS1-15	Peet	Robert
CS7-4, CS7-6	Pennington	R. Toby
MT4-11	Peñuela	Maria Cristina
CS11-1	Pereira	Henrique
PS2-16	Pereira	Taigua
PS5-11	Pereira	Catia
CS7-3, MT4-10, PS10-9, MT1-8	Peres-Neto	Pedro
CS13-6	Pérez-Alquicira	Jéssica
CS12-4	Pergl	Jan
PS2-9	Perry	Danae
CS16-5	Peters	Marcell
MT1-11	Peterson	A. Townsend
MT3-4	Phelps	Nicholas
CS8-2	Phillips	Matt

PS2-9	Phillips	Katrina
CS15-3	Pickles	Brian
PS1-15	Piel	William
MT4-14	Pigot	Alex
PS9-1	Pilgaard	Jeppe
CS7-3	Pinel-Alloul	Bernadette
PS4-3	Pinilla Buitrago	Gonzalo
S3-4	Pires	Mathias
CS15-3	Pither	Jason
MT2-8	Pokorny	Petr
PS1-19	Pokorny	Lisa
CS14-7	Pondaven	Philippe
PS2-4	Popescu	Viorel
CS16-2	Porter	Warren
CS6-1	Potter	Kevin
PS8-8	Poulin	Robert
PS1-2	Presley	Steven
MT2-3	Price	Trevor
CS14-1, CS14-4	Price	Jonathan
CS6-4	Provenzale	Antonello
PS5-5, PS5-3	Psomos	Achilleas
MT4-14	Pyron	Alex
CS12-3, CS12-4	Pyšek	Petr
MT1-11	Qiao	Huijie
PS7-1	Qin	Haining
S3-4	Quental	Tiago
MT3-8	R. Pertierra	Luis
CS2-8	Raczka	Marco
CS8-6, CS7-1, CS13-4, MT2-11, CS13-7, PS2-10, S1-6	Rahbek	Carsten
PS5-8	Ramachandran	Vivek
PS5-8	Ramakrishnan	Uma
MT2-4	Ramirez	Kelly S
PS3-14, PS4-11	Ramirez-Valdez	Arturo
CS6-6	Rampedi	Isaac
S1-6	Rangel	Thiago
PS9-6	Rapacciuolo	Giovanni
CS10-6	Rasbury	E.
CS13-1	Rattis	Ludmila
PS2-9	Rautsaw	Rhett
MT2-3	Rawat	Gopal Singh
S3-8	Real	Raimundo
PS2-20	Rebbas	Khellaf
CS5-4	Recoder	Renato
PS1-15	Regetz	Jim
CS4-6	Renaud	Julien
MT4-8	Renema	Willem
PS2-14	Reyna-Hurtado	Rafael
CS7-6	Rezende	Vanessa
PS2-17	Ribeiro	Eraldo
MT4-5	Rickart	Eric
PS6-8, PS1-11	Ricklefs	Robert
CS10-1	Riddle	Brett
MT4-7	Ries	Leslie
MT3-1	Rigal	Francois

CS12-3	Rillig	Matthias
PS10-6, PS10-13	Rinaldi Colli	Guarino
CS6-3	Riordan	Erin
CS1-5	Ripplinger	Julie
S2-5	Rissler	Leslie
PS3-7	Rivera	Danielle
MT1-6	Rixen	Christian
PS8-12, MT2-1	Robles-Fernandez	Angel
PS2-13, PS2-15	Rocha	Yuri
PS8-13	Roderick	George
MT1-5	Rodrigues	Ana
PS3-7	Rodrigues	Miguel Trefaut
PS10-6	Rodrigues Vieira	Cecília
PS8-2	Rogers	William
CS7-1	Rojas	Danny
PS4-3	Rojas Soto	Octavio
PS8-13, MT3-9	Rome	Quentin
CS6-2, CS5-1	Rosauer	Dan
CS1-4	Rosenblad	Kyle
MT4-5	Rowe	Rebecca
CS2-8	Rozas-Davila	Angela
PS2-4	Rozylowicz	Laurentiu
PS10-2, PS8-5	Rudgers	Jennifer
CS4-1	Rueda	Marta
PS1-1	Rueda	Juan
CS3-4, MT3-6	Rumpf	Sabine
PS1-12, PS6-5	Rundell	Rebecca
CS14-7	Sachs	Julian
PS3-3	Sage	George
CS7-6	Saiter	Felipe
S3-4	Salamin	Nicolas
CS11-2	Salguero-Gómez	Roberto
PS2-20	Sammut	Paul
CS15-5, MT4-3, CS7-2, PS5-12, PS1-15	Sandel	Brody
PS9-5	Sanders	Nathan
CS10-2	Sanderson	Michael
PS9-3	SantaMaria	Toby
PS3-14	Santamaria-del Angel	Eduardo
MT4-12	Saraf	Sargam
PS5-17	Sarmiento	Fausto
PS5-7	Sasamura	Takashi
CS11-6	Saunders	Paul
CS1-4, CS15-8, PS5-19	Sax	Dov
PS2-20	Scalercio	Stefano
PS2-13, PS2-15	Schacht	Gustavo
PS2-14	Schank	Cody
PS1-2	Scheiner	Samuel
CS14-7, MT2-13	Schiebelhut	Lauren
PS1-15	Schildhauer	Mark
MT3-6	Schneeweiss	Gerald
MT1-3	Schneider	David
CS1-6	Schroeder	Katlin
PS4-1	Schulp	Anne
CS15-2, CS12-6	Schweiger	Andreas

CS3-5, PS4-8, S1-1	Seddon	Alistair
CS12-4	Seebens	Hanno
MT4-6	Seliger	Benjamin
CS1-8	Sert	Osman
PS2-17	Shadik	Courtney
MT3-5	Shaney	Kyle
PS4-12	Shapiro	Beth
PS9-5	Sheard	Julie
PS8-4	Shen	Zehao
PS10-3, PS8-11, PS2-11, PS1-4, PS1-14	Shiono	Takayuki
PS2-20	Shreeve	Tim G.
CS4-8, CS13-8, PS6-7, PS6-3	Si	Xingfeng
PS2-16	Silva	José Rodrigo
PS6-12	Silva	Rejane
S3-4	Silvestro	Daniele
CS15-3	Simard	Suzanne
CS3-1, MT2-8, CS14-5, CS3-2	Sizling	Arnost
CS3-1, CS3-2, MT2-8, CS14-5	Sizlingova	Eva
CS11-6	Smedjova	Lucie
CS10-6, CS8-5	Smiley	Tara
MT1-1	Smith	Adam
PS4-9	Smith	Alison
CS1-6, PS9-2, S1-3, PS4-16	Smith	Felisa
PS2-9	Smith	Nathaniel
MT3-12	Smith	Thomas
MT4-4	Snell	Sara
MT1-11, PS8-12	Soberon	Jorge
MT1-4, MT1-9	Sofaer	Helen
MT1-5	Somveille	Marius
CS13-8	Song	Xiao
CS15-7	Sorte	Cascade
CS7-4	Souza	Fernanda
PS2-19	Souza	Daniel
PS1-15	Spencer	Nick
CS5-5	Sperling	Felix
PS4-1	Spoor	Fred
CS2-1	Spriggs	Elizabeth
S1-3, PS4-16	Stafford, Jr.	Thomas
PS2-9	Stahelin	Gustavo
PS1-6	Staiger	Kiri
PS5-4	Stauffer	Brett
CS8-4	Steadman	David
CS16-5	Steffan-Dewenter	Ingolf
MT3-3, CS14-2, CS12-6	Steinbauer	Manuel
CS2-5	Stelbrink	Björn
CS14-7	Stibor	Herwig
CS9-4	Stigall	Alycia
CS11-2	Stott	Iain
CS5-4	Strangas	Maria
CS12-6	Strasberg	Dominique
CS10-5	Streicher	Jeffrey
CS13-6	Suárez-Atilano	Marco
PS5-7	Sugimoto	Atsuko
MT1-12	Sun	Hang

S2-6	Supp	Sarah
CS15-5, PS4-6, MT1-2, CS3-7, CS2-3, CS11-2, CS4-7, MT4-3, CS1-7, CS2-2, CS11-4, MT1-13, MT2-14, PS5-12, MT3-3, PS9-1, PS1-15, PS4-16	Svenning	Jens Christian
PS10-12	Swenson	Nathan
CS14-7	Swift	Holly
MT4-2, CS9-1	Szava-Kovats	Robert
CS6-6	Tafirei	Respina
PS2-10	Taheri	Shirin
PS3-3	Talbot	Sandra
MT3-6	Talebi	Amir
CS12-1	Tank	David
CS11-6	Tanner	Amy
PS6-1	Tarr	Simon
PS10-4	Tello	J. Sebastian
CS1-7	Teng	Shuqing
PS10-9	ter Braak	Cajo
PS1-15	Theirs	Barbara
PS5-4, MT3-12	Thomas	Kathryn
PS3-9	Thomassen	Henri
CS16-3	Thorup	Kasper
CS4-6, PS5-15	Thuiller	Wilfried
CS3-6	Tiedt	Sonia
MT1-3	Tingley	Morgan
PS10-8	Title	Pascal
CS14-5, CS3-2, MT2-8, CS3-1	Tjørve	Even
CS14-5, CS3-2, MT2-8, CS3-1	Tjørve	Kathleen
CS3-2	Tjørve	Even
PS2-7	Tockner	Klement
S1-3, PS4-16, CS1-6	Tomé	Catalina
PS7-2	Torres-Perez	Fernando
PS10-4	Torrez	Vania
PS1-8	Tószögyová	Anna
PS9-5	Tøttrup	Anders
PS10-13	Tourinho Dantas	Pedro
PS5-10, S1-1	Tovar	Carolina
CS9-2	Treml	Eric
MT3-1, CS14-3	Triantis	Kostas
MT2-12	Trucchi	Emiliano
CS7-2, PS1-15	Tsirogiannis	Constantinos
PS2-6	Tuanmu	Mao-Ning
CS8-3, PS4-13	Tuff	Ty
PS5-10	Ulloa	Carmen
MT4-14	Upham	Nathan
CS2-8	Valencia	Bryan
CS7-6, CS14-4	Valente	Arthur
PS10-1	Valls	Luis
PS8-6	van der Heijden	Geertje
CS12-4	van Kleunen	Mark
CS11-6	Vander Wal	Eric
MT3-3, S2-1	Vandvik	Vigdis
CS13-6	Vázquez-Domínguez	Ella
PS8-14	Vera	Pablo
CS3-8, PS2-1	Vetaas	Ole

MT4-11	Vicentini	Alberto
PS2-20	Vila	Roger
MT2-10, PS4-13, CS8-3	Vilela	Bruno
PS4-10	Villaseñor	Amelia
MT3-9	Villemant	Claire
CS11-2, PS1-15	Viole	Cyrille
PS2-20	Voda	Raluca
PS2-9	Volk	Dan
MT3-7	Vollering	Julien
CS2-5	von Rintelen	Thomas
PS4-1	Vonhof	Hubert
CS9-3	Wagner	Philipp
PS8-6	Waite	Catherine
CS16-1	Wallace	Cynthia
CS10-5	Walls	Ramona
PS6-4	Walsh	Seana
CS4-8	Wang	Siyu
CS16-2, PS4-12	Wang	Yue
MT3-10	Wang	Lifei
PS8-2	Wang	Hsiao-Hsuan
PS3-2, MT2-5	Warren	Dan
MT1-14, CS14-4, CS12-1, CS12-4	Weigelt	Patrick
CS6-3	Weiss	Stuart
CS11-2	Welk	Erik
CS7-1	Wenstein	Ben
CS1-6, PS9-2	Westover	Marie
CS10-2	Whiteman	Noah
MT3-1, CS14-4, CS14-3, CS6-5, CS14-1	Whittaker	Robert
CS5-6, CS10-5	Wiens	John
CS11-6	Wiersma	Yolanda
PS2-8	Wikelski	Martin
MT1-10	Wilder	Benjamin
S1-1	Wilebore	Beccy
CS16-3	Willemoes	Mikkel
CS16-3	Williams	Heather
S1-4, MT1-2, PS5-21, S1-2, CS16-2, PS4-12, CS15-3	Williams	John
PS4-14	Williams	J. Eric
PS1-2	Willig	Michael
S1-1, CS3-5, CS6-5, PS4-8, PS2-18	Willis	Kathy
CS6-5	Wilmshurst	Janet
CS16-8	Wilson	Adam
CS14-7	Wilson	Jesse
CS10-2	Wing	Rod
CS11-1, CS12-4, MT2-12	Winter	Marten
MT1-6	Wipf	Sonja
PS1-15	Wiser	Susan
MT1-3	Withey	John
CS10-2	Wojciechowski	Martin
PS4-12	Wooller	Matthew
CS4-8	Wu	Yiru
PS3-8	Wu	Hua
PS6-7	Wu	Lingbing
CS4-6, MT1-14	Wüest	Rafael O.
S3-3	Xiao	Xiao

CS1-7	Xu	Chi
PS8-7	Yacobucci	Margaret
CS11-6, CS11-3	Yalcin	Semra
PS2-2	Yan	Yujing
PS3-10	Yanahan	Alan
MT4-8	Yasuhara	Moriaki
PS1-4	Yasumuro	Haruhiko
CS6-6	Yessoufou	Kowiyou
MT2-4	Yguel	Benjamin
CS5-3	Yin	Xue
CS16-4	Zambrana-Torrelio	Carlos
PS2-7	Zarfl	Christiane
CS4-8	Zeng	Di
PS1-10	Zhang	Yuxin
PS1-10	Zhang	Shuang
CS4-8	Zhao	Yuhao
PS3-8	Zhao	Mian
PS7-1	Zhao	Lina
MT1-11	Zhu	Gengping
CS3-4, MT1-14, PS5-5, PS5-15, PS5-3	Zimmermann	Niklaus
CS9-1, CS12-3	Zobel	Martin
PS5-15	Zurell	Damaris
CS9-3	Zwaan	Roelof E.