Frontiers of Biogeography

Title

Conference program and abstracts. International Biogeography Society 6th Biennial Meeting – 9-13 January 2013, Miami, Florida, USA

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6th Biennial Meeting – 9-13 january 2013, Miami, Florida, USA

Conference Program and Abstracts

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Conference Program and Abstracts

International Biogeography Society 6th Biennial Meeting – 9-13 January 2013, Miami, Florida, USA

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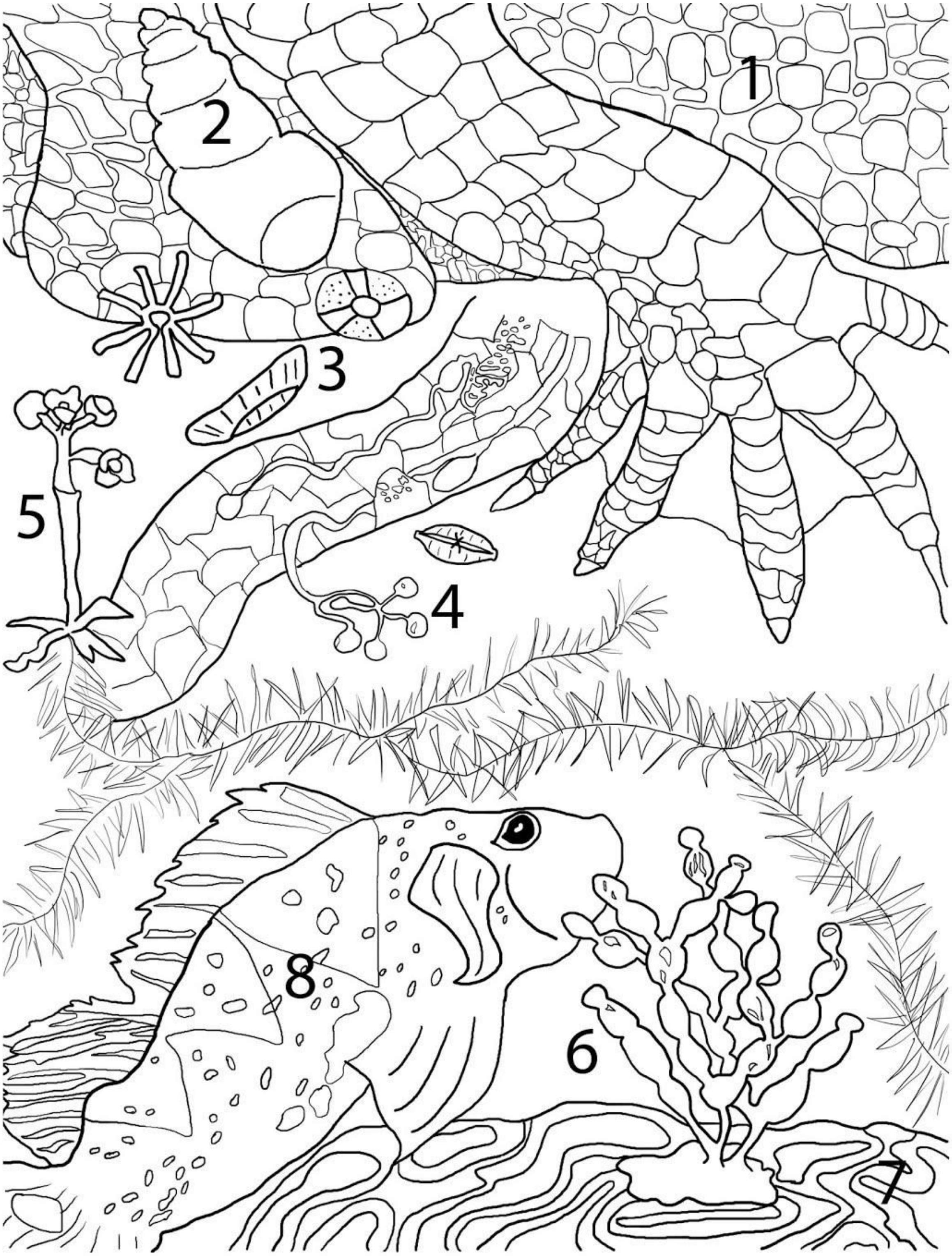

1- American Alligator (*Alligator mississipiensis*)
2- Florida Tree Snail (*Liguus fasciatus*)
3- Diatoms, assorted species
4- Arbuscular mycorrhiza (*Glomus sp.*)
5- Leafy Bladderwort (*Utricularia foliosa*)
6- Red Macroalgae (*Botryocladia sp.*)
7- Brain Coral (*Diploria labrynthiformis*)
8- Peacock Bass (*Cichla ocellaris*)

cover art by Klara Scharnagl, Florida International University

General Index

ISSN 1948-6596

Sixth biennial conference of the International Biogeography Society

an international and interdisciplinary society contributing to the advancement
of all studies of the geography of nature
Miami, Florida, USA
9 – 13 January 2013

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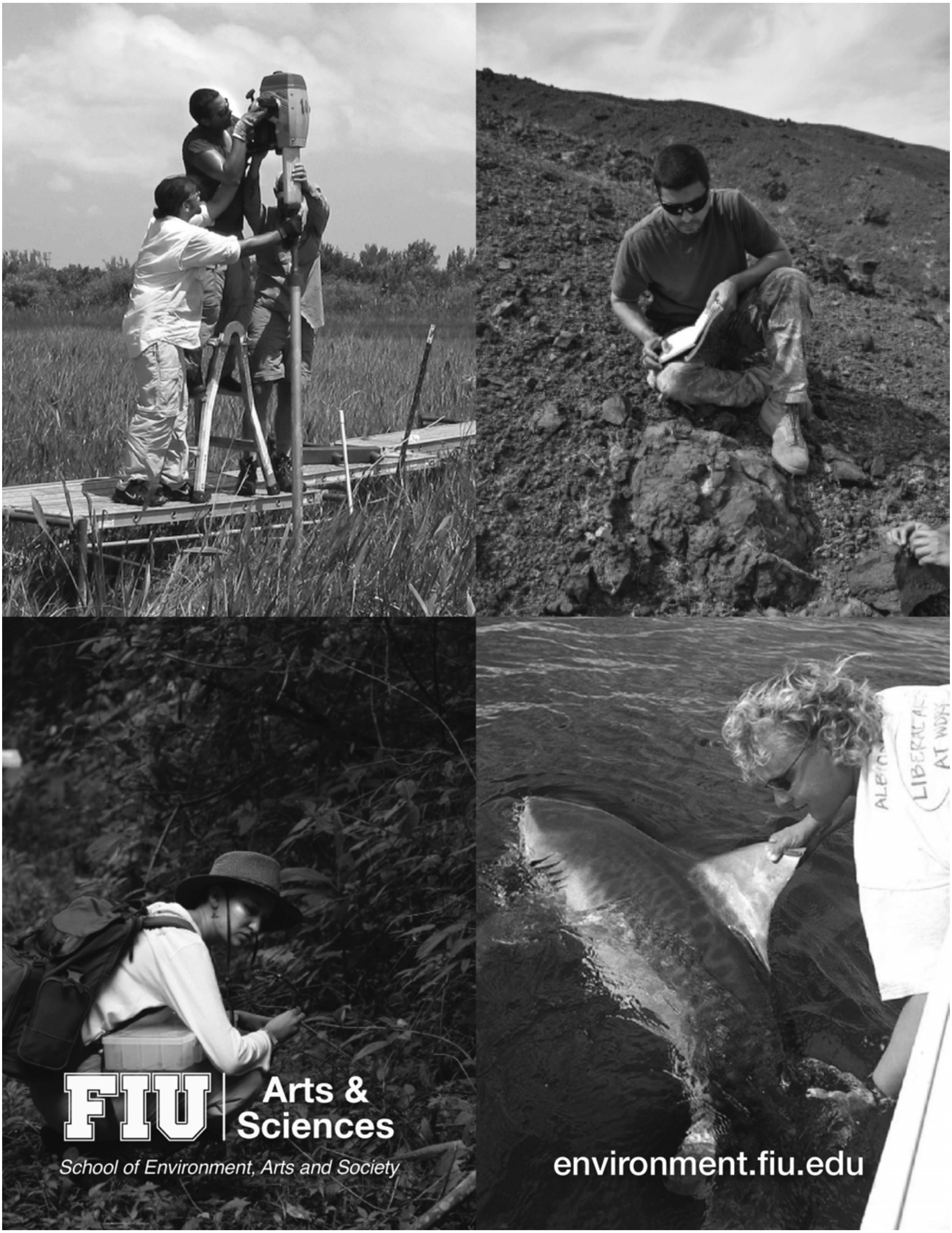
Biogeography, the study of the geography of life, has a long and distinguished history, and one interwoven with that of ecology and evolutionary biology. Traditionally viewed as the study of geographic distributions, modern biogeography now explores a great diversity of patterns in the geographic variation of nature — from physiological, morphological and genetic variation among individuals and populations to differences in the diversity and composition of biotas along geographic 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. Therefore, the International Biogeography Society (IBS) was founded in 2001, and incorporated as a non-profit organization in 2002, with the following mission:

- Foster communication and collaboration between biogeographers in disparate academic fields - scientists who would otherwise have little opportunity for substantive interaction and collaboration.
- Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers.
- Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world’s biota.

More information at the IBS website: http://www.biogeography.org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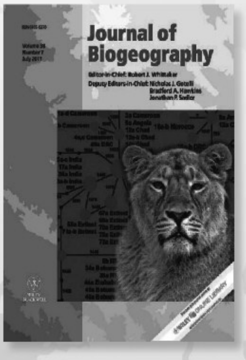
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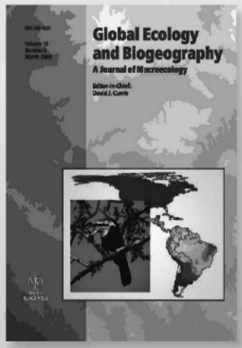
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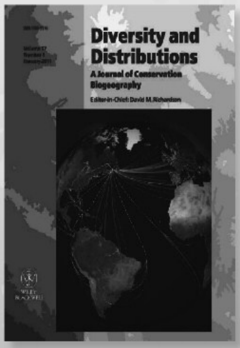
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A Journal of Conservation Biogeography

frontiers of biogeography

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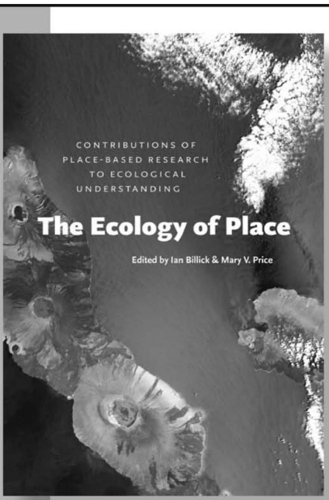
CONTRIBUTIONS OF PLACE-BASED RESEARCH TO ECOLOGICAL UNDERSTANDING
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Edited by Ian Billick & Mary V. Price

Location of Newport Beachside Hotel and Kovens Conference Center

The conference reception will be held on January 11th at the Newport Beachside Hotel

Wolfe Student Center (workshops)

Kovens Conference Center

AC1	Academic One
AC2	Academic Two
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BH1	Bay Vista Housing
CU	Central Utilities
EL	Ecotoxicology Lab
HL	Hubert Library
HM	Hospitality Management
KCC	Roz & Cal Kovens Conference Center
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T2	Trailer 2
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OR	Outdoor Recreation
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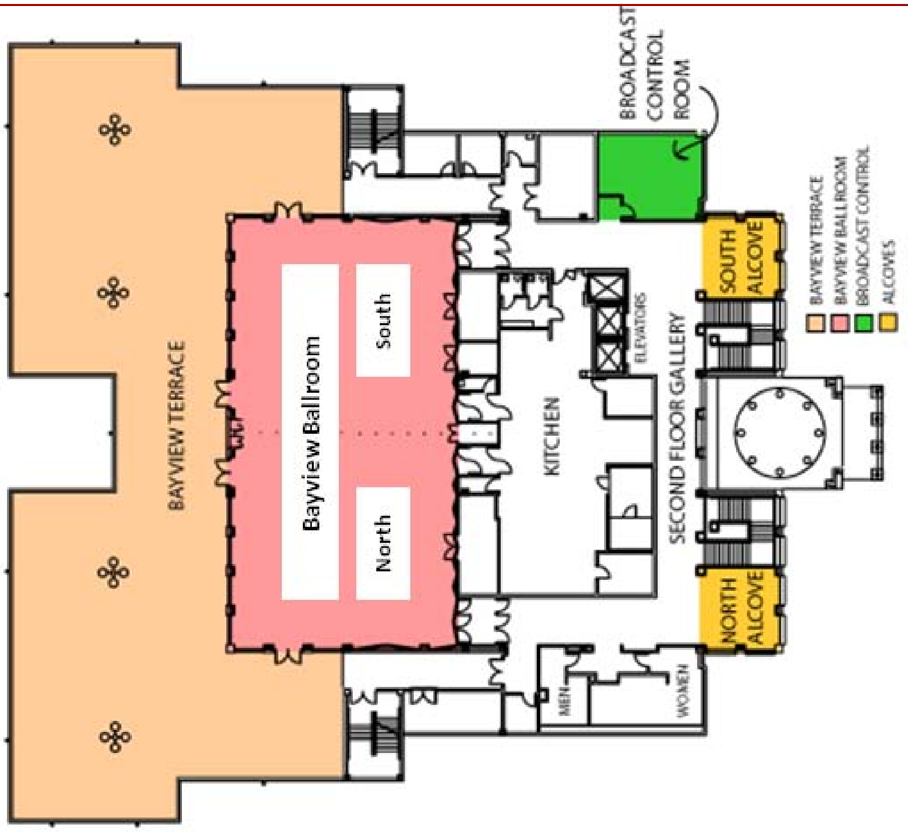
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CONFERENCE PROGRAM

Wednesday, 9 January 2013 Field trips and pre-conference workshops

Workshops: Wolfe University Center (WUC)

8:30 – 12:00	*Biogeography of Stress (WUC Room 157)* Leslie Rissler, University of Alabama Michael Hickerson, City College, CUNY Michael Angilletta, Arizona State University Michael Hood, Amherst College Justin Calabrese, Smithsonian
8:30 – 12:00	*Communicating Biogeography (WUC room 223)* Robert Whittaker, Oxford University
9:00 – 17:00	*Biodiversity Informatics (WUC room 221)* Robert Guralnick, University of Colorado Rosemary Gillespie, University of California, Berkeley David Bloom, University of California, Berkeley Walter Jetz, Yale University
12:00 – 13:00	*Lunch (on own in student center)*
13:00 – 17:00	*Introduction to Bayesian Modeling (WUC room 157)* Brian Beckage, University of Vermont
13:00 – 17:00	*Popular Science Writing (WUC room 223)* Sarah Perrault, University of California, Davis

Field trips: Depart from Newport Beachside Hotel*

8:00 – 16:00	*Everglades Airboat Ride and Swamp Tromp*
8:30 & 13:00	*Historic Oleta River Canoe Trek (~3 hours)*

***NB:** Changes in time or pick up location changes will be sent via email to those registered for field trips

Thursday, 10 January 2013 Plenary Sessions, Bayview Ballroom

08:00 **Opening ceremony**

08:15 *Javier Ortega* Introductory Lecture: "The Biogeography of the Caribbean"

Symposium 1

Island Biogeography: New Syntheses

Conveners: Kostas Triantis and Robert Whittaker

08:40	*Kostas A. Triantis and Robert J. Whittaker*	Introductory Remarks
08:45	*Lawrence R. Heaney, Danilo S. Balete and Eric A. Rickart*	Biodiversity dynamics in oceanic archipelagoes: A call for integration of biological and geological phenomena.
09:10	*François Guilhaumon, Kostas A. Triantis and Robert J. Whittaker*	Species-area relationships.
09:35	*Knud Andreas Jønsson*	Evolution and phylogenetic expansion of core corvoid passerine birds across the Indo-Pacific archipelagos.
10:00	Break	
10:30	*Lenore Fahrig*	Rethinking patch size and isolation effects: the habitat amount hypothesis.
10:55	*Jens M. Olesen, Jakob Hemdorff, Claus Rasmussen and Kristian Trøjelsgaard*	Dynamics of biotic interactions on islands and the role of generalists.
11:20	*Alison G. Boyer, Jonathan Belmaker and Walter Jetz*	Beyond species richness: The island biogeography of functional diversity.

11:35 **Lunch and Poster Session 1** (to 14:00)

Phylogeography (1A–32A)
Geospatial Techniques and Land Cover (33A–39A)
Biodiversity Gradients and Macroecology (42A–83A)
Biogeography of Traits (85A–93A)
Island Biogeography (101A–135A)

Symposium 2

Beyond Bergmann: New Perspectives on the Biogeography of Traits

Conveners: Adam C. Algar and Nathan G. Swenson

14:00	Conveners	Introductory Remarks
14:05	*Jonathan B. Losos and Adam C. Algar*	Traits, function, and biogeography: An evolutionary perspective with anolis lizards.
14:30	*Nathan J. B. Kraft*	Towards a mechanistic understanding of functional diversity patterns within communities.
14:55	*Folmer Bokma*	"Rate of evolution" is not the same as "rate of evolutionary diversification".
15:20	Break	
15:50	*Trevor D. Price*	Morphological and species diversification of Himalayan songbirds.
16:05	*Katrin Böhning-Gaese*	Using traits to illuminate the mechanisms behind macroecological relationships.
16:30	*Nathan G. Swenson*	Mapping the distribution and diversity of woody plant function on continental scales.

16:55 **Poster Session 1 (continued)** (2 hours)

Friday, 11 January 2013 Plenary Sessions, Bayview Ballroom

Symposium 3

The Convergence of Conservation Paleontology and Biogeography

Conveners: Edward Davis and Jenny McGuire

08:00	*Edward Davis and Jenny McGuire*	Introductory Remarks
08:05	*Elizabeth A. Hadly*	Whither biodiversity? Using the past to forecast Earth's future.
08:30	*Jessica L. Blois* et al.	Can space substitute for time in predicting climate-change effects on biodiversity?
08:55	*Susanne A. Fritz* et al.	The integration of palaeontological and neontological research in ecology and evolution.
09:10	Break	
09:40	*Sara Varela*	Species distribution models and palaeontology.
10:05	*A. Michelle Lawing*	Using the past to inform future expectations of species response to climate change.
10:30	*Robert Guralnick, Jessica Metcalf and Stefan Prost*	An integrative data and modeling framework to investigate range-wide demographic and distributional patterns and drivers in the Late Quaternary.

10:55 **Poster Session 2** (until 1:00)

Neotropical Biogeography (1B–18B)
Conservation Biogeography (20B–62B)
Disturbance and Disease Biogeography (65B–70B)
Climate Change Biogeography (71B–118B)
Historical and Paleobiogeography (121B–137B)

12:00 Lunch (and continued poster session)

Symposium 4

Predicting Species and Biodiversity in a Warmer World: Are We Doing a Good Job?

Conveners: Antoine Guisan and Niklaus E. Zimmermann

13:00	*Antoine Guisan*	Introductory Remarks
13:05	*Niklaus E. Zimmermann and Antoine Guisan*	Projecting species ranges at large spatial scales.
13:25	*Yvonne M. Buckley*	Demo-geography: how can spatial population dynamics help us predict species response to global change?
13:50	*James S. Clark*	Inference to prediction in high-dimensional systems: the interactions behind biodiversity response to global change and resource competition.
14:15	Break	
14:45	*Lauren B. Buckley*	How do traits and their variation over space and time affect species' response to environmental change?
15:10	*Richard G. Pearson* et al.	Linking ecological niche models, demographic models, and climate model ensembles to estimate species' extinction risks due to climate change.
15:30	*Jens-Christian Svenning and Brody Sandel*	Vegetation responses to future climate change - pervasive non-equilibrium dynamics?
15:50	*Antoine Guisan*	Concluding remarks

15:55 Break

16:10 Robert Ricklefs introduces The MacArthur & Wilson Award

16:15 **The MacArthur & Wilson Award Keynote Lecture**

Miguel B. Araújo "Revisiting the effects of climate and biotic interactions on species distributions"

17:00 **Poster Session 2 (continued)**

19:00 **Beach Party and Auction at the Newport Beachside Resort** (to 21:00)

Saturday, 12 January 2013 Contributed Papers: 8:30 – 10:00

CP 1: Phylogeography Seminar Room 115

Chair: Katharine Marske

08:30	*Katharine Ann Marske, Carsten Rahbek and David Nogués-Bravo*	Phylogeography: spanning the ecology-evolution continuum.
08:45	*Andres M. Cuervo and Robb T. Brumfield*	Historical assembly of a diverse bird fauna: Diversification in the linear "archipelago" of Neotropical cloud forests.
09:00	*VV Robin, Pooja Gupta and Uma Ramakrishnan*	Comparative phylogeography of the entire understorey bird community in a sky island reveals differential impacts of island structure on population structure.
09:15	*Roberta Damasceno* et al.	The geography of divergence and disparity: how landscapes help understand the decoupling of genetic structure and phenotypic diversity.
09:30	*Rosalía Piñeiro* et al.	Comparative phylogeography of two shade-tolerant and a light-demanding African rainforest tree.
09:45	*Jennafer Hamlin and Michael Arnold*	Testing range expansion and hybridization in two Louisiana irises.

CP 2: Marine Biogeography Seminar Room 122

Chair: Ben G. Holt

08:30	*Hannah Lloyd et al.*	Intercontinental patterns in marine biodiversity.
08:45	*Brezo Martínez* et al.	Assessing projections of species distribution models under global warming using thermal thresholds.
09:00	*Isabelle Rombouts and Gregory Beaugrand*	Global biogeography of body size in marine copepods.
09:15	*Jonathan Belmaker, Valeriano Parravicini and Michel Kulbicki*	A biogeographic perspective on species invasion: Red Sea fish introduction into the Mediterranean.
09:30	*Alex Dornburg* et al.	Asymmetric responses to shifting biodiversity hotspots: evidence from squirrelfishes and soldierfishes (Holocentridae).
09:45	*Ron I. Eytan and Thomas J. Near*	Historical biogeography of recently diverged coral reef fish lineages.

CP 3: Biogeography of the Anthropocene

Bayview Ballroom North

Chair: Alycia Stigall

08:30	*Anthony D. Barnosky*	Defining the Anthropocene: A paleontological and biogeographical perspective.
08:45	*Naia Morueta-Holme* et al.	In the footsteps of Humboldt – elevation shifts of Chimborazo's vegetation over 210 years.
09:00	*Simon J. Goring* et al.	Estimating pre-settlement vegetation in the American Midwest. Exploring climate relationships and links to proxy data for robust data assimilation.
09:15	*Carolina Tovar* et al.	Influence of prehistoric human burning on Central African Rainforest.
09:30	*Kim C. Diver* et al.	Potential effects of sea level rise on island biodiversity in the Coiba National Park archipelago, Republic of Panama.
09:45	*Blaise Petitpierre* et al.	Climatic niche shifts are rare among terrestrial plant invaders.

CP 4: Hot Topics I

Bayview Ballroom South

Chair: Elisa Bonaccorso

08:30	*Matthew C. Fitzpatrick and Stephen R. Keller*	Molecular biogeography: Spatial analysis of adaptive genetic variation using community-level modeling approaches.
08:45	*Diego Nieto-Lugilde* et al.	Large-scale biotic interaction effects - tree cover interacts with shade tolerance to affect distribution patterns of herb and shrub species across the Alps.
09:00	*Regan Early and Dov Sax*	Combining data on species' native and naturalized ranges informs invasion potential abroad and conservation concern at home.
09:15	*Krishnapriya Tamma, Anirudha Marathe and Uma Ramakrishnan*	The relatively recent assembly of mammalian fauna in the Indian subcontinent: support for 'Out of Asia' origins.
09:30	*Zhiheng Wang et al.*	Tropical niche conservatism and large-scale tree diversity patterns in China.
09:45	*David Storch and Antonín Macháč*	Is the metabolic theory of ecology able to predict geographical diversity patterns?

Saturday, 12 January 2013 Contributed Papers: 10:30 – 12:00

CP 5: Island Biogeography Seminar Room 115

Chair: Liliana Dávalos

10:30	*Michael N Dawson* et al.	Island biogeography in the marine realm: of microbes, phytoplankton, and macroinvertebrates.
10:45	*Liliana M. Dávalos and Amy L. Russell*	Long-term disequilibrium and short-term equilibrium dynamics in West Indian biogeography.
11:00	*Søren Faurby and Jens-Christian Svenning*	The island rule re-re-revisited.
11:15	*Kevin C. Burns*	Network super-generalism on islands: evidence from fruit-frugivore webs.
11:30	*Ana M. C. Santos, Marcus V. Cianciaruso and Paulo De Marco Jr.*	Climate, species pool and dispersal effects on the functional diversity of island parasitoid assemblages.
11:45	*Manuel J. Steinbauer* et al.	Elevation-driven ecological isolation.

CP 6: Neotropical Biogeography Seminar Room 122

Chair: Alexandre Antonelli

10:30	*Hanna Tuomisto*	Floristic and species diversity gradients across Amazonia.
10:45	*André Luis Casarin Rochelle, Lucia Garcez Lohmann and Fernando Roberto Martins*	The Age and Area Hypothesis revisited: Do older species have larger geographic ranges?
11:00	*Elisa Bonaccorso* et al.	Biogeography of *Ochthoeca* Chat-tyrants: A window into the history of Andean avifaunas.
11:15	*Roberto Alonso Bosch* et al.	The GAARlandia hypothesis and Caribbean historical biogeography: A perspective based on geological, paleontological and molecular genetic evidence.
11:30	*Héctor T. Arita*	Species-to-genus ratios reveal latitudinal asymmetry in the diversification of New World bats.
11:45	*Brian Tilston Smith* et al.	Barriers, time, and ecology explain the origins of lowland Neotropical bird diversity.

CP 7: Global Change Biogeography I — Bayview Ballroom North

Chair: Regan Early

10:30	*Raimundo Real* et al.	Fuzzy logic as a key conceptual tool for modelling the distribution of interacting species in climate change scenarios.
10:45	*John-Arvid Grytnes* et al.	Is there more than climate warming causing the upward movements of high-alpine plants in Europe?
11:00	*Morgane Barbet-Massin and Walter Jetz*	Global perturbations of functional structure and diversity in bird assemblages under future climate change.
11:15	*Ruth Kelly* et al.	Combined global climate and local landscape models improve precision of invasion risk models in an island context.
11:30	*Saija Piiroinen* et al.	Range expansion to novel environments: adaptation and cross-generational effect of stress in the invasive Colorado potato beetle.
11:45	*Recently canceled—to be determined*	——-

CP 8: Hot Topics II — Bayview Ballroom South

Chair: Jean-Philippe Lessard

10:30	*Juliana Chacón,_Annika Vinnersten and Susanne S. Renner*	When do models that account for changing continental connectivities make a difference? An example from the Colchicaceae.
10:45	*Scott J. Steppan, John J. Schenk and Kevin C. Rowe*	Continental colonizations, adaptive radiations, and global biogeography of muroid rodents: the role of geographic and ecological opportunity.
11:00	*Roland Jansson, Genoveva Rodríguez-Castañeda and Larisa E. Harding*	What can multiple phylogenies say about the latitudinal diversity gradient? A new look at the tropical conservatism, out-of-the-tropics and diversification rate hypotheses.
11:15	*Julie M. Allen and Jill E. Jankowski*	Multiple radiations of Passerines in the Andes? A phylogenetic perspective on species distributions.
11:30	*Andrés Baselga* et al.	The fractal geometry of biotic ranges across multi-hierarchical clade levels reveals a spatiotemporal continuum of biodiversity.
11:45	*Ben G. Holt* et al.	An update of Wallace's zoogeographic regions of the world.

12:00 Lunch

Saturday, 12 January 2013 Contributed Papers: 14:00 – 15:30

CP 9: Historical and Paleo-biogeography Seminar Room 115

Chair: Daniel Gavin

14:00	*Bradford A. Hawkins, Marta Rueda, Thiago F. Rangel, Richard Field and Alexandre F. Diniz-Filho*	Community phylogenetics at the continental scale: cold tolerance, phylogenetic niche conservatism and the structure of North American forests.
14:15	*Alycia L. Stigall*	When and how do species achieve niche stability over long time scales?
14:30	*Jessica A. Oswald*	The abiotic processes driving patterns of bird species endemism in dry forest communities.
14:45	*Christine D. Bacon* et al.	New insights on an older model: the Isthmus of Panama and the Great American Biotic Interchange.
15:00	*Jacquelyn L. Gill* et al.	Novelty in space and time: Linking pattern and process to understand the drivers of late-glacial no-analog plant associations.
15:15	*Hongyan Liu, Yi Yin, Guo Liu and Qian Hao*	Responses of forests to Holocene climate change in semi-arid North China.

CP 10: Conservation Biogeography Seminar Room 122

Chair: And Davidson

14:00	*Ana D. Davidson*	Forecasting extinction risk in global mammals.
14:15	*Fernanda Thiesen Brum* et al.	Clade-specific human land use impact on Neotropical primates.
14:30	*Mindy M. Syfert* et al.	Applying species distribution models to help inform IUCN Red List assessments.
14:45	*Ivis Chan Aguilar* et al.	Predicting the effect of habitat loss on tree species diversity in the Mesoamerican region.
15:00	*M. Allison Stegner* et al.	Species nestedness as an indicator of biodiversity conservation within Colorado Plateau protected lands.
15:15	*W. Daniel Kissling* et al.	Global hotspots of diversity and threat for palms under recent and future land cover change.

CP 11: Global Change Biogeography II

Bayview Ballroom North

Chair: Leslie Rissler

14:00	*Dov F. Sax, Regan Early and Jesse Bellemare*	The fundamental, realized and ‘tolerance’ niche: new considerations in the context of climate change.
14:15	*Christian Hof*	Understanding impacts of interacting global threats on biodiversity: It’s not just climate change!
14:30	*Marta A. Jarzyna, Brian A. Maurer and William F. Porter*	Is the temporal β-diversity of avian communities a result of climate change?
14:45	*Alessandro Catenazzi and Rudolf von May*	Critical thermal maxima of montane tropical frogs: biogeographical and conservation implications.
15:00	*Carl Beierkuhnlein, Jürgen Kreyling and Anke Jentsch*	Modification of organismic responses to climate change by intraspecific diversity.
15:15	*Christy M. McCain and Sarah R. B. King*	Not all mammals are responding similarly to climate change: the importance of body size and activity times.

CP 12: Global-Scale Biogeography

Bayview Ballroom South

Chair: Roland Jansson

14:00	*Eline D. Lorenzen, Rasmus Heller and Hans R. Sigismund*	Comparative phylogeography of sub-Saharan African savannah ungulates.
14:15	*Craig R. McClain* et al.	Increased energy promotes size-based niche availability in marine mollusks.
14:30	*Brian J. Enquist* et al.	The commonness and distribution of rarity: Quantifying the botanical diversity of all plant species in the Americas.
14:45	*Marina S. Ascunce and David L. Reed*	Geographic genetic structure of human lice provides insights into human migrations around the globe and past ecological interactions among hominids.
15:00	*Gabriela Ibarguchi, Vicki Friesen and Pete Convey*	Cold-hardy terrestrial, marine and aquatic global diversity: overlooked lineages out of Antarctica and its ancient mountains.
15:15	*Alexandre Antonelli* et al.	SUPERSMART: Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa.

15:30 Break

Saturday, 12 January 2013 Closure: 16:00 – 18:00

IBS Business Meeting and Wallace Award Lecture

16:00 IBS Business Meeting followed by Student Awards Ceremony

16:55 President introduces The Alfred Russel Wallace Awardee

17:00 **Closing Keynote: The Alfred Russel Wallace Award Lecture**

James H. Brown "Clades, species, cultures: Why are they most diverse in the tropics?"

17:50 Close of Meeting

Sunday, 13 January 2013 Post-Conference Field Trips

Field trips: Depart from Newport Beachside Hotel*

8:00 – 16:00	*Everglades Airboat Ride and Swamp Tromp*
8:00 – 16:00	*Fakahatchee Strand Swamp Tromp*
8:00 – 13:00	*Bird Watching Tour*
8:30 – 15:00	*Sea Kayak and Snorkel Trip*

***NB:** Changes in time or pick up location changes will be sent via email to those registered for field trips

Symposia and oral presentations

Introductory Lecture

Brief Introduction to the Biogeography of the Caribbean Islands

Javier Francisco-Ortega

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The Caribbean Islands are one of the biodiversity hotspots and the largest insular system of the New World. These islands have had a complex geographical history and have been shaped by volcanism, tectonic uplifts and displacements, and eustatic sea-level changes. These historical factors have resulted in unique "islands-within-islands" biogeographical patterns. For example, habitats restricted to the serpentine soils of Cuba do not form a continuous landscape but are on a highly fragmented "archipelago" that is located within a matrix that is dominated by volcanic or limestone substrates. Molecular phylogenies are helping to understand the origin and evolution of species restricted to these unique ecosystems. Every year the region is affected by hurricanes and therefore ecological disturbance is another important component to understand the biogeography of these islands. The Caribbean has been a major arena to discuss vicariance versus dispersal avenues for species diversification. This debate has been fueled by the GAARlandia land-bridge hypothesis. Proponents of this hypothesis indicate that during the Eocene-Oligocene transition the terrestrial ecosystems of northern South America and portions of the Greater Antilles were connected by an area that was above sea level involving the current Aves Ridge.

MacArthur & Wilson Award Lecture

Revisiting the effects of climate and biotic interactions on species distributions

Miguel B. Araújo[1,2,3]

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[2]'Rui Nabeiro' Biodiversity Chair, CIBIO, University of Évora, Portugal
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A central tenet of biogeography is that the broad outlines of species ranges are determined by climate, whereas the effects of biotic interactions are manifested at local scales. If true it would follow that broad-scale assessments of climate change on species distributions would not require information on biotic interactions. I revisit these statements using a mix of empirical and modeling studies. Firstly, using ongoing field and laboratory experiments, I show that climatic fundamental niches of species are both conserved and adaptive. Specifically, tolerance to heat is largely conserved across lineages while tolerance to cold varies markedly between and within species. This pattern challenges the longstanding view that physiological tolerances of species change continuously across climatic gradients, and portrays an alternative view in which climatic fundamental niches would overlap across species more than typically expected. An important consequence of strong conservatism of upper thermal tolerances is that estimated realized niches for cold-adapted species will probably underestimate their upper thermal limits, thereby potentially inflating assessments of risk from climate change. In contrast, species whose climatic preferences are close to their upper thermal limits will unlikely evolve physiological tolerances to increased heat, thereby being predictably affected by warming. Secondly, using mathematical models that predict co-occurrence between pairs of species subject to all possible types of biotic interactions, I show that patterns of co-occurrence arising from positive interactions, such as mutualism and commensalism, are manifested across scales. In contrast, negative interactions, such as competition and amensalism, generate patterns that are discernible mainly at finer resolutions. Scale dependence in consumer-resource interactions depends on the tradeoff between the strength of positive and negative interactions between species. I conclude that evidence is inconsistent with the widely held view that climate alone is sufficient to characterize species distributions at broad scales, but it is consistent with the view that competition is unlikely to structure species ranges beyond local to regional scales.

Keywords: conservation paleontology, paleophylogeography, species distribution model

Alfred Russel Wallace Award Lecture

Clades, species, cultures: Why are they most diverse in the tropics?

James H. Brown

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Known for centuries, the geographic pattern of increasing biodiversity from the poles to the equator is one of the most pervasive features of life on Earth. Biogeographers should have been able to reach consensus on the primary factors that generate and maintain high diversity in the tropics. Over the nearly half-Century of my career, however, many “historical” and “ecological” hypotheses have been proposed and debated, but there is still little consensus. Current discussions center around two main phenomena, phylogenetic niche conservatism and ecological productivity. My current thinking is that while these two factors play important roles in some taxa and habitats, the single most important factor is kinetics: the temperature dependence of ecological and evolutionary rates. The relatively high temperatures in the tropics generate and maintain high diversity because “the Red Queen runs faster when she is hot”. Theoretical motivation comes from considering the effect of temperature on the pace of life and the role of metabolism in ecology and evolution. Empirical support comes from using “natural experiments” to expand the scope of studies beyond terrestrial animals and plants to microbes, marine organisms, and human cultures, and beyond latitude to other environmental variables.

Keywords: kinetics, latitude, niche conservatism, productivity, species diversity

Conveners: Kostas Triantis and Robert Whittaker

Biodiversity dynamics in oceanic archipelagoes: A call for integration of biological and geological phenomena

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Most islands occur in groupings, due to the geological processes that produce them, and most organisms that are endemic to islands occur within oceanic archipelagoes, not on isolated islands. Although oceanic archipelagoes occupy a small proportion of the earth's surface, they support a disproportionately large percentage of its biodiversity. The dynamics of species richness within such archipelagoes is usually strongly influenced by rare colonization from outside the archipelago, relatively frequent colonization within the archipelago, and by a combination of colonization and vicariance within single islands, operating on a time-scale of millions of years. These biological dynamics are, in turn, heavily influenced by the geological dynamics of the archipelagoes, and much evidence indicates that much/most species richness develops through phylogenetic diversification on the same time-scale and within the context of the long-term geological history of the archipelago. If consistent geological processes produce volcanoes that have somewhat regular spacing, and/or erupt for somewhat regular periods of time, they will strongly influence the rate and cumulative amount of speciation of some organisms. Hot-spot archipelagoes and plate-margin archipelagoes have different geological characteristics that may cause the latter to have higher levels of species richness and endemism, and to have more extensive phylogenetic diversification, than the former. We advocate for further development of models of island biogeography that more fully and extensively integrate biological and geological phenomena, as a likely means of increased understanding of biodiversity dynamics in oceanic archipelagoes.

Keywords: diversification, endemism, island biogeography, integrative models, volcanism

Species-area relationships

François Guilhaumon[1,2,3], Kostas A. Triantis[2,4] and Robert J. Witthaker[5,6]

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Species are not uniformly distributed in space, this has been established since the XIXth century with the first scientific expeditions. If we just observe, the variety of living forms that coexist may let think that their spatial distribution is the result of chance alone. But if we look carefully, it turns out that the geographical distribution of biodiversity follows a small number of unifying rules, patterns and processes. Among those, the species-area relationship (SAR), the change in species numbers with increasing area, is certainly the oldest pattern recognized in ecology. From a theoretical point of view, the SAR is central to ecology as its' shape responds to numerous ecological (e.g. structure of assemblages, spatial distribution of individuals) and observational (e.g. sampling design, scale of observation of the pattern) properties. From a more applied perspective, the SAR is an essential tool for conservation biology. It has been used, among others, to compare the richness of regions of varying area in order to guide conservation strategies and to predict species extinctions as a consequence of habitat destruction. In this talk I will discuss recent syntheses and applications of SARs, with a specific focus on the mathematical modelling of the pattern and its' implications. A central point of the talk will be the log-linear power law SAR model, I will prodive evidence for its suitability in theoretical and applied studies. The last part of the talk will cover a so called "hot topic" of the SAR literature : the estimation of species extinctions.

Keywords: island biogeography, modelling, patterns, conservation biology, species extinctions

Evolution and phylogenetic expansion of core corvoid passer- ine birds across the Indo-Pacific archipelagos.

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Earth history such as palaeogeography, ocean circulation and climate, is considered important in driving evolutionary processes thereby shaping distributions of biota. Likewise, species interactions might also be important in shaping distributions because species compete for resources and may even predate one another. The transition zone between Australia and Asia, known as Wallacea, is part of the most tectonically dynamic region of the world – the Indo-Pacific – and the geology and palaeogeography of the region has continuously and rapidly changed throughout the Cenozoic. The Indo-Pacific, which is heavily influenced by past geological changes, represents a continuously changing plethora of opportunities for animals and plants as islands emerge, change and disappear. Islands with different geological histories and in various sizes and distances from continents provide an opportunity to investigate the important factors that have shaped the contemporary distributions of species. I present an overview of the current knowledge of systematics and biogeography of a large (>750 species) and highly diverse passerine bird group, the core Corvoidea, which originated in Australo-Papua and later dispersed to all continents (except Antarctica) and archipelagos on Earth.

Rethinking patch size and isolation effects: the habitat amount hypothesis

Lenore Fahrig

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I challenge (i) the assumption that habitat patches are natural units of measurement for species richness, and (ii) the island analogy, with its assumption of distinct effects of habitat patch size and isolation on species richness. I propose an alternate view of the relationship between habitat distribution and species richness, the ‘habitat amount hypothesis’, and suggest ways of testing it. The habitat amount hypothesis posits that the patch size effect and the patch isolation effect are driven by a single process, the sample area effect. The patch size effect is due to the sample area represented by the area of the patch itself, and the patch isolation effect is due to the sample area represented by the habitat in the landscape surrounding the patch, influencing colonization rate. The hypothesis predicts that species richness in equal-sized sample sites should increase with the amount of habitat in the 'local landscape' (the area within an appropriate distance) of the sample sites. The habitat amount hypothesis replaces two predictor variables, patch size and isolation, with one variable, habitat amount. It implies that species richness should be sampled and analyzed in equal-sized sample sites, not variable-sized habitat patches. If supported it would mean that, for understanding the relationship between habitat distribution and species richness: (i) distinguishing between patch-scale and landscape-scale habitat effects is unnecessary; (ii) distinguishing between patch size effects and patch isolation effects is unnecessary; (iii) considering habitat configuration independent of habitat amount is unnecessary; and (iv) delineating discrete habitat patches is unnecessary.

Keywords: SLOSS, habitat patch concept, matrix quality, species-area relationship, edge effects

Dynamics of biotic interactions on islands and the role of generalists

Jens M. Olesen, Jakob Hemdorff, Claus Rasmussen and Kristian Trøjelsgaard

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Models of island species diversity have a long history, spanning back in time from at least MacArthur & Wilson's "Theory of Island Biogeography" (1967) and up to Whittaker et al.'s "General Dynamic Theory of Island Biogeography" (2008). These theories focus upon species dynamics, but biotic interactions are also basic components of island biodiversity. In this presentation I focus upon (i) variation in the structure and dynamics of pollination interaction networks on islands varying in age, area and isolation; (ii) a detailed explanation of the network roles played by specific functional groups on islands, such as network hubs or generalists, and finally, (iii) a discussion of the possibility of merging island biology, network analysis and food web theory in future empirical studies. As examples I will use a pollination network study from the Canary Islands (K. Trøjelsgaard, unpubl. data), a food web study from the Canary Islands (J. Hemdorff, unpubl. data), a pollination and seed dispersal study from the Galápagos Islands (Heleno et al., 2012. Proc. Roy. Soc.; A. Traveset et al., unpubl. data) and a global dataset about island vertebrates and bees as pollinators (C. Rasmussen & J. M. Olesen, unpubl. data). Trøjelsgaard, for example, finds that richness of biotic interactions has a hump-shaped relationship with island age, thus confirming predictions stated by Whittaker et al. (2008). Rasmussen and Olesen conclude that certain bird, lizard, bat and bee groups are over-represented on islands where they may serve as interaction hubs.

Keywords: bee, biodiversity, biogeography, bird, distributions, network, pollination

Beyond species richness: the island biogeography of functional diversity

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Functional diversity, measured as the combination of ecological attributes in a community, is a critical component of biodiversity, linking species composition to ecosystem function and services. However, little is known about the biogeographic distribution of functional diversity in island and mainland vertebrate communities. We quantified the functional diversity of landbirds found on 45 Pacific islands (including all known extinct species) and compared them to 400 bird communities from continental settings around the world. We examined four complementary metrics of ecological function in each community: functional diversity (FD), functional richness (FRic), functional evenness (FEve), and functional divergence (FDiv). Each metric was calculated in R v. 2.15.0 based on 15 functional variables encompassing body mass, activity period, diet, and foraging location. After controlling for strong correlations with species richness, island isolation was the best predictor of FD and FRic, with higher functional diversity on less isolated islands. Communities on small, low islands showed higher FEve, with nearly equal functional spacing between species. FDiv was related only to annual precipitation with the most divergent communities found on dry islands. Both island and mainland communities had higher FD than expected based on a random draw of species from the global pool, however, dispersal limitation of FD in island communities was apparent. Mainland communities were more overdispersed than island communities. This work demonstrates that accounting for species functional roles allows a more integrative understanding of biodiversity and ecosystem function in a rapidly changing world.

Conveners: Adam C. Algar and Nathan G. Swenson

Traits, function, and biogeography: an evolutionary perspective with *Anolis* lizards

Jonathan B. Losos[1] and Adam C. Algar[2]

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Understanding the evolution of biological diversity requires more than examining patterns of species distribution. Investigating the match between organismal phenotype and the environment has long been a staple of evolutionary biology, but since the 1980's, evolutionary biologists have realized that establishing such correlations is only part of the story; what is needed is not only knowledge of phenotype-environment links, but an understanding of the functional and ecological consequences of phenotypic variation. *Anolis* lizards have been a useful group with which to take the approach because they have diversified greatly and repeatedly throughout the Caribbean and mainland Central and South America, and because they are amenable to investigation of the functional and ecological consequences of trait variation. Here we show that by incorporating such information into studies of species distributions, we can assess the role of interspecific interactions, in combination with climatic niche requirements, in determining species distributions. Ongoing work shows that the phenotype-function relationship is often more complicated than it initially seems, and detailed knowledge of this relationship is needed to understand differences in the outcome of evolutionary diversification in different areas.

Keywords: anole, ecomorphology, lizard, performance

Towards a mechanistic understanding of functional diversity patterns within communities

Nathan J. B. Kraft

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Trait-based ecology has seen substantial growth in recent years, particularly in the study of plant communities. Advances in functional ecology, trait sampling efforts and community inventories have uncovered striking patterns of trait variation within and across communities that offer glimpses into variation in the processes structuring communities. Progress, however, depends critically on a deeper understanding of the ecological mechanisms responsible for various functional diversity patterns that are typically detected in trait-based studies. Here I will discuss some of the key challenges in interpreting functional diversity patterns in an ecological context, and present results from experimental community assembly in annual plant communities designed to disentangle the ecological drivers of diversity patterns. I will focus on biotic interactions, as the linkages between competition, species coexistence, and functional diversity patterns within communities are particularly uncertain at this point in time.

Keywords: community assembly, functional traits, coexistence, annual plants, phylogenetic community structure

"Rate of evolution" is not the same as "rate of evolutionary diversification".

Folmer Bokma

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The phenotypes of species are the result of an evolutionary process, and so are the (small- and large-scale) distributions of species with different phenotypes over space. The factors that govern this evolutionary process, leading to differences in the numbers and phenotypic diversity of species remain poorly understood, however. I will present some novel phylogenetic methods that allow inferences to be made about the relation between rates of phenotypic evolution, speciation, extinction, and evolutionary diversification, that, when applied to different groups of species, challenge traditional ideas about the effects of climate change mediated selection on the process of evolutionary diversification.

Keywords: biodiversity, character evolution, macroevolution, phylogenetics

Morphological and species diversification of Himalayan songbirds

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Latitudinal and altitudinal gradients in species diversity may be close to equilibrium, with some locations having lower species carrying capacity than others, or far from equilibrium, in which case the history of species build-up (time, diversification rate and dispersal) is a critical determinant of species numbers. It is difficult to distinguish these alternatives, but one way is through the use of morphology, with greater diversity implying greater "ecological space". I study morphological diversity within communities of the Himalayan songbirds (oscines; total 443 species) in the context of their history, as inferred from a complete molecular phylogeny. This group radiated over the past 32 Ma into an environment occupied by other avian taxa (nonpasserines and suboscines). Oscines peak in diversity at mid-elevations in the east. On a 1000km^2 scale species numbers in the west are about 40% fewer than in the east, and there is no mid-elevation peak in the west; these differences strongly correlate with climate. Substantial slowdowns in morphological evolution imply some approach to equilibrium. The lack of correlation of morphological diversity and species numbers across altitudes as well as regionally may partly reflect non-equilibrium historical build-ups, but is also likely to result from competition with other groups.

Keywords: altitudinal gradients, Himalayas, latitudinal gradients, molecular phylogeny, morphological diversity

Using traits to illuminate the mechanisms behind macroecological relationships

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Macroecology is often criticized because of studying only statistical relationships without taking into account the mechanisms that drive the respective patterns. Similarly, statistical species distribution models are deemed inferior to models that are process-based and take into account more mechanisms. Here, I include various species' traits in macroecological studies with the aim to gain a more mechanistic understanding of large-scale, macroecological patterns. For example, considering the habitat selection of species allows linking geographic distributions of species not only to climatic factors, but also to habitat. Correspondingly, projections on the simultaneous impact of climate and land-use change on future distributions of birds show that considering not only climate but also habitat leads to vast differences in projections of species richness. The dis-

persal ability of species can be quantified across many species using ecomorphological traits. Consequences of the dispersal ability of species are visible also at the range-scale and lead to differences in the degree to which species are able to fill their potential geographic range. Using multiple species' traits and path analysis demonstrates how a complex interplay of morphological, ecological and life-history traits influences directly and indirectly the global range sizes of birds. Analyses of plant-frugivore networks show that tropical interaction networks are significantly less specialized than temperate networks (contrary to general assumptions). These patterns are connected with systematic differences in the traits of tropical and temperate species. Increasingly better data on the traits of species and advances in statistical analyses offer promising avenues for the further development of the field.

Keywords: species richness, geographic ranges, climate, habitat, dispersal

Mapping the distribution and diversity of woody plant function on continental scales

Nathan G. Swenson

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The geographic distributions of species result from species interactions with the abiotic and biotic environment, which are governed by the functional strategies of species. Plant geographers and plant ecologists have advocated a functional approach to studying the distribution and diversity of plant species for over a century. Implementation of this functional approach has been limited by the availability of large-scale geographic and trait databases and by having to rely upon categorical plant functional types. Overcoming these limitations is critical for our understanding of the distribution of plant biodiversity and how it will respond to future global change. In this talk I will present recent work from my laboratory that has integrated large geo-referenced plant specimen and plot databases with large plant functional trait databases to map continental scale patterns of plant functional diversity and to identify the mechanisms underlying these patterns. Using both types of geographic data I will demonstrate that it is now entirely feasible to estimate the geographic distribution of plant functional diversity on continental scales. I will argue that plant biodiversity informatics is primed to transform our understanding of the distribution and diversity of plant function for the betterment of our basic and applied research agendas.

Keywords: Biogeography, Functional Trait, Phylogeny, Functional Diversity

Whither biodiversity? Using the past to forecast Earth's future

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Extracting species' responses to past perturbations is one of the best ways of unraveling how they will respond in the future. Large environmental events provide opportunities for insights into resilience of animals over time. The transition from the Late Pleistocene glacial period to the Holocene interglacial witnessed the extinction of two-thirds of all the large-bodied mammalian genera and global expansion of modern humans. The smaller mammalian survivors of the extinction persisted but showed range changes, species turnover, and diversity decline. Subsequent but smaller climatic events, such as the Medieval Warm Period, continued to exert impacts on animals by causing adjustments in population abundances, body size and changes in genetic diversity. A retrospective view yields predictions for animals of the future. We will certainly lose species, while a few will thrive. Other species will abandon their former homes and occupy new areas. Surviving animals may change in size, behavior and/or genetic diversity. Although past climates exerted evolutionary pressures on animals, the rate and magnitude of changes in the next century suggest perturbations too fast for present species to keep pace with, resulting in a world very different than it has been for millions of years. Yet in addition to climatic changes, our planet faces the added pressure of 7+ billion people and all the resources we require. Charting the future of biodiversity requires not only history, which details the timing, scale, and magnitude of past global state shifts, but also should be combined with systems theory to forecast our planet's future.

Keywords: biodiversity, genetic diversity, paleobiology, population size

Can space substitute for time in predicting climate-change effects on biodiversity?

Jessica L. Blois[1], John W. Williams[2], Matthew C. Fitzpatrick[3], Stephen T. Jackson[4] and Simon Ferrier[5]

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Space-for-time substitution is widely used in biodiversity modeling to infer past or future trajectories of ecological systems from contemporary spatial patterns. However, the foundational assumption— that drivers of spatial gradients of biodiversity also drive temporal changes in biodiversity— is rarely tested. Here, we empirically test the space-for-time assumption by constructing orthogonal datasets of compositional turnover of plant taxa and climatic dissimilarity through time and across space from late-Quaternary pollen records in eastern North America, then modeling climate-driven compositional turnover. Predictions relying on 'space-for-time' substitution were approximately 85% as accurate as 'time-for-time' predictions. However, space-for-time substitution performed poorly during the Holocene when temporal variation in climate was small relative to spatial variation, requiring subsampling to match the extent of spatial and temporal climatic gradients. There are many good reasons to exercise caution when applying empirically calibrated models to project biodiversity responses to 21st-century climate change, including the prospect of shifting realized niches and emergent species interactions, the challenge of extrapolating models to no-analog climates, and the overarching question of whether ecological systems are computationally irreducible. Nevertheless, this research complements studies that have focused on modeling changes in species richness and adds growing support to the prospect of projecting impacts to biodiversity as a result of climate change.

Keywords: paleobiogeography, fossil-pollen, late Quaternary, compositional turnover

The integration of palaeontological and neontological research in ecology and evolution

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Present-day patterns of biological diversity are strongly influenced by both historical and present-day factors, yet research in ecology and evolution is largely split between palaeontological and neontological studies. We argue that this separation has impeded our understanding of how fundamental processes shape biodiversity. We outline how integration can be achieved by capitalizing on data and methodologies from both disciplines. We present a conceptual framework based on six fundamental processes shaping diversity in space and time: species' interactions with the abiotic environment, biotic interactions, dispersal, trait evolution, speciation, and extinction. We illustrate our framework with four examples of key questions, which have not been addressed with both contemporary and fossil data: 1) which mechanisms generate spatial and temporal variation in diversity; 2) how do traits evolve; 3) how do species-environment and biotic interactions shape community structure; and 4) what factors influence the temporal dynamics of geographical ranges and ecological niches. The proposed integration of palaeontological and neontological data and methods is timely because large data sets and new methods are increasingly available in both fields. We will demonstrate our ideas with a large compilation of mammalian species' distributions across the Northern Hemisphere, from the Neogene to the present. The proposed framework serves as a guideline for combining palaeontological and neontological perspectives to unravel the fundamental processes shaping Life on Earth.

Keywords: diversification, ecological niche, environmental factors, fossils, trait evolution

Species distribution models and palaeontology

Sara Varela

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The increasing availability of open-access biodiversity databases, world-wide high resolution climatic variables, and the accessibility to different modelling techniques, have exponentially incremented the use of Species Distribution Models (SDMs) in the latest years. Out of this boom, new software and ecological models appeared, followed by a heated debate about SDM methodology. As a result, SDM predictions about the current geographic ranges of species have improved significantly. Palaeontologists, however, have largely ignored spatial ecology and therefore the use of spatial models is not as overspread as it is in current ecology or biogeography. When used, SDMs have been mostly applied to predict the spatial dynamics of mammals during the Pleistocene. Consequently, the theoretical framework for using this kind of models with fossil records is still narrow and it needs to be improved. Here, I will focus on two questions that are fundamental for stepping forward in Paleobiogeography and for producing better species distribution predictions for the past: the selection of the calibration datasets from fossil records and the use of the new environmental variables potentially available from General Circulation Models (GCMs).

Using the past to inform future expectations of species response to climate change

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Paleophylogeogrpahic species distribution modeling provides a historical context to how species respond to climate change by integrating rich geological evidence, paleoclimatic data, phylogenetic comparative methods, and species distribution models. I projected paleophylogeographic species distribution models over the last three glacial-interglacial cycles for rattlesnake species within the genus *Crotalus*, which indicates these species were not able to adapt as fast as climate changed. The rate of geographic displacement of suitable habitat for rattlesnakes over the next century will be two to three orders of magnitude faster than it was over the last 320 ky. A deep time perspective of spiny lizard (*Sceloporus*) response to climate change, early Miocene to present, shows that origins, diversification, and subsequent species richness are not coincident in geographic space. Instead, the first lineages to diverge tracked their habitat by moving south as the climate cooled after the Miocene climatic optimum and evolved adaptations such as viviparity to cope with the new environments. Because the climatic and geographic context of North America changed so dramatically during the history of these species, important insights can be gained from their history that will lead to a better understanding their evolution and their fates as future climates return to a Miocene-like state. This work provides a deeper understanding to the biology of climate change by explicitly addressing how species responded to climate change in the past to inform expectations of how they will respond in the future.

Keywords: conservation paleontology, paleophylogeography, species distribution model

An integrative data and modeling framework to investigate range-wide demographic and distributional patterns and drivers in the Late Quaternary

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A grand goal of historical biogeography is to determine the relative importance of species' demographic and distribution change drivers (e.g. abiotic change, biotic interactions, fitness). Isolating these causal variables is challenging, however, given the complex and interdependent interactions between climate and landscape change, species' fitness, and the biotic environment. In the best of all worlds, the multiple types of data necessary to make appropriate inferences, drawn from disparate fields such as paleoclimatology, paleobiology, genetics, and spatial ecology, would be combined into a single modeling framework. However, such exemplar study systems are rare and the methods are not well established. Here we present a strong modeling framework that integrates fossil spatiotemporal data, species distributional modeling, ancient DNA, and paleoclimatological reconstructions in order to strongly test alternate models of demographic and distributional changes. We focus on late Pleistocene and early Holocene subfossil and fossil deposits because they provide an ideal temporal window rich with data for paleontologists, ecologists, climatologists and phylogeneticists to test assumptions and ground-truth synthetic approaches. The late Quaternary (~ last 50,000 years) is not only an ideal time period for synthetic studies due to the richness of available data, but also because it was a period of dramatic climatic and biotic change. We show examples of such approaches utilizing late Quaternary and modern data collected from American Bison, arctic voles, lemmings and shrews.

Keywords: Ancient DNA, Ecological Niche Modeling, Late Quaternary climate change, model testing, paleobiogeography

Conveners: Antoine Guisan and Niklaus E. Zimmermann

Projecting species ranges at large spatial scales

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Many approaches exist to map the current distribution and to project the fate of species and populations at local to regional scales under changing environmental conditions, such as e.g. following climate change. At large spatial scales, species distribution models (SDMs) – a statistical method that calibrates often primarily climatic properties of the realized niche – are used abundantly (and almost exclusively) to achieve this goal. The SDM methodology is well established, and the advantages and limitations are known and explored. Currently, several new approaches are developed that extend the SDM method so that some of these limitations can be mitigated. These novel approaches offer new insights into the likely future of species and biodiversity, and offer better ways to test ecological and biogeographical hypotheses. We summarize the current state of SDM modelling and we provide an overview of current trends and novel approaches around SDMs

Keywords: biodiversity, climate change, ecological niche, global change, species distribution models, SDMs

Demo-geography: how can spatial population dynamics help us predict species response to global change?

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Species exist as collections of populations. Extinction, persistence, invasion and range expansion are conventionally attributed to species but are processes that operate at the level of populations. In order to predict species responses to climate change we need to be able to predict how birth, death and growth rates vary in space and time with the abiotic and biotic variables likely to change with climate. Our knowledge of the geography of demography however is still rudimentary. The most comprehensive synthesis of spatial and temporal variation in population growth rates to date has shown that population growth rates are more variable through time than through space; however, the available spatial distribution of replicate populations within a species is extremely restricted. Decades of work on invasive species has shown that changes in species distribution and population dynamics in response to novel abiotic and biotic conditions are sometimes predictable but are context dependent. Species distribution models predict probability of occupancy from explanatory variables hypothesized to best explain or predict species occupancy. The same explanatory variables may determine individual birth, death and growth fates so there is a potential link between species distribution models and demographic models. However, modelled probabilities of occurrence do not necessarily correlate with population processes. I will present a framework for using species distribution models to inform demography and outline key gaps in knowledge which, if filled, would greatly improve our knowledge of demo-geography. In particular I will draw examples from invasion ecology to outline how analogous systems can be used to fill in some of those gaps.

Keywords: biodiversity, demography, population dynamics, spatial, temporal

Inference to prediction in high-dimensional systems: the interactions behind biodiversity response to global change and resource competition.

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Efforts to understand biodiversity impacts of global change confront the challenge of long-lived and complex organisms responding synthetically to the changing combination of growing season length and drought, while embedded in a local competitive environment. Recognition that such interactions are responsible for the richness of natural ecosystems makes it imperative to address this complexity. High-dimensional inference seeks to accommodate the uncertainty in noisy data, necessarily crude process models, heterogeneity within populations, and the many interactions that control multivariate responses. I discuss emerging tools to directly evaluate biodiversity response to interactions, where the processes operate at the scale of individuals, in this case, tree populations in eastern North America. A hierarchical framework allows for coherent synthesis, meaning that analysis invokes no more assumptions than accepted distribution theory. Posterior inference is transparent and traceable directly back to model, data, and prior understanding. It admits observations and models at different scales, spatio-temporal dependence structure, and process-based relationships. The daunting challenge of thousands of potential models is addressed with techniques similar to those finding recent application in genomics. Application shows how diversity can be affected by interactions involving climate and species competition, and it identifies the life stages sensitive to each combination of temperature, drought, and competition. Inference at the individual scale contrasts with regional scale modeling in a number of ways. Results are consistent with potential savannification in the southeastern US.

How do traits and their variation over space and time affect species' response to environmental change?

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Mechanistic niche models translate an organism's phenotype and environmental conditions into energetics and population dynamics. These models predict more pronounced and individualistic responses to climate change than environmental niche models. I will describe research testing mechanistic models by hindcasting responses to climate change in two Colorado alpine systems over the last 50 years: *Colias* butterflies and grasshoppers. We are repeating historic lab and field studies and examining museum specimens to investigate how butterfly phenotypes determine ecological and evolutionary responses to climate change. For grasshoppers, we are investigating what phenotypic traits have resulted in differential responses among communities. I will additionally discuss research for lizards demonstrating the energetic implications of morphological and physiological variation and how behavior can buffer these implications and modify species' distributions. Our research suggests that considering morphology, physiology, and life history will be essential to accurately forecast responses to climate change.

Keywords: biodiversity, biogeography, distributions, paleobiology, phylogeography

Linking ecological niche models, demographic models, and climate model ensembles to estimate species' extinction risks due to climate change

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Correlative, static ecological niche models (species distribution models) have been widely applied to estimate species' vulnerability to climate change; however, these models suffer limitations including not accounting for demographic processes and life history traits. A major challenge is to develop dynamic tools that are more biologically realistic. We will describe a novel modeling approach that links ecological niche models (ENMs), generic demographic models, and downscaled global climate model ensembles with annual time steps. We develop ENMs using a combination of "dynamic" climatic variables and "static" variables such as land cover and hydrology. The outputs of ENMs are then linked to demographic models, which are standardized stochastic models with upper and lower bounds for each of a set of life history parameters. These demographic models are sampled with a Latin hypercube design and each sampled model is linked with results of an ENM to form stochastic metapopulation models with dynamic spatial structure. Analysis of simulation results reveals interacting effects of life history changes and range shifts on the vulnerability of species to climate change. We will demonstrate this approach using a case study of 40 species of North American reptiles and amphibians, and will describe how the model results can inform conservation prioritization initiatives, including the IUCN's Red List. We will discuss strengths and weaknesses of the approach, and will put forward that these coupled models provide an important step toward better understanding biodiversity responses to climate change.

Keywords: biodiversity, biogeography, conservation, species distribution modeling, metapopulation model

Vegetation responses to future climate change - pervasive non-equilibrium dynamics?

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During the coming decades and centuries anthropogenic climate changes are likely to elicit major vegetation changes. Complex non-equilibrium responses - which occur when vegetation comes out of equilibrium with climate - may potentially play a key role in these dynamics. Understanding these dynamics is crucial for our ability to accurately predict future vegetation and related ecosystem functioning on time scales relevant to conservation planning and society. Unfortunately, many predictive studies have rather focused on equilibrium end-points with only slight consideration of transient trajectories. We review what is to be expected in terms of non-equilibrium vegetation dynamics over the next 50-200 years, integrating information from paleoecology, biogeography and macroecology, landscape ecology, vegetation and plant ecology, invasion biology, global change biology, and ecosystem ecology. We conclude that near-future climate changes are likely to induce strong non-equilibrium in many aspects of vegetation conditions due to migrational lags at local to continental scales, delays in local population build-up, lagged community development due to protracted successional dynamics and extinction debts, time constraints on evolutionary responses, and delays in ecosystem development. Other global change factors such as habitat loss and biological invasions are likely to strengthen near-future non-equilibrium dynamics. The expected prevalence and complexity of vegetation non-equilibrium constitutes a key challenge for forecasting near-future ecological dynamics as well as for future conservation management.

Keywords: climate change; dispersal limitation; range shifts; time lags; transient dynamics

Phylogeography: spanning the ecology-evolution continuum

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Synthesis of ecological and evolutionary concepts and tools has led to improved understanding of how diversification, dispersal, community assembly, long-term coexistence and extinction shape patterns of biological diversity. Phylogeography, with its focus on millennial-scale interactions within and between populations, can help elucidate the processes acting between the evolutionary time-scales on which species arise and the ecological time-scales on which members of an assemblage interact with each other and their environment. Still, it has yet to be widely incorporated in that synthesis. Here, we identify three areas where integration of phylogeography with ecological and evolutionary approaches can provide new insights into key questions. First, phylogeography can help clarify the roles of phylogenetic niche conservatism, niche divergence and environmental stability in the generation of species richness. Second, phylogeography can help isolate the effects of millennial-scale dispersal limitation from other factors driving community assembly and spatial turnover. Third, phylogeography can help identify key processes leading to and resulting from extinction events, including the population dynamics of species range reduction and its effects on the strength and temporal flexibility of interaction networks. We conclude with an outlook on establishing specific data-gathering protocols as part of a collaborative, interdisciplinary research agenda.

Keywords: speciation, coexistence, communities, dispersal, extinction

Historical assembly of a diverse bird fauna: Diversification in the linear "archipelago" of Neotropical cloud forests

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We investigated the tempo and geography of diversification of the avifauna of the Neotropical cloud forests and examined the influence of elevational zonation and the degree of range fragmentation in population differentiation of multiple bird species. First, we elucidated phylogeographic patterns in 40 species using mtDNA sequences for >3,400 specimens collected from across their shared distribution. Overall, we found remarkable phylogeographic structure and although a few geographic themes were shared among a number of species when examined at a large spatial scale (e.g. north-to-south differentiation), there was substantial individuality in the timing of divergence, as well as in the spatial pattern when examined at a finer scale. Second, we tested two complementary hypotheses on the role of elevational range on genetic divergence. To do this, we sequenced over 2,700 specimens collected along elevational transects (1000-3100 m) on both sides of a number of putative Andean barriers and representing over 130 species. Genetic divergence was correlated positively with mean elevation, and negatively with the amplitude of elevational distribution. However, there was high turnover in the species pool diverging at different biogeographic breaks along the Andes as a result of the interplay between elevational zonation, the idiosyncratic dynamic of individual species histories, and the time of lineages evolving in the Andean landscape. The present-day cloud forest Andean avifauna is the result of constant flux of lineages and ongoing diversification, where the effect of physical barriers is modulated by zonation of bird distributions along elevational gradients.

Keywords: Andes, elevational zonation, lineage accumulation, phylogeography

Comparative phylogeography of the entire understorey bird community in a sky island reveals differential impacts of island structure on population structure

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Sky island systems provide an excellent opportunity to study species distributions with the effects of isolation and connectivity, resulting from the interactions between topography and paleo-climate. In such systems, breaks in mountain ranges cause vicariance (isolation), while paleo-climatic changes cause changes in dispersal (connectivity) between populations. We previously studied a montane forest species in the Western Ghats sky islands that revealed deep phylogenetic breaks at ancient geographic divides, and population divergence roughly corresponded to paleo-climatic events. We proposed to examine if this paradigm was consistent for several montane species in this system. We sampled almost the entire understory bird community from the *Shola* habitat (matrix of natural forests and grasslands) from all six major 'islands' in the Western Ghats sky island complex, covering most of the endemic species' range. Four mitochondrial gene sequences (~3kb, 253 samples, 23 species) using standard primers were assembled. Maximum likelihood and bayesian trees revealed a deep divergence for several endemic species across ancient geographic divides. There is evidence for cryptic speciation and possible delimitation of new species. Phylogeographic signatures were stronger and divergences deeper for montane forest and grassland specialist species. Correspondingly, widespread and migratory birds (both long-distance and elevational) showed less phylogeographic structure. Divergence times across species varied and were not consistent with a break caused by a single climatic event. Our study is the first of its kind in this biodiversity hotspot, and provides evidence that species ecology may interact with processes like vicariance and dispersal to drive evolution across such a landscape.

Keywords: Western Ghats, *Shola* habitat, biogeography, endemic birds, ecology

The geography of divergence and disparity: how landscapes help understand the decoupling of genetic structure and phenotypic diversity.

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Landscapes, both their topography and geography, determine the spatial pattern of species persistence through past climate change, habitat fragmentation, and environmental gradients. Opportunities for geographic isolation and divergent selection in heterogeneous landscapes affect the correspondence between genetic divergence and phenotypic disparity within species, possibly leading to speciation. We present a novel approach that integrates species distribution modeling, phylogeographic and phenotypic analyses of populations spanning across geographic and environmental ranges, as well as different levels of paleo-climatic stability and isolation. We apply it to the low vagility, widespread lizard *Leposoma* spp. from the Brazilian Atlantic Forest. We assess two aspects of phenotype, eco-morphology and thermal physiology, which likely responded to past climate change. There is strong phylogeographic structure at local to regional scales, even without overt evidence of geographic isolation. Concordance between high genetic divergence and phenotypic disparity in macroclimate, microhabitat use, and morphology, but not thermal physiology, is found in populations at the southern periphery of the distribution and in geographic isolates. Populations inhabiting a large and climatically stable area - the core of *Leposoma* distribution - show discordance: high genetic divergence and low phenotypic disparity. We hypothesize that microclimatic niche tracking and divergent selection played an important role in *Leposoma* persistence during past climatic oscillations, with changes in morphology and microhabitat use resulting from either divergent adaptation or adaptive plasticity. These results demonstrate value of integrated genetic and phenotypic analyses in the context of current and past climatic gradients in multiple scales across landscapes.

Keywords: phylogeography, Brazilian Atlantic Forest, phenotypic disparity, Leposoma, eco-morphology

Comparative phylogeography of two shade-tolerant and a light-demanding African rainforest trees

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The evolutionary history of African rainforests has been largely conditioned by the last Pleistocene glaciations. Pollen records have clearly shown that the dry environmental conditions between 20000 and 14000 BP (before present) in Central Africa lead to the contraction of rainforests in favor of savannas or mountain forests. Rainforest species would have thus survived in local refugia and subsequently expanded in the postglacial period to reach their current distributional ranges. Based on the rate of endemism, the location of these refuge areas in Africa has been proposed. However, the theory of rainforest refugia needs further evidence to be validated. In this study we use nuclear microsatellites and chloroplast markers to characterise the spatial genetic variation of three rainforest trees: *Lophira alata* (Ochanceae), *Greenwayodendron suaveolens* subsp. *suaveolen*s (Annonaceae), and *Scorodophloeus zenkeri* (Caesalpinioideae, Fabaceae). The last two species are shade-tolerant, widely-distributed in Central Africa, and characteristic of mature rainforests, which makes them more suitable to trace the impact of past climatic changes on these habitats than commercially exploited trees, usually light-demanding, for which most genetic resources have been developed. Our results reveal a significant geographical structure of the genetic variation in Central Africa. Testing for genetic signature of demographic expansion or contraction and comparisons of the spatial genetic variation across species with GIS tools may significantly contribute to understand the natural history of African rainforests from West and Central Africa.

Keywords: African biogeography, demographic expansion tests, nuclear microsatellites, Quaternary glaciations, rainforest refugia

Testing Range Expansion and Hybridization in Two Louisiana Irises

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Regions such as the Southeast US provide an ideal backdrop to test hypotheses regarding contemporary and historical species distributions. One biogeographic barrier that has influenced the distribution of species is the Mississippi River, where populations of species may be isolated on opposite sides of this waterway. However, in areas where boundaries have periodically disappeared, isolated populations may have become admixed. In this study, we focus on the Mississippi River discontinuity with regards to the biogeographic and genetic distinction of two closely related hybridizing species: *Iris fulva* and *Iris brevicaulis*, which are part of the Louisiana Iris species complex. While much work has been published on their association in southern Louisiana, the extent of hybridization and genetic structure of these two species moving northward along the Mississippi River has not been documented. Assessing the phylogeography of each species will allow a description of species-level genetic structure along the Mississippi River; also by using two closely related species, we will be able to address whether both species show similar distribution patterns northward from their southern terminus in the state of Louisiana. In addition, we will test for the extent of hybridization and the role hybridization may have played in these species distributions beyond the well-documented hybrid zone. The incorporation of novel alleles via hybridization or introgression may be expected to allow populations to persist in or extend to other parts of their ranges.

Intercontinental patterns in marine biodiversity for IBS 2013 meeting in Miami, Florida, USA

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Habitat provision and latitudinal variation are recognised as important drivers of biodiversity patterns. However the interaction between the two and their hierarchical contribution to high diversity is not well understood. As the positive relationship between habitats and associated communities is spatially heterogeneous, to quantify the value of specific habitat-forming species we must consider (1) how the structure (traits) of habitats vary throughout their distribution and (2) how spatially distributed abiotic conditions contribute to diversity patterns. This study quantified variation in the morphology of a suite of temperate rocky-intertidal biogenic habitats (macro-algae) and the diversity of their associated invertebrate communities, in 18 locations along 2 coastlines, sharing similar latitudes in Australia and New Zealand. The traits of habitat-forming species were related to variation in abiotic conditions (e.g. wave exposure) to determine how habitat structure and environmental conditions influence diversity and how those relationships vary across latitude. Habitat traits (length, biomass, patch size) and spatially distributed abiotic variables were related to invertebrate diversity using spatial regression analysis. The results highlight the need for spatially explicit studies to identify important drivers of community change. As understanding complex issues such as how marine ecosystems will be impacted by climate change requires an understanding of how species will respond to changing environmental conditions throughout their distribution. To ascertain the conservation value of individual habitats we must also understand how biodiversity varies in response to changes in habitat structure with respect to latitudinal and localised environmental gradients.

Keywords: habitat-forming species, intertidal, latitude, spatial-scale, trait

Assessing projections of species distribution models under global warming using thermal thresholds

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Species distribution models (SDMs) can be a useful tool in predicting species range retractions in response to global warming. However, they do not explore the mechanistic causes of species shifts, making difficult to predict outside the environmental gradient were the model was trained. In this study, we assessed the projections of SDMs using thermal thresholds suggested by mortality and growth experiments as proxies of the fundamental niches of two target species: intertidal seaweed *Himanthalia elongata* (predicted to become extinct in response to coastal warming in southern Europe) and *Bifurcaria bifurcata* (predicted to spread). Results suggest that *H. elongata* is highly sensitive to the ocean temperatures that the species currently encounters at its distribution limit in N Spain, whereas *B. bifurcata*’s lethal threshold is far from current and projected temperatures. We used these thresholds to produce geographic projections of these species’ distributions to assess projections obtained using SDMs. The predictions obtained by both methods were robust in geographic areas where the species shows high or low dominance. Physiological thresholds represented unfavorable climatic conditions for the species and thus may explain the retraction of distributional boundaries in response to environmental extremes. In areas of intermediate prevalence of the species, both approaches were limited by a lack of information on biotic interactions. We present a simple example of how integrating correlative and mechanistic approaches provides a better understanding of species distribution and more robust predictions of species distribution under climate change.

Keywords: biogeography, species distribution models, climate change, ecophysiology, ocean warming, macroalgae, mechanistic modelling

Global biogeography of body size in marine copepods

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Marine copepods are of prime importance in the functioning of marine ecosystems because of their direct link between phytoplankton and fish and their role in biogeochemical cycling. Changes in their body size can influence the energy transfer in the pelagic food web and the amount of material exported to the deep ocean. For example, larger animals produce larger faecal pellets and thereby increase the rate of export in organic matter in the water column. Since many copepod species have a cosmopolitan distribution and cover a wide range of sizes, they are particularly suitable to study the geographic variations in body size and their controls at a circum-global scale. Plankton body size is likely to be related to one or multiple independent environmental parameters. Several physical and chemical properties of seawater such as temperature, nutrient and oxygen availability have already been linked to variations in plankton size locally but, to date, an ocean-wide analysis has not been carried out. Using a comprehensive database of copepod body sizes, we first tested the latitude-size variation at the intra-specific level, also known as Bergmann's rule. Secondly, the relationships between the geographical variations in body size and environmental factors were assessed at the same spatial extent. Understanding the controls on copepod body size could hopefully yield a key insight on the causal mechanisms for its geographic variation so that the response to external forcing can be anticipated in the context of climate change.

Keywords: latitude, traits, Bergmann's rule, temperature, primary productivity

A biogeographic perspective on species invasion: Red Sea fish introduction into the Mediterranean

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Alien species are considered one of the prime threats to biodiversity, driving major changes in ecosystem structure and function. Identifying the traits associated with alien introduction has been largely restricted to comparing indigenous and alien species or comparing alien species that differ in abundance or impact. However, a more complete understanding may emerge when the entire pool of potential alien species is used as a control, information that is rarely available. In the eastern Mediterranean the marine environment is undergoing an unparalleled species composition transformation, as a flood of aliens have entered from the Red Sea following the opening of the Suez Canal in 1869. We compile data on species traits, geographical distribution and environmental affinity of the entire pool of reef associated fish species in the Red Sea and Indo-Pacific. We use this extensive data to identify the prime characteristics separating Red Sea species that have become alien in the Mediterranean from those that have not. Alien species occupy higher maximum temperatures in their native ranges. Thus, contrary to previous predictions, increased water temperatures may actually decrease invasion rate as less species survive the increasingly hot summers in this region. We further find that ecological trait diversity of alien species is substantially higher than expected from random sampling from the pool of Red Sea species pointing at additional processes, such as competition, promoting alien trait diversity. We use these results to provide a first quantitative ranking of the potential of Red Sea species to become established in the Mediterranean.

Keywords: biodiversity, biogeography, alien species, Lessepsian species, traits

Asymmetric responses to shifting biodiversity hotspots: evidence from squirrelfishes and soldierfishes (Holocentridae)

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One of the most striking contemporary biodiversity patterns is the uneven distribution of marine species-richness, with species diversity in the Indo-Australian Archipelago (IAA) vastly exceeding any other marine area. However, the IAA formed fairly recently in geologic time, and marine biodiversity hotspots have shifted across nearly half the globe in the last 50 million years. Understanding how the diversification dynamics of marine lineages have been influenced by the rise and fall of biodiversity hotspots represents a necessary historic perspective on the formation and maintenance of global marine diversity. However, evolutionary inferences are often challenged by a lack of fossil evidence that would facilitate insights into historic patterns of abundance and diversity. Squirrelfishes and Soldierfishes (Holocentridae) provide an exception to this. Holocentrids are among the most conspicuous fishes in the nocturnal reef fishes and reach their greatest diversity in the IAA. Holocentrids also represent some of the most numerous fossil taxa in deposits from the Eocene West Tethyan biodiversity hotspot. We sample DNA sequence data from most genera and over fifty percent of extant holocentrid species for multiple single copy nuclear genes and one mitochondrial gene and integrate this data with a morphological character matrix that includes stem holocentrine and myripristine lineages from the West Tethys and Cretaceous stem holocentroid fossils. We utilize a Bayesian time-calibrated phylogenetic framework and estimate a similar origin of extant holocentrids to predictions based on the fossil record. Our study further demonstrates how inferences of biogeographic history can potentially be misled in the absence of fossil data.

Keywords: Phylogeny, reef fishes, fossil, molecular, phylogeography

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Historical biogeography of recently diverged coral reef fish lineages

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It is difficult to employ phylogenetic models of historical biogeography for nascent species due to population genetic processes such as incomplete lineage sorting, which result in paraphyletic or polyphyletic phylogenetic trees. Species tree methods accommodate incomplete lineage sorting; however, it is difficult to assign individual gene sequences to a putative species for recently diverged and morphologically cryptic taxa. One approach to overcoming the problem of incomplete lineage sorting is to delimit species using multi-locus DNA sequence data prior to phylogenetic analyses. In this study we combine species delimitation methods with species tree inference and likelihood based analyses of the historical biogeography of a group of recently diverged lineages of the Caribbean reef fish species *Acanthemblemaria spinosa.* By combining these methods, we are able to determine the timing and direction of colonization of *A. spinosa* lineages throughout the Caribbean. Specifically, we ask if lineages have dispersed in the direction of prevailing surface currents and if colonization has been stepwise throughout the Caribbean. The methods we employ here may provide a useful framework for inferring the historical biogeography of recently diverged lineages.

Keywords: Caribbean, reef fish, species tree, species delimitation, historical biogeography

Defining the Anthropocene: A paleontological and biogeographical perspective

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Paleontology formed the basis of definition for most of the geological eras, periods, epochs, and ages that are commonly recognized. By the same token, the Anthropocene can be defined by diverse paleontological criteria, including the occurrence and first and last appearances of various organic remains and unique biogeographic assemblages, in accordance with commonly accepted biostratigraphic and biogeographic practice. Here I focus on the utility of defining the Anthropocene by its distinctive fossils (or potential fossils of the future), with special reference to biogeographic issues. Among the useful criteria are changes in the abundance of certain taxa (especially humans and domestic animals), geologically sudden (and human-mediated) spread of taxa that result in homogenization of the global biota, and extinctions. Also discussed are comparisons of how the magnitude of paleontological changes that can define the Anthropocene compare to those that characterize earlier stratigraphic units, and the consequent implications for formally recognizing the Anthropocene as a new epoch in the geological time scale.

In the footsteps of Humboldt – elevation shifts of Chimborazo's vegetation over 210 years

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Climate change is often associated with shifts in species' spatial distribution along latitudinal and elevation gradients. Documenting the response of biotic communities to recent global warming requires historical data that can be very limited in the time frame covered. The legacy and works of Alexander von Humboldt include not only the foundation of the entire field of biogeography, but also what is likely the oldest dataset of observed elevation distributions of plants, along the slopes of Mt. Chimborazo and the Andes. These data provide the unique opportunity to study vegetation changes since 1802. We revisited the southeastern slope of Mt. Chimborazo in June 2012, exactly 210 years after Humboldt's own exploration of the area. We sampled plant community composition along transects for every 100 meters of elevation between 3,800 and 5,200 m. Most resampled plant species show dramatic upward shifts in their maximum elevation limit, providing further evidence of the strong impacts of global climate change on biodiversity since the time of the industrial revolution.

Keywords: elevation distributions, biodiversity, biogeography, climate change, range shifts

Estimating pre-settlement vegetation in the American Midwest. Exploring climate relationships and links to proxy data for robust data assimilation

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The development of robust estimates of vegetation composition, stem density, basal area and biomass prior to major European land-use conversion presents an opportunity to link paleoecological proxy data to modern vegetation distributions and future projections of climate and vegetation using either species distribution models, or more complex dynamic vegetation models. We present results from the first phase of the PalEON project that have produced estimates of presettlement vegetation, along with preliminary uncertainties for these estimates. We show that forest classification of the pre-settlement forest differs strongly from prior model-based estimates (BIOME3 classification for example), and shows much greater homogeneity. The use of various structural measures of forest composition (stem density, basal area) also affects the classification of forest types. The influence of land-use conversion has strongly affected the distributions of a number of species in the Upper Midwest. Prairie and Savanna taxa are particularly affected by conversion to agriculture. We show how land use conversion can affect the apparent vegetation-climate relationships for some of these species across the upper Midwest.

Keywords: biodiversity, biogeography, distributions, paleoecology, land-use, species distribution models, dynamic vegetation models

Influence of prehistoric human burning on Central African rainforest

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Four major forest types are currently present in the Central African rainforest; mixed forest, Marantaceae forest, mono-dominant forest and swamp forest. These forest types span vast areas and demonstrate highly significant differences in diversity and productivity; yet factors responsible for their formation are poorly understood. One hypothesis is that they are as a consequence of different intensities of past human activity, in particular burning. Here we present results from fossil charcoal contained in 12 sediment cores spanning the last 2500 years and covering a spatial area of 900 km^2. First, the lack of spatial relationship between fire events of the different cores (discontinuous and asynchronic) and the low values of charcoal suggest that fires at the end of the Holocene are predominantly human-made for this region. Second, these records demonstrate clear evidence that prehistoric burning influenced current forest type with Marantaceae forest undergoing more frequent and large burning events over the past 1000 years. Whilst the large spatial scale of prehistoric activities on the South America rainforest is now widely acknowledged, these results indicate the significant impact that early human populations also had on the Central African Rainforest; a legacy that is still seen today.

Keywords: fossil charcoal, Holocene, Congo, African forest types

Potential effects of sea level rise on island biodiversity in the Coiba National Park archipelago, Republic of Panama

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Coastal areas and islands are at an increased risk of losing habitats with rising sea levels, potentially affecting species that rely on those locally threatened habitats. We utilized field work, geographic information systems (GIS), and island biogeography theory to evaluate potential consequences of sea level rise on island area and habitat diversity for eighteen islands within the Coiba National Park and its Special Zone of Marine Protection UNESCO World Heritage Site in the Pacific Ocean off the coast of the Republic of Panama. Using GIS techniques and satellite imagery, we calculated loss in island area and habitat diversity at particular time series based on data from sea-level prediction scenarios incorporated with digital elevation models (DEMs). The islands will likely lose 2 to 100% land area with a sea level rise of 1 m, and 11 to 100% with a sea level rise of 10 m. Due to habitat compression, we predict that the archipelago will lose "sangrillal" habitat completely with a sea level rise of 10 m. Beach, mangrove, and "alcornocal" habitats will be partially lost. Predicted decreases in island area and number of habitats are discussed in reference to the Choros model for predicting plant species richness on islands. A 1 m sea level rise in Coiba over the next century has the potential to cause extirpation of approximately 9% of plant species per island due to area and habitat losses. Caveats of the results are discussed in terms of endemic species, ecological adaptation, and shoreline configuration.

Keywords: biogeography, habitat diversity, islands, Panama, sea-level rise

Climatic niche shifts are rare among terrestrial plant invaders

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Biodiversity is put at threat by global change. Ecological niche modeling (ENM) is widely used to predict or to assess the effects of global change through predictions of potential species distribution under different climate or invasive species range. However, ENM relies on the pivotal assumption of niche conservatism (i.e. species ecological niche is conserved through space or time). This assumption has been challenged recently by evidence of niche shifts between native and invaded range of some invasive species. Here, we report the first large-scale test of niche conservatism for 50 terrestrial plant invaders between Eurasia, North America, and Australia. We show that when analog climates are compared between regions, fewer than 15% of species have more than 10% of their invaded distribution outside their native climatic niche. These findings reveal that substantial niche shifts are rare in terrestrial plant invaders, providing support for an appropriate use of ecological niche models for the prediction of both biological invasions and responses to climate change.

Keywords: niche conservatism, global change, biological invasions, ecological niche model

Molecular biogeography: Spatial analysis of adaptive genetic variation using community-level modeling approaches

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An emerging frontier in biogeography is the application of spatial modeling techniques to explore the environmental causes of intraspecific variation and to visualize this diversity at landscape scales. At the same time, advances in molecular ecology and genomics are providing unparalleled, genome-wide insight into the molecular diversity present within species that can be used to identify gene-environment relationships and the molecular basis of local adaptation. While the merging of spatial biogeographical modeling and molecular ecology is already underway, key challenges remain. Chief among these are (1) accommodating non-linearity in the exploration of gene-environment relationships, (2) handling large genomic datasets that include numerous rare, low frequency alleles, and (3) generating maps of how adaptive genomic diversity is predicted to vary across the landscape. These problems are similar to those faced by biogeographers when modeling the environmental relationships driving compositional turnover in diverse assemblages of species, some of which are rarely recorded. In this study, we explore how these problems can be addressed using community-level modeling techniques, such as Generalized Dissimilarity Modeling and Gradient Forests, that simultaneously model all species in an assemblage (or SNPs in a genome), and which we argue could be powerfully applied to the analysis of intraspecific genomic variation. Using balsam poplar (*Populus balsamifera*) and Atlantic salmon (*Salmo salar*) as case studies, we demonstrate that these new community-level modeling techniques offer unique strengths for exploring and mapping adaptive genomic variation that are complimentary to or improve upon the currently available techniques in landscape genetics.

Keywords: traits, intraspecific variation, genomics, evolution, landscape genetics

Large-scale biotic interaction effects - tree cover interacts with shade tolerance to affect distribution patterns of herb and shrub species across the Alps

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While often ignored in large-scale studies of species distributions, there is an increasing interest in the role played by biotic interactions. The effect of competition for light in vegetation dynamics and succession has long been recognized. However, its role for large-scale plant species distributions has scarcely been investigated. Here, we used species distribution modeling (SDM) to assess the effect of tree cover on the elevational range limits of 1,378 herb and shrub species across the Alps, based on 18,798 vegetation plots. We hypothesize that tree cover will have a negative effect on the occurrence on light-demanding species via size-asymmetric competition for light, but a facilitative effect on shade-tolerant species. In order to compare the relative importance of tree cover, four models with different combinations of variables (climate, soil and tree cover) were run for each species. Then, we simulated a removal experiment by comparing the elevational distribution of each species under high and low tree cover. Tree cover improved model performances and species' response curves to a tree cover gradient varied depending on their shade tolerance, supporting the hypothesized antagonistic role. Results indicated that high tree cover causes range contraction, especially at the upper limit, for light-demanding species, whereas it causes shade-tolerant species to extend their range upwards and downwards. Tree cover thus drives plant-plant interactions to shape plant species distribution patterns, with varying effects according to shade tolerances. These findings have strong implications for the biotic responses of herbs and shrubs to future climate change with expected range-shift debts.

Keywords: facilitation, light competition, size-asymmetric competition, species distribution models, traits

Combining data on species' native and naturalized ranges informs invasion potential abroad and conservation concern at home

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Species distribution models (SDMs) of climate niches are heavily relied-upon tools to predict species distributions under climate change or during invasions. This fundamentally requires that observed distributions reflect species' climatic tolerances, that climate niches are conserved in different time periods or regions, and that SDMs can be accurately transferred across space or time. Recent research suggests that these requirements are supported for widespread or weedy species. However, the species of most concern under climate change and many problematic invasives are rare, poor competitors in their current native distribution. Therefore, we investigated niche conservatism and SDM transferability between species native and introduced ranges, and the consequences for predicting both invasions and native distributions under climate change. We studied 52 European native plant species naturalized in the USA, which range from rare to widespread and specialised to generalised in Europe. Native distributions rarely reflect climatic tolerances, and native SDMs greatly underpredict US distributions. In Europe, species are absent from large areas that are within their dispersal capabilities and within the climate conditions occupied in the USA. Niche conservatism and SDM transferability vary widely between species, but some trends lend hope to the improved application of SDMs. First, native climatic niche breadth is positively correlated with niche conservatism and SDM transferability. Second most species in the US occur within one niche diameter of their native niche breadth. In conclusion, SDMs appear unsuitable for a broad range of species without additional validation. Confidence is higher for species with very large native ranges and niche-breadths.

Keywords: Species distribution model, climate change, niche conservatism, niche shift, climate change

The relatively recent assembly of mammalian fauna in the Indian subcontinent: support for 'Out of Asia' origins

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Patterns of species richness at regional scales vary considerably. Geologic history might be particularly important for dynamic regions like the Indian subcontinent, which became a part of the Asian landmass relatively recently. Given the timing of the Indian subcontinent's collision with Asia, it has been suggested that mammalian assemblages in the subcontinent have arisen from colonization events 'Out of Asia'. We investigated the importance of environment, area and history in driving patterns of species richness for relatively less mobile mammalian species (rodents). We calculated rodent species richness in 2°x2° grid cells based on all available presence data. Area explained 29% of the observed richness pattern. Environmental and habitat variables had low explanatory power. However, model fits were better when the species were divided into three groups based on biogeographic history ('eastern', palearctic' and 'western'). Further, species richness declined with distance from eastern-most, western-most and northern-most cells, supporting an 'Out of Asia' origin for rodents in the Indian subcontinent. Other mammalian groups (bats, herbivores, carnivores and primates) reveal similar results. Most importantly, phylogenies that include populations of species from outside and inside the Indian subcontinent also support an 'Out of Asia' hypothesis, suggesting that most mammals have colonized India relatively recently. Our results pose interesting questions regarding endemic species. We speculate how species from different biogeographic realms may respond to future climatic change in the Indian subcontinent.

Keywords: small mammals, dispersal, deconstruction analyses, colonization, sink

Tropical niche conservatism and large-scale tree diversity patterns in China

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The environment and evolutionary mechanisms underlying large-scale patterns of species richness is a fundamental yet controversial question of biology since the time of Wallace and Darwin, and has been the cornerstone of macroecology. With a rich flora, broad environmental/geological gradients, China provides a "natural lab" for testing the mechanisms of species richness patterns. Here, we compiled the distribution maps of 11,405 woody species in China, and, in combination with the current phylogeny of angiosperms, we 1) demonstrated the large-scale patterns of woody species richness cross China, 2) evaluated the effects of contemporary climate, particularly environmental energy, water–energy dynamics and winter coldness, and 3) explored how long-term evolution influences current species richness patterns by detecting the phylogenetic structures in local floras. We found that species richness decreases from southern China to northern China and the Tibetan Plateau. Species become younger and more derived towards the north. Winter temperature is the best predictor of species richness and species age. These results support the tropical niche conservatism hypothesis (also known as freezing tolerance hypothesis), and suggest that the patterns of woody species richness are mainly resulted from the increasing intensity of winter coldness from the equator to the poles.

Keywords: biogeographical affinities, China, freezing tolerance hypothesis, niche conservatism hypothesis, phylogeny, woody plants, water-energy dynamics

Is the metabolic theory of ecology able to predict geographical diversity patterns?

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Dozens of hypotheses try to explain species richness variation on earth surface, but they rarely make any quantitative predictions. One exception is the metabolic theory of ecology (MTE) which derives its predictions from temperature-dependence of individual metabolic rate and consequently all biological rates including the rate of diversification. Quantitative MTE predictions concerning diversity patterns are nevertheless extremely difficult to test, and although the crucial role of temperature for diversity patterns has been demonstrated, more specific tests of the MTE have been so far contentious. However, MTE provides one prediction which can be tested quite readily, namely that diversification (and consequently diversity) increases with environmental temperature only in ectotherms. We have performed a phylogenetic analysis based on well-resolved phylogenies and geographic distribution data, which reveals that diversification rates indeed increased with temperature across ectotherm clades, but not in endotherms, in accord with the prediction of MTE. However, these patterns of diversification are not followed by geographic patterns in diversity of these clades. The MTE may be thus an appropriate theory of diversification rates, but diversity patterns appear largely decoupled from diversification patterns. In contrast, diversity patterns seem to be driven by the capacity of different environments and regions to maintain different numbers of species. However, if there is such a diversity limitation, it is not clear in which spatial and taxonomic scale it applies and which factors actually limit diversity.

Keywords: latitudinal diversity gradient, evolutionary diversification, phylogenies, QuaSSE, environmental determinants

Island biogeography in the marine realm: of microbes, phytoplankton, and macroinvertebrates

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Whether there are ecological and evolutionary patterns that apply across all realms and all sizes of organisms remains an open question. In recent years, studies addressing this question have examined whether microbes have biogeography similar to macrobiota, including the species-area relationship (SAR) which characterizes island biogeographic patterns. In parallel, island biogeography theory, which for 40 years was considered largely irrelevant in the marine realm, has been revisited. We bring these two research agendas together to compare biogeographic patterns of microbes, phytoplankton, and macroinvertebrates, and to explore their shared and unique causes, in millennial-long 'natural experiments' in Indo-West Pacific marine lakes. We find that macroinvertebrates show an SAR characteristic of islands, their species diversity decays with colonization distance, and species studied to date illustrate the 'island rule', release from predation, reduced dispersal ability, and peripatric evolution and punctuated equilibrium. Phytoplankton also show an island-like SAR, a colonization-distance diversity relationship, and reduced dispersal ability. Microbes too displayed an SAR across lakes, as well as the related distance-decay of community similarity. We conclude that general patterns do exist across all realms and sizes of organisms. Whether these parallel patterns arise from parallel processes, and whether unique patterns arise from unique mechanisms and/or unique responses of macroinvertebrates, phytoplankton, and microbes is a fundamental next line of enquiry toward understanding the extent to which general ecological and evolutionary processes bridge realms.

Keywords: evolutionary ecology, island evolution, species richness relationships

Long-term disequilibrium and short-term equilibrium dynamics in West Indian biogeography

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In the half century since its first formulation, the equilibrium theory of island biogeography (ETIB) has been invoked to explain current patterns of diversity across countless archipelagoes. However, limitations in the fossil record, coupled with a fragmentary understanding of colonization dynamics, have limited the application of the ETIB in geological time. Here, we use dated phylogenies for the majority of endemic extant mammalian lineages and fossil deposits from the Greater Antilles and the Bahamas to infer colonization and extinction dynamics in the West Indies. Using a maximum likelihood approach to compare the series of colonization events by independent bat lineages to that expected given ETIB, we found colonization slowed 20-fold since the mid-Miocene to about 2 lineages/million years from the high colonization rate that prevailed since the Eocene. Although the drivers of this shift are unclear, the timing is consistent with the fossil-based pattern of colonization throughout the Tertiary for the land mammal fauna. We also combined bathymetric estimates with estimates of faunal diversity at the Last Glacial Maximum, and show that most of the extinction events observed throughout the Quaternary can be explained by the loss of area experienced as a result of post-glacial sea level rise. This is in contrast with the multiple ad-hoc explanations for island extirpation involving competition, or specific habitats. Together, our findings demonstrate the power of the ETIB as a null model for historical community dynamics and constitute one of two known examples of long-term historical disequilibrium in colonization.

Keywords: island biogeography, Caribbean, non-equilibrium

The island rule re-re-revisited

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The "Island rule" states that large animals generally decrease in size on islands while smaller animals increase in size and is one of the most famous patterns in both island biology and body size evolution. It is, however, also one of the most debated patterns and its very existence have been questioned in several recent papers which suggested that while larger animals decrease in size on islands, no overall pattern exists for smaller species. Using a new improved species-level phylogeny of all mammals and a new nearly complete database of the body size of all mammals we show that the island rule is true after all. The apparent lack of pattern for smaller species, suggested by others, appears to be the result of different body size optimum for one specific clade with unique physiological constraints. Our results predict a very strong effect of body size on the directionality of body size changes ranging from more than 90% chance or size increase for the smallest species to more than 90% chance of size decline for the largest. Furthermore our results suggest that the point where size increases and decreases are equally likely is inseparable from suggested mammalian optimal body size of 1 kg which previously has been predicted based on energy allocation arguments.

Keywords: evolution, biogeography, body size, mammals

Network super-generalism on islands: evidence from fruit-frugivore webs

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Species interactions are hypothesised to be 'super-generalised' on islands. For example, island pollinators are thought to visit greater numbers of flowering plant species relative to mainland pollinators. However, the island super-generalism hypothesis has yet to be fully tested and the processes underpinning super-generalism are unknown. I observed birds forage for fruit in a New Zealand forest for six consecutive years and searched the literature for similar data from other biogeographic locales. Data from 16 fruit-frugivore webs are then used to test the super-generalism hypothesis by comparing network 'connectance' (the fraction of potential species interactions that are actually realised) between islands and the mainland. I also explore why connectance might increase in island environments. After controlling for sampling effects and species richness (network size), island networks had higher average connectance values, supporting the super-generalism hypothesis. Additional analyses indicated that elevated connectance in island networks is linked to more equitable interaction frequencies among fruit and frugivore species, which may arise from density compensation - a common island phenomenon.

Keywords: Ecological networks, Island biogeography, Mutualism, Seed dispersal

Climate, species pool and dispersal effects on the functional diversity of island parasitoid assemblages

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Islands may help to understand pattern and process in the assembly of communities because their isolated nature may allow identifying the effects of particular mechanisms. Colonization filters as well as convergent evolution, adaptive radiation and competition may affect the assembly of island biotas thus determining their trait structure. Here we assess the global patterns of functional diversity in island parasitoids (Hymenoptera, Braconidae), identifying its main correlates and ascertaining potential mechanisms behind community assembly through species pool-based null models. We found that spatial variation in functional diversity correlates with climatic variables: islands with high precipitations and temperatures host assemblages with higher functional diversity. Although many island parasitoid assemblages show similar functional structure to their regional pool, more than a third of the studied islands host functionally clustered communities. These islands tend to be located near the tropics and to host species with largest body sizes, longer wings, and that attack certain types of hosts. These results suggest that community assembly on these islands is mainly driven by filters acting during the colonization process (by habitat and/or dispersal filtering). A small number of islands host functionally overdispersed communities that may be structured by competition. These non-random patterns might be caused by factors acting at different scales.

Keywords: Braconidae, community assembly, island biogeography, species traits.

Elevation-driven ecological isolation

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Elevational gradients in species diversity are among the most fascinating patterns in biogeography. However, there is still a sever lacks in identifying causalities and processes that are responsible for those patterns. The degree of diversification on islands or island like mountains is suspected to be positively influenced by isolation, time and environmental heterogeneity. A differentiation of these influences is often hindered by a correlation among variables. We show, that elevation specific data on endemism can be used to disentangle different drivers of species diversity. Especially the percentage of single island endemic species can provide information on changes of diversification along elevational gradients. With data from different island systems (oceanic and continental) and at different resolutions (within islands and on entire archipelagos) we found evidence for an *elevation-driven ecological isolation*, that leads to distinctly higher diversification in high elevated ecosystems. The geographic distance to source ecosystems is larger for high elevation ecosystems in comparison to low elevation counterparts. Consequently these high elevation ecosystems on island or island like mountains support a higher degree of endemic species. High elevation ecosystems also pose a special opportunity when investigating the basic processes of island biogeography, as they are the part of an island that is fastest eroded in the ontogeny of an oceanic island. This leaves the highly specialised biota the least time to establish and move on to a newly emerging island within the archipelago.

Keywords: altitudinal gradients, diversification, island biogeography, speciation

Floristic and species diversity gradients across Amazonia

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Historically, Amazonia used to be considered a relatively uniform forest area where obvious dispersal barriers (other than rivers) are currently lacking, and species composition changes gradually over large distances. However, several recent studies have documented considerable floristic turnover across sites at the landscape to regional scales. Much of this variation has been related to differences in soil properties, such as nutrient content, which in turn reflects the underlying geology. This becomes biogeographically interesting because Amazonia can be subdivided into geochemically different regions, of which central Amazonia is characterized by nutrient-poor soils and western Amazonia by nutrient-rich soils. Even so, edaphic heterogeneity within western Amazonia is known to be considerable, and our recent studies indicate that central Amazonia is also heterogeneous in this respect. To date there is little information on how the floristic-edaphic relationships that have been observed within one region scale up to the entire Amazon basin. I will address this issue using ferns as an example group. The data reveal both similarities and differences in how the flora relates to soil gradients in the two major regions, and additional patterns related to climatic heterogeneity within the rain forest realm.

Keywords: beta diversity, climate, ferns, soils, tropical rain forest

The Age and Area Hypothesis revisited: Do older species have larger geographic ranges?

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We tested the hypothesis that plant geographic ranges are positively correlated with species phylogenetic age - the "Age and Area Hypothesis" - as originally proposed by J. C. Willis in 1922. We expected that endemic species would be younger while older species would be more widely distributed. We used the dated molecular phylogeny of 104 species from the tribe Bignonieae (Bignoniaceae) to infer species age and a large dataset (complemented with herbarium records) to calculate their geographic range size. We used simple linear regression to evaluate correlations between those variables. Species ranged from central Argentina to the south region of United States. We found no correlations between the phylogenetic ages of the species and the extents of their geographical ranges. Possible relationships between age and area reported for some taxonomic groups by other authors may have been due to other factors that also influence species geographic ranges. In the case of the tribe Bignonieae, the main factor could be species dispersal efficiency, which is considered an important driver of geographic distribution, especially among species with wind-dispersed seeds. A better understanding of the factors that shape species distributions is important to conservation efforts, especially in terms of the tropical region, which is largely composed of species with limited distributions (endemics). Our results differ from other studies with neotropical species, which highlights the importance of additional studies integrating phylogeny, biogeography and conservation.

Keywords: Bignonieae, biogeography, distributions, phylogeny, phytogeography

Biogeography of *Ochthoeca* Chat-tyrants: A window into the history of Andean avifaunas

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The tropical Andes harbor the world's highest diversity of birds. This astonishing diversity is partially attributed to the action of deep river valleys that dissect the cordillera transversally into well-defined physiographical units. However, the true dimensions of Andean bird diversity and the importance of these valleys are only beginning to be understood. *Ochthoeca* Chat-tyrants are ideal organisms for studying biogeographic processes affecting Andean birds. Most species are allopatric, their geographic ranges are fragmented, and an important proportion of potentially isolated population shows evidence of morphological change. Here, we approach the biogeographic history of this group using a phylogenetic analysis based on rich sampling of species and populations across the tropical Andes and related mountain ranges. Results indicate that species of *Ochthoeca* are not monophyletic and split into two clades. The first clade includes some species in genus *Myiophobus*; the second is integrated only by species of *Ochthoeca*. Nonetheless, the topology of both clades suggests the importance of two major barriers promoting speciation and isolation of populations: the Táchira depression, in western Venezuela, and the Huancabamba depression, in northern Peru. Other barriers in eastern Colombia, southern Ecuador, and central Peru coincide with genetic breaks observed within some species. Biogeographic analyses point towards the Central Andes, as possible ancestral area for both clades, with posterior dispersals into the Northern Andes, northern Venezuela, Bolivia, and Argentina. Time-divergence analyses suggest that genetic diversification of species and populations, has occurred at different time scales.

Keywords: Andes, phylogeography, Neotropics, Tyrannidae, ND2, Dispersal-Vicariance analisis, time-divergence.

The GAARlandia hypothesis and Caribbean historical biogeography: A perspective based on geological, paleontological and molecular genetic evidence

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When and how the different lineages of plants and animals colonized the West Indies are two of the most important questions in the study of Caribbean historical biogeography. The GAARlandia hypothesis suggests the existence of a chain of islands or dry land connection between northern South America and the Greater Antilles during the Eocene–Oligocene transition (35–33 Ma). This short-lived landspan may have facilitated the overland dispersal of the terrestrial biota from South America to the Greater Antilles. Given the persistent skepticism concerning the importance and even existence of GAARlandia in explaining Caribbean biogeography, we review known geological and paleontological information and highlight recent molecular genetic studies. We compiled published information on phylogenetic relationships of elements of the Caribbean terrestrial biota and the estimated times of divergence for Greater Antillean versus continental taxa obtained from molecular clock analyses. Based on the congruence between geological scenarios and divergence times, we find support for both parts of this model: GAARlandia likely facilitated overland or island-hopping dispersal of terrestrial organisms (insects, spiders, freshwater fishes, amphibians, reptiles, mammals and some lineages of plants), and its subsequent break-up promoted island-island vicariance and the formation of the current endemic biota of each of the islands of the Greater Antilles, Cuba-Hispaniola-Puerto Rico.

Keywords: Caribbean biogeography, overland dispersal, phylogenetic relationships, times of divergence, island-island vicariance

Species-to-genus ratios reveal latitudinal asymmetry in the diversification of New World bats

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The tropical niche conservatism hypothesis (TNCH) has been proposed to explain the high species richness in Neotropical vertebrates. Under the hypothesis, most clades have a tropical origin and fail to disperse to extratropical areas; clades of temperate origin, in contrast, tend to occur also in the tropics, thus contributing to the diversity there. Here I test the hypothesis for the New World fauna of bats (Chiroptera) by analyzing the latitudinal gradient of diversity of the nine families. The gradient of richness for the 341 species shows a pattern consistent with the TNCH, but the gradient for the 89 genera reveals subtler patterns: (a) higher than expected species-to-genus ratios both at the southern and northern extremes of the continent; (b) a low ratio in Central America and Mexico, but not in the corresponding latitudes in South America; (c) a symmetrical Rapoport pattern for genera (more genera with small ranges near the equator); but (d) a highly asymmetrical pattern for species (with an over-representation of restricted species in the extreme south); (e) a rather uniform distribution of endemic species; but (f) a higher than expected number of endemic genera in North America but not in South America. In general, results support the TNCH, but also reveal the effect of the geological history of the area. In particular, I hypothesize that some of the genera traditionally considered of South American origin might have originated in North America prior to the Great American Biotic Interchange (GABI).

Keywords: Chiroptera, diversity gradients, higher taxa, Neotropics, niche conservatism

Barriers, time, and ecology explain the origins of lowland Neotropical bird diversity

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The Neotropical lowlands harbor extraordinary avian diversity. Most models proposed to explain the diversification of this avifauna invoke large-scale, tumultuous historical events (e.g. uplift of the Andes, Pleistocene forest refugia) that fragment the distributions of widespread species. Although phylogeographic analyses often detect genetic variation that is structured by prominent geographic barriers, it is unclear if these barriers played a primary role in diversification or are simply structuring genetic variation that arose via other processes. A growing number of comparative phylogeographic studies in other organisms are finding that species having the same distribution rarely exhibit the same temporal or spatial patterns. Instead, individual evolutionary histories may reflect idiosyncratic responses that are driven by species ecology and stochasticity. Here, we present a comparative phylogeographic analysis of 27widely distributed lowland bird lineages. We calculated levels of genetic structure in each lineage, and tested spatial and temporal patterns of diversification across prominent biogeographic barriers. We found a high degree of variation in patterns of phylogeographic structure and divergence times across biogeographic barriers, observations that are inconsistent with shared history. Analyses designed to detect the sources of this idiosyncratic spatial and temporal variation found that geographic origin and species ecology play important roles in determining the amount of genetic structure across the landscape and the timing of diversification across barriers. Our results suggest that cataclysmic events are not needed to explain the diversification of the Neotropical avifauna. Instead, a population model invoking heterogeneity in historical and contemporary landscapes and time may be sufficient.

Keywords: biodiversity, comparative phylogeography, speciation, biogeography, assemblage

Fuzzy logic as a key conceptual tool for modelling the distribution of inter-acting species in climate change scenarios

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Spatial modelling is a typical tool for assessing biogeographical responses of species to environmental conditions and predicting the evolution of their geographical distributions in climate change scenarios. Species distribution models customarily yield local suitability outputs for individual species according to autecological conditions, being the inclusion of species interactions a challenge for spatial modelling in this context. Fuzzy logic is a form of many-valued logic whose variables may have a truth value that ranges in degree between 0 and 1, and climatic favourability may be considered a fuzzy concept which should be treated accordingly. The favourability function was conceptually conceived to apply fuzzy logic to spatial modelling, by assessing and removing the effect of prevalence on each value of probability of species presence, so enabling direct comparison and combination of models built for several species. This characteristic makes the favourability function particularly useful in the spatial modelling of interacting species. In particular, we here show how the fuzzy intersection of favourability for different species has been proved to be useful to assess the biogeographical relationship between parapatric hare species in Europe and between monophagaus butterflies and their corresponding host plant in the Iberian Peninsula. We also evaluate the effect of these interactions on the predicted modification of the species distributions in the context of climate change.

Keywords: Butterflies, Favourability function, *Lepus*, parapatric species, host-parasite relationships

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Is there more than climate warming causing the upward movements of high-alpine plants in Europe?

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Species ranges have shifted northwards in latitude and upwards in altitude in recent decades. The observed shifts in species ranges have commonly been explained as a response to recent climate warming. However, several alternative hypotheses have been proposed to explain these altitudinal shifts, including increased deposition of atmospheric nitrogen, changes in precipitation or moisture availability, and dispersal limitation. We amalgamated observed shifts in the upper range-limit of alpine plants on 115 European mountains from Svalbard in the north to Italy in the south and evaluated different driving forces. On these 115 mountains nearly 70% of the species that showed detectable change in their upper range-limits between surveys had shifted their range-limits upwards, and the same species tend to move up on different mountains. When relating change in temperature to the proportion of species shifting upwards we find no indication that temperature

increase causes the upward movement of species. Correspondingly, warmth-demanding species do not move upward more frequently than expected by random chance. In fact, the average temperature indicator value is higher for the species shifted down than expected by randomness. A lower proportion of species migrated upwards on those mountains which experienced the highest increase in summer precipitation. The only trait variable related to species moving up is whether the species is a snowbed species or not. This may indicate that changes in amount of precipitation and timing of snowmelt may be more important than the direct effect of temperature for the observed range shifts of high-alpine plants.

Keywords: mountain summits, range shifts, precipitation, nitrogen deposition

Global perturbations of functional structure and diversity in bird assemblages under future climate change

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Human-induced global climate change is of major scientific and political concerns, especially when considering potential impacts on biodiversity, ecosystem processes and human well-being. One of the major aims of global change research is the development of reliable predictions on future geographic distributions of species. To date, projections tend to be focused on changes in species richness level. However, biodiversity has many facets, and one critical of them in the context of ecosystem services and function is functional diversity (FD). Indeed, animal assemblages fulfill a critical set of ecological functions for ecosystems that may be altered substantially under future climate change. Here, we integrated species and community perspectives to assess the consequences of projected geographic range changes for the diverse functional attributes of avian assemblages worldwide. Using 1° resolution data and species distribution modeling, we modeled current and future (2080-2099) ranges of all bird species (excluding marine and pelagic species) within an ensemble forecast framework. Then, using traits data (foraging type, foraging height, nocturnality and body mass) for all species, we calculated both current and future FD. Assemblage functional structure was projected to change highly unevenly across space with sometimes substantial losses of functional diversity that could have severe consequences for ecosystem health. Range expansions may counter losses in high-latitude regions, but offer little compensation in many tropical and sub-tropical biomes. Future management of local community function and ecosystem services thus relies on knowledge about global dynamics of species distributions and cross-scale approaches that include the biogeographic context of species traits.

Keywords: distributions, traits, dispersal

Combined global climate and local landscape models improve precision of invasion risk models in an island context

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Climate change and invasive species are widely considered to be among the most important threats to biodiversity. Climate change may disproportionately benefit invasive species, exacerbating their negative impacts on global biodiversity and ecosystem function. However, invasive species may also become less vigorous within parts of their current range, affording opportunities for ecosystem restoration. Here, we combine global climate data with local scale environmental and human impact data to estimate the current and future potential niches of 15 'high risk' invasive aquatic plant species within the island of Ireland. The global ranges of the majority of invasive plants examined were determined by climatic tolerances set largely by mean annual temperature and minimum temperature of coldest month. However, their potential range within Ireland was generally restricted by interactions with local land use, environment and human influence. Hence, global climate models predicted consistently larger potential ranges for all species than models which also incorporated local factors. All eight species currently established in Ireland occupied only a small proportion of the predicted suitable range under current conditions, suggesting that all have the potential to increase their ranges irrespective of climate change. The two species currently present that were identified as most likely to benefit from climate change were the water fern *Azolla filiculoides* and *Myriophyllum aquaticum*. In addition, three further species not currently established in Ireland (*Egeria densa, Hydrilla verticillata* and *Ludwigia grandiflora*) are likely to expand their range under future climate scenarios. Additionally, risk of multiple invasions at the same sites increased under climate warming scenarios.

Keywords: species distribution models, MaxENT, aquatic, plants, niche

Range expansion to novel environments: adaptation and cross-generational effect of stress in the invasive Colorado potato beetle

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Adaptation to stressful conditions is among the most important factors influencing species range expansion to novel environments. As invasive species expand their range to new areas they have to tolerate and adapt to various stressors such as changes in temperature, photoperiod and stress imposed by human action. The Colorado potato beetle, *Leptinotarsa decemlineata,* an invasive pest of potato, has expanded its range from ancestral ranges in northern Mexico to very high latitudes in Europe. We show that beetles, which invaded northern Europe (60°N) only about 30 years ago, are well adapted to the local conditions. They possess several life-history adaptations relating to the shorter growth season, and generally higher cold tolerance than more southern populations. We also show that the range expansion potential of the beetles may be complicated by exposure to other stressors experienced by the preceding generations. Parental stress, cold temperature or insecticide, can result in pre-adapted offspring having traits beneficial for the overwintering survival of the beetles. However, parental cold temperature stress impaired tolerance to insecticide stress. Taken together, both genetic and plastic responses to stress can play important roles in range expansions.

Keywords: adaptive phenotypic plasticity, anthropogenic stress, cold tolerance, invasive species, species range

When do models that account for changing continental connectivities make a difference? An example from the Colchicaceae

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Ancestral area reconstruction (AAR) using likelihood models (Lagrange software; Ree et al., 2005; Ree & Smith, 2008) can incorporate information about past area connections. For example, the temporal boundaries of a land bridge may be used to assign higher or lower likelihoods of dispersal during certain times. However, assigning connectivity likelihoods and time slice definition are *adhoc*, models may be overparameterized, and it is unclear what metric to use to assess model fit. A handful of (empirical) studies so far have compared AARs with or without time-slice models, reporting no consistent benefit of time-slices modeling. We studied the effect of modelling changing area connectivity in the lily family Colchicaceae, which has 250 species in 16 genera on all continents except South America and Antarctica. The common ancestor of Colchicaceae/Alstroemeriaceae lived in East Gondwana (75.3–102.5 Ma); initial radiation (at c. 75 Ma) occurred in Australia. Colchicaceae reached southern Africa during the Paleocene. As Africa moved north and the Tethys Sea was closing, the ancestor of the *Disporum*/*Uvularia* clade dispersed to Southeast Asia probably via Arabia and from there to North America (28–16 Ma) via the Bering land bridge. AAR models that accounted for the changing connectivity between Australia, Africa, and Eurasia over the past 100 Ma resulted in more plausible results for at least this expansion event than did a model without time slices. The presentation will compare models of past connectivity so far published and will provide some guidelines for when their use may be appropriate.

Keywords: Colchicaceae, likelihood-based ancestral area reconstruction, time-slice models, East Gondwana, Bering land bridge

Continental colonizations, adaptive radiations, and global biogeography of muroid rodents: the role of geographic and ecological opportunity

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Ecological opportunity (also known as geographic opportunity) is one of the main explanations for differences of taxonomic diversity among clades. We test for ecological opportunity (rapid diversification of a clade in response to niches made available by expansion into new regions) in the globally-distributed muroid rodents, the most species-rich clade of mammals. Based on a robust, 300-species molecular phylogeny, we reconstruct ancestral distributions, identify changes in net diversification rates, and fit density-dependent models of diversification to clades that have colonized continental landmasses. We identify at least 28 continental colonizations, most leading to significant endemic radiations, including 5-7 of Africa, five of North America, four of Southeast Asia, two of South America, two of Sahul, one of Madagascar, and 8-10 recolonizations of Eurasia. All colonizations were of adjacent areas, requiring no long-distance dispersal. Of the three “virgin” colonizations (of areas lacking muroids or close relatives), only the first colonizations of South America and Sahul match the model predictions and appear to be large-scale adaptive radiations. None of the secondary colonizations led to bursts of diversification, a pattern predicted by our model that includes the inhibitory affect of incumbent radiations on subsequent colonizers. Land area was not correlated with either the rate or size of diversifications. Geographic shifts can be critical for evolutionary history by promoting adaptive radiations, but only under restrictive conditions. We discuss the conditions and mechanisms explaining why adaptive radiations occur in some regions but not others, and thus in part, global biodiversity patterns.

Keywords: phylogeny, historical biogeography, S-Diva, South America, Sahul

What can multiple phylogenies say about the latitudinal diversity gradient? A new look at the tropical conservatism, out-of-the-tropics and diversification rate hypotheses

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We reviewed published phylogenies and selected 111 ones representing mammals, birds, insects and flowering plants. We then mapped the latitudinal range of all taxa to test the relative importance of the tropical conservatism, out-of-the-tropics and diversification rate hypotheses in generating latitudinal diversity gradients. Most clades originated in the tropics, with diversity peaking in the zone of origin. Transitions of lineages between latitudinal zones occurred at 16-22% of the tree nodes. The most common type of transition was range expansions of tropical lineages to encompass also temperate latitudes. Thus, adaptation to new climatic conditions may not represent a major obstacle for many clades. These results contradict predictions of the tropical conservatism hypothesis (i.e., few clades colonizing extratropical latitudes), but support the out-of-the-tropics model (i.e., tropical originations and subsequent latitudinal range expansions). Our results suggest no difference in diversification between tropical and temperate sister lineages; thus, diversity of tropical clades was not explained by higher diversification rates in this zone. Moreover, lineages with latitudinal stasis diversified more compared to sister lineages entering a new latitudinal zone. This preserved pre-existing diversity differences between latitudinal zones and can be considered a new mechanism for why diversity tends to peak in the zone of origin.

Keywords: ancestral area reconstruction, evolutionary time, latitudinal-zone transitions, sister group analysis, tropical origination

Multiple radiations of Passerines in the Andes? A phylogenetic perspective on species distributions.

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Species turnover is exceptionally high along Andean elevation gradients—individual species have narrow elevational ranges of a few hundred meters, and complete replacement of a given bird community can occur within 1000 meters moving up or downslope. This aspect of beta diversity makes a critical contribution to the immense regional diversity observed in Andean landscapes. Patterns of species turnover are often related to contemporary ecological drivers such as climate, vegetation, and species interactions. While such factors may reinforce elevational ranges, they offer limited insight into the role of evolutionary history in shaping observed patterns of species turnover. Here we apply a newly developed phylogenetic tree for all birds to provide an evolutionary perspective to patterns of species turnover and diversification in the Southeastern Peruvian Andes, which boasts a regional pool of over ~900 bird species. We quantify community phylogenetic structure and phyloenetic beta diversity along two 3000-m elevation gradients from the Amazonian lowlands to treeline to identify regions with a strong signal of phylogenetic turnover within the Andean bird fauna. We find clustering in the higher elevation communities for many Passerine families, which correspond with areas of phylogenetic turnover. We couple this analysis with knowledge of Andean uplift events to better understand the historical role of Andean elevation gradients in generating observed diversity across tropical bird families.

Keywords: phylogenetics, community structure, species turnover, Andes, Passerines

The fractal geometry of biotic ranges across multi-hierarchical clade levels reveals a spatiotemporal continuum of biodiversity

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The proposed correlation of species and genetic diversity in community ecology may indicate the action of uniform processes determining biodiversity patterns across hierarchical levels. DNA sequencing of whole assemblages permits the study of spatiotemporal patterns of biodiversity across hierarchical levels of species, genealogies, and individual genotypes. Using a fragment of mtDNA from > 5000 individuals sampled from 23 assemblages of predatory aquatic beetles from across Europe, we tested a key aspect of neutral theories in ecology that predict self-similarity of diversity patterns across hierarchical levels. Community similarity at all levels decreased exponentially with geographic distance, and initial similarity was correlated with the age of nested groups, consistent with a molecular clock. Log-log linear correlations between lineage age and the number of lineages, and between the number of lineages and their range sizes, revealed a fractal geometry in time and space, respectively, indicating a spatio-temporal continuum of biodiversity across scales. Simulations show these findings to mirror dispersal-constrained models of haplotype distributions. These novel macroecological patterns may be explained by neutral evolutionary processes, acting continuously over time, to produce multi-scale regularities of biodiversity. Our results link neutral evolutionary processes with neutral patterns of community assembly and support the hypothesis of dispersal and mutation as major determinants of biodiversity patterns at this continental scale.

Keywords: beta diversity, distance decay of similarity, DNA barcoding, nested clade analysis, neutral theory

An update of Wallace's zoogeographic regions of the world

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In 1876, Alfred Russel Wallace published the first map of global terrestrial zoogeographic regions based on the distributions and taxonomic affinities of broadly defined vertebrate groups. Despite relying on limited information and lacking a statistical basis, Wallace's original map is still in use today. Whilst the field of systematics has progressed immeasurably since Wallace's time, modern attempts to produce biogeographic maps focus on the distribution of species and are typically drawn without phylogenetic considerations. With the increasing availability of large phylogenetic trees, the opportunity now exists to use

phylogenetic information for grouping assemblages of species into biogeographic units on a global scale. We generated a global map of terrestrial zoogeographic regions by combining data on the distributions and phylogenetic relationships of 21,037 species of amphibians, birds and mammals. Our map distinguishes 20 distinct zoogeographic regions, which are grouped into 11 larger realms, showing both consistencies and inconsistencies with regions previously defined based on distributional data. In addition to permitting a sound delimitation of biogeographic regions, phylogenetic information allows quantifying phylogenetic affinities among species assemblages and zoogeographic regions. Examining global patterns of spatial turnover in the phylogenetic composition of vertebrate assemblages, we found that turnover was higher in the southern than in the northern hemisphere. Our results show that the integration of phylogenetic information provides valuable insight on historical relationships among regions, detailing key global patterns of vertebrate diversity.

Community phylogenetics at the continental scale: cold tolerance, phylogenetic niche conservatism and the structure of North American forests

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The tropical conservatism hypothesis, founded on a limited ability of woody clades to adapt to mid-Tertiary global cooling, is a prominent explanation for major global biogeographic patterns. Focusing on the phylogenetic structure of the tree species recorded in *ca*. 175,000 forest plots (each 0.4 ha) across the contiguous United States, we derived four predictions from this hypothesis: (1) local tree communities to the south are composed of species from older families than communities to the north; (2) the phylogenetic structures of cold tolerance and associated tree traits conform to expectations for trait evolution under a niche-conservatism constraint; (3) cold tolerance is the trait most strongly associated spatially with average clade age; and (4) of 12 environmental variables structured at either broad or local scales, minimum temperature in the coldest month best describes variation in mean clade age. Mean clade age showed a strong latitudinal pattern consistent with prediction 1, with some regional longitudinal and local patterning superimposed on the main latitudinal trend. Using a phylogenetic signal representation curve, the curves were consistent with a niche conservatism interpretation of trait evolution under an Ornstein-Uhlenbeck process, supporting prediction 2. Using Random Forest classification and regression trees and spatial GLMs, our results were also consistent with predictions 3 and 4, accounting for two thirds of the variation and almost all the spatial structure in the data. We conclude that tropical niche conservatism in the face of long-term climate change may drive local community phylogenetic structure of forests across the US.

Keywords: dispersal type, forest phylogenetics, leaf phenology, precipitation, seed size

When and how do species achieve niche stability over long time scales?

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Recent syntheses of ecological niche modeling analyses suggest that individual species may conserve the parameters of their ecological niches over long intervals of time. Evidence for niche stability has been documented across both abiotic environmental changes (e.g, climate or sea level) and biotic changes (e.g, species invasions) and for time scales ranging from years to hundreds of thousands of years. Yet, niche conservation is not ubiquitous among all species or all environmental changes. Within the same community, species respond to a specific change in environmental conditions with varying degrees of niche stability. Explaining the underlying reasons for these individualistic responses is important for conservation efforts and requires comparing multiple clades and styles of environmental change. To examine this issue, niche stability was analyzed for a suite of shallow marine taxa that inhabited the shallow epicontinental seas of North America during the Late Ordovician Period (~450 Ma). Niche stability was assessed for a broad set of taxa including: trilobites, brachiopods, echinoderms, mollusks, and bryozoans. These taxa experienced environmental changes including sea level fluctuations, a shift in ocean chemistry, and a wave of species invasions, during nine time slices over an interval of~3 million years. Niche models were generated with Maxent and stability was assessed via ecological, geographic, and parameter similarity between time slices. Taxa exhibited high similarity during intervals of gradual abiotic change and increased niche evolution during the interval of biotic invasion. Eurytopic taxa had highest stability and accomplished this primarily by narrowing niche variance during environmental perturbations.

Keywords: paleobiology, species distribution model, ecological niche model, climate change, invasive species

The abiotic processes driving patterns of bird species endemism in dry forest communities

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Across the Neotropics, seasonally dry forests are patchily distributed and contain low diversity relative to adjacent humid forests but have a high number of endemic species. Nowhere is bird species endemism higher than in the fragmented tracts of dry forests in northwestern Peru. High endemism is resultant from long-term isolation, which is thought to be an indication of limited gene flow into or out of these forests. I am using integrative approaches by using late Pleistocene passerine fossils, paleoniche modeling, and quantifying the levels of genetic divergence in bird species, to determine the role of Quaternary climate fluctuations and the uplift of the Andes Mountains had in shaping species distributions. Each approach is used to generate hypotheses and validate the results of the other approaches. All three methods indicate that dry forest bird species had more extensive distributions during the Pleistocene, likely during glacial periods, compared to today. The goal of this research is to unravel the abiotic mechanisms responsible for the modern levels of endemism and diversity found in little known Peruvian dry forests, and to preserve these forests and species according to future climate change scenarios.

Keywords: Pleistocene passerine fossils, Neotropical biogeography, Quaternary climate change, Paleoecology, Phylogeography

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New insights on an older model: the Isthmus of Panama and the Great American Biotic Interchange

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The formation of the Isthmus of Panama and the land connection that ended the 'splendid isolation' of South America and spurred the Great American Biotic Interchange (GABI) was a defining event of the Cenozoic. Previous understanding based primarily on the mammalian fossil record supported a Pliocene – Pleistocene closure of the Central American Seaway and onset of the GABI. New geological and paleobiological data are changing the existing model of the Isthmus of Panama with evidence supporting it is approximately five times older than previously accepted and was completed by 15 Ma. We conducted a meta-analysis of all dated molecular phylogenies addressing both terrestrial and marine taxa in the region to examine patterns of dispersal across the landbridge through time. Our results highlight the gradual evolution of the hyper-rich Neotropics and show a sharp increase of crossing events between Central and South America at 10 Ma. While marine data were fairly consistent through time, terrestrial taxa show a significant shift in crossing rates, particularly for a north to south pattern. Despite issues with current methodologies for meta-analysis and fine-scale understanding of paleoclimate, these results lend insight into one of the most significant geological events during the Cenozoic and its biological and geological implications.

Keywords: Biogeography, dispersal, diversification, land bridge, Miocene, Neotropics

Novelty in space and time: Linking pattern and process to understand the drivers of late-glacial no-analog plant associations

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The Pleistocene-Holocene transition in North America (17 ka BP to 8 ka BP) was a time of widespread environmental change, including the arrival of humans, the extinction of 35 genera of megaherbivores, and individualistic shifts in species' ranges and abundances in response to climate change and melting ice sheets. The widespread formation of novel plant associations during this interval is presumed to be the result of novel environmental conditions, but the relative importance of various proposed causal mechanisms remains unclear. We present a synthesis is of 7 well-dated, high-resolution pollen records from new and re-cored classic sites in the Great Lakes region of the Midwest, USA. Dissimilarity analysis indicates that the late-glacial no-analog plant associations were more narrowly constrained in this region (14.5 ka BP to 11.8 ka BP) than reported in previous sub-continental-scale syntheses (17 ka BP to 11 ka BP). A nonmetric multidimensional scaling analysis was conducted to reconstruct the trajectory of the sites in ecological space through time. Results reveal 1) abrupt changes in vegetation and increased variability within and between sites during the no-analog interval, 2) a distinct northwest-southeast time-transgressive pattern, as well as 3) interregional phenomena within the no-analog interval. Between-site differences in the behavior of key pollen types (e.g., *Fraxinus nigra*-type, *Ostrya*-type, and *Picea*) suggest that local site factors may have influenced the individualistic response of taxa to extrinsic abrupt forcing, including megafaunal extinction and climate change, resulting in particular novel plant associations that were unique to the region.

Keywords: paleoecology, novel communities, Pleistocene megafaunal extinctions, pollen analysis

Reponses of forests to the Holocene climate change in semi-arid North China

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Semi-arid forests that are of global climatological and environmental significances have been predicted to decline under estimated climate warming in the forthcoming decades. These predictions are based on the assumption that forests respond rapidly to climate change, which has not been validated at the tree species level over long time periods. We systematically investigated 10 sediment sequences and collected 42 Holocene pollen sequences from the monsoon-influenced North China to reconstruct the Holocene dynamics of three main forest types mono-dominated by pine (*Pinus*), oak (*Quercus*) and birch (*Betula*), as well as steppe and desert respectively indicated by *Artemisia* and Chenopodiaceae. Vegetation distribution as well as forests cover during the Holocene in North China was reconstructed. Charcoal from sediment was employed as proxy of fire intensity. We found that: (1) Forests were sensitive to both temperature and precipitation during 12-5 ka BP, but their sensitivity to temperature has markedly decreased since about 5 ka BP. The differentiated sensitivities across species, time and region, were accounted for by non-directional climate change, the different climatic niches of species, and pre-existing vegetation patterns during the late-glacial. (2) Forest cover had declined as a prompt response to climate drying during the mid- to late Holocene whereas forests had remained as dominant vegetation till 2 ka BP; (3) Both climate drying and openness of forest contributed to unusually high fire frequency and drought during 3.5 to 2 ka BP, which eventually lead to a steppe-dominated landscape in the semi-arid North China.

Keywords: vegetation sensitivity, forest resilience, time lag, fire, climate drying

Forecasting extinction risk in global mammals

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One-quarter of all mammals are in danger of extinction, and over half of all mammal populations are in decline. A major priority for conservation science is to identify those species that are most vulnerable to extinction and map their spatial distribution around the globe. Here, I: 1) used powerful machine-learning and spatial modeling approaches to understand the interactions of intrinsic and extrinsic drivers of terrestrial and marine mammal extinction risk; 2) used this information to predict risk across all mammals, including IUCN "Data Deficient" species; and 3) conducted a spatially-explicit assessment of these results to understand how risk is distributed across the globe. I found that intrinsic and extrinsic variables interact strongly to predict extinction risk across mammals, and that there are critical thresholds in these variables at which risk rapidly increases. Overall, for both terrestrial and marine species, intrinsic traits are the best predators of risk. I also identify regions of high current and latent risk, and show how these areas overlap with human impacts and protected areas.

Keywords: biodiversity, macroecology, conservation, IUCN Red List, random forest models

Clade-specific human land use impact on Neotropical primates

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Nearly half of the world's primates are threatened principally due to human activities, as deforestation and hunting. Here we perform a broad-scale evaluation of the association between human land use and phylogenetic distribution of Neotropical primates aiming to answer the following question: which sort of land use-related human impacts the primate clades are currently facing in the Neotropics? We used the IUCN range database to obtain the occurrence of the Neotropical primates in a 1° × 1° grid. For each grid cell we compiled the cover of six land use categories, which represent a gradient of human population density. We synthesized phylogenetic composition patterns of all cells in the two first axes of a principal coordinates analysis, which accounted for almost 50% of all phylogenetic variation. The spatial distribution of clades was associated with the cover of land use categories in each cell by correlation. The Atelidae clade was more representative in sites with higher cover of urban, villages and cropland areas. Since two third of this family is currently endangered, the advance of agricultural and colonization frontiers could be increasing extinction rates of species belonging to this clade. Cebidae, Callitrichidae and Aotidae were more correlated with rangelands, generally used to cattle-ranching, which also leads to forest loss and fragmentation. The Pithecidae showed strong association with wild areas, so that land use appears not to be an issue for them currently. Primate clades are probably facing different land use pressures, what implies in the need of a clade-specific conservation planning.

Keywords: Phylogenetic composition, conservation, human impact.

Applying species distribution models to help inform IUCN Red List assessments

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Characterising a species' geographical range is central to many conservation assessments, including those of the International Union for Conservation of Nature's (IUCN) Red List of Threatened Species. IUCN currently recommends that extent of occurrence (EOO) is quantified by drawing a minimum convex polygon around known or inferred species localities. Rarely do these assessments incorporate information from species distribution models (SDMs). A key impediment to this stems from uncertainty about how SDM predictions relate to EOO- commonly used for Red List assessments. This is especially true when data are scarce, as with many plant species. We address this issue by comparing the spatial overlap between EOOs derived from specimen localities and EOOs built around the edges of ranges derived from SDMs, for plant species with and without well-known distributions occurring in Costa Rica and Panama. For species with well-known distributions we show that EOOs derived from SDMs based on subsamples of the data are relatively invariant to sample sizes and match the true EOO more closely than an EOO drawn around subsampled data (< 20 localities). For the species with less well-known distributions, EOOs derived from SDMs correlate strongly with, but tend to be larger than EOOs derived from specimen localities. This implies that in some cases EOOs derived from SDMs are more representative of "true" EOOs than those drawn around known localities. We conclude that, if interpreted with due caution, SDMs can provide useful information when deriving EOOs and complement the present process of Red List assessments.

Keywords: MaxEnt, IUCN Red List, geographic range, distributions

Predicting the effect of habitat loss on tree species diversity in the Mesoamerican region

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Biodiversity loss driven by expanding anthropogenic activity poses a threat to natural communities and the ecosystem services that they underpin. Understanding how communities of species vary across space is essential to predicting the impacts of human-induced changes on biodiversity. This knowledge can be used to plan conservation areas that more effectively represent biodiversity. We use generalized dissimilarity modelling to predict spatial turnover patterns in community composition (beta diversity) of tree species within the Mesoamerican region. We map the effect of habitat loss on species turnover patterns by combining our predictions of beta diversity with a continuous measure of habitat condition known as mean species abundance (MSA), derived from land use maps in the year 2000. We then apply the species-area relationship to estimate the proportion of tree species lost due to habitat loss in the same year. We compare our estimate of species loss using this spatio-temporal method to an estimate derived using the species richness index (SRI). The SRI provides an estimate of species loss by calculating the fraction of the original species that survives land use change. Areas of high species turnover most affected by habitat loss include the Chiapas region, Costa Rica and Panama. Conservation efforts should therefore maximize the protection of these areas of taxonomically distinct tree species assemblages. Estimates of tree species loss in Mesoamerica up to the year 2000 varied from 5% using the SRI method to 15% using the spatio-temporal method. We discuss methodological issues which give rise to this difference in estimates.

Keywords: biodiversity, beta diversity, land use change, conservation biogeography, mean species abundance

Species nestedness as an indicator of biodiversity conservation within Colorado Plateau protected lands

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Public lands have been established, in part, to preserve biodiversity. One way to assess how this objective has been met is by examining patterns in species nestedness. Nestedness occurs when smaller communities are subsets of larger communities within the same biotic region; a nested pattern may indicate that some lands better maintain biodiversity. We quantified nestedness in mammals in a range of managed land types throughout the Colorado Plateau to: 1) determine if species assemblages are nested, 2) clarify which factors drive nestedness, and 3) assess whether differences in management impact biodiversity conservation. To quantify nestedness, we used the NODF metric and compared the true nested pattern to simulated nested communities using a species frequency-constrained null model (r0) and 500 simulations. We performed sensitivity analysis to determine if the nested patterns are robust or artifacts of individual management areas. Here, we show that mammals in protected lands on the Plateau are significantly nested, but neither IUCN park status nor management type are adequate predictors of nested rank or total diversity. We also tested the relationship between nestedness and 9 descriptive variables using Spearman rank correlation: year of land unit desingation, budget, latitude, longitude, minimum elevation, maximum elevation, elevation range, visitation, and area. Only maximum elevation and elevation range had marginally (without a p value adjustment) positive correlations with nestedness. These results suggest that inherent physical attributes of protected lands are most important for biodiversity conservation, and differences in management style may not have an impact on overall biodiversity.

Global hotspots of diversity and threat for palms under recent and future land cover change

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Land-use change and habitat degradation are among the major threats to terrestrial biodiversity in the present century. Here, we use data on past anthropogenic habitat conversion, current tropical deforestation rates, and projected future land cover changes due to land use and climate change and combine them with unique data on the global distribution and phylogenetic structure of palms (Arecaceae), a plant family of key importance for ecosystems and human livelihoods in tropical regions. Using both taxonomic and phylogenetic aspects of diversity (species richness, endemism richness, phylogenetic diversity, and biogeographically weighted evolutionary distinctiveness), we then identify global hotspots where centers of high diversity and pronounced levels of recent and future land cover change spatially coincide. These areas are simultaneously characterized by high biodiversity and strong anthropogenic global change and therefore represent regions where habitat restoration and conservation efforts will likely result in disproportionally high benefits for global biodiversity conservation. We highlight the importance for other organisms and human society and the disparities and similarities of these hotspots against other global conservation prioritization schemes.

Keywords: biodiversity, conservation prioritization, evolutionary history, global land cover, Millennium Ecosystem Assessment

The fundamental, realized and 'tolerance' niche: New considerations in the context of climate change

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The current distributions of species are often implicitly assumed to represent the total set of environmental conditions under which species can survive. When this assumption is incorrect, the estimates of extinction risk generated from species distribution models will be misleading. Further, the degree to which species can tolerate or thrive under conditions found beyond their historical distributions will inform the suite of conservation management options available. Empirically characterizing the realized, fundamental and tolerance niches of species can advance our understanding of extinction risks and management options, particularly in the face of global climate change. Although these relationships have not previously been characterized over geographic scales for any large group of species, we suggest that this could be done for many plant species by comparing native, naturalized and horticultural distributions. Doing so will advance our understanding of how niches map onto geographic space, will inform which species are at no, immediate or delayed risk of extinction from climate change, and will inform the application of management strategies such as managed relocation and managed stasis.

Keywords: niche syndromes, managed relocation, managed stasis, conservation

Understanding impacts of interacting global threats on biodiversity: It's not just climate change!

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Current and future climate change is widely expected to have unprecedented effects on Earth's biodiversity. In fact, studies with predictions of distribution changes, population declines and species extinctions are rapidly accumulating. However, in addition to climate change other threats may impose even greater challenges to species and ecosystems, namely habitat fragmentation and destruction, caused by anthropogenic land-use changes. Here, I assess the potential impacts of global threats to biodiversity using different analytical approaches. Firstly, in a study on the geography of future threats for global amphibian diversity I show that the spatial additivity of different threat factors could jeopardize amphibian diversity more than previous, mono-causal, assessments have suggested. In a second study I demonstrate how observed changes in the abiotic and biotic conditions (e.g. changes in temperature, precipitation and vegetation) across breeding and wintering ranges of migratory birds influence their population dynamics. Finally, I will discuss species' chances to respond successfully to anthropogenic threats from climate change and the continuing destruction and fragmentation of natural habitats.

Keywords: species' responses to global change, macroecology, amphibian declines, migratory birds, land-use change

Is the temporal β-diversity of avian communities a result of climate change?

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Global temperature and precipitation changes resulting from climate change have a potential to greatly affect biodiversity. While individual species have been shown to be affected by the recent climate warming, our understanding of the community-level consequences of changing climate is limited. Our objectives were to test whether temporal changes in bird communities are a result of climate change, and to evaluate the role of habitat disturbance as a confounding factor. We used 1980 and 2000 New York State Breeding Bird Atlas data to evaluate changes in avian communities as a function of recent climatic and land-cover trends. We calculated indices of temporal β-diversity to reflect changes in the entire avian communities as well as the dynamics of specific guilds. We evaluated linear and non-linear responses of communities to a suite of climatic temporal trend variables as well as variables indicating habitat disturbance, while accounting for spatial dependence. We found that changes in community diversity are significantly correlated with the trends in climatic conditions, but the responses differ among the examined guilds. The responses also differ among different levels of habitat disturbance, indicating that habitat disturbance confounds the impacts of climate change on avian community composition. We conclude that bird communities are affected by climate change, but their responses are confounded by other environmental and biotic factors.

Keywords: Avian guilds, bird communities, biodiversity, habitat disturbance

Critical thermal maxima of montane tropical frogs: biogeographical and conservation implications

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Tropical montane organisms often have small elevational ranges, and are thus expected to be vulnerable to climate change. Amphibians are one of the most threatened groups of vertebrates. To better understand the potential effects of widespread temperature increases in frogs, we measured critical thermal maxima (CT_{max}) in 15 species of strabomantid frogs along the steep elevational gradient of Manu National Park in the eastern slopes of the Andes of southern Peru. Strabomantidae includes over 550 species of terrestrial-breeding frogs that are continuously distributed along the Andes. These frogs are generally small in size, have low vagility, and often have small geographic distributions on mountaintops. Frogs were captured between the cloud forest at 1200 m and the high-Andean grassland above 3300 m and up to 3800 m. We used the loss of righting response as a measure of CT_{max}. We used the difference between CT_{max} and the mean temperature a frog experiences in nature as a measure of tolerance to high temperatures. We produced a phylogeny for the 15 species and traced the CT_{max} on the phylogeny to explore the evolutionary relationship between species' distribution and physiological tolerance . We found that tolerance to temperature stress increased with elevation, suggesting that frogs at higher elevations may be less sensitive to rising temperatures. We used climate scenarios predicted for our study area to evaluate the future distribution of these species. We discuss the ensuing extinction risks for species along the wide elevational gradient at Manu National Park.

Keywords: elevational gradient, physiological ecology, threatened species, tropical Andes

Modification of organismic responses to climate change by intra-specific diversity

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Responses of organisms to climatic changes are depending on various aspects such as individual age, population dynamics, community structure. Monitoring of species in the field, climate envelope modeling, and climate change experiments have been set up in order to identify the direction and intensity of species-specific responses especially for key species (e.g. dominating ecosystem processes) and target species (e.g. in nature conservation). However, the relevance and validity of modeling results and experimental findings is only granted if all populations of a considered species are showing comparable response patterns, which is not likely to occur. Little attention has been paid until now to the intra-specific variability of ecological responses across species distribution ranges. Here, we test European trees and grasses that control the functioning of spatially and economically important ecosystems such as deciduous forests and grasslands. We selected provenances of seeds along biogeographical and climatic gradients and exposed even-aged cultivated juvenile plants to expected climatic extremes and warming. The juvenile phase is a bottleneck for regeneration and population dynamics. Replicated losses of juvenile cohorts support demographic disequilibria and finally community turnover. Extreme climatic extremes such as periods of drought, heavy rain, late frost events are expected to become more and more important as a result of climate warming. Combinations of warming and extremes are likely to aggravate organismic stress. Under controlled experimental conditions (EVENT-Experiment in Bayreuth, Germany), we can identify that important species show strong provenance effects. Unexpected responses are found for combined extremes and for combinations of trends and events.

Keywords: climatic extremes, bioclimatic envelopes, grasslands, deciduous forests, EVENT-experiment

Not all mammals are responding similarly to climate change: The importance of body size and activity times

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Mammalian traits like body size have been linked to differential ability to shelter from climate change during the K-T and Pleistocene extinction events. Here we present the first evidence that mammalian responses to current climate change are stronger among larger-bodied mammals, as well as those without the ability to shelter behaviorally from climate. Among the 69 mammal species in North American measured for responses to recent climate change (local population extirpations; range contractions; range shifts; changes in abundance, phenology, body size, and genetics) only about half have responded as predicted. Mammalian responses increase with body size for all predicted responses and just among responses indicating a higher extinction risk (extirpations, range contractions, decreasing populations) using phylogenetic and ordinary logistic regression. Similarly, large mammals are more likely to contract their elevational ranges, whereas smaller mammals to expand their elevational ranges. Mammals with obligate diurnal or nocturnal activity times respond to climate change more than mammals with activity flexibility for all predicted responses and only extinction risk responses. Lastly, responses to climate change increase among species with higher latitudinal ranges. In conclusion, body size and behavior appear to mediate species interactions with climate, and including such species traits in predictive models will improve mammalian predictions of climate change risk.

Keywords: behavior, biogeographic range, phylogeny, population size, temperature change

Comparative phylogeography of sub-Saharan African savannah ungulates

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The savannah biome of sub-Saharan Africa harbours the highest diversity of ungulates (hoofed mammals) on Earth. To elucidate the biogeographic history of the region, we compile population genetic data from 19 co-distributed ungulate taxa, and find striking concordance in the phylogeographic structuring of species. Data from across taxa reveal distinct regional lineages, which reflect the survival and divergence of populations in isolated savannah refugia during the climatic oscillations of the Pleistocene. Data from taxa across trophic levels suggest distinct savannah refugia were present in West, East, Southern and South-West Africa. Furthermore, differing Pleistocene evolutionary biogeographic scenarios are proposed for East and Southern Africa, supported by palaeoclimatic data and the fossil record. Environmental instability in East Africa facilitated several spatial and temporal refugia and is reflected in the high inter-and intraspecific diversity of the region. In contrast, phylogeographic data suggest a stable, long-standing savannah refuge in the south.

Keywords: biodiversity, biogeography, distributions, herbivores, Pleistocene refugia, regional structuring

Increased energy promotes size-based niche availability in marine mollusks

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Variation in chemical energy, that is food availability, is posited to cause variation in body size. However, examinations of the relationship are rare and primarily limited to amniotes and zooplankton. Moreover, the relationship between body size and chemical energy may be impacted by phylogenetic history, clade-specific ecology, and heterogeneity of chemical energy in space and time. Considerable work remains to both document patterns in body size over gradients in food availability and understanding the processes potentially generating them. Here, we examine the functional relationship between body size and chemical energy availability over a broad assortment of marine mollusks varying in habitat and mobility. We demonstrate that chemical energy availability is likely driving body size patterns across habitats. We find that lower food availability decreases size-based niche availability by setting hard constraints on maximum size and potentially on minimum size depending on clade-specific ecology. Conversely, higher food availability promotes greater niche availability and potentially promotes evolutionary innovation with regard to size. We posit based on these findings and previous work that increases in chemical energy are important to the diversification of Metazoans through size-mediated niche processes.

Keywords: morphological evolution, body size, variation, size clines, energy, productivity

The commonness and distribution of rarity: Quantifying the botanical diversity of all plant species in the Americas

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The study of commonness and rarity at biogeographic scales can elucidate mechanisms driving gradients in biodiversity and has implications for conservation priorities. However, efforts to quantify the total number of species and the nature of rarity at increasingly larger scales are impeded by informatics challenges and taxonomic issues. Here we utilize new botanical informatics tools and apply them to a suite differing data sources to quantify, for the first time the diversity and 'patterns of commonness and rarity' for all the plants of the Americas. We combined disparate data sources from 760 data providers to analyze 22.5 million botanical observations. We estimate that approximately 43% of the estimated global Embryophyte diversity is in the Americas. The distribution of observations across species is highly skewed and reveals that rarity is commonplace. We find that rare species disproportionately clustered around mountainous regions, especially in the tropics (Andes, the Sierra Madre in Mexico and Central America) indicating that mountainous regions harbor a disproportionate number of the total species in the Americas. Further, globally rare species also cluster in isolated regions including the Mata Atlantica region along the southeastern coast of Brazil. Lastly, there is a relative dearth of rare species throughout the Amazon confirming past claims that the Amazon consists of widespread species. Lastly, we assess the distribution of commonness and rarity to assess several prominent theories for variation in diversity across gradients and the role of topography in maintaining and creating botanical diversity.

Keywords: biodiversity, informatics, diversity gradients, latitude, tropical

Geographic genetic structure of human lice provides insights into human migrations around the globe and past ecological interactions among hominids

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The extent to which modern humans and archaic hominids interacted directly is a key question in anthropology. Recently, host-specific parasites have been used to better understand the ecology and evolution of humans. For example, mitochondrial DNA (mtDNA) of the human louse (*Pediculus humanus*) revealed evidence of a population expansion that coincided with the out-of-Africa expansion of modern humans roughly 100,000 years ago. However, this is the case for only one of the three known louse mtDNA haplogroups. Previous studies suggest that the three louse haplogroups (A, B, C) evolved on different hominids as early as 2 million years ago and later switched to modern humans when they co-occurred with other hominids. Here we use both mtDNA sequences and nuclear markers in more than 200 lice from around the world to determine whether the nuclear genome supports the ancient patterns of divergence seen in the mitochondrial genome. Bayesian clustering analyses assigned lice to distinct genetic clusters that were geographically structured. We will discuss the association, or lack of, between each mtDNA haplogroups and nuclear genetic clusters in each continent. These data allow us to assess recombination at the nuclear level in each geographic region and can provide insights into when lice from each mtDNA clade became in contact, thus reflecting host ecological interactions.

Keywords: phylogeography, biogeography, genetic diversity, humans, parasites.

Cold-hardy terrestrial, marine and aquatic global diversity: overlooked lineages out of Antarctica and its ancient mountains

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Antarctica is often described as a continent depauperate in biodiversity compared to other regions of the world. However, since the onset of cooling over 30 million years ago (Ma), and even until recent times, isolated Antarctica may have served as an overlooked but important centre of diversification for taxa in and around the continent, and globally. New hardy endemic species are being described on the continent and in the Southern Ocean, while many other species in cold regions around the world are being identified as sister taxa with perplexing disjunct distributions; many have yet to be considered true cold-adapted Antarctic lineages. In addition, and analogous to the biodiverse modern Andes and the Himalayas today, ancient ranges present in Antarctica prior to the final break-up of Gondwana, such as the Transantarctic Mountains and other highlands, may have promoted the early divergence of alpine lineages and pre-isolation of taxa now in disjunct regions globally. Here, examples of Antarctic contributions to global biodiversity are reviewed including un-tested taxa ranging from alpine species to seabirds. Antarctica may have directly and indirectly promoted the diversification of a significant portion of the biodiversity in the Southern Hemisphere and elsewhere, serving as an important evolutionary core until more recently than was previously considered possible.

Keywords: polar, alpine, temperate, deep-sea, Transantarctic Mountains

SUPERSMART: Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa

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Understanding the historical assembly of biomes and the response of biodiversity to past episodes of climate change may help us prioritize clades and regions for conservation. Vast amounts of biological data are being deposited at public databases, holding the potential for powerful assessments of large-scale evolutionary processes. Yet, there have been surprisingly few attempts to merge and synthesize data within and among databases, and apply them in macro-evolutionary and biogeographic research. In this talk I will present SUPERSMART, which aims at merging data from major biological databases and providing users with a flexible, open-source platform for a wide range of evolutionary and biogeographical questions and analyses. In particular, we are linking DNA sequences, species distribution data, fossil records, and climatic variables. For these purposes we are *1)* further developing the PhyLoTa browser in order to produce genus-level, fossil calibrated mega-chronograms for plants, animals and fungi; *2)* from these trees, producing hundreds of species-level, multi-gene datasets of directly comparable crown ages; *3)* applying a newly developed Bayesian meta-analysis approach to estimate rates of speciation, extinction, and migration within and among user-defined operational areas; and *4)* testing for correlations between diversification, migration, and environmental niche evolution. The bioinformatics pipeline developed for this purpose is distinctly modular and can easily be modified and extended as new methods and software become available. There are several interactions between SUPERSMART and other on-going initiatives in North America and Europe. I will provide some highly relevant empirical examples of the use of this platform in biogeographic research.

Keywords: Historical biogeography, species diversification, biome evolution, bioinformatic tools, dated tree of life.

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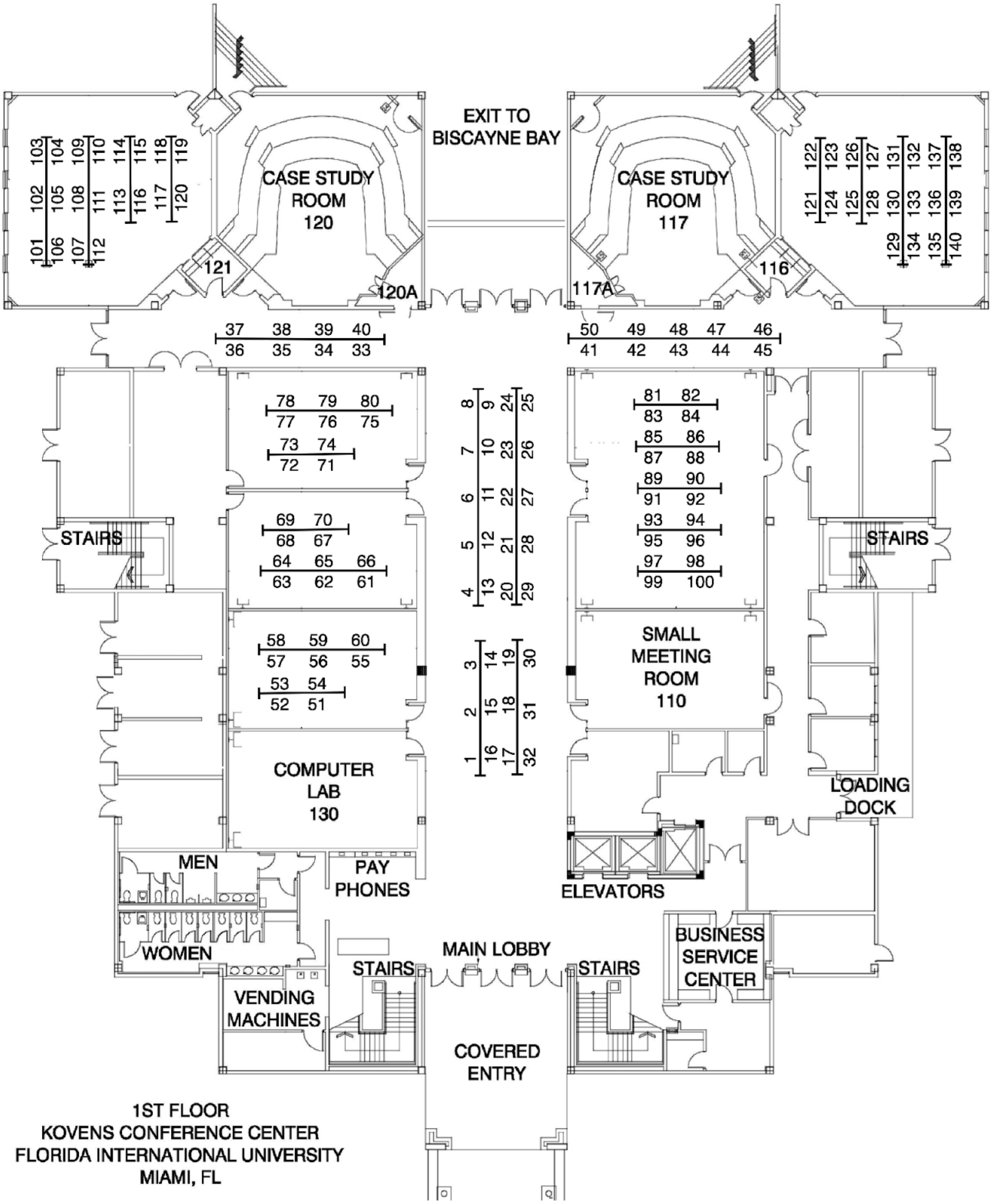

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1A Phylogeography of *Aequorea victoria* and *Aurelia labiata* within Puget Sound, Washington: a repeated sampling approach

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In Puget Sound, Washington, the water has acidified, has elevated sea surface temperature, and reduced dissolved oxygen. The area is inhabited by two species of blooming jellyfish (*Aequorea victoria* and *Aurelia labiata*). Puget Sound therefore provides a microcosm in which to study the relationship between global change and jellyfish blooms, which may have additional consequences for commercial fisheries by consuming larvae, aquaculture by destroying equipment and stock, and power stations by compromising equipment all of which are economically important to Puget Sound. The integration of population genetics and dynamics in a new framework to identify endemic versus transient blooms allows a critical knowledge gap to be addressed: since blooms are characterized by increased jellyfish biomass ascribed to habitat conditions, the exposure over time, not just at present, is important. Thus, one must ascertain the required foundation of population genetics (presented here) to then incorporate ecological conditions to tease out bloom causation. To accomplish this, a suite of nuclear and mitochondrial genetic markers were amplified: cytochrome *c* oxidase subunit I, 16S ribosomal RNA, histone 3, and actin to estimate pairwise sequence distance, nucleotide and haplotype diversity, and generate haplotype networks for samples collected at identical locations in 2011 and 2012. *A. victoria* and *A. labiata* have high gene flow between regions within Puget Sound evident from low pairwise sequence distance, low nucleotide diversity between and within populations, and moderate to high haplotype diversity. Understanding population genetic structure within Puget Sound will provide a case study framework to solidify jellyfish bloom causes.

Keywords: hydrozoan, jellyfish blooms, scyphozoan

2A Hybridisation, introgression and phylogeography of Icelandic birch

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Birch woodland is an integral component of the tundra biome, which covers expansive areas of the Arctic. In natural woodland in Iceland two species of birch co-exist: the diploid dwarf birch *Betula nana* and the tetraploid tree birch *B. pubescens*. Both species are extremely variable, morphologically, and this is believed to be due to introgressive hybridisation between the two species. In this paper an overview of our research on Icelandic birch over the past ten years will be presented. Qualitative and quantitative assessments of morphological variation of birch in natural woodlands clearly indicate introgressive hybridisation, and this, as also shown by the extensive sharing of maternally inherited cpDNA haplotypes across ploidy groups, is supported by the statistical analysis of introgression indices and the variation components. The molecular data also reveal a geographical structure of introgression and phylogeographical patterns, both within Iceland and in relation to Europe. By using ploidy-based morphometric standards on pollen in peat sediments from different sites in Iceland, we have further shown that birch hybridisation occurred since early on, from the time birch vegetation began to develop soon after the deglaciation. In conclusion, our botanical, cytogenetic, palynological and molecular studies show that hybridisation between *B. nana* and *B. pubescens* is widespread in Iceland; the resulting gene flow via introgressive hybridisation is bi-directional; and that the process is continuous through time and space. Present-day birch in Iceland is most probably post-glacial in origin, migrating from Western Europe and colonizing Iceland in the early Holocene.

Keywords: botany, cytogenetics, hybrid zone, molecular genetics, palynology

3A Estimating asymmetry of dispersal and intensity of migration in time within a Bayesian framework (R implementation)

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Bayesian methods for reconstructing evolution of geographic ranges can integrate various types of uncertainty by sampling from posterior distribution of phylogenetic trees differing in topology, divergence time estimates and reconstructed scenarios of area inheritance. This wealth of information may serve not only for calculating posterior probabilities of alternative reconstructions but it can also be used to investigate dispersal pattern in space and time. We propose simple methods of measuring dispersal asymmetry and of identifying temporal dispersal windows and we provide their implementation using R statistical environment ('cot' package available from the authors). Both methods use stationary distribution of trees resulting from Bayesian analyses using Markov discrete phylogeographical model. For each tree and each migration route, a dispersal asymmetry index (DAI) is calculated; its mean ranging between 0 and 1 is a measure of asymmetry while its posterior distribution over set of trees is used to evaluate the significance of asymmetry. To show the temporal distribution of dispersals, each tree is divided into time slices and a relative measure of intensity of migration along a particular route is scored and summarised as mean and 95% HPD.

4A Investigating phylogeography and population structure in the relict dragonfly *Tanypteryx hageni*

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The dragonfly family Petaluridae consists of 11 species distributed in Australia, New Zealand, Chile, the Appalachians in eastern North America, the Pacific Northwest of North America, and Japan. Recent work suggests that this group distributed to their current locations prior to the break up of Pangaea, with clades on Gondwanaland and Laurasia that separated over 100Ma. These species are unique among dragonflies for two reasons: their use of fens for larval habitat—larvae in most species dig a burrow in saturated soils in which they live—and their extended larval development times, taking 5-9 years (depending on species) to go from egg to adult. Adults live from 3-6 weeks during the summer months, and are observed each year. With these long development times and short adult lifespans we are left with the question: what is a population in these species? Do individuals at any single fen represent five temporally separated cohorts? Here we present work on the Black Petaltail, *Tanypteryx hageni*, found in mountain habitats from northern California to British Columbia. Samples were taken from over 500 larval and adult specimens from sites throughout this range. We determined age of larvae through morphometrics, and compared haplotype data across these groups to determine levels of reproductive isolation. We also analyzed adult coloration in individuals from different sites and from different years for pattern diversity.

Keywords: biogeography, population structure, life history

5A Worms out west: Revealing faunal assembly for pinworms (Nematoda: Oxyurida) and chipmunks (Mammalia: Rodentia) in the American West

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An understanding of evolutionary history among hosts and their associated parasites has wide-ranging implications. Such a background contributes a framework to define the consequences of climate change on zoonotic pathogens and parasites, the role of biotic complexity in pathogen emergence, and improve the resolution of host phylogeographic history. Our current understanding of genetic relationships among chipmunks (including multiple instances of mitochondrial introgression) suggests that a complex and dynamic history produced patterns of contemporary diversity and distribution. We generated phylogenies for two pinworms (*Syphacia eutamii* and *Heteroxynema cucullatum*) associated with western North American chipmunks (genus *Tamias*, subgenus *Neotamias*) to address questions about the history of this host-parasite assemblage. In particular, does phylogeographic history for pinworms and chipmunks suggest similar responses to past changes in populations, such as expansion and isolation? Is there evidence of host-switching, possibly due to patterns of recurrent expansion and subsequent isolation in host populations at varying spatial and temporal scales? Phylogeographic relationships suggest that within both pinworm species some genetic lineages have been associated with a host species or host lineage, whereas others are independent and structured geographically. Although both species of pinworms are associated with the same host subgenus, each parasite species has a different phylogeographic history, suggesting independent evolutionary trajectories over time. Unraveling the parasites' biogeographic histories will provide additional insight into the complex history of these hosts.

Keywords*:* phylogeography, hosts, parasites

6A Phylogeography of the American hog-nosed skunk, *Conepatus leuconotus*

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Recent advances in phylogeographic studies, including paleo-ecological niche modeling (PENM), are helping to rapidly advance the field of phylogeography as one of biology's most integrative disciplines. One important contribution PENMs have made to our understanding of phylogeography is in developing spatially-explicit hypotheses for subsequent testing using methods of statistical phylogeography. PENMs also provide alternative techniques for identifying Pleistocene refugia for taxa lacking sufficient fossil data. Such is the case for the American hog-nosed skunk, *Conepatus leuconotu*s (Lichtenstein, 1832), a mesocarnivore currently distributed from southern Colorado to Nicaragua. Using PENM, we established five *a priori* hypotheses regarding the demographic history of *C. leuconotus*. PENMs indicated the possibility of at least four potential Pleistocene refugia. Using statistical phylogeographic methods and mitochondrial DNA sequence data, we plan to test for the existence of these four refugia in addition to three alternative demographic hypotheses and one time since divergence hypothesis. To date, 78 modern samples of *C. leuconotus* from across their distribution have been sequenced for cytochrome -b, D-loop, and ND5 genes. Due to reduced availability of modern tissue samples, we have augmented our modern dataset with historic tissues from museum specimens (1891 – 1998). To date, 100 historic samples have been successfully extracted and are awaiting sequencing for the cytochrome-b, D-loop, and ND5 genes. The 2000-plus base-pairs from these 178 individuals will enable us to statistically test for genetic signatures of putative Pleistocene refugia in *C. leuconotus*, furthering our understanding of how past climatic conditions have helped shape the evolutionary history of this enigmatic carnivore.

Keywords: Refugia, Pleistocene, ecological niche modeling

7A Four pulses of diversification and differential migration rates across the Andes explain the structuring of genetic diversity in an assemblage of lowland Neotropical birds

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Comparative phylogeographic studies may arrive at spurious conclusions when species-specific variation in population parameters is not taken into account. To avoid these biases, coalescent-based analyses allow population parameters to be modeled while testing alternative hypotheses about the evolutionary history of entire community assemblages. We apply coalescent-based phylogeographic approaches to understand the role of the Andes as a biogeographic barrier that influences patterns of genetic variation between populations of lowland Neotropical birds. mtDNA sequence data from 24 taxa with populations co-distributed across the Andes was used to test for simultaneous divergence employing an approximate Bayesian computation method. We also used an information-theoretical approach for five species with multilocus data to evaluate the hypothesis that gene flow across the Andes is influenced by foraging strata (understory versus canopy). We found that four pulses of cross-Andes diversification dating from the Miocene to Pleistocene are more probable than a single, simultaneous, assemblage-wide divergence across the Andes. Understory birds exhibit low migration across the Andes, whereas canopy species show evidence for substantial cross-Andes migration. These results confirm that Andean uplift likely had an important initial influence on the genetic divergence of lowland Neotropical birds, but that species did not all respond to this event in the same way. Climatic fluctuations during the Pleistocene, in particular, appear to have facilitated episodic crossing of the Andes in some species and not in others.

Keywords: Phylogeography, Approximate Bayesian Computation, Information-theoretical.

8A Can phylogeography explain the growing dominance of cattails (*Typha* spp.) in wetlands around the world?

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Cattails (*Typha* spp.) are important members of wetland communities around the world, but in recent years there has been growing concern about the dominance of *Typha* in some geographical regions. We hypothesized that increased dominance is related to the cryptic introduction of non-native lineages, and used chloroplast sequences to reconstruct the global phylogeography of two widespread species: *T. latifolia* and *T. angustifolia*. We found that haplotype lineages in *T. angustifolia* are characterized by relatively recent divergence within and between regions (Asia, Europe, North America). *Typha latifolia,* on the other hand, yielded two divergent clades: one in Asia, and the other in North America and Europe. Both species show evidence of recent long-distance dispersal between continents, and these introductions may at least partially explain their increasingly invasive behaviour.

Keywords: *Typha*, phylogeography, cryptic introductions, long-distance dispersal

9A Molecular epidemiology of avian malaria of Sympatric nesting grounds in the Midwest

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The potential of migratory bird facilitated disease spread is not only of public health but also of conservation concern. Migratory birds traverse the globe each year, utilizing a wide array of habitats, which potentially exposes them to a diverse range of pathogens. Avian malaria is caused by *Plasmodium*, a protozoan blood parasites that is transmitted via mosquitoes. Using molecular detection tests, we confirmed the presence of avian malaria in Greater Prairie-chickens (GPC) and Upland Sandpipers (UPSA) that nest sympatrically in the Flint Hills of Kansas. While both exhibit different ecologies (one is migratory, one is not), a shared habitat during the breeding season creates potential for disease transmission. Since both species nest sympatrically, we predicted that vector-borne pathogens would be exchanged among the species. We screened a total of n=1225 GPC and n=605 UPSA for avian malaria using polymerase chain reaction to amplify DNA of blood-borne pathogens. Positive samples were sequenced. We found that the majority of *Plasmodium* infections were haplotypes unique to each species, but we also found haplotypes shared between the two avian species suggesting transmission of *Plasmodium* has occurred in the Flint Hills. In addition, a transmission event appears to have occurred in South America. Two *Plasmodium* species found in UPSA in Kansas were also found in the endangered Galapagos Penguin.

Keywords: avian malaria, *Plasmodium*, migration, disease transmission, blood parasites

10A Tropical Eastern Pacific may also be a hotspot for pelagic invertebrates

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The roles that pelagic predators such as scyphomedusae play are not well understood because their diversity, distributions, and phylogenetic relationships are poorly known. In the Tropical Eastern Pacific (TEP), relative to other taxa, scyphomedusae appear to have few roles, which are poorly contextualized; only three species have been documented previously, without any description of their evolutionary relationships or biogeographic affinity. We made new collections in the TEP (from the Pacific coasts of Mexico and Central America), constructed phylogenies using 4 molecular markers (mitochondrial 16S and COI; nuclear 18S and 28S), and estimated community similarity using Jaccard and Sørensen indices. We found 20 new species in the TEP, including 5 species of *Chrysaora* (which illustrate the genus is paraphyletic), 5 species of *Stomolophus*, and 3 species of *Aurelia*—each genus diversified across the Panamanian Isthmus (e.g. new Pacific species of *Stomolophus* constitute the sister taxon of Atlantic *S. meleagris*). New species of Lobonematidae and Catostylidae, previously known only for the Western Pacific and/or Atlantic basins, suggest diverse biogeographic origins of the TEP scyphofauna. Within the TEP, community similarity indices suggest 4 biogeographic regions: one in the Golfo de California (GCA), and three in Central America separated by Golfo de Tehuantepec and Golfo de Chiriqui. In the northern and southern extremes, 25% of new species may be endemic to the regions of the GCA and Golfo de Panama. These phylogenetic and biogeographic findings build a foundation for future ecological studies into the possibly diverse roles of many pelagic predators in the TEP.

Keywords: comparative phylogeography, diversity, jellyfish, marine biogeography, scyphozoa

11A The *Ototylomys* journey along Central America during the GABI: determining the emerging-participant-spectator status of a rodent

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Central America (CA) has an extraordinarily intricate geological and biogeographical history that renders it ideal to study patterns of historical divergence, genetic differentiation and structuring of endemic biota populations. CA current fauna includes a complex mixture of North and South American components, many associated with the Great American Biotic Interchange (GABI), the major migration process in the region. *Ototylomys phyllotis*, the big-eared climbing rat, is the only extant member of the *Ototylomys* genus and its distribution ranges from Costa Rica to southern Mexico. Information for this species showed an incomplete genetic structure, unknown origin and controversial migration history and subspecies division. We explored it further under a phylogeographic framework by analyzing 770 pb of cyt b from 132 individuals within 47 localities along its complete distribution. We found that *O. phyllotis* shows a high (0.990±0.003) and moderate (0.0448±0.0019) haplotype and nucleotide diversity values, a strong genetic structure corresponding with four major phylogeographic lineages (genetic distance 4-8% between them). Our results support that the predominant evolutionary processes acting on *O. phyllotis* lineages were allopatric fragmentation with restricted gene flow from Costa Rica to Chiapas, while range expansion/colonization in the Yucatan peninsula. Phylogenetic results point out its origin from an ancestral population in El Salvador-Honduras, followed by several migration pulses towards its southern and northern distribution limits. Our estimated divergence times prove that this climbing rat was both a spectator and a participant of the major CA biogeographical event.

Keywords: phylogeography, Quaternary, Middle America, Muridae, diversification

12A Genetic structure of marginal populations of green turtles nesting in the northwestern Pacific Ocean

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The green turtle (*Chelonia mydas*) is a long-lived reptile with a circumtropical distribution. Previous studies have indicated there are phylogeographical population structures of nesting green turtle females maintained by strong maternal philopatric behavior towards their natal regions. Japan is located at the northern limit of the Pacific breeding area, and nesting sites exist in the Ryukyu Archipelago and the Ogasawara Islands. Previous studies were suggested that there were three genetically differentiated stocks nesting in the Ogasawara Islands and Yaeyama Islands situated in the southern Ryukyus. These populations were also differentiated from two Taiwanese nesting populations. In the present study we analyzed the green turtles nesting in islands further north in the central Ryukyus, and compared them with reported populations. The haplotypes detected in the northwestern Pacific Ocean belonged to three divergent clades, corresponding to the three of five clades detected in the Pacific Ocean. Although several divergent haplotypes were shared within nesting populations, the haplotype compositions showed significant differentiation among regions. Each regional population showed high genetic diversity. These results suggested that the populations in this area had their origin in the emigration of individuals with ancestral haplotypes from lower latitudes. The present nesting populations in the northwestern Pacific Ocean might have been formed by a balance between their natal philopatry and historical long dispersal.

Keywords: Ryukyu Archipelago, northern limit, historical immigration, genetic diversity, phylogeography

13A Phylogeography and population genetics of three Florida mangrove species

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Mangroves are able to mitigate some of the detrimental results of global climate change, such as sea level rise and increasingly severe storm surges during hurricanes. Furthermore, mangroves provide habitat to many marine and coastal species, from invertebrates to fish to birds, as well as ecosystem services such as filtering water and cycling nutrients. In Florida, overdevelopment of coastal real estate and increased shipping has had a negative impact on mangroves over the last century. If current trends continue, many areas of Florida will have no natural protection from rising sea levels, and coastal habitats and real estate will be destroyed at an increasing rate. Red (*Rhizophora mangle*), black (*Avicennia germinans*), and white (*Laguncularia racemosa*) mangroves co-occur in Florida. Protecting these mangrove species and effectively restoring degraded coastal habitats must become conservation priorities. Significantly, when evaluating conservation strategies, studies have shown that restoration efforts are more effective when local propagules are used to restore degraded habitats. Surprisingly, no genetic data are currently available for these three mangrove species in their native range in Florida. In this study, we sampled 10 individuals in each of 15 populations from each of the three species. We are conducting phylogeographic analyses using microsatellites, single copy nuclear genes and chloroplast DNA sequence markers. These markers will provide the first insights into genetic variation within and among populations of the three species of mangroves in Florida and facilitate reconstruction of the phylogeographic history of each species. Here, we present our preliminary genetic data and phylogeographic analyses.

Keywords: climate change, conservation, *Rhizophora*, *Avicennia*, *Laguncularia*

14A Diversification and demography of the Oriental garden lizard (*Calotes versicolor*) on Hainan Island and the adjacent mainland

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Calotes versicolor is one of the few non-gekkonid lizards that are geographically widespread in the tropics. To date, little is known about its phylogeographic and demographic past. We investigated the impact of cyclic upheaval and submergence of land bridges during the Pleistocene on the diversification and population dynamics of *C. versicolor* on Hainan Island and the adjacent mainland. We analyzed mtDNA (*ND2–COI*; 2663 bp) from 212 individuals sampled from 35 localities on Hainan Island and 4 localities on the adjacent mainland. Bayesian phylogenetic analysis supports two distinct lineages, A and B, which are estimated to have coalesced about 0.26 million years ago. The estimated coalescence times within each of the lineages A (0.05 Ma) and B (0.13 Ma) correspond to dates of ephemeral Pleistocene land bridges. Lineage A contains individuals mainly from central and southern Wuzhi Mountain on Hainan Island, whereas lineage B mainly comprises individuals from other sites on the island plus the adjacent mainland. Two distinct population groupings: A, primarily containing linage A, and B, mainly consisting of lineage B, were identified by spatial analysis of molecular variance. Neither the Wuzhi Mountain nor the Qionzhou Strait and Gulf of Tonkin act as barriers to gene flow among *C. versicolor* populations. Coalescent simulations suggest that there may have non-physical barriers to gene flow in the Pleistocene. A stable size through time for Group A, and moderate expansions and contractions in population size during the end of the Pleistocene for Group B were inferred by demographic analyses.

Keywords: historical demography, non-physical barrier, Pleistocene sea-level, phylogeography, population structure

15A Genetic variation in arid regions of southern California: a study of the California vole (*Microtus californicus*)

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Temporal variation in environmental conditions results in continuous change to both landscapes and patterns in species distribution. During the Pleistocene, wetter and cooler conditions prevailed on the east side of the Sierra Nevada in California. As conditions became more arid, mesic taxa became isolated. One such species is the California vole (*Microtus californicus*), which is commonly found in grasslands and oak woodlands, but also inhabits desert oases. The current desert regions host numerous pockets of mesic habitat, including narrow canyons, springs, and ponds. Given the isolation of these patches, this species likely invaded the desert region during periods when the climate and habitats were more suitable for colonization. Present anthropogenic changes (i.e. irrigation, water diversion, wastewater treatment) to the environment also play a role in their isolated distribution. In this study, we assess how changes in the environment affect genetic diversity in and among these desert populations using nuclear microsatellite and mitochondrial DNA markers. The microsatellite data show significant population structure among populations in the desert and between those from the contiguous part of their range. However, the mitochondrial sequence data do not show structure among desert populations. These genetic patterns suggest long-term occupation by *M. californicus* in the desert and subsequent separation due to geographic barriers to dispersal.

Keywords: phylogeography, gene flow, barrier, dispersal

16A Exploring signals of historical demography in North American boreal mammals through statistical comparative phylogeography

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Biota have responded to past glacial and climactic fluctuations resulting in distinct evolutionary (genetic) and ecological (niche) signatures. Debate persists whether communities respond to climate perturbations as cohesive units or individualistically, revealing either consistent or stochastic signatures, respectively. Within a comparative phylogeographic framework, we assessed variation among ten species of boreal mammals from western North America using a multilocus coalescent-based lineage context for each taxon. Phylogenetically informed species distribution models were developed and hypotheses of Last Glacial Maximum distributions were tested for alternative demographic scenarios of diversification. Signatures consistently revealed four distinct and often reciprocally monophyletic lineages (Northern, Southwestern, Coastal, and Eastern). We were unable to reject a model of long-term fragmentation during glacial advances supporting an independent refuge model. We also documented a consistent signature of demographic expansion for Northern lineages, indicative of populations tracking glacial retreat. Finally, episodes of divergence leading to monophyletic clades are consistently coincident with the periodicity of major glacial cycles. Taken together, these signatures suggest consistency between ecological and evolutionary divergence for boreal mammals. Our comparative approach provides novel insight to conservation of fragmented populations that face further climate warming and potential habitat loss within the next century.

Keywords: climate fluctuation, historical biogeography, independent refuge, paleo-distribution, species distribution model

17A The ecology of Malagasy formicine diversification: widespread waifs and undocumented endemics

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The tropical regions of the world house a disproportionately high amount of the world's biodiversity. Though the reasons for this are not well understood, a number of hypotheses have sought to explain these high rates of speciation; most focusing on the well-studied biota of the Neotropics. Due to its isolation, Madagascar is well suited to exploring how organisms diverge (speciate) and persist in fragmented habitats without the confounding influence of migration to/from adjacent areas. By applying multi-locus sequence data to an exploration of the evolutionary history of the formicine fauna of Madagascar we seek to understand the factors that have driven diversification on this microcontinent. Our findings reveal a startling array of speciation patterns and intraspecific levels of differentiation. Molecular data support preliminary morphology-based indications of high levels of cryptic diversity and remarkable variation in levels of gene flow among codistributed species.

Keywords*:* biodiversity, biogeography, Madagascar, ecology, phylogeography, ants

18A ABC, *not* as easy as 1, 2, 3: the potential perils of model choice via approximate Bayesian computation

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Approximate Bayesian computation (ABC) is rapidly gaining popularity in many subfields of biology, including biogeography. One example, msBayes, infers the temporal distribution of divergences among pairs of taxa, allowing biogeographers to test hypotheses about historical causes of diversification in co-distributed groups of organisms. We used msBayes to infer the distribution of divergence times among 22 pairs of vertebrate taxa distributed across the Philippine Archipelago. Our objective was to test whether sea-level oscillations during the Pleistocene caused diversification across the islands. To help guide our interpretation of the empirical results, and determine the accuracy and power of msBayes, we performed a suite of simulation-based analyses. Our empirical results strongly support a recent simultaneous divergence event for all 22 taxon pairs, consistent with the prediction of the Pleistocene-driven diversification hypothesis. However, our simulations reveal low power of the method to detect random variation in divergence times and bias toward supporting clustered divergences. For example, we demonstrate that msBayes will infer one simultaneous divergence event with strong support even if the 22 taxon pairs diverged randomly over the past three million generations. We also find the method is sensitive to the prior distributions placed on parameters. Our results demonstrate that analyses exploring power and prior sensitivity should accompany ABC model-selection inferences. We suggest the behavior of the method may be improved by using uniform priors over divergence models (rather than classes of models) and more flexible prior distributions on demographic and divergence-time parameters.

Keywords: Approximate Bayesian computation, msBayes, model selection, simultaneous divergence, Philippines

19A Phylogeographic patterns on mountaintop vertebrates: a study model on small mammals of the Coast and the Andes of central Chile

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We evaluated the phylogeographic patterns of two sigmodontine rodents of central Chile mountaintops, *Abrothrix olivaceus* and *Phyllotis darwini*. We evaluated if these species experienced genetic differentiation between the Andes and the Coast mountains due to the habitat shifts of the Last Glacial Maximum (LGM). We used nuclear and mitochondrial markers, and sequence data were analyzed through maximum-likelihood and Bayesian analyses, as well as network and splitstree methodology. In addition, to evaluate the genetic structure of populations we performed the Geneland analysis for each species. Finally, for each taxon we performed a niche modelling analysis to reconstruct the expansion and contraction history on the mountaintop lineages. The results showed two well supported clusters for *P. darwini* grouping haplotypes from the Coast and from the Andes, although we also recovered shared haplotypes between both mountains. A similar pattern was observed for *A. olivaceus* although not that evident as that recovered for *P. darwini*. The network and splitstree analyses also recovered a comparable pattern of differentiation for each species to that obtained with phylogenies. Although the Geneland results in *P. darwini* and *A. olivaceus* exhibited population structuring, the clusters recovered are not neccesarily congruent with the grouping of the intraspecific phylogeny and the network analyses. We hypothesized that the latter would be due to the shared haplotypes between the Coast and the Andes. Finally, the niche modelling for both species suggest that part of the high Andean distributional range it would have dissapeared during LGM between 26° and 32°S.

Keywords: biogeography, sigmodontine rodents, Andean Cordillera, Coastal Cordillera, phylogeography

20A Molecular phylogeography and genetic structure of alien species raccoon dog (*Nyctereutes procyonoides*) in Europe

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The raccoon dog is alien species in Europe that spread rapidly into many European countries and has significant ecological impact on native ecosystems. The size of raccoon dog population in Europe varied in different periods, and today this species is widely spread. In many countries raccoon dog is declare as invasive species and hunting is permitted throughout the year. The aim of our study was to investigate genetic variability and phylogenetic relationships of raccoon dog using molecular markers. Tissue samples of 269 raccoon dogs were collected by hunters during period 2007-2011 from different locations in Lithuania. Short tandem repeats and mitochondrial DNA control region were used as molecular markers to evaluate the distribution of genetic variation among *Nyctereutes procyonoides* collected from Lithuanian, Finland, Poland, Germany, Hungary, Russia, China. In total, eight haplotypes were found in raccoon dogs in Lithuiania. Phylogenetic relationships between the haplotypes demonstrated presence of two haplogroups. However these haplogroups were not related with spatial geographic structure of the population. Six of 15 canine microsatellite loci displayed a polimorphic alleles. The numbers of alleles per locus, allele frequencies, observed and expected heterozygosity at the locus were estimated, and the distances between analyzed populations were determined. Analysis of molecular variance (AMOVA) showed that genetic diversity of the populations yielded highly significant differences within populations and among populations. The present data revealed a high level of molecular genetic variation in microsatellite loci and mtDNR control region and showed that raccoon dog population is heterogenic and consisted of separate maternal lineages.

Keywords: mtDNA control region, microsatellite, genetic variation, phylogeography

21A Once upon a time in Anatolia: population history of the Anatolian nuthatch

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In this study, the main aim was to understand how Anatolian nuthatches (*Sitta krueperi*) have responded to global climate changes through the latest Quaternary glacial-interglacial cycles. For this, we used a molecular phylogeography, together with ecological niche modelling. Using previously published and new sequences of the mitochondrial COI gene, we investigated phylogeographic structure in Anatolian nuthatches. In addition, using the maximum entropy machine learning algorithm in the MAXENT software, we developed an ecological niche model (ENM) to predict the potential geographic distribution of *S. krueperi* under reconstructed past [the last glacial maximum (LGM), 21 000 years ago] and present (1950 to 2000) bioclimatic conditions. This study represents a first attempt to combine molecular phylogeography and ecological niche modelling for a bird species in Anatolia, a region in which high levels of intraspecific genetic differentiation are observed and which is an important source and refugium of genetic diversity for European biota.

Keywords: mtDNA, last glacial maximum, refugium, phylogeography, *Sitta krueperi*

22A Build and test more realistic historical demographic hypotheses with Species Distribution Modeling and coalescence simulation based methods (already known Approximate Bayesian Computation and a new "phylogeographic simulation" method)

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The use of species distribution modeling (SDM) techniques to propose historical demographic hypothesis as species response to Quaternary climatic changes has become a common procedure offering a complementary source to genealogical information. Given the known limitations of SDMs, hypothesis testing is a delicate following step bearing in mind that quality of tested scenarios is essential. Defining species boundaries of two sister species of cold adapted leaf beetles (Chrysomelidae; *Gonioctena*), we studied their potential current and past geographic distribution in addition to inter and intra-species genetic variation patterns. Concretely, the inference of past geographic distributions in Europe during the Last Glacial Maximum (LGM) and the previous interglacial period for both species suggests different evolutionary scenarios, even for a same species, mainly differentiating on population's connectivity during the LGM. Our study involves an Approximate Bayesian Computation (ABC) method and another coalescence simulation based approach directly integrating geographical information as outputted with SDMs to infer the most likely demographic history for each species. The former method allows us to simulate and then evaluate quite complex historical scenarios while the second was used to directly integrate mapped models of species geographic distribution along the genealogy simulation procedure. Overall, using a multilocus and multispecies source of DNA sequences data, we intend to explore the more likely demographic response to glaciation-interglaciation cycles and explain current distribution of genetic variation for these two closely related cold-adapted species while offering different approaches to discriminate among several SDM approach outputs.

Keywords: phylogeography, cold-adapted species, SDMs, Coalescence simulation

23A Is the Brahamputra river valley a barrier for avian fauna in northeastern India?

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The northeastern region of India is a biodiversity hotspot and harbors around 8% of the global avifaunal diversity. A dominant feature in this region is the river Brahamaputra, which has been proposed as a biogeographic divide based on the presence of sister species on either side of this river. However, the role of the river and associated valley as a phylogeographic divide has yet to be been tested. We sampled bird species from three populations, two north, and one south, of the river valley, and used genetic data (2200 bp of mitochondrial DNA and 600 bp of nuclear DNA) and phylogenetic analyses to investigate the role of the river valley in population differentiation and cryptic speciation. On average, populations that were further apart but on the same side of the river show less genetic difference than closer locations on opposite sides of the river. Phylogenetic analyses also suggest that the river valley is a biogeographic divide for four of the six species. The extent to which the river valley is a barrier depends upon species ecology: sedentary species reveal higher levels of differentiation than less sedentary species. Our dataset also reveals the presence of two cryptic species in this biodiversity hotspot. Finally, we test whether species' ecology can predict the extent of genetic differentiation across the Brahamaputra valley using genetic data from seven additional species from two sites. Our study implicates vicariant patterns (across the river valley) in this region, and suggests that species respond differentially to such barriers based on their ecology.

Keywords: biodiversity, biogeography, distributions, river, phylogeography

24A Doe elevation shifts promote diversification of montane species within Anatolian mountains: The case of the Caucasus endemic bush-cricket *Phonochorion*

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Localized up-down altitudinal shifts and subsequent isolation-admixture of montane species in response to glacial cycles has been proposed as a mechanisms for the high diversity along Anatolian mountains. However specific predictions of the proposed mechanism (the elevation shift model) has yet to be tested. Here we provide a first assesment of this model for promoting inter and intraspecific genetic diversity in the bush-cricket genus *Phonochorion* endemic to the West Lesser Caucasus hotspot. Mitochondrial genes were analysed by bayesian MCMC inferences and coalescent simulations. Timing of diversification was estimated using a multi-species coalescent model. Divergence with gene flow was tested using an isolation with migration model and coalescent based tests separating gene flow from incomplete lineage sorting. Demographic history was assessed using mismatch distributions and extended bayesian skyline plots. Key biogeographic events were evaluated using statistical dispersal-vicariance analysis. Speciation events corresponded both to the Miocene and Pleistocene while intraspecific divergence was Pleistocene based. Paraphyly and haplotype sharing between species was best explained by incomplete lineage sorting rather than gene flow. Overall diversification patterns within the genus are best explained by the fragmentation of a wide ranging ancestor with subsequent dispersal events and demographic expansions coinciding with the Pleistocene. Diversification patterns within the genus *Phonochorion* agree well with the predictions of the elevations shift model. Genetic patterns of diversification were driven mainly by Pleistocene glacial cycles and reflected the nature and distribution of sky-islands with demographic expansion coinciding with glacial cooling. However there was no evidence for divergence with gene flow.

Keywords: Glacial expansions; Pleistocene climatic oscillations; statistical phylogeography; gene flow; incomplete lineage sorting

25A The influence of pelagic duration on population genetic structure: a look at the appropriateness of global analysis

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Pelagic duration (PD) is expected to affect the frequency and spatial scale of migration and thus influence population genetic structure, but recent global analyses have concluded that PD is poorly correlated with marine population genetic structure. However, taxonomic and geographic subsets of species within the global syntheses do show the predicted positive correlation between PD and gene flow. This internal inconsistency suggests considerable heterogeneity in the patterns and processes of evolution and/or their measurement. For example, geographic location significantly influences Fst, as does the geographic scale of observation. Thus, global syntheses, which have applied “treat-as-one-trial” analyses as opposed to meta-analyses of effect size, likely confound many variables and therefore may not adequately describe the effect of dispersal on marine population genetic structure. Here we re-analyze the data previously aggregated in global syntheses, extracting datasets normalized for the effect of molecular marker and including only co-occurring species. We find high correlation between PD and Fst and also effects of fecundity and census population size. Similar analyses in other regions also find a close relationship between dispersal related attributes and Fst. Inability of previous analyses to detect this relationship suggests a problem with the analytical framework, which may be corrected by using comparison of sympatric sister species or synchronously diverging co-distributed species, which are amenable to meta-analyses.

Keywords: dispersal, Fst

26A Generation of biodiversity: Phylogeography of *Agalychnis* and *Dendropsophus* Tree frogs in Mesoamerica

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The amphibian fauna of Mesoamerica is highly diverse yet also highly endangered due in large part to anthropogenic environmental change. The overall aim of this study was to understand the ecological and historical factors leading to the generation of this rich biodiversity and to identify how it may be conserved in the long term. Mitochondrial sequence data was generated from *Agalychnis* and *Dendropsophus* tree frog species from Panama, Costa Rica, Nicaragua, Honduras, Belize and Guatemala. The high morphological diversity in *Agalychnis callidryas* corresponds to high genetic diversity in mitochondrial DNA. Analysis of mitochondrial sequence data using the general mixed Yule-Coalescent (GMYC) model indicates several divergent clusters indicating the presence of several previously unrecognized species.

Comparative phylogeographical analysis of both *Agalychnis* and *Dendropsophus* species combined with species palaeo-distribution modeling enabled the identification of dispersal routes through Mesoamerica from the ancestral home of these genera in South America. Species distribution modeling based on contemporary and predicted future climatic and environmental variables identified sites of conservation importance that could contribute to a regional conservation strategy.

Keywords: climatic change, dispersal, environmental niche modeling, phylogeography, speciation

27A Re-evaluation of a classic phylogeographic barrier: new techniques reveal the influence of microgeographic climate variation on population divergence

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We evaluated divergence and relationships within *Geomys pinetis* to assess the status of formerly recognized *Geomys* taxa. Additionally, we integrated new hypothesis-based tests in ecological niche models (ENM) to provide greater insight into causes for divergence and potential barriers to gene flow. We amplified mtDNA sequences from 58 individuals of *G. pinetis* collected across the southeastern US to reconstruct their phylogenetic relationships and test the time of divergence. ENMs for eastern and western lineages of *G. pinetis* were evaluated using a randomization analysis to estimate niche identity and background similarity statistics between each modeled lineage. Additionally, we used ENM tests to assess the Apalachicola River Discontinuity (ARD) as a geographic barrier contributing to lineage divergence in *G. pinetis*. Sequence data strongly supported two lineages within *G. pinetis* occurring east and west of the ARD with an estimated divergence of 1.37 Ma (1.9 Ma – 830 ka). Predicted distributions from ENMs were consistent with molecular data and defined each population east and west of the ARD with little overlap. ENMs also support the hypothesis that the ARD represents a ribbon of unsuitable climate between more suitable areas where these populations are distributed. The estimated age of divergence between eastern and western lineages of *G. pinetis* suggests that the divergence was driven by climatic conditions during Pleistocene glacial-interglacial cycles. The ARD forms a ribbon of unsuitable habitat at the contact zone of eastern and western lineages of *G. pinetis* forming a significant barrier promoting microgeographic isolation that helps maintain ecological and genetic divergence.

Keywords: Apalachicola River, Florida, geographic barrier, *Geomys pinetis*, phylogeography

28A Nuclear and mitochondrial markers reveal different levels of phylogeographic structure for *Boa constrictor imperator* populations from Mexico and Central America

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Phylogeography focuses on the understanding of how population and historical processes may influence genetic diversity in extant populations. Complex geology and climatic history of the Middle American region make it an ideal setting for studies of evolutionary and ecological processes. Our principal aim was the analysis of genetic diversity and phylogeographical structure of *Boa constrictor imperator* in Mexico and Central America, and the identification of historical key events responsible of their current distribution and diversity. Based on 145 individuals, we combined molecular data from mitochondrial cyt*b* and nuclear ODC intron sequences and microsatellites, implementing analyses of phylogenetic inference, spatial genetics and model-driven methods. Analyses of microsatellites reveal the presence of five main genetic clusters with moderate but significant levels of structure (F_{ST}= 0.043-0.085), while cyt*b* and ODC indicate the presence of two monophyletic linages (D_{XY}= 0.04) with a consistent east-west geographical pattern. Results are in agreement with phylogeographic histories of other Neotropical organisms dispersal across the Panama Isthmus. Our results are relevant for the boa's conservation given its unresolved taxonomic status with respect to all South American subspecies.

Keywords: Phylogeography, Neotropics, Middle America, Boidae, *Boa constrictor*, Great American Biotic Interchange

29A Phylogoegraphic evidences for the drainage evolution in Sino-Himalaya for IBS 2013

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The modern of major rivers drainages Jinshajian and its tributaries, Salween, Mekong, Yarlu Tsangpo and Honghe in Sino-himalyas were once tributaries of a single southward flowing system of Honghe. Historical hydrographical exchanges deeply carved landscapes, and left an imprint on the genetic structure of organisms. To check the imprint, we selected two species *Terminalia franchetii* and *Buddleja crispa*, which both strictly occur in the valley of the region, to study the relationship with river capture events. We used cpDNA sequences (Trn*L-F*, *pet*L-*psb*E) in *T. franchetii* to investigate the relationship between the modern phylogeographic structure and geological changes in drainage patterns. The results indicated that a disjunctive distribution dominant haplotypes between northern and southern valleys are corresponding to the geography of past drainage systems, which provided an evidence that the modern disjunct of *T. franchetii,* and associated patterns of cpDNA haplotype, result from vicariance caused by these historical rivers separation and capture events. Molecular dating inferences of splits times among river systems was in Pleistocene agree with previous time estimate of the drainage re-arrangement in the region. In *B. crispa* , by two cpDNA(trnL-F, psbA-trnH) analyzing, we detected that a disjunctive distributions of single and closely related haplotypes, as well as phylo-groups strongly indicate the historical relationships of present-day discontinuous drainages. Our inferred timings of these events mostly are also Pleistocene. The phylogeographic analyzing of the two plants elicited the similar conclusions which provide the evidences from plants for proving the historical river capture events in Sino-himalayas.

Keywords: Phylogeography, Terminalia franchetii, Buddlejia crispa, river captures, Sino-himalaya

30A Fine-scale connectivity between arctic crustacean populations

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Understanding how species have survived to Quaternary climatic changes might be important in a global warming context in terms of predicting its effects on species distribution and survival. Successful dispersal among populations leaves genetic signatures that can reveal the effects of historical and contemporary processes on genetic diversity. Even though several studies have been conducted in the Arctic Ocean, marine crustaceans are largely underrepresented. With the advent of next generation sequencing techniques and new population genetic methods, it is easier to develop a large number of markers that enable the investigation of gene flow between populations in non-model organisms. Here, we investigate the population genetic structure of peracarids, an important order of crustaceans, and the connectivity between populations in the Arctic Ocean. Six species of benthic and pelagic peracarids have been sampled from different locations in the Arctic Ocean, and using a 454 platform, a hundred microsatellites have been characterized for each species including a dozen polymorphic microsatellites necessary to conduct this survey. Patterns of intra and interpopulation genetic variation with microsatellites, a mitochondrial gene (cytochrome c oxydase subunit 1, CO1), and nuclear gene 18S will be measured and the level of gene flow will be assessed at different time scale using classical genetic approach and a Bayesian method. This study will give an overview of the historical and contemporary processes that have shaped the present distribution of arctic peracarid species, and will serve as a baseline for monitoring changes in the Arctic Ocean.

Keywords: marine biodiversity, Arctic, gene flow, phylogeography, genetic structure

31A Taxonomic, phylogenetic and functional betadiversity in South American hummingbirds

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The difference in species composition between assemblages, betadiversity is a fundamental measure of biodiversity. Betadiversity has historically been quantified solely through differences in taxonomy. This compositional betadiversity is information poor, since it conveys little about species functions in an assemblage. Furthermore, all species are not equally related, such that turnover between sister species may be the result of different biogeographic mechanisms than turnover between distantly related species. Functional and phylogenetic betadiversity supplement compositional diversity and are gaining recognition in the study of biodiversity. Partitioning species assemblages into their phylogenetic, functional, and compositional dimensions permits novel insight into the mechanisms influencing betadiversity. Using hummingbirds from Northern Latin America, we propose a framework to test mechanistic explanations governing the dimensions of diversity. By comparing dimensions of betadiversity with environmental dissimilarity, distance, and connectivity, we seek to identify the underlying ecological controls of assemblage turnover in this diverse system. Finally, we evaluate which phylogenetic groups are associated with turnover in each combination of dimensions. We find that compositional and phylogenetic turnover is better predicted by environmental dissimilarity than distance metrics. Cost distance was a stronger predictor of taxonomic turnover than Euclidean distance, suggesting current species assemblages are limited by geographic barriers. Clade level analysis showed that betadiversity was not even across phylogenetic groups. This predictive framework advances the study of betadiversity by providing a priori expectations for why compositional, functional, and phylogenetic diversity differs across space.

Keywords: betadiversity, hummingbirds, phylogenetic community structure

32A Genetic divergence by historical vicariance during the Quaternary in a temperate shrub, *Rhododendron weyrichii*, distributed in the Islands of Japan and South Korea

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Continental islands are unique in terms of geographical complexity, and distribution of many species in the islands have been changed to geographical continuity and discontinuity responding to the past climatic oscillations and sea-level changes. *Rhododendron weyrichii* is a shrub that distributed in continental islands of southwest Japan (Kii Peninsula, Shikoku, and Kyushu) and South Korea (Jeju). The glacial periods may have affected genetic diversity and structure in *R. weyrichii*, and existence of geographical barrier between the islands may have affected its genetic structure. In this study, we examined phylogeographic history in *R. weyrichii* by sequence analysis on nine nuclear genes and four regions of chloroplast DNA using 18 sampled populations, and palaeodistribution modeling. Nucleotide diversity was low values in Shikoku, and the variation of chloroplast microsatellite repeats was high in Kyushu. The sequence analysis on nuclear genes and cpDNA revealed clear divergence between the islands, and a limited admixture of cpDNA haplotypes in each population. Especially, the populations between Shikoku and Kyushu showed clear divergence at cpDNA and nuclear genes, and between Kyushu and Jeju were divergent at nuclear genes. The ecological niche modeling predicted that suitable regions were separated into three regions (Kii, Shikoku, and Kyushu) during the Last Glacial Maximum, although there are no large differences between the predicted range at the LGM and the range at present. These results suggest that genetic divergence of *R. weyrichii* has been caused by historical vicariance due mainly to seed dispersal limitation.

33A Improving the ecological meaning of remote sensing predictors in species distribution models

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Detailed knowledge of species distribution patterns is recognized as being of core interest in the fields of biogeography, conservation biology and many related disciplines. Given the accelerated loss of biodiversity and the decline in associated ecosystem functioning worldwide, scientists are racing against time to accumulate information on species distributions. In the last two decades, an increasing number of studies used remote sensing data to augment the performance of correlative species distribution models (SDMs). However, voices critical of this application have also been increasing, pointing out problems with the ambiguous relationship between habitat suitability and remote sensing variables and the unclear specification of the modeling purpose (i.e. mapping actual or modeling potential species distribution). Here, we elaborate on the potential reasons for frequent misconceptions about remote sensing data in SDMs and discuss the differences between the "horizontal" approach of geographers versus the "vertical" approach of ecologists. We provide further suggestions to improve the ecological relevancy of remote sensing predictors and illustrate them with two case studies on the distribution of Mexican tree species. Specifically, we analyze the fundamental differences between categorical land cover classification and continuous remote sensing data, and show how the selection of ecologically meaningful remote sensing predictors effects final SDM predictions. Improving the application and interpretation of remote sensing data in SDMs is crucial for further development of the discipline.

Keywords: Mexico, trees, land cover, interdisciplinary

34A A high spatial resolution satellite-based cloud climatology for biogeographical applications

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Cloud cover strongly affects the evapotranspiration, especially in the tropics and subtropics. This poster describes a near-global 250m pixel resolution daytime cloud climatology developed using 10 years of MODIS imagery from two sun-synchronous polar-orbiting NASA satellites. Our simple thresholding procedure to extract cloudiness from individual visible images and average them to produce monthly, seasonal and multiannual means has some limitations but is reliable over most of the tropics and subtropics. Our thresholding procedure is not as reliable where snow cover is frequent. The most important results from our work are that mean daytime cloudiness is strongly controlled by small topographic features throughout the moist tropics and that the underlying vegetation in many regions closely mirrors the mean cloudiness patterns. Thus, these cloud climatologies should be useful for not only improving the mapping of high-rainfall cloud forest distributions, but may be even more important in low-rainfall regimes, such as along the coasts of Peru, Chile, and Baja California, and parts of southern Arabia and eastern Africa. Many taller oceanic islands also show prominent stratocumulus-controlled moist environments (e.g. the Galapagos, Cape Verde, and Canary Islands and some others regions that are partially cloud-controlled such as Hawaii and Socotra). In addition to providing a better understanding of the climatic controls on vegetation (and the associated fauna) at high spatial resolution, these cloudiness products may be useful for conservation and restoration efforts in cloud-controlled regions where the original vegetation cover has been altered.

Keywords: biogeography, climatology, MODIS, cloud, precipitation

35A Modeling species distribution using niche-based proxies derived from composite bioclimatic variables and Modis NDVI

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Vegetation mapping based on niche theory has proven useful in understanding the rules governing species assemblages at various spatial scales. Remote-sensing derived distribution maps depicting occurrences of target species are frequently based on biophysical and biochemical properties of species. However, environmental conditions, such as climatic variables, also affect spectral signals simultaneously. Further, climatic variables are the major drivers of species distribution at macroscales. Therefore, the objective of this study is to determine if species distribution can be modeled using an indirect link to climate and remote sensing data (NDVI time series). We used plant occurrence data in the US states of North Carolina and South Carolina and 19 climatic variables to generate floristic and climatic gradients using principal component analysis. We further modeled the correlations between floristic gradients and NDVI using Partial Least Square regression. We found strong statistical relationship between species distribution and NDVI time series in a region where clear floristic and climatic gradients exist. If this precondition is given, the use of niche-based proxies may be suitable for predictive modeling of species distributions at regional scales. This indirect estimation of vegetation patterns may be a viable alternative to mapping approaches using biochemistry-driven spectral signature of species.

Keywords: floristic and climatic gradients, species composition, Partial Least Squares regression, remote sensing, vegetation mapping and modeling

36A Study of zoogeomorphic activity of Brandt's vole (*Microtus brandtii*) and its role in the degradation of Mongolian steppe

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Our study examined pastureland degradation in the Mongolian plateau by comparing the grazing types of traditional nomadic cultures and recent settlements using a zoo-geomorphological approach. We hypothesized that the activity of Brandt's vole (*Microtus brandtii*) softens the soil near colonies, increases the organic and nitrogen content of the soil, changes the plant species composition, and increases the amount of aboveground biomass in degraded pastureland.

Keywords: satellite imagery, zoo-geomorphologic activity, Brandt's vole, *maximum entropy method,* Local Convex Hull (LoCoH) method.

37A Remotely sensed spatial heterogeneity of species habitat

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Understanding biodiversity patterns and their relationships with environmental factors is a fundamental question in biogeography. Spatial heterogeneity of species habitat has long been recognized as an important determinant of species distribution and diversity. However, since field measurements of habitat heterogeneity are limited in terms of spatial coverage and temporal frequency, broad-scale studies usually rely on metrics derived from categorical land cover maps. Remote sensing provides spatially continuous and sometimes temporally consistent observations on the land surface, and thus is an excellent tool for characterizing habitat heterogeneity and monitoring its dynamics. With Oregon as a test site, we evaluated the potential of remote sensing image texture for quantifying species habitat heterogeneity and modeling species richness. Correlation and regression analyses showed that first- and second-order texture measures derived from Landsat imagery explained up to 50% and 74% of the variation in the spatial heterogeneity of forest canopy height and aboveground biomass, respectively. In contrast, landscape metrics derived from 30-m categorical land cover data explained < 20% of the variation. Furthermore, models built with texture measures also explained > 35% of the variability of bird species richness among Breeding Bird Survey transects. Categorical land cover data require human interpretation that is not without error and may not be most pertinent for organisms. It also is limited in spatial grain and availability. Remote sensing image texture may thus be a vital tool for capturing ecologically relevant habitat attributes for modeling global biodiversity and addressing ecological questions at finer spatial scales.

Keywords: bird species richness, image texture, Landsat imagery, landscape patterns, vegetation characteristics

38A Species distribution modeling using novel spaceborne remote sensing datasets

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To date, the primary dataset used for species distribution models is the WorldClim database. This dataset consists of interpolated grids derived from station data primarily recorded during the years 1960-1990. While these grids have been successfully applied to many modeling studies with diverse applications, it is possible that their performance is suboptimal in regions with few weather stations or topographically complex regions where interpolation methods may struggle. We have generated novel bioclimatic layers derived from remote sensing and remote-sensing/station-based composite sources (AMSR-E and MERRA, respectively) which we use to generate species distribution models for a set of South American vertebrates. We compare models using remotely sensed data with models generated from WorldClim-based bioclimatic variables. Similar datasets will likely become increasingly useful, as more remote sensing datasets with increasing spatial and temporal resolution become available, particularly because such datasets are measuring climate change currently underway.

Keywords: distribution modeling, niche modeling, remote sensing

39A Incorporating satellite derived cloud climatologies to improve high resolution interpolation of daily precipitation

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Conservation of biodiversity demands comprehension of evolutionary and ecological patterns and processes that occur over vast spatial and temporal scales. A central goal of ecology is to understand the factors that control the spatial distribution of species and this has become even more important in the face of climate change. However, at global scales there can be enormous uncertainty in environmental data used to model species distributions. Even 'simple' metrics such as mean annual precipitation are difficult to estimate in areas with few weather stations and available data sets do not quantify uncertainty in these surfaces. We are developing a global, 1km resolution, daily meteorological dataset for 1970-2010 by leveraging relatively high quality station observations with spatially continuous but indirect satellite observations. While several satellite derived precipitation products exist, all are relatively coarse ($\geq 0.25^{o}$). An alternative approach is to use higher resolution multi-spectral satellite data to estimate other cloud parameters that are more directly related to precipitation. Precipitation will fall when cloud particles achieve sufficient mass to overcome updraft winds and when the clouds have sufficient vertical extent to facilitate the growth of these particles. The MODIS Cloud Product (MOD06) includes estimates of effective radius and optical thickness at 1km resolution. These parameters are theoretically related to precipitation and we are exploring their utility in the interpolation of station precipitation observations. Improving high resolution estimates of precipitation will facilitate analysis of geographic and/or environmental shifts in species distributions in response to global climate change.

Keywords: biogeography, climate, modeling, meteorology, time series

42A Selection and the 3rd dimension of marine biogeography: contemporary sympatric population partitioning along a razor-thin depth gradient

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Broad-scale biogeography has been wildly successful in identifying spatial isolation as a primary driver of biodiversity. In the marine realm, where roughly 80% of species have a dispersive pelagic larval phase and there are few impermeable dispersal barriers, there is much debate about the importance of fine-scale drivers of reproductive isolation in the generation of biodiversity. Here, we investigate the relationship between disruptive natural selection along a narrow depth gradient and the genetic partitioning of broadcast-spawning *Cellana talcosa* limpet populations on the scale of a few meters. *C. talcosa* is one of three endemic, monophyletic and vertically-stratified Hawaiian limpets. The weight of available ecological and genetic data is consistent with a sympatric origin of *C. talcosa* as its ancestors pushed progressively deeper into shallow subtidal habitats and experienced drastic increases in predation pressure by crushing predators. We test for contemporary sympatric divergence between the predator-protected intertidal and the predator-exposed subtidal *C. talcosa* on two islands across 37,000 homologous restriction site associated DNA sequence contigs from 100-1400 bp in length with at least 10x coverage to measure the level of selection and genetic partitioning. Overall, in the heterogeneous marine realm there are a myriad of selective pressures pulling populations apart, particularly along depth gradients, as dispersal simultaneously acts to hold the populations together. Finely-scaled biogeographic studies, in combination with genome-wide DNA analysis can help to elucidate this dynamic and its importance in the generation of biodiversity.

Keywords: phylogeography, genomics, RADseq, speciation, SNPs

43A Assembly of plant communities in climate space

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We propose a conceptual framework for identifying the importance of multiple climate-linked processes (climate lags, biotic interactions, and environmental filtering) to the assembly of local communities. We develop a set of orthogonal metrics (observed-inferred niche distance, species-inferred distance, community niche volume, respectively) that can be calculated for the multidimensional climate niches of species in communities, and also relative to multiple approaches for delineating regional species pools (global, geographic dispersion field, environmental dispersion field) corresponding to increasingly complex assembly scenarios. We then test this framework with the a plant occurrence database (BIEN), using data from 578 census plots (0.1 ha) and 5,329,509 occurrence records for 89,780 species distributed across the New World. We show that patterns are strongly contingent on the use of a null model, and there are significant strong effects of each underlying process in almost all communities studied. However the sign and magnitude of these effects is highly idiosyncratic and not predictable from multiple current- or paleo- climate variables. Broadly our study indicates that inference about assembly processes requires robust null modeling and high-quality occurrence data.

Keywords: community assembly, niche, regional pool, source pool, null model

44A Species richness and diversity of predatory wasps along a latitudinal gradient in the Atlantic rain forest, Brazil

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The Atlantic Rain Forest is regarded as a conservation hotspot, since it is one of the most diverse and threatened ecosystem of the world. Its high biodiversity is generated mainly by latitudinal and elevational gradients along the Brazilian coast. Predatory wasps have a fundamental role in ecosystem maintenance, controlling populations of other arthropods. The present study aimed to describe the species richness and variation in diversity of predatory wasps along a latitudinal gradient covered by the Atlantic Rain Forest. Seventeen areas, between 7° and 27° of latitude south,, were sampled with a standardized protocol based on three different collecting methods. The species richness was estimated by rarefaction, and the species diversity was estimated by the Shannon index and by the fundamental biodiversity number (ϑ). Moreover, the Pielou's equability and the immigration rate (m) were estimated to help understand the variation in the species richness and diversity. Generalized additive models (GAM) were applied to correlate the estimates to latitudinal variation. These models indicate a peak of species richness and diversity of predatory wasps between 20° and 23° latitude south. Moreover, both species richness and diversity are explained by the latitudinal variation and the immigration rate combined. The values estimated by the Pielou's equability index and by the fundamental biodiversity number were not explained by latitudinal variation. Our results suggest that the heterogeneity of the predatory wasp community is higher around the Tropic of Capricorn and it is highly influenced by the species richness.

Keywords: Hymenoptera, biodiversity pattern, tropical forest, Neotropical Region.

45A Cross-scale phylogenetic structure in coastal dune-plant communities across the globe

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Dune plant communities occur along coast-lines world-wide. We assessed their evolutionary and ecological assembly across scales using phylogenetic and functional data from temperate dune plant communities on five continents. We calculated phylogenetic clustering (Net Relatedness Index, NRI and Nearest taxon index, NTI) of regional dune floras to estimate the amount of in-situ diversification relative to the global dune species pool and evaluated the relative importance of land and climate barriers for these diversification patterns by geographic analyses of phylogenetic similarity. We then tested if dune plant communities exhibit similar patterns of phylogenetic structure within regions due to consistent coastal disturbance gradients. We therefore calculated NRI for local communities relative to the regional species pool and tested its correlation to disturbance-related functional traits, plant height and seed mass. Regional species pools were phylogenetically clustered relative to the global pool, indicating local diversification, and clustered together on either side of the tropical climate barrier. Local NRI plot values confirmed that most communities were phylogenetically clustered within regions. NRI values were negatively correlated with plant height, indicating greater phylogenetic clustering in low-growing, more disturbed communities, consistent with environmental filtering along disturbance gradients. Height and seed mass both showed phylogenetic signal. Generally, low NRI plots tended to represent coastal scrub and forest, while high NRI plots tended to represent more herb-dominated vegetation. In conclusion, global dune plant communities are build up by regionally localized diversification processes, with coastal disturbance gradients driving convergence in local community structure among geographic regions.

Keywords: biogeography, functional traits, NRI, plant community assembly, plant height

46A Geographical distribution of angiosperm lineages influences community assembly of Neotropical and Afrotropical trees

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The phylogenetic structure of local ecological communities is often interpreted in terms of niche-based mechanisms of community assembly. Here we evaluate how the geographical distribution of major angiosperm lineages influences the phylogenetic structure of local tree communities in Neotropical and Afrotropical forests. We compiled tree species abundance data from a series of 1-ha plots from seven sites. Net relatedness index (NRI) was used as a measure of phylogenetic structure for 400-m^2 subplots based on plot and site species pool sizes. Phylogenetic composition of each subplot was determined relative to the complete species pool for the seven sites, using principal coordinates of phylogenetic structure (PCPS). We related phylogenetic composition and local phylogenetic structure using linear regression. Magnoliids were associated with phylogenetic overdispersion in the Afrotropics, while monocots and eudicots were associated with phylogenetic clustering in the Neotropics. Increasing species pool size from plot to site level increased NRI values in three sites and decreased it in four sites. Phylogenetic composition significantly accounted for the variation in local phylogenetic structure in all but two sites. The local phylogenetic structure of tropical tree communities appears to be determined principally by the phylogenetic composition of the regional pool of species, which is an outcome of the biogeographic history of the tropical tree flora. At the same time, the patterns found in some of the communities might be attributed to site-level neutral dynamics or local niche-based assembly processes. Our study provides new evidence that biogeographic history has a profound influence on local community assembly.

Keywords: community phylogenetics, historical biogeography, neutrality, niche, rainforest

47A Global biogeography of grassland Auchenorrhyncha (Insecta: Hemiptera)

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Patterns of grassland biogeography were inferred using molecular phylogenetic analysis of 3 lineages of grass-specialist sap-sucking insects. Because they are hyperdiverse and globally distributed, but with a high degree of local endemism, these organisms have the potential to elucidate patterns in the evolution of the grassland biota that are much more detailed than those based on previously studied grassland vertebrates or plants. Preliminary phylogenetic results based on DNA sequence data from three gene regions indicate that biogeographic patterns of grassland leafhoppers and planthoppers are more complex than those of previously studied groups of grassland organisms, with multiple invasions of various grassland regions within each lineage. While all lineages are inferred to have Old World origins, patterns of spread are quite variable. One lineage, Deltocephalini + Paralimnini, originated in the Oriental region then spread throughout the Old World before invading and radiating in the New World. The other two lineages, Hecalini and Caliscelidae, both originated in the Palearctic and had two main clades; one of which spread to the Nearctic then south into the Neotropics while the other clade spread through the Old World (and in one lineage also invaded the Neotropics then spread north into the Nearctic). This study has implications for conservation. Grasslands are rapidly being destroyed and identifying regions possessing many unique lineages would allow these regions to be targeted for further protection.

Keywords: leafhoppers, planthoppers, insects, phylogenetics

48A Global species richness patterns and their drivers among the order Anseriformes

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Birds (class Aves) follow the latitudinal gradient in species richness (more species are found closer to the tropics). However, by reducing the taxonomic scale to the order level other patterns can emerge which can be instructive about mechanism. For example, in the order Anseriformes the pattern is reversed so richness increases towards higher and lower latitudes. This divergence from the latitudinal gradient in species richness, as well as the divergence from other marcoecological rules (e.g. Lack's rule), calls for a study of the drivers of species richness in this order. Here we studied the spatial pattern of species richness among Anseriformes during breeding season. As in other studies of birds, we found variability in productivity (measured by NDVI) to be the most important predictor when using univariate models to predict richness. However, allowing for non-stationarity in the relationship between predictors and response by using regression trees we found day length in the breeding season to be the most important predictor followed by annual actual- or potential evapotranspiration conditioned on short or long days respectively. Predictors commonly used to explain large-scale richness patterns of birds, such as annual mean temperature and topographic heterogeneity, explained little or none of the variation in richness among Anseriformes. We discuss several possible mechanisms for this pattern. We highlight the importance of using methods allowing for non-stationarity in the processes driving richness patterns, especially on a global scale where the strength of the predictors are likely change.

Keywords: waterfowl, Anatidae, non-stationarity, biogeography, distributions

49A Quantifying the fundamental unit of biogeography: Assessing different methods to measure geographic range size and why it matters

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Geographic range size is a fundamental property of a species and a key criterion in determining conservation status and prioritization. Yet, many methods of measuring range size exist in the literature, occasionally confounding the area of a species' outermost limits with the area over which it actually occurs. As different methods can cause drastic differences in species richness and extinction risk estimates, how we measure range size is profoundly important. We used a very large dataset of New World plant species to investigate several popular approaches of estimating the geographic range sizes and distributions of species, from methods estimating the size of a species' geographic extent, through methods approximating the size of a species' occupied range, to methods estimating both a species' occupied range and distribution. We explored how combinations of environmental layers and different thresholds influenced the range size estimates of Maxent models. For each approach, we computed geographic range size and accuracy metrics and compared the resulting sizes with those of expert-drawn maps. We found that for range size measures derived solely from occurrence data, the area defined by a convex hull was a fairly good predictor of range size. Range size estimates derived from Maxent models were significantly improved when combining spatial filters with bioclim layers, and sensitive to the threshold used to create presence/absence maps. As species richness maps created from range maps of various approaches were markedly different than maps derived using expert range maps, we offer some best practices for estimating geographic range size.

Keywords: biodiversity, biogeography, distributions, richness, maxent

50A Speciation rate is constrained by lack of persistence of divergence processes and diverging populations

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The mechanisms behind variation in species numbers remain elusive. Diversification rate is determined by the balance between production of new species and persistence of these species. Persistence is, however, also of crucial importance in determining speciation rate. We argue that persistence of processes leading to divergence, and of the diverging populations themselves through the entire time period needed for speciation, have generally been too little appreciated. Speciation studies tend to focus on how factors affect gene pool separation only. This neglect has consequences for our perception of how different factors affect diversification and thus how we interpret biogeographic patterns in species diversity. We introduce a framework explicitly distinguishing how various factors affect lineage splitting from how they affect persistence of lineages and processes during speciation. Some traits that promote lineage splitting, such as specialization, simultaneously reduce persistence of the products of the splits. The opposite is true for other traits: dispersal ability is predicted to curb splitting but promote persistence. A trait could therefore have positive or negative net effects on speciation rate in different situations, depending on the relative strengths of the promoting and hindering processes. Environmental factors may also affect persistence. For example, climate change may initiate splitting by isolating gene pools in refugia and by providing novel environments with vacant niches. Recurrent climate change may, however, also interrupt isolation and/or cause extinction of diverging gene pools. An explicit acknowledgement of the role of population and process persistence will make discussions on controls of speciation and diversification clearer.

Keywords: diversification, lineage splitting, biogeographic patterns

51A Determinants of species diversity patterns in European liverworts (Marchantiophyta)

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The determinants of spatial diversity patterns are a long-standing subject of biogeography, and have been studied extensively for many groups of organisms including vascular plants. However, other important groups of land plants have not been studied in the same way due to a lack of appropriate data. Liverworts (ca. 7,500 extant species) diverged from the other land plants >475 millions of years ago, and may thus provide important independent insights into the determinants of plant species richness. A new database of liverwort and hornwort species occurrence, compiled as part of the Early Land Plants

Today project (www.elpt.org), now allows macroecological analysis of liverwort diversity. This dataset holds records of liverwort and hornwort species occurrence in geo-political units worldwide. We used presence-absence data of all European liverwort species (n=462) in 346 units throughout Europe to calculate species richness and relate it to current and past environmental conditions. Preliminary results indicate that current climate is the most important driver of liverwort species richness, which appears to be most strongly related to temperature seasonality/continentality and annual/wet season precipitation. Habitat complexity (topographic and edaphic diversity) seems to play an intermediate role. There is little evidence for an independent effect of past environments (Quaternary temperature- and precipitation stability, glacial cover). We are currently investigating those factors in more detail. Our results indicate that diversity patterns in liverworts and vascular plants are not necessarily subject to the same constraints, pointing to an important role of ecological and life history differences.

Keywords: biodiversity, climate, land plants, macroecology, species richness

52A Dependence on biogeographical region, activity time and use of space

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Bergmann’s rule was originally explained by a mechanism that is unique to endotherms. Nevertheless, geographic variation of body size of poikilotherms, including snakes, is increasingly studied. Such studies usually focus on assemblages of species in a region, ignoring species’ ecological and biological traits.

We examined the relationship between environmental temperatures and body size of Australian (n=126) and North American (n=102) snakes. We also considered phylogeny, activity time (diurnal/nocturnal, cathemeral species were deleted) and use of space (surface active /burrowers/aquatics). For each species we calculated the mean annual temperature across its distribution range and a mean body mass, using family-specific allometries we developed. As a sole predictor, temperature is unrelated to mass. With ecological traits, however, there is a relationship between mass and temperature, which varies between regions and ecological traits. In Australia, size of burrowers and of surface-active diurnal species decreases with temperature, whereas that of nocturnal species increases. In North America size of diurnal surface active species increases with temperature, whereas that of nocturnal surface actives and burrowers is temperature-independent. Our results indicate that “putting all snakes in one basket” is misleading. Biogeographical regions and ecological traits profoundly affect the geographic variation of snake body size. One reason for this may be that even sympatric snake species experience different environmental conditions, including thermal conditions. Thus different factors shape spatial variation of snake body size.

53A Cryptic diversity of a “cosmopolitan” harpacticoid copepod: the “meiofauna paradox” remains

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Many meiofaunal species are widespread or cosmopolitan, despite these tiny benthic organisms typically have limited dispersal ability and no pelagic propagation stages (“meiofauna paradox”). Recent molecular-based studies have revealed that some species formerly considered to be cosmopolitan are flocks of cryptic species. We present a case study of harpacticoid *Nannopus palustris*, which was formerly assumed to be a single, cosmopolitan but highly variable species. Several geographically distant populations (North, Black and White seas, Indian Ocean and South Carolina, USA) were compared by means of morphological and genetic analyses. Both mitochondrial and nuclear gene trees were in compliance with the morphological data and demonstrated significant differences between populations. Only North and Black Sea populations were genetically similar and morphologically indistinguishable, all other populations had remarkable morphological peculiarities, and none of them entirely fitted the “canonical” description of *N. palustris*. Average genetic divergence was extremely high – 47–66% by Cyt*b* and 2–4% by 28S DNA. Thus, “*N. palustris*” is in fact a complex of pseudo-sibling species which represent the whole spectrum of phylogeographical situations: from local sympatry to broad-range entirety of distant populations. At finer spatial scales, little genetic variation was observed between conspecific populations, indicating high genetic exchange. Moreover, geographic and genetic distances between populations were not correlated, contradicting the gradual “isolation by distance” model of speciation. No single explanation can be provided for this phylogeographic pattern. “Meiofauna paradox” is thus a complex phenomenon involving several evolutionary mechanisms.

Keywords: meiofauna, Harpacticoida, cryptic diversity, morphology, biogeography

54A Global variation in altitudinal diversity patterns across latitudes

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Recently, vertical gradients of species diversity (altitudinal or elevational, water depth) have gained attention, offering much needed complements to horizontal (latitudinal) gradients with a longer history of study. The increase in accumulated data, especially during the last two decades, involving a wide range of organisms and most large mountains around the world, enable us to closely examine how the latitudinal and altitudinal patterns are intertwined. Here, using data from 443 altitudinal gradients worldwide, we investigate how altitudinal diversity patterns differ across latitudinal zones due to differences in the length (extent) and start/end positions of the sampled climatic gradients. The results show that intermediate latitudes had higher proportions of unimodal diversity patterns than low and high latitudes. In general, mountains with greater elevational extents had proportionally more unimodal patterns. Most altitudinal diversity curves showed positive skews and the elevation of their peaks increased with the elevation of the mountain base sampled and to a lesser extent with the upper sampling limit. More inclusive taxonomic groups tended to exhibit hump-shaped relationships between diversity and altitude whereas relationships for smaller groups were highly variable. Altitudinal patterns in precipitation and human impact are suggested as explanations for the mismatch between latitudinal and altitudinal diversity patterns. Overall, the uneven distribution of mountains across the earth’s surface appears to have profound effects on global latitudinal diversity patterns. We discuss the possible effects of underlying gradients of mountains on diversity patterns across latitudes and make several suggestions that may improve future sampling and research.

Keywords: Comparative studies, elevation, gradient range and positions, horizontal vs. vertical patterns, mountains.

55A Phylogeny and biogeography of Ruscaceae with a focus on possible family origins and distribution patterns in tribe Dracaeneae

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Ruscaceae (Asparagales; lily-of-the-valley, solomon's seal, beargrasses, and dragonblood trees) comprise a monocot group in which most tribes are boreotropical in distribution. One group (tribe Dracaeneae) including the woody genera *Dracaena* and *Sansevieria* is pan-Pacific (except S.A.) as well as in Africa. Forest understory herbs in tribe Polygonateae (*Maianthemum, Polygonatum, Convallaria*) are all boreotropical genera. Many genera have bird-dispersed fruits or seeds and may be dispersed over long distances, while Nolineae are wind dispersed over potentially long distances, but only occur in North America. Previously, relationships among well-supported tribes in the family have been unresolved. To better portray relationships in Ruscaceae a phylogeny will be presented based on ITS and 18S nuclear ribosomal DNA, as well as *ndh*F, *mat*K, *ycf*1, and *rbc*L genes, and *psb*A-*trn*H intergenic spacer of the chloroplast, sampling 129 taxa with increased sampling in tribe Nolineae and Dracaeneae in particular. *Eriospermum* (African) is sister to remaining Ruscaceae with high support. While the positions of Nolineae and Dracaeneae receive low support they are likely to be sister to remaining tribes. A group conforming to Dracaeneae includes *Ruscus, Dracaena,* and *Sansevieria* with high support, while Central American species of *Dracaena* are sister to the *Dracaena-Sansevieria* clade. Other relationships within the family will be presented, while using the phylogeny in an ancestral area reconstruction in a likelihood framework, focusing on major contributors to distribution patterns seen in *Dracaena* (including *Pleomele* and *Sansevieria*) and *Maianthemum*. An out-of-Africa diversification will also be discussed.

Keywords: pan-Pacific, boreotropical plants, Asparagales

56A Deconstructing biodiversity gradients into species- and assemblage-level processes: Climate and body size species sorting plus macroecological effects on the species richness of European scarab dung beetles

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Biodiversity gradients are known to be determined by processes occurring at both assemblage and species levels. While ranges are constrained by environmental conditions, dispersal limitation and other historical processes, the composition of local assemblages depends on species-sorting processes that are related to local productivity and species traits and interactions. Here we study how the distributions of the 106 European Scarabaeoidea dung beetles – known to be affected by temperature gradients rather than dispersal limitation – and the diversity of their assemblages are affected by environmental gradients and processes occurring at the landscape level. To do this, we use the recently proposed SESAM protocol, comparing the results of stacking species distribution models (SDM) with those of macroecological models (MM) based on the same variables. Although we find strong environmental impacts on both species ranges and assemblages, the effects of different predictors vary between these two levels, even showing opposite relationships. Temperature, altitude or landscape configuration seem most important at the species level, while soil characteristics are most important for assemblages. The differences between SDM and MM predictions are related to the body size of the species present in each area, their phylogenetic relatedness, productivity and habitat diversity. This evidences that the diversity of dung beetles is determined by the interplay of environmental constraints acting on their distributions and limitations to their coexistence acting at the landscape level.

Keywords: species distributions, community assembly, environmental constraints, SESAM protocol, Western Palearctic Scarabaeoidea

57A Does the Energy Equivalence Rule apply to soil invertebrates?

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The energy equivalence rule assumes that the scaling of population density with body mass, $N \mu W^{-a}$, is inversely proportional to the scaling of individual metabolic rate $M \mu W^{a}$. As a result, the total population energy use (PEU), calculated as the product of individual metabolic rate and population density, is independent of body mass: $MN \mu W^{a}W^{-a} \mu W^{0}$. Since its introduction, the energy equivalence rule has been repeatedly tested but seldom applied to invertebrates. Here we evaluated the validity of this rule at the scale of a single community of soil invertebrates. In order to do so, two series of soil samples were collected from a deciduous forest of Kampinos National Park (Poland). Invertebrates were extracted, counted, weighed and identified to the genus level. In addition, metabolic rate was estimated on the basis of regressions found in the literature. Strong linear dependencies were found between log-transformed metabolic rate and log-transformed body mass. The slope of this relationship was found to be 0.84 for both series of samples. Similarly, strong linear dependencies were found between log-transformed body mass and log-transformed density. The slope of this relationship was found to be –0.77 and –0.79 for the first and second series of samples respectively. As predicted by the energy equivalence rule, the absolute values of these slopes did not significantly differ. Moreover, no correlation was found between body mass and PEU. The energy equivalence rule does seem to apply to soil invertebrates.

Keywords: scaling relationships, body mass, density, metabolic rate

58A Biogeography and evolution of the fauna in the Tibetan Plateau and the Himalayas

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The history of the Tibetan Plateau and the Himalayas (QTPH) region makes it a ‘living laboratory’ for understanding how the Earth’s abiotic evolution has shaped regional biotas. Geographic distributions of many animal groups indicate an asymmetric and marginal pattern. Several major diversity centers based on both species richness and endemism have been found in the marginal areas of the QTPH, including the eastern Himalayas, the western Himalayas, north-western Hengduan Mountains, and the north-eastern mountainous areas of the plateau. There is a noticeable congruence between patterns of endemism and patterns of species richness in these areas. Phylogeographic and phylogenetic studies have revealed some glacial refugia that are spatially coincident with the diversity centers in the marginal areas as well as recolonization pathways after the glaciations. Analyses based on the global distributions of the QTPH species of a insect group have identified general macro-scale biogeographical patterns and biogeographical affinities of the QTPH terrestrial fauna in a global context. Current evidence suggests that historical mechanisms such as faunal exchanges, vicariance due to the uplift of geographical barriers (e.g. the Himalayas), environmental heterogeneity and Quarternary glaciations have shaped the biogeographic patterns and the fauna in the QTPH.

Keywords: bird, distributions, global scale, insect, phylogeography

59A Hot and wet, but mostly productive – What do turtles like?

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We know little about global reptile distribution and richness patterns. To ameliorate this we mapped and analyzed the species richness of all 316 extant species of terrestrial and freshwater turtles. We analyzed richness globally and in four regions – America, Eurasia (including N. Africa), Sub-Saharan Africa and Australia, and used simultaneous autoregression (SAR) models to control for spatial autocorrelation. We tested several hypotheses regarding the drivers of richness patterns: 1. Richness increases with higher ambient energy and water availability (which we measured by mean annual temperature and precipitation); 2. Richness increases with increasing resource availability (measured by mean net primary productivity (NPP)); 3.Richness is high in climatically stable regions (measured by temperature and precipitation seasonality); 4. Richness increases with increasing elevation range and habitat variability. NPP and mean annual temperatures predicted richness best, lending support to the productivity and climatic constraints hypotheses. Richness also generally increased with precipitation. Temperature is the best predictor in America and Eurasia, but in Australia it is NPP, and in the Afrotropic it is temperature seasonality. Habitat heterogeneity only slightly affects richness. Our results highlight that different factors affect turtle richness across the globe. Since other climatic factors characterize each region, the mechanisms and forces selecting for increased richness also differ.

Keywords: species richness, temperature, precipitation, NPP

60A Downscaling of geographical distributions of individual species and species richness

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Reliable methods to identify diversity hotspots and individual species distributions at resolutions (grains) finer than resolution of the available data hold great potential benefit for ecology and conservation. We introduce a novel, effective and statistically tractable approach to downscale coarse-grain maps of species richness and maps of individual species distributions to fine-resolution maps. The approach is based on hierarchical Bayesian modelling. It treats putative (unknown) distribution of an ecological property (species richness or an individual species distribution) as a latent variable which is modelled as a function of observed fine-grain environment. The fine-grain ecological property is then upscaled and stochastically linked to the observed coarse-grain values of the same ecological property. Our method directly incorporates some of the well-known macroecological scaling relationships (such as species-area relationship) into the model structure. The method is simple and can be readily used in other geographical disciplines to produce the most probable fine-resolution maps of a given variable in poorly surveyed areas.

Keywords: biodiversity, biogeography, distributions, scale, betadiversity

61A Ecological limits on the diversification of the Himalayan core Corvoidea

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Within geographic regions clades often differ greatly in species richness. Such variation must ultimately reflect differences in one or more of the following factors; the timing of colonization, rates of net diversification and/or rates of immigration. We examine these alternatives by assessing historical causes of the low diversity of a bird parvorder in the Himalayas (the core Corvoidea, 57 species present), relative to its more species rich sister clade (the Passerida, ~400 species present), which together comprise the oscine passerines within this region. The core Corvoidea represent an ecologically diverse clade, and within the Himalayas species span a large range of body sizes and elevations, traits which we found to be correlated within the group; large species are found at high elevations, and small species at lower elevations. In contrast, the Passerida contain many small-bodied species spanning all elevations, while in the other orders of birds (the nonpasserines) many large bodied species are found at lower elevations. Cladogenetic events leading to ecological differences between species of core Corvoidea in body size and shape mostly occurred millions of years ago, and the rate of evolutionary change has declined toward the present. Elevational distributions have been evolutionarily more labile, but are also associated with ancient speciation events. We suggest the core Corvoidea occupy a restricted volume of ecological space in competition with other bird species, and this has limited *in situ* diversification and/or immigration.

Keywords: Adaptive radiation, Diversity-dependence, Ecological controls, Phylogeny, Passerida

62A The latitudinal richness gradient in New World woody angiosperms is consistent with the tropical conservatism hypothesis

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Plant diversity peaks in the tropics, where climatic conditions are warm, wet, and seasonally stable, and it declines towards the temperate and polar zones as conditions become colder, drier, or more variable. The tropical conservatism hypothesis invokes evolutionarily conserved environmental tolerances, climatic limitations on dispersal and establishment, and paleoclimatic history to explain this latitudinal diversity gradient. Here, we use latitudinal distributions for over 12,000 woody angiosperm species, a fossil-calibrated supertree, and null modeling to test predictions generated by the tropical conservatism hypothesis. Species in the northern temperate zone are generally clustered within younger families, and those "temperate families" tend to be nested within more tropical lineages. Interestingly, many of the oldest families (>100 MY) also tend to have temperate distributions, suggesting that they are relicts of recently documented periods of global cooling during the otherwise generally warm Cretaceous. Climate and evolutionary history are often considered alternative explanations for the latitudinal gradient, but they are linked by the evolutionarily conserved environmental adaptations of species and the history of Earth's climate system. The recent explosion of phylogenetic and paleoclimatic information promises an increasingly fine-grained view of the biodiversity dynamics over broad extents of space and time. By linking physiological tolerances of species to evolutionary and biogeographic processes, phylogenetic niche conservatism may provide a theoretical framework for a generalized explanation for Earth's predominant pattern of biodiversity.

Keywords: biodiversity, paleoclimate, phylogenetic conservatism, ecoinformatics, SALVIAS

63A Population-level scaling of avian migration speed with body size

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Optimal migration theory suggests specific scaling relationships between body size and migration speed for birds at the individual level based on the minimization of time, energy, and risk. Here we test if the quantitative predictions originating from this theory can be detected when migration decisions are integrated across individuals. We estimated population-level migration speeds daily for the combined period 2007-11 using the eBird dataset for 114 North American birds. Species were categorized into three flight mode: powered, soaring, and mixed. Across flight modes and in accordance with time-minimization predictions, spring migration speeds were faster than autumn migration speeds. Relative to mixed and soaring fliers, powered fliers arrived later on the breeding grounds and the initiation of autumn migration started earlier and the overall migration period in the autumn lasted longer. In accordance with optimality predictions, migration speeds of powered flyers scaled negatively with body mass. Mixed-mode fliers had similar relationships. Powered and mixed-mode fliers with longer migration journeys also had faster migration speeds. Predictions for soaring fliers were poorly supported but not completely refuted. In total, our findings indicate powered and mixed fliers employed a migration strategy that, when examined at the population level, was in compliance with optimality predictions. These results suggest that the integration of migration decisions across individuals does result in population-level patterns that agree with theoretical expectations developed at the individual level, indicating a role for optimal migration theory in describing the mechanisms underlying broad-scale patterns of avian migration, especially for species that use some form of powered flight.

Keywords: eBird, macroecology, North America, optimal migration theory

64A Evolutionary uniqueness of vertebrate assemblages worldwide

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Phylogenetic trees contain essential information on the evolutionary relationships of species and have become increasingly available in recent decades, such that the opportunity now exists to use phylogenetic information to identify regions comprising species assemblages with unique evolutionary histories. Combining distributional and phylogenetic information allows quantifying phylogenetic affinities among biogeographic regions and to quantify the amount of "evolutionary uniqueness" harbored in one given region. Here, we used distributional and phylogenetic data on over 20K species of amphibians, birds and non-marine mammals, and pair-wise values of phylogenetic beta diversity (hereafter “pβ”) to quantify phylogenetic relatedness among all pairs of terrestrial zoogeographic regions in the world. We quantified the phylogenetic or “evolutionary” uniqueness of each region based on mean inter-region pβ values. Using this approach, the Australian, Madagascan and South American regions comprised the most phylogenetically distinct assemblages of vertebrates. These evolutionarily unique regions harbor radiations of species from several clades that are either restricted to a given region, or only found in a few regions. Our new phylogenetic-based approach provides a new outlook on the organization of biological diversity on Earth and a baseline for identifying conservation priority areas.

Keywords: biogeographic regions, phylogenetic beta diversity, global diversity, conservation priority, vertebrate assemblages

65A Distance decay of floristic composition along temperature and moisture gradient in Taiwan

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Vegetation patterns in Taiwan are influenced by temperature and moisture gradients. In cooler areas, one vegetation type can occur across the whole island, while in warmer areas vegetation types exhibit remarkable local variation. Does distance decay of similarity in floristic composition increase from cool to warm areas? If so, what is possible explanation for this pattern? To answer these questions, we used the National Vegetation Database of Taiwan with 5018 forest vegetation plots covering an altitudinal range of almost 3500 m. The dataset was stratified using a randomly moving window, generating spatially structured subsamples. Mantel tests and variance partitioning were used to calculate adjusted R^2 of the relationship between a vegetation similarity matrix and geographic distance or a environmental similarity matrix, respectively. The results show that distance decay of floristic composition is stronger in warmer and/or wetter habitats in Taiwan. In warmer habitats, it can be explained by the dispersal limitation or unknown spatially structured environmental factors; in wetter habitats by the spatially structured environmental factors.

Keywords: altitudinal gradient, dispersal limitation, mantel test, spatial structure, variance partitioning

66A Do Rapoport effects apply to epibiont aquatic invertebrates? The case of ostracod Entocytheridae commensal on freshwater crustaceans

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The Rapoport pattern, observed in a wide variety of taxonomic groups, states that species having geographic distributions with higher mean latitude or altitude would exhibit wider latitudinal or altitudinal ranges, respectively. One of the main explanations proposed for this pattern suggests that at higher altitudes/latitudes, the reduction in species richness facilitates increased ranges because of reduced competition. Studies testing Rapoport’s rule are mainly based on free-living organisms. The distribution of non free-living species, however, may be strongly cued to particular factors such as host specificity, richness or dispersal abilities. To check for Rapoport effects on a group of epibiont organisms, we built a geographic database of Entocytherid ostracods, commensal on other crustaceans, which constituted of >2100 sites located between 15 and 50 º of latitude, and altitudes of 0-3000 m a.s.l., including 220 ostracod species and 243 hosts, mostly crayfishes. The altitudinal Rapoport relationship seems to hold both for commensals and their hosts, parallel to an expected reduction in species richness. However, although the hosts seem to loosely follow the latitudinal pattern of Rapoport's rule, their commensals do not show a clear pattern. This could be due to a peculiar latitudinal distribution of species richness in both groups, which present a peak at intermediate latitudes (30-40º). The biogeographic history of crayfish hosts, together with strong dispersal barriers such as Central American dessert areas, could strongly affect the geographic distribution of the entocytherids.

Keywords: ecogeographic rules, host, richness geographic patterns, crayfish, Ostracoda

67A Null models identify non-random beta diversity patterns in time, but not in space, across a regional diversity gradient

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Beta diversity metrics, which quantify the dissimilarity among samples, are often used to investigate community assembly mechanisms. When compared across sites or regions, however, null models must be used to detect if differences in beta diversity reflect differences in the relative importance of assembly mechanisms, or if they simply reflect differences in regional and/or local diversities (or sampling effects). Despite the increasing application of null models in spatial beta diversity research, the same approach is rarely taken in comparing temporal beta diversity among regions. To explore community assembly processes across a local and regional diversity gradient, I collected zooplankton from eight pond regions in 2009 and again in 2011. In contrast to many studies, I found no relationship between spatial beta diversity and regional diversity, either before or after the stochastic null model was applied. However, investigating temporal beta diversity relayed a different story. Prior to the null model analysis, observed temporal beta diversity was negatively related to local and regional diversity. After accounting for sampling effects using the null model analysis, this trend reversed, indicating that more diverse systems are compositionally more unstable. This study therefore shows that 1) studying temporal beta diversity can reveal determinism in community assembly that is not detected in space, and 2) local and regional diversity is actually negatively related to community stability when using a null model approach.

Keywords: beta diversity, temporal turnover, community assembly, stability

68A Nestedness in Ozark stream fish communities: spatiotemporal variation and underlying mechanisms

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Nestedness is a characteristic of metacommunity structure. Significant nestedness has been documented in freshwater systems, although it appears to be highly variable. We evaluated patterns of nestedness for main stem and tributary sites in two river systems of the Ozarks: the Buffalo River and its tributaries within the boundaries of the Buffalo National River, Arkansas (BUFF) and the Current River and Jacks Fork and their tributaries within Ozark National Scenic Riverways, Missouri (OZAR). We used the NODF nestedness metric (nestedness metric based on overlap and decreasing fill) and evaluated the potential mechanisms likely to contribute to the observed nestedness. Six environmental variables were evaluated by ordering the main stem sites according to gradients in these variables and re-calculating NODF scores. Significant nestedness was found consistently for main stem sites at OZAR and tributaries of both river systems. Significance of nestedness for the main stem sites at BUFF depended upon the year and null model used. The Current River and Jacks Fork at OZAR are fed by numerous springs, and annual base flow conditions are relatively constant. The Buffalo River is subject to much lower annual base flows, which vary among years, and this may drive the variability in nestedness observed over time. Ordering tributaries and main stem sites by variables indicative of size (width, depth, and watershed area) always yielded higher nestedness scores than ordering tributaries by habitat variables. Overall, the high degrees of nestedness observed suggest that immigration-extinction dynamics may primarily underlie the nested patterns.

Keywords: immigration-extinction dynamics, environmental gradient, nested subsets, NODF metric, river system

69A Geographic patterns of beta-diversity. The problem of calling any measure of diversity differentiation: beta-diversity

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Since its inception, beta-diversity has been a controversial term. Recently, there has been a renewed interest in comparing the relationships between diversity measures whereas attempts to explore how they differ in their spatial patterns are still lacking. Here, we compared the spatial patterns of several metrics of diversity differentiation, including the true beta-diversity. We used Whittaker's multiplicative and additive formulas, Simpson dissimilarity, Sørensen dissimilarity and its nestedness-resultant component, Jaccard dissimilarity, and its turnover and nestedness components, as well as the range edge density and the mean dispersion field. Although it may seem obvious that these metrics measure different things, they have been used indistinctively and interchangeably. Therefore, we evaluated the spatial patterns for each beta diversity measure to assess their potential use based on the qualities, constraints and relationships among them. We divided the metrics in two sets: pool-dependent and pool-independent. We used data from IUCN distribution maps for amphibians (6,188 species), mammals (5,276 species) and reptiles (2,357 species), and from Birdlife international for birds (>10,000 species). Patterns varied among taxonomic groups. Nevertheless, it is probable that diversity differentiation metrics reflect different aspects of one single phenomenon common to all taxonomic groups under study.

Keywords: dispersion field, dissimilarity, nestedness, range edge density, spatial turnover

70A Distribution of gelatinous macrozooplankton species in the northeastern Baltic Sea

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The brackish Baltic Sea is suitable for few species of marine origin and hence the diversity of Cnidarians and Ctenophores is low. However, some new invaders have been recorded there during recent decades. Records of *Mnemiopsis leidyi* from the Baltic Sea have recieved the most publicity, because its infamous invasion to the Black Sea two decades before. The occurrence of cryptogenic *Mertensia ovum* in the northern Baltic is currently less studied and there are only few reports of hydromedusa *Maeotias margina* from the Baltic Sea. Native scyphomedusaes *Aurelia aurita* and *Cyanea capillata* occur in the northern Baltic Sea on the edge of their salinity tolerance. Most of the medusas appear in the north in late summer as

migrants from the south, but at least some *A. aurita* are probably born much closer. The abundance of jellyfish in the north still depends on the success of reproduction in southern areas, but the pattern of water movement are likely crucial. The abundance of jellyfishes in Estonian waters varies among years and has never reached real bloom level, but even average densities may have some top-down impact.

Keywords: invasive species, jellyfish blooms, ctenophores

71A Variation in avian diversification rate, species richness and elevation across mountain systems

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Tropical mountain systems are often much more species-rich than lowlands with similar area, and have been categorized as “hotspots” of biodiversity. Explaining why highlands harbor the highest bird richness has received considerable attention, however, little, if any, general consensus has emerged. Key processes for the variation in species richness include net diversification rates, immigration, and local evolutionary history. Given the consistent pattern of high species richness in tropical mountain systems, highland location should affect at least one of the above-mentioned processes. Effectively understanding these differences requires consideration of both geographic and evolutionary history. Here, we integrate a time-calibrated phylogeny of all extant bird species with their respective elevation distributions and analyze separate mountain systems of the world as replicates. Additionally, we use a species-level measure for diversification rate, which allows for an adequate trait comparison. We explore the different evolutionary processes that might underlie current patterns of biodiversity at different elevations by asking the following questions. Is altitudinal species diversity best explained by past recurrent vicariance events caused by mountain climate stratification and topographic heterogeneity? Does the climatic stability of mountains result in lower extinction rates? To which degree are higher elevations suited for temperate immigrants? Is a clade’s age related with the number of species in that lineage ?

Keywords: biodiversity, elevation, phylogeny, birds, diversification

72A Biogeography of the rocky intertidal fish community in the western coast of the Baja California peninsula, Mexico

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The taxonomical composition, ecological attributes and biogeographical aspects of the rocky intertidal fish communities of the western coast of the Baja California peninsula, Mexico, were studied at 16 sites between Medio Camino (32° 10’ N) and Los Cerritos (23° 20’N), during June 2006 to February 2010. The rocky intertidal fish assemblage was composed by 42 species, 33 genera and 19 families. A discontinuous pattern in the ecological attributes of the fish community was recognized along the geographic gradient, which was mainly composed by those assemblages located within the Sebastian Vizcaino and

Todos Santos Bays. Woolly sculpin (*Clinocottus analis*) and opalaye (*Girella nigricans*) were the most abundant species both in the northern and central sub-areas, while the notchfin blenny (*Entomacrodus chiostictus*), Mexican night sergeant (*Abudefduf declivifrons*) and porehead blenny (*Labrisomus multiporosus*) dominated the southern sub-area. Based on distribution and density of permanent species, the area encompassed between Punta Abreojos and San Juanico represents the distributional boundary for northern (warm-temperate) and tropical fish elements. Most of the species (85%) have distributional ranges that include the California marine faunal region and its Californian province, followed by those species with distributions into the tropical eastern regions of the Mexican province (58%) and Cortez province (56%). The known northern most geographical ranges are extended for *Muraena lentiginosa*, *Sargocentron suborbitalis*, *L. Multiporosus* and *Bathygobius ramosus*; while the southernmost ranges extended for *C. analis*, *Oligocottus rubellio* and *Amphistichus koelzi*. The latitudinal gradient showed a significant correlation with the fish species diversity.

Keywords: biodiversity, community ecology, biogeographic patterns, transitional zone

73A Large-scale patterns of biodiversity in epiphytic foraminiferans

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This study investigated the diversity and distribution of epiphytic foraminiferal species living on the seagrass *Thalassia testudinum* at different spatial scales, ranging from within a single sampling unit to between ecoregions of the Tropical Northwestern Atlantic Province. Epiphytic foraminiferal communities were censused from 18 sites in Belize and 9 sites in the Bocas del Toro Archipelago, Panama. Diversity indices calculated for each site include: species richness (S), Shannon's H, evenness (E), density, Whittaker plots, and k-dominance plots. Large area species richness was higher in Belize (S=56), compared to Panama (S=25). Sample species richness was highest at the Twin Bays site in Belize (S=35), and lowest at Bocas del Drago, off Isla Colon (S=2), and at Hospital Point, off Isla Solarte (S=2) in Panama. Between-site similarity was analyzed using the Czekanowski Similarity Index. In Belize, the highest similarity indices were observed between mangrove sites located within the Main Channel at Twin Cays (86%). In Panama, the highest similarity indices were observed between mangrove sites located in Hospital Bight and Boca Torito (87%). Similarity indices calculated for Belizean vs. Panamanian sites were generally low (<20%), with the highest similarities observed between pairs of mangrove sites. Only two epiphytic foraminiferal species, *Planorbulina acervalis* and *Iridia diaphana*, were present at all sites sampled.

Keywords: Foraminifera, microbial eukaryotes, seagrass epiphytes, marine biogeography

74A From local to global patterns of herbivory: environmental and ecological determinants of herbivory by specialist herbivores on host plants

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There is a current paradigm which states that specialist herbivores are correlated with the distribution of their host plants. However, specialist herbivore distribution is also governed by other factors, such as variation in plant quality and pressure from natural enemies. Further, the factors behind variation in the distribution of specialist herbivores are also likely to be dependent on the scale at which the plant-herbivore interaction is studied. Here we evaluate this paradigm by combining a global meta- analysis with a field based population density study of two distinct landscapes in New York. At the global scale we found that specialist herbivores had a stronger negative effect on plants at locations with high mean annual precipitation and high total annual precipitation (i.e., tropical wet ecosystems). However, the control of herbivore abundance was also stronger under these climatic conditions as predation and plant defenses also increased with environmental temperature.

Across the 89 locations within two distinct landscapes we found that specialist herbivore abundance did not follow host plant abundance or its reproductive output; rather canopy cover was amongst the most important factors predicting specialist herbivory rates between landscapes. At the local scale, closer distances between populations seemed to favor higher abundance of specialist herbivores. Working from local to global scales it becomes clear that the different processes that limit plant-herbivore interactions range from co-evolutionary mechanisms acting over long time at the global scale, to physiological constraints and behavioral preferences at landscape and local scales.

75A Analysis of sympatry networks: theoretical foundations, software implementation and applications

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Locality points are the empirical evidence about the distribution of species. Those records become informative when sympatry relationships can be inferred from them across various taxa. Traditionally, areas of distribution are created by enclosing the points within polygonal figures. Then, the strength of sympatric association is estimated through the amount of overlap between those elementary geometric objects. Although commonly accepted, this strategy is intrinsically unrealistic and potentially misleading. The innovative contribution of this work is: 1) to provide quantitative guidelines for measuring the strength of the sympatric association between species, but based solely on dot maps; 2) to model the totality of pairwise scores into a weighted sympatry network. Here, I present a network approach to identify cohesive groups of species connected by sympatry links, called units of co-occurrence. These units fulfill the following duality: 1) within-group connectivity sustained by co-extensive sympatry and 2) between-group allopatry (or weak sympatry). I have implemented the new approach on the R package SyNet freely available on the web. I discuss here an unpublished analysis of 6,500 records of aquatic insects from southern South America. The main findings are: 1) Patagonia and Northwestern Argentina are complex entities composed of many units of co-occurrence which are nested and latitudinally organized. 2) The biotic vicinity of Uruguay is located at the Northeastern Argentina instead of Buenos Aires province. So, the inclusion of Uruguay into a Pampas region should be revised. 3) The trace of the pleistocenic arc (firstly proposed for trees) is recovered here.

Keywords: endemism, distributions, cleavogram, connectivity, dot map

76A Linking present environment and reproductive modes segregation (geographic parthenogenesis) in *Eucypris virens* (Crustacea: Ostracoda)

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The distribution pattern of the freshwater ostracod Eucypris virens shows geographic parthenogenesis: sexual populations are restricted to the Mediterranean area, whereas parthenogens extend much wider toward Northern Europe. By means of an extensive sampling campaign - from Estonia to Morocco and from Portugal to Turkey - we analysed the associations between the presence and relative abundance of males in E. virens populations and an array of environmental factors. We applied multivariate statistical tools to our dataset which included biotic and abiotic variables, in order to uncover the main factors linked with the presence of sexual reproduction. Altitude, water chemistry and biological communities are the most significant environmental features affecting this pattern of presence/absence of sexual populations. These features may actually be related to water temporality, habitats harbouring exclusively parthenogenetic populations being characterised by long standing water invertebrate communities. We hypothesise that the distribution of reproductive modes in E. virens is related to distinct reproductive mode specific abilities to cope with habitat unpredictability. The observed link between environment and type of reproduction suggests that current adaptation is notably involved in geographic parthenogenesis, besides historical reasons related to climatic cycles or differential colonisation success of sexual and asexual lineages. In this framework, spatial structure seems also important as the high altitude habitats are also more isolated.

Keywords: Sex, niche, adaptation, post-glacial dispersal, asexual reproduction

77A Revisiting climatic drivers of plant family richness with macroecological simulation models

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Different mechanisms have been proposed to explain observed patterns of species richness. One reason why it has been dificult to reach consensus regarding the proximal mechanisms driving richness is that all tend to generate similar predictions. This problem is aggravated when regression techniques are used because collinearity between predictors makes it difficult to identify those factors directly affecting richness. The use of null models in macroecology in this context is especially meaningful because it allows for falsification of hypothesis via mechanism simulation and randomization, enabling a direct and comparable test among competing hypothesis. In this study we test several hypothesis explaining plant family richness using spatially explicit Monte Carlo simulation models. In the simulation process, a variable surrogate of the hypothesis being tested is used as a probability of origin and cell colonization of the family. The degree of range cohesiveness is tested by changing colonization algorithm ranging from total scatter range to cohesive range. Finally, we evaluate our simulations against the observed richness to unveil the most important factors driving plant richness patterns. Results suggest that dispersal mechanisms greatly influence the degree of matching the observed patterns and that contemporary climate alone cannot explain the mechanism of distribution at the family level.

Keywords: richness patterns, global simulation models, climate, plant families

78A Species-temperature relationship: the role of taxonomic level

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Species richness of most major taxa increases from poles towards equator. This increase is often explained by the positive effect of temperature on speciation rate. The species-temperature relationship as described by the metabolic theory of ecology (MTE) provides unique quantitative predictions of species richness. However, this theory has gained only limited

support when confronted by data. One of the reasons may be is that that the relationship between MTE and richness depends on the size and the delimitation of the taxon. For example temperature can affect speciation rate only within the space defined by the climatic tolerance of a given taxon. Using the database of tree distribution of North America, we analysed relationships between species richness and temperature simultaneously for variously delimited clades. We tested whether the slope of the species-temperature relationship varies with the clade size, area occupied by the clade, clade age, and both ancestral and current climatic conditions suitable for the clade. The support for the prediction of the MTE steeply increased with the increasing clade size. The value of the slope of the species-temperature relationship was further affected by the environmental conditions of the clade distribution, but clade size remained the best predictor for the variability in the species-temperature relationship. These findings indicate that the species-temperature relationship is not – and actually cannot be - universal.

79A Diversity and geographic distribution of marine heterotrophic flagellates

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World-wide diversity and distribution of marine benthic heterotrophic flagellates (HFs) were studied using a comprehensive database with 368 species compiled from 150 sources. Sixteen percent of the species were found in a single region only, whereas 62 % of the species and 81 % of the genera had wide geographical distributions covering both hemispheres. Less than 3 % of each regional HF biota were endemics, a value much lower than for macro-organisms. The species richness of HFs in temperate and tropical regions was higher than in polar and equatorial ones. However, the diversity per geographic area correlated strongly with sampling effort (number of studies) ($r^2 = 0.71$). Comparison of taxonomic composition of species and genera revealed large differences between the Northern and Southern Hemispheres, although the Antarctic and Arctic regions were similar. Tropical and temperate regions of the Southern Hemisphere demonstrated significantly lower taxonomic distinctiveness, with more Excavata but fewer Opisthokonta and Chromalveolata representatives, compared to the Northern Hemisphere. No clear geographical correlates in taxonomic composition were found at super-genera levels. Thus, the Gondwanian-Laurasian delimitation appears to be the only biogeographical boundary for these organisms. Our capacity to draw robust conclusions on the distribution of marine benthic HF was hampered by under-sampling and under-reporting. We suggest, however, that there are only a few morphospecies of free-living HFs, and that most of these morphospecies have a cosmopolitan distribution, in general agreement with the “moderate endemicity” model proposed by Foissner.

80A Phylogenetic fields of species: cross-species patterns of phylogenetic structure and geographic coexistence

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The coexistence of species underlies geographic patterns of biodiversity and, typically, approaches for understanding such patterns are either ecological or historical, but not both. Recently, there has been an effort in macroecology and phylogenetic community ecology to integrate both ecological and historical approaches. However, macroecology is mostly non-phylogenetic, whereas community phylogenetics is largely focused on local scales. Here we propose a conceptual framework to link macroecology and community phylogenetics by exploring the evolutionary context of large-scale species coexistence and introducing the phylogenetic field concept. The phylogenetic field is defined as the phylogenetic structure of species co-occurring within a focal species’ geographic range. We develop concepts and methods for analysing phylogenetic fields and

apply them to the study of coexistence patterns in the bat family Phyllostomidae. Our analyses show that phyllostomid bats coexist mostly with closely related species, revealing a north-south gradient from overdispersed to clustered species' phylogenetic fields. Patterns at different phylogenetic levels (i.e., all species vs. close relatives only) confirm the overall geographic gradient. Results support the tropical niche conservatism hypothesis, potentially mediated by higher speciation rates in the region of origin coupled with shared environmental preferences among species. The phylogenetic field approach enables species-based rather than site-based community phylogenetics, allowing the description of historical processes at more appropriate macroecological and biogeographical scales.

Keywords: biodiversity, macroecology, community phylogenetics, niche conservatism, historical processes, bats

81A The geography of evolutionary rates: bird song evolves more rapidly and in a less constrained fashion at depauperate latitudes

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Just as features of the physical and biotic environment constrain evolution of ecological and morphological traits, they may also affect evolution of communication systems. Here we analyze constraints on rates of vocal evolution, using a large dataset of New World avian sister taxa. We show that species breeding in tropical forests sing at generally lower frequencies and across narrower bandwidths than species breeding in open habitats, or at high latitudes. We attribute these restrictions on birdsong frequency to the presence of high-frequency insect noise and greater degradation of high-frequency sounds in tropical forests. We fit Ornstein-Uhlenbeck models to show that recent evolution of song frequency has been more greatly constrained in tropical forests than elsewhere, i.e., songs have shown less tendency to diverge over time in tropical forests, consistent with inferred acoustic restrictions. In addition, we find that song frequency has evolved more rapidly overall at high latitudes in both forest and open habitats. Besides a larger available sound window, other factors contributing to more rapid divergence at high latitudes may include an overall increased intensity of sexual selection, occupation of more divergent habitats, and the presence of fewer competing species. These results suggest that evolution of traits important for reproductive isolation – like avian song – evolve fastest not in the tropics, but in depauperate high latitude faunas.

Keywords: Latitudinal Diversity Gradient, Reproductive Isolation, Nearctic, Neotropics

82A The Synthesis Centre within the new German Centre for Integrative Biodiversity Research

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One of the central missions of the German Centre for Integrative Biodiversity Research (iDiv; **http://**www.idiv-biodiversity.de) is the promotion of theory-driven synthesis and data-driven theory in biodiversity sciences.

It is located in the city of Leipzig and jointly hosted by the Martin Luther University Halle-Wittenberg, the Friedrich Schiller University Jena, the University of Leipzig, and the Helmholtz Centre for Environmental Research – UFZ. It is supported by the Max Planck Society, the Leibniz Association, and the Free State of Saxony. The four overarching *iDiv* questions of biodiversity science are: How can we detect and quantify biodiversity ("detection")? How does biodiversity emerge ("emergence")? What are the consequences of biodiversity for the functioning of ecosystems ("consequences")? How can we safeguard biodiversity ("conservation")? Embedded in an active research environment, the Synthesis Centre for Biodiversity Research, sDiv, offers national and international workshops, short-term postdoc positions and a sabbatical programme to foster theoretical and synthetic thinking. sDiv will boost scientific developments in this young discipline by bringing together researchers from different projects and disciplines as well as providing conditions that promote the creative process. Here, we present some key characteristics of sDiv and iDiv in their unique combination of a research and a synthesis centre.

Keywords: biodiversity, synthesis, theory, workshops

83A Did we measure enough environmental variables? Insights from multiscale spatial analysis

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Variation partitioning of species composition into components explained by environmental and spatial variables is often used to identify a signature of niche- and dispersal-based processes in community assembly. Such interpretation, however, strongly depends on the quality of available environmental data. Spatially structured variation not explained by environment (component [c]), which is believed to carry legacy of dispersal-based processes, contains unknown proportion of variation attributable to unmeasured environmental variables. We can never measure everything, but it is useful to know if we measured really too little or we are getting close to perfect. To evaluate this, we used multiscale spatial analysis of component [c], based on PCNM analysis. The prevalence of broad-scaled spatial patterns indicates lack of important environmental variables influencing species composition, while dominance of medium- and fine-scaled patterns is more likely to result from dispersal and other population processes. We demonstrate the method using vegetation data from permanent plots in subtropical broadleaf forest in Taiwan with detailed environmental information including topographical and soil variables. Results show that if only topography is included, [c] is represented by substantial amount of broad-scaled spatial variation, indicating that yet other environmental variables were not considered. Including soil variables into analysis, however, considerably increases importance of medium- and fine-scaled spatial patterns. Recent studies of forest permanent plots often use only topography to quantify environmental control imposed on vegetation; our results indicate that topography itself is poor surrogate for environment and that other variables, such as soil, need to be considered.

Keywords: Lienhuachih, forest permanent plots, PCNM, environmental control, vegetation

85A Climate as a determinant factor in the seasonal activity of species with fossorial habits: the case of the lowland burrowing treefrog (Smilisca fodiens)

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The importance of climatic conditions in shaping the geographic distribution of Amphibians species is mainly associated to their high sensitivity to environmental conditions. How they cope with climate gradient through behaviorally adaptations along its distributions is still a valid question based on the ecological and evolutionary implications for population viability. Due to their low dispersal abilities, the response to seasonal changes of climate may not be associated with movements, but to behavioral and physiological adaptations. Here we analyzed if the activity period of the fossorial Lowland Burrowing Treefrog (Smilisca fodiens) is predicted, on the basis of the seasonal variation of climate along its distribution. We employed Ecological Niche Modelling (ENM) to perform a monthly analysis of spatial variation of suitable climatic conditions (outlined by July conditions, month of major activity), and we then evaluate the geographical correspondence of monthly projections with the occurrence data per month. We found that the species activity corresponds with the latitudinal variation of suitable climatic conditions, throughout a high geographical correspondence of the species' occurrence data with the climate variation along its distribution. Due to the behavioral response of this fossorial frog to seasonal variation of climate, we suggest that precipitation and temperature have played a major role in the definition of geographical and temporal distribution patterns, as well in shaping behavioral adaptations to local climatic conditions. This result highlights the influence of macroclimate in shaping activity patterns facing climatic gradients and the important role of the fosorial habit to maintain ecological requirements in these anurans.

Key words: Climate, gradient, latitude, adaptation, fossorial, anurans, niche modelling

86A Integrating physiological data to fine-tuning of ecological niche models

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Ecological niche modeling (ENM) correlates environmental characteristics with species' occurrences to identify conditions that permit a species to occur. ENM is widely used by ecologists, however, to our knowledge, tests of model agreement with species' physiological traits (PTs), observed in controlled environments, are uncommon. We tested if ENM reflects species' physiological limits using Maxent and a PT (temperature) of an African species, *Bagrada hilaris*, that has invaded southwestern USA. The models obtained had high predictive power (AUC=0.893), low omission rate (0.09), and recovered known invasive range, with additional potential for invasion in South America, Mediterranean basin, China, and New Zealand. Laboratory data suggest that *B. hilaris'* survival rate is temperature-dependent. Our ENM experiments recovered the effect of PT: mean temperature of the driest quarter and mean temperature of coldest quarter had the first and third most contribution to building the models, respectively. Although Maxent generally underestimates a species' niche, in our study it slightly overestimated the known distribution of *B. hilaris* when masked according to PT lab data. These preliminary results support the use of PTs to refine ENM predictions with species' physiological limitations. Future work is needed to understand to what degree ENM recovers PTs.

Keywords: commission error, invasive species, Maxent, model improvement, potential distribution

87A Evaluating body size changes in relation to elevation and latitude in torrent ducks (Merganetta armata, Anatidae): a test of Bergmann's and Allen's rules

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Adaptive strategies to overcome challenges imposed by cold environments are diverse, and many mechanisms that help organisms to deal with such environments have been well documented. Among the most studied strategies are Bergmann's Rule and Allen's Rule, which indicate that organisms living in colder habitats, including those at high elevations, tend to be larger and to have smaller limbs, respectively, to minimize heat loss through their body surface. Although evidence for geographic patterns in body shape supporting both rules has been found in different organisms, all the work has been done studying either elevational or latitudinal temperature gradients, but has rarely considered the effect of both kinds of gradients determining body shape of populations. A good model to evaluate differential effects of both elevation and latitude would be a widespread species that also occupies a wide range of elevations within a single mountain. We tested for the effects of temperature on body size and limb size in Torrent Ducks using replicated elevational gradients at different latitudes, from Colombia to Argentina. We found a strong, negative relationship between body size and temperature across latitude concordant with Bergmann's rule, but a positive relationship is observed when the elevational gradient in temperature is taken into account. We did not find evidence for variation in limb size supporting Allen's rule. We discuss the ecological implications of the observed patterns and highlight the importance of studying replicated gradients to completely understand how environmental factors affect the biology of species.

Keywords: biogeography, adaptation, Andes, temperature, ecological gradients

88A Geographical patterns in breeding traits of European birds

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Breeding strategies of birds is a commonly studied area in avian ecology. In particular, clutch size and number of broods are often studied as they can reveal how much energy individuals allocate to breeding, and because they are easy to measure. We described geographical patterns in these two traits in European birds and explored their relationships to environmental variables (namely the length of breeding season, total productivity measured by NDVI during breeding season, and the difference between maximum and minimum productivity during breeding season and over the entire year), using data from the EBCC European Breeding Bird Atlas. We calculated mean values of the traits for quadrates 50x50 km in size and related them to environmental characteristics using OLS and GLS regression. We analyzed passerines and precocial nonpasserines separately. Clutch size increased with total productivity, in accordance with Lack's hypothesis that clutch size is mainly dependent on the amount of food which parents are able to obtain for the young. Clutch size also increased with the difference in productivity over the year but only in precocial birds, in accordance with Ashmole's hypothesis that clutch size depends mainly on the variance in food supply over the year. Number of broods per season increased with the length of the breeding season but was independent of total productivity and clutch size. These results indicate a lack of a trade-off between clutch size and number of broods, and that different factors may affect clutch size in altricial and precocial birds.

KeyWords: clutch size, number of broods, productivity, latitudinal gradients, spatial statistics

89A Back to the future: prospects for Bergmann's and other ecogeographical rules in the 21st Century

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In 1847, Bergmann called attention to the physiological, ecological and evolutionary implications of body size for the biogeographic distribution of species. Nowadays, Bergmann's rule (BR) is perhaps the best known ecogeographical rule. Contrarily to other rules linking life-history trait variation to environmental gradients, which have been very little explored, BR remains a topic of much interest and debate. Recent claims, however, suggest that BR tests should be restricted to the original conditions: the study of interspecific size clines in closely related endothermic vertebrates, with the classical heat-conservation mechanism as an integral part of the rule. Here, I advocate a different, pluralistic, approach to the exploration of ecogeographical rules, in general, and BR in particular. Within the BR framework we can develop more synthetic and comprehensive approaches to the study of patterns and processes in the geographic variation of biological traits. We should explore BR at different levels of biological organization, describe patterns for a diversity of systems and organisms (including endotherms and ectotherms) and avoid the conflation of patterns and processes, by suggesting and testing alternative explanations with regard to the underlying physiological mechanism. I will show how the narrowness of the epistemological scope we adopt, and the confusion surrounding the wide variety of methods and terminological used, affects our perceptions of the status and validity of BR. In sum, BR is not a rule to be forgotten and deserves a prominent place in future empirical investigations of the biogeography of life history traits.

90A Diversity of Tiphiidae (Hymenoptera: Vespoidea) along an elevational gradient in the Atlantic Rain Forest, Brazil

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Tiphiidae include idiobiont parasitoid wasps of coleoptera larvae, and their diversity is practically unknown in South American ecosystems. The Atlantic Rain Forest is one of the most diverse and threatened ecosystems of the world. Elevational gradients are one of the components responsible for the high biodiversity of the Atlantic Rain Forest. Despite the fact that understanding factors driving variation in biodiversity along gradients is one of the oldest issues in biogeography, most studies have been only assessed species richness and have disregarded important aspects of the community structure. This study described the diversity (species richness and relative abunance) of Tiphiidae along an elevational gradient in a well preserved area of the Atlantic Rain Forest. Species richness was estimated by rarefaction, species equability by the Pielou's index and species diversity by the Shannon index. The values estimated by such indeces were correlated to elevational variation using generalized additive mixed models (GAMM). Species richness of Tiphiidae in the Atlantic Rain Forest is not explained by elevation. However, the species equability and diversity presented a linear relationship with elevation, being higher in the lowlands than in the highlands. Such results suggest that the Atlantic Rain Forest highlands have more

dominant species of Tiphiidae than the lowlands, and the variation in the species diversity along the elevational gradient is determined by the species equability.

Keywords: Biodiversity pattern, Neotropical Region, parasitoids, tropical forest, insect

91A Relating geographical patterns in species traits to environmental variables in South African birds

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A comprehensive understanding of organism trait-environment linkages is essential to explain patterns and processes in communities. We investigated the effect of environmental variables on the geographic distribution of morphological traits, life-history characteristics, and plumage coloration of South African birds. Geographical patterns in the distribution of species traits were affected mainly by the east-west gradient in productivity, and additionally by vegetation character and availability of food resources. Life-histories associated with environmental predictability and low adult mortality (comprising altricial, sedentary and territorial birds) were characteristic for humid savanna. Species in such environments are often multi-colored with more saturated and vivid plumage. Habitats with dense vegetation and high rainfall are preferred by species with longer bills, feeding on invertebrates and often being cavity nesters. At the opposite end of the gradient, arid and unpredictable environments are characterized by more frequent occurrence of carnivorous species, and species with longer tarsi and wings, being ground breeders and often nomadic. The plumage is mostly pale and bright. Grasslands and fynbos have higher representation of granivorous species breeding on the ground, with large clutches, precocial young, which are often vagrant or migranting. Our study provides deeper insight into links between life-history traits and environmental variables, and allows precise definition of functional groups.

Keywords: life-history strategies, plumage coloration, trait-environment relationship, bird macroecology, spatial statistic

92A Biogeography of avian life history traits: an elevational perspective

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Studies examining elevational variation in avian life history traits are taxonomically and geographically restricted, and focus on either one or a few traits in isolation. This study explores interrelationships between elevational parameters (range and mid-point) and a selection of morphological, reproductive, and life-history traits, using a new global avian species-level dataset. Interestingly, whereas previous studies have consistently concluded that birds shift in life history from a high reproductive strategy at lower elevations to a high survival strategy at high elevations, our results show the opposite pattern. We found avian elevational range and mid-point to be positively associated with clutch size and broods per year (annual fecundity), and negatively associated with traits including adult body weight, egg weight, incubation period, fledging time and adult survival. To investigate the robustness of our results, we confirmed this pattern on subsets of the global dataset: species assemblages within biogeographic realms, within the richest mountain ranges for avian diversity, endemics, higher taxonomic levels, and using phylogenetically independent contrasts. Fast life histories at high elevations may result from avian species occupying higher elevations being exposed to more harsh seasonal environments compared to lowland birds.

93A Global warming favors lightly colored insects in Europe

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Climate is a major driver of the geographical distribution and patterns of diversity of species. Climatic characteristics also determine morphological traits of species, and such relationships have been used to reconstruct paleoclimates from pollen fossils and to model changes of vegetation through time. Similar links are less well established for animals. Using distribution data of European butterflies and dragonflies, we found that due to thermoregulatory constraints dark and lightly colored insects are favored in cool and warm climates, respectively. Comparing distribution maps of dragonflies from 1988 and 2006, we found that the overall color lightness of species assemblages was consistently correlated to the thermal environment and increased with global warming. We document that an ecophysiological phenomenon can cause noticeable biogeographical patterns when applied to large clades of insects. Our results provide support for a mechanistic link between climate, functional traits and the distribution of species at larger geographical scales and may provide the foundation for better forecasting of the effect of climate change on insects. Thus, we predict that lightly colored insect assemblages will be favored by global warming, which will lead not only to a change in the appearance of assemblages but perhaps also to new evolutionary trajectories.

Keywords: assemblage approach, ecogeographic rules, macrophysiology, phylogenetic eigenvector regression, thermal melanism.

101A Niches, traits, and natural history: assessing drivers of small-mammal diversity in the sky islands of northern Venezuela

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We use trait data, natural history information, and ecological niche models to study the biogeography of small non-volant mammals in montane “sky islands” of northern Venezuela. First, we conducted species-area and faunal-nestedness analyses among major ranges. We then focused on two peripheral elements: the Serranía de San Luis and the tiny Cerro Santa Ana, which is found on the adjacent Península de Paraguaná. For these two ranges, we tested hypotheses of differential immigration from San Luis and differential extinction on Santa Ana using trait data (including body size and fidelity to mesic microenvironments). Finally, we made niche models for rodents found on Santa Ana using Maxent and climatic data. We used these models to assess whether peninsular populations are likely allopatric with respect to the “mainland” and to test for niche evolution under isolation. Overall, the faunas are highly nested, and most deviant “idiosyncratic” species appear to have speciated in situ. Lower richness tightly accompanies decreasing area. We detect only a weak insinuation of differential (lesser) immigration to Santa Ana by species with high mesic fidelity, but find a strong pattern consistent with differentially high extinction of small-bodied species there. Niche models for the rodents present on Santa Ana suggest current low connectivity relative to “mainland” populations, especially when considering natural history information for mesic-forest species that occasionally inhabit gallery forests within a drier matrix. Models based on localities from the “mainland” predict known records on the peninsula, failing to detect any niche shift under isolation.

Keywords: allopatry, extinction, immigration, nestedness, niche evolution

102A Morphometric differences among populations of *Lottia gigantea* of Isla de Cedros

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Isla de Cedros is an Eastern Pacific island that is located in the transitional zone between the Californian and Mexican biogeographic marine provinces. There are very few studies regarding the macroinvertebrates from this island. *Lottia gigantea* is a macroinvertebrate that inhabits the rocky intertidal zone. Random sampling, which yielded an average of 30 individuals per population, were performed in four different populations: San Agustin(SA), Punta Prieta (PP), Punta Norte (PN) and Punta Morro Redondo (PM) at Isla de Cedros.. Morphological analysis was based on seven morphometric shell characteristics used to compare the populations. Results from the statistical analysis (PERMANOVE-PW) show that the

northern population (PN) is significantly different from southern populations (SA, PP, and PM). PP (t=7.3627; p=0.0010) is the population that presents the most marked difference with respect to PN. The analysis of macroinvertebrates, like *Lottia gigantea*, on Isla de Cedros will help in the understanding of the ecological processes affecting the island.

Keywords: macroinvertebrates, intertidal, island biogeography, Baja California, limpet

103A Phenotypic and genetic structure in forest thrush, *Turdus lherminieri*, an endemic and vulnerable bird in Caribbean Islands

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Understanding the mechanisms underlying population structure is a crucial issue in evolutionary biology and ecology. Identifying the processes driving biodiversity is also needed to provide guidelines for population management and conservation planning. Particular attention is given to insular systems due to the presence of endemic species characterised by small population sizes and small distribution areas. These species are consequently more vulnerable to strong environmental changes. The forest thrush, *Turdus lherminieri*, is an endemic and understorey bird present in four islands of Lesser Antilles: Montserrat, Guadeloupe, Dominica and Saint-Lucia. Four subspecies have been described on each island on the basis of feathers coloration but no study has quantified the divergence between these subspecies. In addition, bird numbers on these islands have declined for the last 15 years and forest thrushes are now protected on Dominica, Montserrat and Saint Lucia. In Guadeloupe however they are still actively hunted by humans. The aims of this study are to study the spatial structure (phenotypic and genetic) and genetic variability in the forest thrush in order to try to identify optimal management strategies. We identified strong morphological and genetic structure among islands. In addition, an uncommon level of differentiation at a fine scale, i.e within island for Guadeloupe, was found between Grande-Terre and Basse-Terre (two parts of Guadeloupe separated by an isthmus). Genetic diversity and allelic richness varied between islands, with higher levels in Guadeloupe followed by Montserrat and Dominica. Dominican birds had the lowest genetic diversity and allelic richness but contained the most unique alleles. Our results show that it is better to have specific management strategies for each sub-species.

Keywords: speciation, insularity, endemism, forest thrush, conservation

104A Host plant affiliation vs. geography as drivers of diversification in a radiation of *Pseudoloxops* plant bugs (Heteroptera: Miridae) from French Polynesia

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Despite its status as one of the world's biodiversity hotspots, the native invertebrate fauna of Polynesia remains poorly known. Through their isolation and topographic complexity, the Polynesian islands have played host to numerous radiations of endemic insects, such as plant bugs (Heteroptera: Miridae) in the genus Pseudoloxops. Distributed across the Old World and Oceania, Pseudoloxops has diversified exceptionally within the archipelagoes of French Polynesia. We first document the diversity itself, using an integrative taxonomic framework to describe new and revise existing species from molecular and morphological data. Using a unified species concept as our underlying ontology, we use three lines of evidence to operationally delimit species for a sample of 192 specimens: (1) phylogenetics, using a dataset of 1,977 base pairs (two

mitochondrial and one nuclear gene) and 20 morphological characters, followed by testing of species hypotheses under the coalescent model; (2) geometric morphometrics, using ordination-based analysis of shape data of male genitalia; (3) traditional morphometrics, using ordination- and frequency-based statistical analysis of continuous morphological data. These methods reveal a total of 14 species distributed across 9 islands. In order to examine the role of host plants and geography in driving the radiation, we generate a time-calibrated phylogeny for the group and map on island distributions and host plants. By reconstructing ancestral character states using maximum likelihood, we assess the relative probability of host-switching vs. geographic isolation for each speciation event. Preliminary analyses indicate some role for host-driven speciation, with switches between angiosperms and ferns as the most likely mechanism.

105A Dispersal ability determines the scaling properties of arthropod species abundance distributions

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The shape of the species abundance distribution (hereafter SAD) changes as a function of sample size. Our previous work with spatially explicit computer simulations using the basic tenets of neutral theory showed that, though qualitatively similar, the pace of the evolution of the SAD as a function of sample size depends on the species dispersal ability. Here we use data on arthropods communities of Laurisilva forests in the archipelago of the Azores, Portugal, to study the evolution of the SADs as a function of sample size and species' dispersal ability, by dividing the data into two guilds: high and low dispersal species. In agreement with the simulations, the empirical data show that the evolution of the SADs differs considerably for the two guilds. In particular, and like in the simulations, both SADs are monotonically decreasing functions for small sample sizes, ie, with the maximum occurring for the singletons class, but as sample size increases, SADs of high dispersal species retain a larger proportion of rare species for the same sample size, while low dispersal ability species develop a maximum for intermediate abundance classes earlier. In addition, we use the scaling properties of the moments of the SADs to forecast their shapes for larger sample sizes. Our results show the importance of studying the evolution of SADs as a function of sample size as a mean to understand patterns and processes of species diversity.

Keywords: biodiversity, biogeography, Laurisilva forest, Azores, moments

106A Temporal change in arthropod forest assemblages in the Azores: contrasting response in predators and herbivores

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Once entirely covered by forest, in the last 600 years the Azorean islands suffered dramatic human mediated habitat changes, including destruction and fragmentation of native forest. As a consequence of these actions, only 3% of the original forest remains and many exotic species have been introduced throughout the years. Destruction of native habitats and species introductions are known to have a great impact on community structure, particularly in insular ecosystems. The goal of this study is therefore to understand how local native forest arthropod communities change over time. We conducted a standardized survey in 16 native forest fragments in seven Azorean islands and compared taxonomic and functional diversity of several guilds sampled 10 years apart (2000-2010). We found that epigean and canopy arthropods (spiders, herbivores) decreased in richness, abundance and functional diversity. Interestingly, not all species within each guild were equally affected, and such changes were only statistically relevant for exotic spider species and indigenous (endemic plus native) herbivore species. Unexpectedly, our results indicate that dominant indigenous predator communities are more resilient than exotic predators to the ongoing processes of plant invasion, land-use changes and climatic variations. Our findings also suggest that exotic spiders are not in equilibrium: they are composed by a diverse regional meta-community, where many of the species found in native forests seem to be tourists that can disappear locally. In contrast, indigenous herbivores mainly composed by specialist feeders are less resilient than exotic generalist phytophagous, suggesting that this group could be more dependent of bottom-up processes.

Keywords: Azores, islands biogeography, arthropods, community, native, exotic

107A Frogs on Southeastern Brazilian islands: composition species, endemism and island biogeography

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This study considers the species composition, endemism and patterns of species richness, island area, island isolation and breeding habitat availability for frog faunas of 18 continental islands off the southeastern coast of Brazil. Each island was visited at least three times and frogs were located by visual and acoustic searching. We consider five categories of breeding habitats: leaf litter, bromeliads, streams, freshwater seeps, and temporary ponds. Island area varied from 6 to 700 hectares, island isolation varied between 0.5 and 35 km, and breeding habitat diversity from 2 to 5. Seventeen species were detected on islands, of which five were endemic to single islands. Two additional species occur on 60% of the sampled islands, and remaining species occur 7- 45% of islands. The island with highest diversity was Buzios with seven species, followed by Mar Virado and Vitoria four species. Our results are consistent with other islands systems, with high endemism and low number of species. There is a positive correlation of island area and habitat diversity on frog species richness, but not a relationship between richness species and island isolation. Breeding habitat diversity predicts the diversity of frog communities on islands. Therefore, the relationship between species richness and area is probably a consequence of the relationship between habitat diversity and area. Strong habitat-diversity effects are expected in taxa with high degrees of habitat specialization, such as frogs.

108A Exploring biogeographical patterns of island floras with process-based models

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Recent studies indicate that together with classical ecological factors, namely colonization and extinction, geological and evolutionary factors are main drivers of insular biodiversity. However, island biogeographical patterns have been rarely investigated by mechanistic modeling and, thus, complex interactions between ecological, evolutionary and geological processes remain untested. We present a stochastic model that simulates population-level (demography, dispersal, interspecific competition, speciation) processes for plants under a metabolic framework over the geological lifespan of volcanic islands. We investigated the emerging properties of species richness, immigration, speciation and extinction rates under different isolation and island size scenarios. Species richness revealed a hump-shaped trend over time. Immigration and extinction rates were similar to one another, but varied in trend and in predominance depending on age and isolation of the island. Speciation rates showed complex dynamics, but generally revealing a hump-shaped trend over time with large initial variation. Proportional endemism increased over time for anagenetic endemics, whereas cladogenetic endemics showed a slightly hump-shaped trend. Isolation decreased immigration and extinction rates, total richness and the number of anagenetic endemics, but increased the number of cladogenetic endemics, radiating lineages and species per radiating lineage. Increasing island area generated higher total, anagenetic and cladogenetic richness. Whereas most findings confirmed theoretical predictions (e.g. General Dynamic Model of Island Biogeography), important divergences were detected. This was possible by simulating local-scale processes, from which large-scale community and biogeographical patterns emerged. Hence, this mechanistic model may guide further theoretical investigations connecting island biogeography with population, niche and community ecology.

Keywords: island biogeography, interspecific competition, mechanistic models, metabolic theory, speciation

109A Assessing a marine biogeographic transition zone: biogeographic patterns of the tidepool fishes of Isla De Cedros, Mexico

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Isla de Cedros (IC) has particular relevance in the context of marine biogeography due to its location in one of the most dynamic transition zones of the Eastern Pacific. Community composition, structure and biogeographic relationships of the rocky intertidal fish fauna were explored in three sites of the island, one in the north end (Punta Norte) and two in the south region of the IC (Coloradito and Punta Prieta), between February 2010 and November 2011. The fish assemblage was composed of 18 species, 17 genera and 11 families. The analysis of the ecological attributes showed seasonal differences in the composition and structure of the three communities, within and between them. The fish community of the southern region showed a strong subtropical influence while Punta Norte community represents a typical transitional site with seasonal differences in the species composition. Blenniidae was the family best represented in species (3 spp) and Cottidae was the more abundant. The sculpin *Clinocottus analis* was the most abundant species in all three sites and during the entire period of study. The rocky intertidal fish community of IC as a whole consists of a combination of species of warm temperate (65%) and subtropical (35%) affinities. The environmental dynamics of a biogeographic transition zone and habitat heterogeneity are the two drive factors for the composition and structure of intertidal communities.

Keywords: biogeography, rocky intertidal, ecotone, Baja California Peninsula

110A Latitudinal distribution of rocky shore macroinvertebrates of Baja California Pacific Islands

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We analyze the latitudinal distribution patterns of macroinvertebrates from the rocky intertidal zones of Baja California Pacific islands. The data were based on the sampling of species in the field, the review of the scientific collection from the Natural History Museum of Los Angeles County, California, USA, from the electronic databases of scientific collections of other museums in the U.S. (Smithsonian Institute, Santa Barbara Museum), Mexican scientific institutions (UNAM-ICMyL), and the compilation of specialized information. We obtained the first compendium of benthic invertebrates from Baja California Pacific islands, comprising 151 species, 101 genera, 65 families and 27 orders / clades, 11 classes, and 5 phyla. We identified five patterns of distribution integrated by 14 biogeographic groups in the Eastern Pacific, according to the isotherms and ocean surface currents. Thus, the islands differ in taxonomic composition and species richness. This highlights the importance of updating the lists of species for other taxa and confirms their presence in the region in the Eastern Pacific. This is important because species are more sensitive to environmental changes, particularly temperature, which influenced their geographical amplitudes. Such species can be used as bioindicators for thermal anomalies caused by ocean warming in addition to oceanographic phenomena such as ENSO.

Keywords: island biogeography, marine invertebrates, rocky intertidal, Eastern Pacific

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111A Evolution and biogeography of the endemic *Roucela* complex (Campanula, Campanulaceae: Bellflowers) in the Eastern Mediterranean

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The Roucela complex is a group of 12 rare, mostly narrow endemic Campanula species found primarily in the Aegean Archipelago. Little is known about the evolution of endemic Campanulaceae in these continental islands. This region has a complex climatic and geologic history with numerous sea-level changes and tectonic events causing connections and disconnections between islands and the mainland across time. Our phylogenetic analyses based on both plastid and nuclear genes recovered three clades within a monophyletic Roucela. Two most basal clades form a grade and are composed exclusively of taxa found east of the mid-Aegean trench. These are successively sister to a clade that includes primarily taxa found west of the trench. Our results indicate that the mid-Aegean trench is historically significant in shaping the evolution of this group. Dating analyses found the Roucela clade to be much older than predicted by often made claims that speciation in the Mediterranean is largely recent and driven by the onset of the Mediterranean climate. Results show that diversification is likely the product of vicariance events that occurred during the Early Miocene. The break-up of the Aegean landmass played a significant role in the diversification of the clades found in the eastern side of the trench, while the Messinian Salinity Crisis contributed to the divergence within the clade occurring in the western side of the trench. Results from distribution modeling analyses corroborate our hypothesis of geologic events and dispersal barriers being responsible for current distributions and driving ancient diversification.

Keywords: continental islands, Aegean Archipelago, niche modeling

112A Comparative biogeography of dune restricted insects in North America

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Sand dunes of the North American deserts are a continental archipelago. Using probabilistic methods to explicitly test, not only the pattern of divergence, but also the divergence dates among taxa is a marked departure from previous parsimony based methods. I will examine the patterns between seven independent lineages in dune systems. I hope to synthesize the results from multiple unrelated taxa to test alternative dispersal patterns in this island system. I will also address questions of species delimitation and how that plays an integral part in how we define biogeography and phylogeography. Finally I will compare the barriers to dispersal in sand dunes relative to oceanic islands.

Key Words: Island Biogeography, Lagrange, Uma, Continental Islands

113A Phylogeography of the Tailless Whip Scorpion genus Phrynus Lamarck, 1801 in Puerto Rico

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Amblypygids, commonly known as tailless whip scorpions, are tropic and sub-tropically distributed arachnids typically found in cryptic habitats. The genus Phrynus Lamarck, 1801 currently contains 28 living species primarily distributed from the southern USA to northern South America (Weygoldt 2000, Harvey 2003). The island of Puerto Rico has records of two species: *Phrynus marginemaculatus* C.L. Koch (1841) and *Phrynus longipes* Pocock (1893). For this study 170 specimens from the genus were collected from 33 sites on the islands of Puerto Rico, Mona, and Hispaniola. Phylogenetic and phylogeographic analyses were conducted using data from five mitochondrial and nuclear loci. The results of these analyses indicate the population structure of the island is directly correlated to the distribution of granite and limestone bedrock. Additionally, interspecific pairwise divergences greater than 20% for Phrynus species on the island of Puerto Rico were observed. While it has been documented that cave species are often limited in their habitat and their ability to disperse between suitable habitats, resulting in relatively small geographic ranges and high degrees of endemism in comparison to surface species (Snowman et al 2010, Porter 2007, Culver et al 2006), pairwise divergences of this order of magnitude are unexpected and indicate that the diversity of the group has been considerably underestimated. This study represents the first phylogeographic analysis of Amblypygi and of Caribbean cave arachnids. Additionally, it provides evidence for correlation of bedrock composition and population structure in troglophilic arachnids.

Keywords: biodiversity, caves, Amblypygi, Caribbean, island biogeography

114A Ecological gradients and recent speciation events in Javanese shrews

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Java Island, Indonesia, offers an outstanding opportunity to understand how ecological gradients generate species. The island's relatively simple shape spanning ~10° longitude, but only 2° latitude generates a strong east-west moisture gradient. Java's numerous volcanoes also result in replicated elevational gradients. We inventoried shrews on four mountains in Java and sequenced nine independently evolving loci in >100 specimens from these collections. Combining morphological and molecular evidence, we find strong support for the occurrence of five species on the island. Among these five species, two pairs of recently evolved sister species are evident. One pair is divided among high and low elevation areas, while the other appears to be divided by Java's longitudinal gradient. Members of each species pair occur in sympatry at some sites, and gene flow appears to occur rarely. The potential connection between these speciation events and Java's ecological gradients will be discussed.

Keywords: biodiversity, biogeography, island, phylogeography

115A How different are diversity and distribution of tree species between islands and mainland in tropical forests?

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Herein we analyze the diversity and distribution of tree species in continental islands (0.2 to 828 ha in size, and 0.4 to 34.8 km of distance from the coast) and coastal localities throughout 400 km of coastal Atlantic Forest in southeastern Brazil. We recorded a total of 552 tree species, including 457 on the mainland and 149 on islands (65 species restricted to islands). Multivariate analysis suggested two groups of assemblages: one for the islands and another for the mainland. Assemblages from geographically close localities were more related among each other in ordination and cluster analysis. The beta-diversity was high among mainland localities (0.74 on average), islands (0.83), all localities (0.86), and even higher when considering only pair wise comparisons between mainland and island localities (0.92). The geographic distances were not correlated to the similarity in species composition considering all localities ($r = 0.04$; $p = 0.27$), mainland assemblages ($r = 0.08$; $p = 0.28$), or islands ($r = 0.33$; $p = 0.06$). We tested for nestedness to verify if species assemblages in islands are subsets of the mainland pool. The observed nestedness metric, NODF, indicated a nested pattern of species occurrences. Thus, even with the high rates of species turnover between localities, the geographic position of islands does not seem to be the most important factor related to the distribution of species. The islands analyzed herein showed a relatively distinct flora but could be considered as subsets of the mainland pool of species.

Key words: Atlantic Forest, vegetation, biogeography, islands, beta-diversity, nestedness

116A Treelines and island biogeography – a global perspective using an innovative research approach

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Treelines have been an important research focus in biogeography for many decades, as tree lines are, per definition, the boarder between the subalpine forest and alpine environments. Theoretically, island treelines experience specific drivers unique to island ecosystems such as isolation-induced absence of adapted high-elevation tree species, immature soils (at least on volcanic islands), exposition to high oceanic winds and only a small Massenerhebungseffekt due to relatively small island area. Here, we test how isolation, island area, island maximum elevation and geology influence the global pattern of island treeline elevations. We collected a global dataset by applying a stratified design using the Global Island Database, GoogleEarth and literature to identify maximum treeline elevations. Islands ranged from 65°N to 55°S. Maximum treeline elevations spanned between 110 and 4061 m showing a single hump near the equator. Island area and island maximum elevation had a positive effect on treeline elevation in contrast to isolation, even when only testing for volcanic islands. When focusing on the subtropics and tropics no latitudinal effect was visible but treelines were significantly higher on continental than on volcanic islands. The tropical peak may be attributed to diurnal temperature regimes, which do not differ strongly between islands and the continent. In contrast to continents the subtropical double hump is lost on islands likely owing to the reduced seasonality and Massenerhebungseffekt. The theory of island biogeography would suggest an influence of geology and isolation, yet it does not seem to play a role in global island treeline patterns.

Keywords: alpine ecosystem, Global Island Database, Massenerhebungseffekt, oceanic-volcanic islands

117A Beta diversity on tropical islands

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Understanding what causes differences in the composition of biotic communities (β diversity) remains one of the central challenges in ecology and biogeography. Previous studies showed that β diversity is driven by variation in habitat conditions, and changes in the overall species pool. While the effects of variation in habitat conditions on beta diversity have been well established, studies on how variation in the species pool influences beta diversity just begun. Using a newly compiled dataset of the diversity (number of species) and composition (identity of species) of fern assemblages in 288 sampling plots along an island size gradient of 15 sampling sites in the Malesian archipelago and New Guinea we investigate within island beta diversity under the influence of different species pool sizes. We show that beta diversity can be significantly altered by the size of the regional species pool and increases with the size of the island. While variation in the environment explains within island beta diversity it does not explain variation in beta diversity along the islands size gradient. We will show possible explanations for the observed pattern and present the major implications for studing community composition on islands.

Keywords: beta diversity, community composition, island biogeography, ferns, Melanesia, New Guinea

118A Patch isolation metrics to quantify road induced habitat fragmentation

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A local population's probability of extinction is mostly determined by its size, which is often associated with patch area. Colonization of an empty patch is mainly influenced by its connectivity to existing local populations. Habitat fragmentation is generally considered to be one of the most important factors affecting species richness because of its influence on extinction and colonization rates. Transportation networks are of significant ecological concern to associated animal populations. Roads contribute to habitat fragmentation by limiting animal movement by physically cutting off individual and population access to neighboring habitat areas. This divides existing populations into smaller more isolated metapopulations. Currently FRAGSTATS computes two metrics adopting an island biogeographic perspective on patch isolation: (1) Euclidean nearest neighbor distance and (2) proximity index. While these metrics quantify patch isolation, they fail to incorporate the fragmenting effects of roads in their formulations. This research presents two new metrics as an improved method for calculating patch isolation in habitats impacted by roads: (1) Euclidean nearest neighbor-roads and (2) number of connected patches. The performance of the new metrics was evaluated using simulated landscape data with different transportation network structures and habitat patch configurations. Comparing output from road-based metrics to existing metrics, as simulated transit network density increased for each landscape; response of new metrics to increased road presence is linear and as expected given metric design. These metrics have successfully captured notable patch, class, and landscape level characteristics and associated responses, which are not available with treatment by conventional measures of habitat fragmentation.

Keywords: species richness, colonization, transportation networks, populations, GIS

119A Long-distance dispersal or large-scale extinction? Explaining the extreme "Rand Flora" disjunction in the bellflower genus *Canarina*

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The "Rand Flora" is a disjunct floristic pattern that chracterizes plant species distributed in the continental margins of Africa (Eastern and South Africa, Northwest Africa) and Macaronesia. One of the most extreme examples is the genus Canarina (Platycodoneae, Campanulaceae), a small genus of three species, one of them endemic to the laurel forests of the Canary islands (Canarina canariensis), and two others distributed in Eastern Africa. *Canarina eminii* is a widely distributed epiphyte in montane forests of the Horn of Africa, Kenya, Tanzania and Uganda, while *Canarina abyssinica*, a rocky dweller of open forests, is apparently restricted to a few sites of Eastern Africa. Here, we use a full Bayesian approach to reconstruct phylogenetic and phylogeographic relationships in genus Canarina, based on seven variable chloroplast markers and 22 populations. Results show that *C. canariensis* and the East African *C. eminii* are sister-species, with *C. abyssinica* as sister to them. Bayesian phylogeographic analysis reveals a strong geographic structure within *C. canariensis*, with several events of inter-island colonization and intra-island segregation (e.g., Teno vs Anaga); *C. eminii* appears also geographically structured into a northern and southern clades. The long temporal gap and large genetic distances separating the Eastern African species and the Canarian endemic suggest that large-scale extinction, probably due to the increasing aridification of North Africa, is more likely to explain this disjunction than a recent long-distance colonization event from East Africa to the Canary Islands.

Keywords: phylogeography, vicariance, relict, island biology

120A Avifaunal patterns in Wallacea: how can we account for the unknown?

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The islands of Wallacea have formed one of the most celebrated case studies in biogeography ever since Alfred Russel Wallace first visited them in the mid-nineteenth century. Despite the region's high scientific and conservation significance, however, Wallacea remains understudied and for even the best-known taxonomic groups, such as birds, basic distributional knowledge is often lacking. We conducted nine weeks of fieldwork on Obi, the eighth largest island in Wallacea, during 2012 and recorded 109 species of bird, 14 of which were previously unrecorded from the island, and three of which likely represent undescribed taxa. These discoveries increase the known avian diversity of Obi by over 10%, and for some families (e.g. Rallidae) substantially alters known distribution patterns within the region. Surprisingly, results such as these are relatively routine for modern ornithological surveys in Wallacea. Here we compare our data with other recent field surveys and a historical reconstruction of known avifaunal patterns to assess the degree to which an incomplete knowledge of

species distributions may be distorting actual patterns of endemism in these islands, as well as masking their affinities to the major continental shelves, both of which confuse the debate over Wallace's Line and constrain the accurate identification of conservation priorities in the region. Understanding where knowledge gaps occur—taxonomically, ecologically, and geographically—can contribute substantially to guiding future research and conservation planning in the region.

Keywords: birds, conservation, endemism, Wallacea, zoogeography

121A Island plant communities: geographic isolation and community function

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Plant functional traits are important drivers of ecosystem processes and are increasingly used to quantify variation in community functioning. Although many studies have examined how plant functional traits change across environmental gradients, few have tested how community functioning changes across a gradient of isolation. Several studies found that island isolation gradients result in varying nested subsets of species based on specific dispersal strategies. The nested subsets along this isolation gradient may also provide a unique composition of functional traits. In this study, we used species composition data from 37 Maine coast islands to generate community weighted mean values of plant traits known to affect ecosystem functioning (e.g. plant growth rate, rooting depth, litter decomposition rate), and explored their variation with respect to island isolation, controlling for area. Our results provide compelling data about plant community functioning on a geographic scale. These data are crucial for the conservation of insular habitats, both for plants and nesting seabirds. These findings are also potentially significant for understanding the ecosystem functioning of fragmented landscapes.

Keywords: continental, trait ecology, dispersal, fragmentation

122A A comparative study on body size of Javan deer: Case study in Peucang Island and Panaitan Island, Ujung Kulon National Park

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Javan Deer in Panaitan Island has been extinct since 1920. Sixteen individual Javan Deer (3 male, 13 female) were captured and moved from Peucang Island (*c.* 450 Ha) to Panaitan Island (*c.* 17500 Ha) during 1978–1982 to reestablish this population. A comparative method was used to measure the difference of body size of adult Javan Deer, land cover, slope, elevation, temperature and humidity on Peucang island and Panaitan Island. We found that the body size of Javan Deer on Panaitan Island is bigger than on Peucang Island. The resources availability of these islands has influenced the body size of the Javan Deer.

Keywords : comparative, body size, Javan Deer, reintroduction

123A Macaronesia: a refugium and stepping-stone for Atlantic bryophyte species in transit from and to Europe

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Oceanic island biotas are typically characterized by high levels of endemism and a suite of life-history traits known as 'island syndromes'. In particular, the loss of dispersal ability characteristic for island taxa has contributed to the hypothesis that islands are evolutionary dead-ends. We investigated whether such a prediction applies to vagile organisms, taking bryophytes as a model. A meta-analysis of life-history traits of island species demonstrated a significant shift from prevailing dioecy on continents to monoecy on islands. Since spores are involved in long-distance dispersal, and owing to the extremely low rates of sporophyte production in dioecious species, this points to dispersal filters for island colonization. In agreement with the loss of dispersal ability hypothesis, lower rates of sporophyte production on islands and increased rates of asexual reproduction, which is assumed to contribute to local dispersal, were further evidenced. Despite this, migration rates derived from population genetic structure in island and continental populations are balanced. The maintenance of a high dispersal ability in bryophytes despite a decreased investment in sexual reproduction in the island setting has substantial consequences for our understanding of the relationships between island and continental floras. In particular, ongoing research demonstrates the substantial role of Macaronesian archipelagos as refugia for the European flora and stepping-stone for a large suite of tropical species in transit to Europe.

Keywords: island syndrome, Last Glacial Maximum, long-distance dispersal, spore-producing plants, reverse colonization

124A Origin and biogeography of New Caledonian Salticidae (Arachnida: Araneae)

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According to the fossil records, salticid spiders have been known at least since Eocene (55 MYA), although some authors suggest its history going back to K-T period. Over the Tertiary the local (continental) salticid faunas have been highly influenced by the geological and climatic history and New Caledonia is one of the most attractive models to show such an influence. Separated from Gondwana some 80 MYA it has the history of long isolation, volcanism and climatic changes which have resulted in the uniqueness of biota and, consequently, in local salticid radiation. Due to long-distance separation from surrounding islands, the possibilities of dispersal have been slight, but the common taxa for the entire western Pacific area raise the question on such likelihood. Analyses made for the species-level show that New Caledonian fauna is highly endemic (70%). The links with Australia, New Zealand and New Guinean refer mostly to wide-spread species. There is no evidence of New Caledonia be the source of fauna for other Pacific archipelagos, but Loyalty Islands. The aims of my study (presentation) are: to analyse the New Caledonian salticid fauna in terms of origin (source), endemism and relations with surrounding faunas of Australia, Fiji, New Zealand and New Guinea; to analyse to what extent the biotic uniqueness and geological history (e.g. multiple sea transgression) influenced the current fauna; to compare the results from morpho-geographical analyses and molecular data of other authors; to discuss the dispersal possibilities for wide-spread taxa and in relation to their biotic requirements.

125A Patterns of compositional dissimilarity in insular systems around the world

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A number of studies have shown that compositional dissimilarity patterns differ among taxa. Taxa with poor dispersal ability tend to have a higher level of compositional dissimilarity than taxa with good dispersal ability. However, this has not been investigated in several different insular systems, and no comparisons have been made between continental shelf and oceanic islands. To do so we used presence-absence matrices from studies that report the distribution of land vertebrates (reptiles, amphibians, birds and mammals) in various insular systems around the world. We calculated a compositional dissimilarity coefficient (Jaccard dissimilarity index) between pairs of islands in each insular system. We applied GLMM to the data, with compositional dissimilarity as a response variable, and taxon, island type (i.e. continental shelf, oceanic), area and elevation differences between islands, and inter-island distance as explanatory variables. Island group was used as a random factor. To assess the significance of explanatory variables we used likelihood ratio tests to compare models with and without the variable, using a bootstrap approach for estimation of p-values. The models applied to the data showed significant differences in compositional dissimilarity patterns among taxa as well as between continental shelf and oceanic insular systems, generally consistent with theoretical expectations.

Keywords: Oceanic islands, continental shelf islands, dispersal ability, community composition, beta diversity

126A Phylogeography of the white-browed shortwing in the Philippines

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The White-browed Shortwing, *Brachypteryx montana*, is a widespread bird distributed across the montane forested areas of southern Asia. We conducted a phylogeographic study of this species within the Philippines using over 200 samples from all the major islands. Using genetic data from mitochondrial and nuclear sequences and environmental niche modeling, we tested different proposed hypotheses for how birds have colonized and diversified in this region. Our results indicate limited gene flow between and differentiation of populations in each of the larger islands, which formed separate monophyletic clades. Populations from Palawan and Mindoro grouped within the Luzon clade, indicating independent colonization of these islands from the larger one. Populations on Mindanao formed two distinct groups that are paraphyletic, suggesting lineages migrated out of Mindanao and one later re-colonized it. This is supported by differentiated songs from these cryptic lineages. We detected both deep and recent divergences across populations on different islands due to periodic connections and isolation of these landmasses, as suggested by the Pleistocene Aggregate Island Complex hypothesis. Our analysis shows that this shortwing colonized the Philippines from Borneo into Mindanao, rather than Palawan, and later migrated northward to the other islands. The biogeography of this shortwing can be compared to other island endemics, as data becomes available, to assess whether this is a general pattern for montane forest species in the Philippines.

Keywords: biogeography, distributions, cryptic species, Asia, birds

127A Islands are dynamic on time scales less than 10 kyr: modeling sea level driven change of Macaronesian archipelago configurations since 120 kyr BP

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Islands vary with sea level changes in size, height and isolation, the rates of which are driven by the sea level change curve and island morphometry. Since the last Myr sea levels fluctuate with a period of ca. 120 kyr and amplitude of 130 m. We modeled and quantified the effects of global sea level cycles on the configuration of archipelagos and volcanic islands of Macaronesia. Between 80 kyr and 15 kyr ago sea levels were at least 80 m lower than present and several islands now isolated were merged or were much larger than present. Recent shrinking of islands due to the sea level rise since the last glacial maximum (20 kyr BP) led locally to more than 50% reductions in island size, drowning of some islands, significant loss of coastal habitat and a significant increase in isolation by the increase of distances between islands and island and continents. Island size reduction must have induced pressures especially on terrestrial ecosystems, inducing upward migrations and interspecies competitions, and probable extinctions. The splitting of merged islands must have led to separations of populations leading to gene flow losses for some biota. Our model produces metrics of sea level-driven island and archipelago changes that can be used to assess its role on biodiversity and biogeography. Island morphometric sea level driven dynamics is another factor suggesting disequilibrium biodiversity of many species. Islands at present are smallest and most isolated and this configuration makes the insular biota even more vulnerable to human impact.

Keywords: biodiversity, biogeography, sea level change, islands, Macaronesia

128A Ecogeographic patterns of body mass variation in fossil and living insular bovids

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Endemic bovids are unusual components of insular faunas. Living species include the Japanese serow (*Capricornis crispus*) and the Formosan serow (*Capricornis swinhoei*), the tamaraw from Mindoro, Philippines, (*Bubalus mindorensis*), and the anoas (*Bubalus depressicornis* and *Bubalus quarlesi*)— species of dwarf buffalos endemic to Sulawesi, Indonesia. Fossil and subfossil endemic bovids are only recorded in some Asian, North American and western Mediterranean islands. The most intriguing species, showing highly endemic features, inhabited the Eastern Balearic Islands (Myotragus), Sardinia (Nesogoral and Asoletragus) and Java (Duboisia). Island bovids show differ in body size relative to their putative ancestors in complex ways that do not conform to a generalized evolutionary pattern. Here we explore the hypothesis that body size evolution of insular bovids is influenced by a combination of selective forces (e.g., time in isolation, island area, distance to mainland, latitude, longitude, and number of predators and competitors) whose relative importance and nature of influence are contextual to clarify which factors played a major role in influencing body size evolution in these mammals. Time in isolation is a key force influencing anagenetic changes in body size within lineages, while it plays a minor role as regards living species, as does isolation from mainland and island area. Analyses of variation in body size among more than 30 insular bovids were consistent with the hypothesis that co-occurring competitors and predators influenced body size evolution in these species, although in different ways on different islands.

129A A first look at biogeography of arbsucular Mycorrhizal Fungi in Pine Rocklands

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The study of arbuscular mycorrhizal fungi (AMFs) has seen a recent surge in terms of molecular research. However, less is known about specific ecological interactions, community composition, and biogeography of AMFs. Pine rocklands are a unique ecosystem in south Florida and parts of the Caribbean. A drier ecosystem than most in south Florida, pine rocklands were diminished under pressure for development for housing and agriculture during early settlement of Florida. As such, they are now a highly fragmented and highly threatened ecosystem. Current efforts include conservation and restoration initiatives. Yet these initiatives are working with little knowledge of the belowground biota of pine rocklands, which could be highly beneficial in restoration efforts [particularly symbiotic microorganisms, such as AMFs]. This poster presents one component [biogeography] of a larger project investigating the questions of AMF diversity, community composition, ecosystem interactions, and biogeography. Soil samples were gathered from pine rockland locations throughout south Florida, the Florida Keys, Puerto Rico [dry forests], the Dominican Republic, and the Bahamas [New Providence]. Soil was sieved and processed, and AMFs were identified using both morphological and molecular techniques. Spores were collected from each soil sample and identified to genus and, where possible, to species level. DNA was extracted from soil samples and run in high-throughput next generation sequencing. This poster will present the results of these analyses; answering the question, how similar are AMF communities across pine rockland ecosystems, despite geographical differences?

Keywords: symbiotic microorganisms, next-generation sequencing, Caribbean

130A The effect of Quaternary climatic oscillations on the biogeography of small rodents from the sky islands of Costa Rica and western Panama

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This research aims to develop a better understanding of the effect of Quaternary climatic oscillations on the biogeography of taxa inhabiting an understudied system of tropical sky islands in Middle America. Based upon fieldwork and existing museum collections, we gathered occurrence records for two species of rodents that inhabit mesic conditions within the mountains of Costa Rica and western Panama: Nephelomys devius and Reithrodontomys creper. We obtained geographic coordinates either with a GPS or by georeferencing, using local maps and original information from collectors. Then, we built ecological niche models using MaxEnt and 19 bioclimatic variables from WorldClim. We projected these models to two extreme climatic scenarios of the late Quaternary, the last interglacial (LIG) and the last glacial maximum (LGM), to obtain predictions of past potential for population connectivity. Models show high environmental connectivity between mountains during the cooler LGM, but moderate to substantial isolation during the warmer climates of the LIG and present. We are currently testing past population connectivity in these species with phylogeographic analyses using cytochrome b. Preliminary results show low genetic structure by mountain, suggesting substantial population connectivity during the past. If so, glacial periods fostered colonization of these mountains but probably hindered speciation by promoting connectivity between cyclically isolated populations. Future analyses will include additional species, nuclear loci, and tests of local refugia and colonization routes.

Keywords: ecological niche models, glaciations, MaxEnt, phylogeography

131A Diversity patterns of oceanic archipelagos: ecology and history reconciled

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The determination of species richness by local conditions of the environment is one of the long-standing paradigms in ecology. This has recently been elaborated by hypotheses stressing the dominant role of regional processes and historical events in species diversification. Using the number of species of native and endemic species of birds, vascular plants, spiders and land snails inhabiting all the major oceanic archipelagos of the globe, we demonstrate the parallel scaling of taxon diversity with ecological space, regardless of differences in ecology and propensity for colonization and dispersal within archipelagos. Our results suggest that diversity on oceanic systems integrates evolutionary and ecological processes and interactions, regulated by the similar geological histories of these systems.

Keywords: biodiversity, biogeography, statistical modeling

132A The early colonization process: favorable traits for successful long-distance dispersal to the Galápagos Islands

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Researchers rely on biogeographic reconstruction estimates to infer colonization of oceanic islands, given that nobody has witnessed early species arrival. We present a new approach that evaluates whether particular traits for long-distance dispersal (hereafter LDD) have been favorable in the natural colonization of the Galápagos Islands by plants. Dispersal syndromes –that is the set of traits related to diaspore LDD by animals, wind and sea currents— of the 251 native genera (509 angiosperm species) presently acknowledged as native were carefully studied, combining data from floristic lists of the Galápagos Islands, diaspore traits and characteristics of continental relatives. Analyses considered only each native plant (corrected by paleobotanical data), each genus as a working unit (corrected by phylogenetic results) and each favorable trait (inferred by LDD traits). A total of 372 colonization events were inferred for the native flora using the latest check-list. The proportions of native colonists grouped into five categories were: endozoochory 16.4%, epizoochory 15.7%, hydrochory 18.6%, anemochory 13.3%, and unassisted diaspores 36.0%. These results were consistent when analysing only the 99 genera that include endemic species in order to rule out any human-mediated introductions. Irrespective of the roles of the different agents involved in LDD, a third of the flora has diaspores with no special syndrome for LDD (unassisted diapores), such as many dry fruits, which have been unexpectedly successful in reaching and colonizing the Galápagos archipelago. This finding leads us to suggest that both unpredictable and so far unknown LDD mechanisms should be further considered in the theory of island biogeography.

Keywords: paleobotanical and phylogenetic corrections**,** floristics, natives, systematics, unassisted diaspores

133A The explosive radiation of *Cheirolophus* in the Canary Islands

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In the last decades, Canary Islands have been key subjects of numerous biogeography studies concerning many diverse plant groups. Particularly, molecular phylogenetic analyses have been significant for addressing some major evolutionary topics on island radiation processes including: (1) relationships between island and mainland floras; (2) inter-island colonization patterns; and (3) intra-island diversification. The genus Cheirolophus, comprising near 20 endemic species in the Canary Islands and distributed over five different islands in the archipelago, presents an ideal scenario to discuss these issues. Here, we employed the latest Bayesian-based phylogenetic tools to analyse the Cheirolophus radiation processes not only in a reliable timescale but also incorporating spatial biogeographic data. nrDNA (ITS and ETS) sequences from 54 samples including continental and insular congeners provided an accurate temporal framework for the colonisation process. Phylogeographic history of Canarian species was inferred by sequencing four chloroplast DNA markers for 34 populations. In our analyses, Macaronesian taxa are grouped in a well-supported monophyletic group that diverged around 8.7 Mya with a crown radiation starting at 1.7 Mya. The case presented here could be considered as one of the most remarkable examples of explosive plant radiation in oceanic islands. Climatic oscillations in the Canary Islands during the last 500,000 years could have enhanced this radiation process. Tenerife, currently containing most of the genetic diversity of the genus in the archipelago, seems to have played a major role in this rapid diversification of Canarian species. Indeed, this island would have been a potential centre of dispersal for inter-island colonization events.

134A Towards a macroecological synthesis of island floras

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Since the early beginning of biogeography, islands have received special attention. Numerous biogeographic, genetic, and ecological studies have contributed to the understanding of colonization, speciation and extinction on islands as drivers of richness and endemism. Increasing comprehensiveness of data on species occurrences and enhanced computational possibilities have enabled macroecologists to reveal global-scale patterns and mechanisms. Here, we review recent progress on the understanding of global plant diversity on islands. We show that species richness can readily be explained by a set of simple physio-geographic variables describing island area, isolation, climate, topography and geology. We revisit island isolation as one of the critical factors, its measurement, and its interactions with area. When looking at alpha, beta, and gamma components of diversity of entire archipelagos, factors like the spatial arrangement and environmental heterogeneity among islands arise as important predictors. Islands are well-known for a high proportion of endemic species. The uniqueness of their floras makes them extraordinarily susceptible to human induced threats. Despite their high conservation value, we still have information for only few of the approximately 180,000 islands worldwide. Compared to mainlands, little is known about their environmental conditions and a useful classification that specifically considers islands is currently missing. We provide perspectives on how to take advantage of available global data sets in delimiting island ecoregions and linking floristics to environments. This framework may prove useful for further studies in island biogeography, macroecology and for environmental assessments that specifically consider islands.

Keywords: island biogeography, macroecology, isolation, archipelago, ecoregions

135A Non-native species extend the functional diversity of Azorean island invertebrate assemblages

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Analyses of species diversity patterns of remote islands have been key to biogeographic theory development, yet we know little about corresponding patterns in functional traits and how, for example, they may be affected by the anthropogenic introduction of exotic species. We collated trait data for spiders and beetles and used a functional diversity index alongside ordination analyses to examine how endemic, native and exotic species contribute to functional trait space patterns across the nine main islands of the Azores (oceanic islands in the mid-Atlantic). In general, for both taxa and for each distributional category, functional diversity is shown to be an increasing function of species richness, which in turn scales with island area. Null simulations confirm that, with exceptions, each distributional group contributes to functional diversity in proportion to their species richness, while those exotic species invading remnant native forest appear to be a random draw of the pool of exotics. While exotic spiders appear to have added novel trait space to a greater degree than have exotic beetles, this may reflect both ecological and analytical causes (e.g. varying trait numbers). The occurrence of linear (not saturating) patterns of trait space increase with richness of exotics suggests the system is open to further colonization by exotic species. We discuss the implications of our results for the long-term maintenance of present-day anthropogenically elevated levels of diversity on these oceanic islands.

Keywords: Exotic species, functional traits, habitat destruction, island biogeography, saturation

1B Testing the role of time and environmental heterogeneity in driving the diversification of the antbirds (Aves: Thamnophilidae)

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The avian family Thamnophilidae is a diverse radiation of insectivorous passerine birds that comprises nearly 220 species mostly restricted to the lowlands and lower montane forests of the Neotropics. Although the Thamnophilidae is considered a widespread group of birds, its distribution is more constrained relative to that of other endemic Neotropical avian radiations. Relatively few antbirds occur in open habitats such as savannas, grasslands, and xeric environments, and no thamnophilids occur at very high elevations or latitudes. Here, we integrate continental-scale distributional and environmental data with the first robust species-level phylogeny of the Thamnophilidae to assess the relative roles of time and environmental heterogeneity in explaining species diversity and distributional patterns of the Thamnophilidae. Model-based approaches evaluated in an information theory environment showed that species diversity patterns in the Thamnophilidae could be explained by the interaction of the effects of time with evolutionary processes that have affected net diversification rates over time. Older lineages tend to exhibit higher species richness, and regions colonized earlier tend to have higher species richness. Also, lineages with broader niches tend to speciate less and lineages inhabiting more seasonal and drier environments tend to speciate more. These results support the role of climatic and habitat changes in explaining diversity patterns in the Neotropics. Their absence in certain Neotropical regions might be associated with extreme environmental conditions that indirectly affect food resources, habitat, or microhabitat requirements of antbirds. A second possibility is that environmental conditions, especially low temperatures, are physiologically challenging, and therefore limit antbird survival.

Keywords: Neotropics, environmental heterogeneity, niche, Thamnophilidae, diversification

2B Genomic ultraconserved elements resolve the comparative phylogeography of five Neotropical birds

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Advances in sequencing technology permit researchers to generate massive genomic datasets, but their application to phylogeographic studies has been limited by the difficulty of generating data from homologous loci across many individuals. Sequence capture of conserved portions of the genome now permits the generation of homologous data across individuals that can then be multiplexed on next-generation sequencing platforms. We evaluated a recently developed class of genomic markers known as ultraconserved elements (UCEs) to determine whether sufficient polymorphism exists in and around these loci to resolve intraspecific relationships and estimate population genetic parameters such as divergence time, effective population size, and migration rate. We apply this method to populations of five Neotropical passerine birds distributed in humid forest throughout the Neotropical lowlands. We successfully align sequences from between 776 and 1516 loci, 23-42% of which are polymorphic, in the five species. We analyze these alignments in a coalescent framework in order to obtain population genetic parameter estimates, construct species trees, delimit species, and model demographic history. Comparisons suggest that poorly dispersing taxa have lower effective population sizes and shallower divergences across barriers, and contain more species, than more vagile taxa. These results are consistent with results from independent datasets, but provide higher resolution of the histories of these populations than was possible previously. Since UCEs can be amplified across a wide array of taxa and can be generated rapidly at low cost, we conclude that they are promising markers for use in phylogeographic and comparative phylogeographic studies.

Keywords: phylogenomics, coalescent, demography, sequence capture, next-generation sequencing

3B The biogeography of an extended phenotype

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Parasites can control the behavior of their hosts, thereby extending their phenotype into host behavior. Zombie ants are ants infected by a specialist fungal parasite that controls host behavior before it dies. The phenomenon is widespread, having been recorded from 27 countries across 5 continents. However, little is known about the distribution patterns and ecological strategies in different habitats. We contrasted the extended phenotype of fungi in ants across 50 degrees of latitude from the deciduous woods (N. America) to the Tropical and Atlantic Rainforests (Brazil). Extensive sampling efforts showed that the diversity of parasitic fungi and infected ants are higher in tropical rain forests. The *Ophiocordyceps unilateralis* s.l. was the only group found in N. America. In temperate deciduous forest, the fungus can grow for more than 18 months. The fungus is able to pause growth during winter, and rapidly returns growing in spring. In tropical systems, the cycle is faster and there is no pause on the fungus development. Importantly, the infected ants in deciduous forests die biting on twigs; in tropical rain forest they die biting on leaves. The extend phenotype expressed by this group of fungi in a group of ants is variable according to environmental conditions, once the trees loose their leaves in deciduous forests and ants pause their activity during winter. We suggest further directions to be taken in studying not only the biogeography of species interactions but also how one species manipulates the behavior of another.

Keywords: Ecological strategies, behavioral manipulation, parasites, fungi, zombie ants

4B Historical fire and bamboo dynamics in western Amazonia

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We examined whether recurrent fire accounts for bamboo-dominated forests that cover about 180,000 km^2 of western Amazonia. We identified bamboo (B+) and closed-canopy forests (B−) using a combination of satellite imagery and field surveys. Local-scale and landscape-scale patterns of historical bamboo dynamics were analyzed by collecting soil cores from B+ and B− sites across three regions. Soil charcoal within cores was used to document previous fire, and phytoliths were employed to reconstruct vegetational patterns through time. Fire occurred in B+ and B− sites with approximately equal frequencies in each region sampled. Between regions, fire signals were most prevalent at Los Amigos, with other regions typically containing only trace amounts of charcoal. Vegetational state remained constant through time in both B+ and B− forests of Cocha Cashu and Acre. The persistence of bamboo through time is less clear at Los Amigos, with bamboo presence changing both spatially and temporally. Fire does not appear to be the driving mechanism behind current bamboo distributions, although it may facilitate bamboo invasion. Once established in an area, bamboo persistently dominates the vegetation structure over historical timescales at some sites, but not at others, which is likely to be a function of patch origin. Increasing human activity, including fire and deforestation, combined with predicted Amazonian drought, may allow bamboo to expand from its current distribution and replace typical Amazonian closed-canopy forests. These structural changes in the forests have important implications for carbon storage, as Amazonian forests are currently the largest terrestrial carbon sink in the world.

Keywords: charcoal, Cocha Cashu, *Guadua*, Los Amigos, phytoliths

5B Biogeography of range sizes of New World oscine passerines (Aves): separating ecology and evolution for migratory and resident clades

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Geographic range size represents one of the major ‘traits’ of species on which macroecologists have focused. Studies on both ecological and evolutionary determinants of range size have concluded that no single ecological hypothesis seems sufficient to explain patterns of range size, and that phylogenetic signal in this trait for extant terrestrial species is weak. However, since range sizes undoubtedly reflect species traits, many of which are strongly conserved during cladogenesis, it would be surprising if there were no phylogenetic signal in range sizes at all. We propose a new eigenvector-based method that allows partitioning the individual and shared associations of phylogenetic, ecological and spatial components with range size variation, while avoiding the reduction of all environmental and spatial variability into summary metrics such as midpoints. We use this method for New World oscine birds, which allows us to compare differences in phylogenetic and environmental signal between migratory and resident clades. We find phylogenetic signal in species-level range size patterns, suggesting that associated traits are not entirely labile. Environmental, spatial and phylogenetic factors can account for up to 95% of the variation in range size, and differ in their relative contributions to patterns of range size in migratory versus resident clades and in breeding versus non-breeding migrants. The breeding ranges of migratory species showed stronger phylogenetic signal than in the other groups, which may result from strong macroclimatic filtering associated with breeding in ‘recently’ deglaciated regions.

Keywords: macroevolution, migrations, eigenvector-based analysis, phylogenetic signal, postglacial recolonization

6B Comparative genetic diversity and species distribution models of two closely related plant species in the tropical Andes

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Phaedranassa (Amaryllidaceae) is a small plant genus of 10 species restricted to the Northern Andes. Seven of the species are native to Ecuador and six of them are endemic to the country. Mountain ridges as the Andes can be barriers for genetic exchange between species. At the same time, recent volcanism could promote the speciation process. We contrasted the genetic diversity patterns with the geographic features of *P. schizantha* and *P. tunguraguae*. Both species are located in the central Andes in Ecuador near the Tungurahua Volcano, one of the most active volcanoes in the country. We found intra-specific and inter-specific genetic variation using microsatellite markers. A coalescent approach indicates that the time of divergence between populations is in general larger for *P. schizantha* than for *P. tunguraguae*. Based on coalescent estimates

of divergence times, for some of the populations climate change events during the Pleistocene might have influenced their current distribution and genetic differentiation. Also, the timing and nature of historical volcanic events in the Tungurahua volcano suggests that volcanism may have played a role in the genetic diversity and distribution, especially for *P. tungurahuae*. Species distribution models showed no distribution overlap among species, suggesting that *P. schizantha* prefers areas with lower altitude, lower precipitation and lower humidity than *P. tunguraguae.* Our study shows that using multiple sources of information we can better explain current species distributions and genetic diversity.

Keywords: Population genetics, microsatellites, phylogeography

7B Niche differentiation in Neotropical singing mice

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Species distributions inferred from ecological niche models (ENM) assume accurate estimation of conditions in which species can survive and their corresponding geographic limits. Sister species of Neotropical singing mice (genus *Scotinomys*) segregate altitudinally in the highlands of Costa Rica and Panamá, where *S. teguina* occurs from ~1000-2900m and *S. xerampelinus* inhabits regions above 2100m. Previous data suggests that *S. xerampelinus* is limited by abiotic factors, whereas *S. teguina* is limited by the presence of dominant heterospecifics. We used ENM and C^{13} and N^{15} stable isotope data from hair samples to further explore the factors mediating altitudinal segregation. Predictive performance of ENM was high for both *S. teguina* and *S. xerampelinus* (AUC= 0.91 and 0.96, respectively). Interestingly, both ENM and isotope analyses showed the niche of *S. xerampelinus* to be nested within that of *S. teguina* (>95% for ENM, 71% for isotopes). Furthermore, the predicted distribution of *S. teguina* was ~30% larger in the absence of *S. xerampelinus*, supporting earlier findings of competitive exclusion. Our data suggest that biotic and abiotic factors interact to mediate the altitudinal distributions of Neotropical singing mice, and highlight the importance of integrating biotic and abiotic data to assess the accuracy and magnitude of niche differentiation.

8B Testing for the existence of a long biogeographical barrier perpendicular to the Amazon River

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In biogeographical discussions about lowland Amazonia, rivers have often been regarded as the main dispersal barriers. Accordingly, biogeographical subdivisions of the area typically follow the courses of largest rivers. A recent study by Higgins *et al.* (2011, Journal of Biogeography) described an erosion process, which can create edaphic borders that typically are oriented perpendicular to main river courses. That study documented how such a barrier of over 100 km in length in Peruvian Amazonia significantly affects the distribution of the majority of plant species. The study also identified on the basis of remote sensing data a potential dispersal barrier of over 1000 km long that goes perpendicularly over the Amazon River in western Brazil. No field data existed that would have allowed for an evaluation of practical significance of this potential barrier to species distributions. In 2012, a three-month expedition from March to June was organised by Brazilian, Danish and Finnish botanists to Juruá and Tarauacá rivers to investigate if the predicted dispersal barrier can be found. In this talk I will present preliminary results of species distribution patterns of Melastomataceae plant species over a stretch of ca. 500 km along the two rivers. According to the results, the predicted dispersal barrier exists and its significance in restricting plant species distributions is comparable to the barrier documented in Peruvian Amazonia.

Keywords: geology, Melastomataceae, rain forest, soil

9B Phylogeography of the Andean Wax Palms (Ceroxylon) based on nuclear and chloroplast genes

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The wax palms are a genus of twelve species that are endemic to the tropical Andes. Previous phylogenetic studies have suggested that speciation within the genus is recent, with several species less than one million years old which exhibit a lack of genetic variability. Despite the fact that these palms are conspicuous elements of the forest, morphology has mislead their taxonomy as all the generic-level variation is conserved within each species, meaning that diversity is not sorted among, but rather within, entities. Two chloroplast, and a nuclear region were sequenced along the entire distributional range of the genus in order to address how haplotype diversity is geographically arranged. Results suggest that diversity is centered in Colombia and Ecuador and that diversification follows a South-to-North pattern. General, tribal-level haplotypes were found to be conserved in the south and center of the distribution, which are subsequently lost in the north. The two isolated mountain ranges in the North (Sierra Nevada de Santa Marta, Colombia and Cordillera de la Costa, Venezuela) exhibit low genetic diversity and/or unique haplotypes. Given that the *Ceroxylon* distribution has likely been highly fragmented since the origin of the group future studies should be conducted to understand how population structure of closely related species correlate with the landscape.

Keywords: Andes, haplotype diversity, biogeography.

10B Distribution of a rediscovered freshwater decapod crustacean within the Mbaracayú Forest of Canindeyú, Paraguay

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The Atlantic Forest of South America is one of the world's 25 recognized biodiversity hotspots, yet only 8% currently remains of its original 1.5 million km^2. The remaining fragments within Paraguay, known as the Interior Atlantic Forest, are being deforested at an estimated rate of 2,885.5 km^2 per year. In 2001, UNESCO designated the Mbaracayú Forest, the largest remaining Interior Atlantic Forest fragment in Paraguay, as a Biosphere Reserve. Few studies within Paraguay's various Interior Atlantic Forest fragments have focused on invertebrates, with even fewer on aquatic invertebrates. In the 1980's, the last confirmed aeglid crab specimens were collected in Paraguay followed by their proposed extirpation in 1999 due to wide-scale deforestation. However, after almost three decades of failed attempts to locate specimens within Paraguay, aeglid crabs were rediscovered within the Mbaracayú Forest in 2009. In 2010 research was conducted to determine the distribution of this freshwater decapod crustacean within the Mbaracayú Forest.

Keywords: *Aegla*, deforestation, decapoda, South America, conservation

11B The biogeography of diversification: how biomes affect intraspecific diversity in tanagers of the genus *Tangara*

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Tropical habitats host incredible biotic wealth. In order to effectively conserve standing genetic diversity it is essential to understand how that diversity arose and how it is distributed. In birds, allopatric speciation is considered to be the primary mode of diversification at the species level. One way barriers to dispersal among populations can arise is through the fragmentation of formerly contiguous habitat. Historical changes in habitat extent, distribution, and connectivity shape intraspecific diversity and have important implications for the speciation process. We study how intraspecific diversity and genetic structure differs between major South American biomes across a large monophyletic radiation of neotropical birds, tanagers in the genus *Tangara.* By studying the demographic and phylogeographic background of broadly sympatric congeners representing each of several habitats, we compare and contrast the evolutionary processes that formed the observed patterns of variation. Using mitochondrial DNA in conjunction with nuclear-encoded microsatellite data, we test the hypothesis that different habitats contain species with predictably different patterns of intraspecific diversity, and examine how orientation and regional stability of biomes through time influences divergence and diversification. Our results show strikingly different patterns of diversity, divergence, and geographical structure between congeners occupying different habitats.

Keywords: Diversification, speciation, phylogeography, Neotropics, *Tangara*

12B The reinvasion of Central America from the south: Historical biogeography of the Neotropical snake genus *Chironius*

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The snake genus *Chironius* is endemic to the Neotropical region. Recent phylogenetic hypotheses suggest that the genus might have originated in South America, and dispersed posteriorly to Central America. Here, we use event-based methods to explore the historical biogeography of the genus and test the hypothesis of a South American origin followed by a subsequent invasion of Central America. We reconstructed two alternative scenarios of ancestral areas of distribution based on two distinct phylogenetic hypotheses for the genus. We considered five biogeographic units within the Neotropical realm: Caribbean, Amazonian, Chacoan, Paranean, and Andean. Reconstructions of optimal ancestral distributions were obtained by Bayesian Binary MCMC Analysis implemented in RASP. Our analyses suggest either an Amazonian or an Andean origin for *Chironius*. Several events of dispersal seem to have defined most of the distributions of the main clades, especially those that invaded open landscapes of the Chacoan Subregion. Also, vicariance seems to have defined disjunct distributions in both Amazonian and Paranean subregions, in two independent events. Additionally, at least two independent events of dispersal explain the invasion of the Caribbean Subregion from South America. Both biogeographic reconstructions corroborate the hypothesis of a South American origin for *Chironius* with a posterior invasion of Central America through dispersal. As a future prospect, further analyses that incorporate a time-calibrated phylogeny could shed light on the possible causal factors related to the diversification of this group of snakes, and provide better grounds for the study of the evolution of South American biotas and their associated landscapes.

Keywords: Serpentes, historical biogeography, Neotropical region, vicariance, dispersal

13B A phylogenetic perspective on the biogeography of avian body size in a South American adaptive radiation.

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Variation in body size constitutes one of the largest sources of morphological variation. Though biogeographic patterns of body size variation are well characterized within species or genera, it is unclear whether such patterns transcend higher taxonomic levels. Bergmann's Rule predicts that body size will increase with latitude and its underlying physiological prediction is that organisms are larger in colder environments. We tested if latitude and temperature are correlated with body size within the bird family Furnariidae. This specious family has undergone an adaptive radiation and occurs in virtually every terrestrial environment in South America. We combined morphometric, environmental, and phylogenetic data for 287 species of Furnariids and tested these correlations using phylogenetic least squares regressions. We found large variation in body size at all latitudes and temperatures and no support for a positive relationship between body size and latitude. However, we found a highly significant, negative relationship between body size and temperature. To determine if these patterns were present at shallower phylogenetic scales we examined nine sub-clades. Once again, we found that no individual clade within Furnariidae showed a positive relationship between body size and latitude, yet five showed a highly significant negative relationship between body size and temperature. These results demonstrate that latitude may be a poor predictor of the biogeography of body size in large specious clades distributed in mountainous tropical environments. Conversely, the biogeography of body size in Furnariids is consistent with the divergent selection driving body size divergence across temperature gradients.

Keywords: Bergmann's Rule, Furnariidae, phylogenetic regression

14B Status and distribution of Rallidae in coastal estuaries from tidal marshes to mangrove forests

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In the western hemisphere, tidal marsh ecosystems in temperate northern regions transition to mangrove forests in subtropical southern regions. In the southern region, mangrove forests transition back to tidal marsh ecosystems. The largest extent of these ecosystems occur within a few estuaries, but they have suffered severe loss and degradation as increasing human populations alter the coastal landscape for agriculture, aquaculture, and development. Tidal marsh and mangrove forests provide habitat for rails and crakes (family Rallidae), secretive bird species that are found in these ecosystems. In the northern region, Clapper Rail subspecies are endemic to tidal marshes. In the southern region, the Plain-flanked Rail is restricted to mangrove forest and coastal marshes and lagoons. There is a varying number of rail subspecies or populations found along the north-to-south gradient. Here, we review the Rallidae species across the American latitudinal gradient to examine their current status and estuarine distribution. Specifically, we consider body size, habitat dependencies, population size, and range extent in relation to habitat availability and the amount of surrounding urbanization. We discuss the variation in their ecology relative to the tidal marsh and mangrove forest ecosystems they use, as well as the differences in their morphology and their apparent adaptation to these ecosystems.

15B Feather growth and the biogeography of stress in Neotropical birds

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How environmental conditions affect physiology and distribution of animals has been a pervasive topic in both ecology and evolution because spatial distribution guides the interactions of organisms, and so is thought to be the primary driver of both speciation and community composition. Physiological response to environment can limit distribution through variation in ability to cope with variation in factors such as temperature, oxygen, photoperiod, and primary productivity. Furthermore, environmental gradients can affect life-history traits through trade-offs in energetic decisions. According to Ashmole's Hypothesis, time invested in breeding increases with increased latitude. Because of this and the fact that most birds molt immediately after breeding and protract molt when they fail to breed or abandon breeding early, I hypothesized that birds in higher latitudes will show higher rates of feather growth. Furthermore, because stress effects the amount of energy a bird invests in parental care compared to individual survival and molt is an essential investment in survival, duration of molt should respond differentially to environmental factors such as elevation and precipitation depending on habitat preferences. I analyzed feather growth rates in 968 individuals of five widespread Neotropical birds. I found significant latitudinal gradients in accordance with my hypothesis, and differential responses to elevation and precipitation. These results suggest feather growth may be useful in studying how environment and physiology interact to affect distribution and energetic decisions. Further work will combine these datasets with phylogeography to investigate the relative roles of geographic features as biogeographic barriers on Neotropical birds.

Keywords: biodiversity, physiology, distributions, energetics, life history

16B Habitat suitability models of Neotropical birds

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Habitat suitability models have the potential to improve the configuration of geographic ranges, which are typically based exclusively on highly subjective 'expert-drawn' knowledge that assume a homogeneous species distribution within range polygons. We used range polygons as a baseline to develop 1- km resolution habitat suitability models for 3,111 known extant Neotropical breeding birds, based on their habitat preferences and elevational range. We then created species richness maps for three components of diversity: all species, threatened species and endemic species. Overlapping geographic ranges on average overestimated bird species richness by a factor of two compared to that estimated by overlapping their suitable habitats. The peak of avian species richness (based on suitable habitat overlap) was found in the tropical Andes and the lowland Amazon. Regions with the highest difference between the two estimators were found in the Andes, north of the Amazon basin and the Brazilian Atlantic forest. The percentage of suitable habitat within geographic ranges was consistent with IUCN species conservation status, decreasing from Least Concern species to Critically Endangered species. Depending on species habitats, flooded forest habitat specialists have less suitable habitat within their ranges whereas forest habitat specialists have more. In general, species richness maps based on expert-drawn geographic ranges showed less detail and appeared smoother than species richness maps based on habitat suitability. These results indicate that the methodology used here could provide a substantial improvement over conventional distribution data for biogeographic and macroecological analysis, and conservation planning.

17B Molecular and morphological diversity of the ectomycorrhizal fungal genus *Clavulina* from the Guiana Shield region

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Clavulina (*Clavulinaceae, Basidiomycota*) is an ectomycorrhizal (ECM) genus of fungi with ~81 species described globally from tropical and temperate forests. In the central Guiana Shield of northeastern South America mycofloristic and root tip sequencing studies demonstrate *Clavulina* is an especially ubiquitous and speciose genus. Fourteen years of fieldwork in rainforests dominated by ECM Leguminous trees have yielded ~25 *Clavulina* morphospecies and 21 additional *Clavulina* species from root tip sequences currently yet as fruiting bodies. These 40+ regional taxa are in striking contrast with c. 10-15 taxa resulting from north and south temperate surveys, where ecosystems have received comparatively much more focused research. Collections and descriptions associated with the Guyana site have contributed significantly to our taxonomic and biogeographical understanding of this group considering that previously only ~65 species had been described worldwide, many resulting from temperate fungal forays. Molecular and morphological data indicate this genus may have diversified or radiated in the Neotropics, a pattern not yet documented for ECM fungi. Molecular phylogenies and relative evolution rate analyses support these hypotheses. Additionally, Guyanese *Clavulina* taxa have micro- and macro-morphologies that differ radically from the traditional generic diagnostic concept, which was based largely on temperate collections. For example, most *Clavulina* are coral shaped, and several Neotropical taxa have been described with funnel-shaped or effused fruiting bodies. Here we present the first large scale multi-locus phylogenetic and molecular evolution rate analyses of the genus *Clavulina.* Insights into evolution of anomolous morphologies and biogeographic patterns will be discussed.

Keywords: *Dicymbe,* morphology, molecular phylogenetics, Neotropics

18B Biogeography of the flora of Peru’s Western Andes: endemicity, origins and conservation

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The Andes Mountains of Peru represent a global hotspot for biodiversity, including high numbers of vascular plant species. This study provides an overview and conservation assessment of the diversity and evolutionary histories of plants found in the western Andes. The habitats in drainages that connect to the Pacific Ocean are primarily arid or semi-arid, with climate systems controlled by the cold waters off-shore, a semi-permanent high pressure cell, and rain shadow effects caused by the mountains. There are numerous specialized species in the hyper-arid landscapes of central and southern Peru, found in seasonal fog vegetation (known as “lomas”) and among succulent plant assemblages. Results from phylogeographic studies suggest that endemism is associated with dispersal and speciation since Miocene times and primarily with origins in the subtropical Andes. The woody vegetation of the northern coast and the Andean versant is predominantly shrubland, with forests mostly found in isolated patches, restricted both by climatic factors and human land use. The highest endemism is among the shrubs and phylogeographic studies, although limited, frequently point to ancient connections to dryland floras found in North and Central America. Another habitat of high endemicity is formed by high mountain peaks of the western Andes, which have led to allopatric speciation in the past in habitat archipelagos that today represent critical sites of environmental change, due to global climate drivers. Overall the flora demonstrates many features that are best explained by processes that predate the Quaternary, while current species distributions highlight the lack of suitable conservation strategies.

Keywords: biodiversity, endemism, Peru, vascular plants

20B Exploring the social networks of bats

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Conservation of populations requires an understanding of their distribution in space and time. This may be achievable for species that are readily observable or easily tracked, but can be extremely difficult for inconspicuous species. Indeed this can be especially more challenging for species that have dynamic social groups which can only be identified though analysis of interactions between individuals over time. Here we present a study of two inconspicuous, social species, Daubenton's bats (*M. daubentonii*) and Natterer's bats (*M. nattereri*) in a British lowland wood over a period of five years. Over one thousand bird boxes spread through the wood, that the bat use as summer roosts, facilitated easy access to the bat population at a high spatial resolution, difficult to achieve in a natural system. Individuals were marked and cohabitants recorded. Using these data social network analyses were used to visualize and quantify the structure of the population. These analyses revealed both species had strong social structure with species-specific differences in the position of males in the networks. Despite occupying a continuous woodland with many available roost sites, social groups of female Daubenton's bats and Natterer's bats (both sexes) had small roost home ranges ($0.23 km^2$ and $0.17 km^2$ respectively) with little conspecific overlap, suggesting these bats may be more reliant on smaller areas of habitat for roosting than previously understood.

Keywords: conservation, population structure, home range, roost, woodland

21B Species-people correlations and the need to account for survey effort in biodiversity analyses

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Positive regional correlations between biodiversity and human population have been detected for several taxonomic groups and geographic regions. Such correlations could have important conservation implications and environmental mechanisms (mainly energy) have been invoked to explain them, with little testing for an artefactual explanation: more populated regions may show higher biodiversity because they are more thoroughly surveyed. We tested the hypothesis that the published herptile-people correlation in Europe is determined by the distribution of survey effort. Without explicit information on the effort associated to each record, we compared herptile-people correlations among three nested regions subjected to different survey coverage. Both mean species richness and human density increased towards better-surveyed regions. Whether or not accounting for latitudinal effects, the relationship between species richness and human population was positive and significant at the lower survey coverage levels, but faded as the analysis focused on better surveyed regions and disappeared in the best-surveyed level. Single-species analyses revealed identical patterns, for both human-avoiding and human-adapted species. These results suggest an artefactual origin for the correlation between herptile diversity and human population in Europe. More importantly, they highlight the importance of addressing sampling artefacts whenever possible in biodiversity analyses, which may be possible even when survey effort is not directly recorded. Our findings also underline the utility of noting survey effort along with biodiversity records, and the need for better surveys of biodiversity in less populated areas. An adequate identification of conservation conflicts requires more rigorous assessments of the effects of survey effort on biodiversity data.

Keywords: artefacts, biogeography, distributions, human influence, macroecology

22B Analysis of the adequacy of protection status of ecosystems in the Nigerian protected area

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This research analyzes the adequacy of Protected Area Systems (PAS) in Nigeria, focusing in particular on assessment of protected areas (Forest Reserves and National Parks) with respect to the extent of their coverage within various ecosystems. The application of gap analysis, within an ecosystem approach, was adopted to determine the extent of protected area coverage for the study region. Eighteen ecosystems were identified and delineated using a Geographic Information System, on the basis of geographic, physiographic and ecological characteristics. A 20% threshold for representation is recommended by the Federal Government of Nigeria and was adopted to determine the sufficiency of coverage of specific ecosystems within the existing PAS network. Findings revealed that only four ecosystems were adequately protected (more than 20% of their area protected). Six ecosystems had fair (10 to 20%) protection, while eight ecosystems had inadequate (less than 10%) protection. The study recommends an increase in the protection status of the ecosystems that had less than 10% protection. Also, existing environmental laws should be revised and seriously implemented, while adequate funds for nurseries, plantations and maintenance of planted stock will improve survival of species. Emphasis should be on native species, to promote ecosystem stabilization.

Keywords: biogeographic regions, ecosystem approach, forest reserves, gap analysis, national parks

23B Transferability of ecological niche modeling predictions: a test using Monk Parakeet worldwide invasions

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Obtaining predictions of species distribution that can be accurately projected across space and time is a major challenge in the field of ecological niche modeling. Invasive species provide a unique opportunity to address this problem because they occupy areas subjected to different ranges of environmental conditions. In this study, I compared the performance of different modeling strategies to examine the invasive potential of the monk parakeet (*Myiopsitta monachus*), a species originally native to Argentina, which has established several stable populations worldwide. My results show that for this species, the best strategy to create reliable transferable predictions is to model the niche of the species from the pattern of occurrences in the native range using complex model settings. In contrast to previous studies, I found that models using both native and introduced records provided good discriminatory power but did not perform better than random models after accounting for overfitting. Simple model settings also resulted in apparently good transferability but the predictions were not significantly better than models based on random geographic records, indicating that seemingly high performance may in fact stem from factors independent of the species distribution. These results thus highlight the need to measure model performance with both overfitting and discriminatory power criteria, and to correctly assess statistical significance. I obtained a single model performing better than random models; its predictions reveal several areas at risk of new monk parakeet introductions and show that most of the currently well established populations are likely to expand to surrounding areas.

Keywords: MAXENT, overfitting, model complexity, null models, *Myiopsitta monachus*

24B Functional traits, types and response groups match grazing gradient and plant community patterns

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We examined traits of dominant and frequent species in previously classified plant communities, in order to reveal the specific impact of livestock grazing on community patterns. First we identified Plant Functional Types (PFTs) to evaluate which traits show a response to grazing impact. Second, we analysed the traits to differentiate the impact of altitude and grazing. We used RLQ analysis and fourth-corner statistic, two three table ordination approaches that circumvent the so called fourth-corner problem. RLQ analysis and the fourth-corner statistic offer exciting opportunities for studying trait–environment relationships. Both analyses calculate correlations among environmental data and species traits, albeit focussing either on multivariate or univariate relationships. Fourth-corner statistic is an exhaustive and precise analysis of the relationship between a species trait and an environmental variable, helping ecologists to identify the relative importance of specific traits. RLQ results may be visualized as ordinations of species and traits onto environmental gradients, and also takes into account the correlation among traits. We clustered the results of RLQ ordination, classified Functional Response Groups (FRGs) of taxa, and analysed their proportionality to previously identified plant communities. RLQ analysis pointed to a high differentiation of plant trait values along the grazing gradient, but not along the altitudinal gradient. Several traits showed a high degree of correlation with grazing. The identified PFTs and FRGs matched very well recently classified plant communities, indicating their potential as a convenient tool for the assessment of rangeland condition. Trait-based analyses can be used to identify adaptations of species to different environmental conditions and in particular related to grazing. In this respect, RLQ and fourth corner analyses of vegetation ecological data are tools with high potential for future pasture management and conservation.

Keywords: gradient analysis, fourth-corner Statistics, grazing impact, rangeland management, RLQ analysis

25B How far from equilibrium are non-native plants? Implications for modeling invasion risk.

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A prominent underlying assumption of species distribution modeling is that the target species is at equilibrium with current environmental conditions. If a species is not at equilibrium, models will underestimate potential range. By definition, the continued spread of invasive plants fails the equilibrium assumption. Yet, modelers often assume equilibrium in order to predict invasion risk. Here, we ask how far from equilibrium are alien and invasive plants in comparison to native plants in the U.S. We obtained herbarium records for the lower 48 states from the Global Biodiversity Information Facility for all plants identified by the USDA PLANTS database as either native or introduced in these states. We calculated equilibrium for each species as the ratio of occupied pixels to climatically suitable pixels, with higher total occupancy of suitable land area suggesting greater climatic equilibrium. For species with less than 1500 regional occurrences, the ranges of both alien and invasive plants were significantly further from equilibrium than the ranges of native plants, which in turn were significantly further from equilibrium than U.S. endemic plants. Only for the most widespread alien and invasive species was equilibrium comparable to that of native species. Aliens and invasives appear to have much broader climatic tolerance than natives, threatening large portions of the central U.S. that are currently under-invaded. Although they are seemingly already wide-

spread, continued spread of the most problematic invasive plants and noxious weeds is likely. Our findings suggest that nearly all models of invasion risk vastly underestimate potential for invasive plant establishment.

Keywords: invasive plant, equilibrium, species distribution modeling, invasion risk

26B Contrasting climatic niche dynamics during the Eastern and Western invasions of spotted knapweed in North America

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Spotted knapweed (*Centaurea stoebe*) is a well-studied plant native to Europe and highly invasive in North America. The species was introduced in the late 1890s almost simultaneously to the eastern and western coast of North America, but the subsequent inland invasions from these two entry ports showed very different patterns of spread both in terms of velocity and habitats colonized. Here we model the spatio-temporal dynamic of the realized climatic niche limits of the two invasions using historical and climatic data. During the eastern invasion, the realized niche gradually increased over time until reaching niche limits similar to the native range. Conversely, in the West the niche abruptly expanded after an extended time lag, colonizing climatic conditions not occupied in the native range. We discuss these differences in the temporal dynamics of the niche patterns in the light of historical, ecological and evolutionary processes evidenced for this species. We suggest that both pre-adaptation and rapid evolutionary change contributed to the invasion success of *C. stoebe* in North America. In the western invasion, a longer time lag was needed to conquer the novel habitat due to climatic isolation. Invasion into the dry rangeland was then favored by enemy release and the less competitive vegetation, combined with post-introduction evolutionary change underlying the increased population growth rate as compared to European *C. stoebe*.

Keywords: Niche limits, niche conservatism, invasion routes, pre-adaptation, *Centaurea stoebe*

27B Edge effects and competitive exclusion: A case of two sympatric species of mouse lemurs in northwestern Madagascar.

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Edge effects are an inevitable and important consequence of forest loss and fragmentation. These effects include changes in species biology and biogeography, though data on how edges affect geographical variation in traits among individuals are lacking. Here, we examine variation in body mass and morphometry for two sympatric species of mouse lemur (*Microcebus murinus* and *M. ravelobensis*) between edge and interior habitats in the dry deciduous forest at Ankarafantsika National Park, Madagascar. Between May and August 2012, we conducted a mark-recapture study on mouse lemurs along edge and interior forest transects within continuous forest adjacent to a large savanna. Of the 37 *M. murinus* captured during our study, 78% (N=29) were trapped in interior habitats. Conversely, 75% (N=60) of *M. ravelobensis* were captured in edge habitats. We found that mean body mass of *M. murinus* and *M. ravelobensis* did not differ between edge and interior habitats. However, female *M. ravelobensis* weighed significantly more in edge habitats (56.6 ± 10.4 g) than in interior habitats (48.1 ± 11.7 g). Complementarily, analyses of overall species morphometry suggest greater access to resources for *M. ravelobensis* at the edge. We propose that edge effects differentially affect resource availability for local mouse lemurs, increasing competitive pressure within and between these female-dominant species. Our study provides some of the first evidence that edge effects on inter- and intraspecific competition influence community and species composition in naturally co-occurring species.

Keywords: fragmentation, competition, biogeography, trait-based ecology, Madagascar

28B The abundant center distribution in terrestrial ectotherms: evidence from pond-breeding North American amphibians

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The abundant center distribution hypothesis predicts that population density decreases as the geographic range edge is approached. This hypothesis forms the basis for many inferences regarding spatial variation in species' ecology, evolution, conservation, and management. However, the extent to which abundant center distributions represent a biogeographical rule is dubious, as such patterns occur in less than half of all species examined and population sampling across the entirety of species' ranges is rarely feasible. In addition, investigations of abundant center distributions among vertebrates are particularly contentious, as many studies utilize large, endothermic species whose vagility and physiological tolerance to suboptimal conditions may obscure otherwise strong relationships between local abiotic conditions and local population density. To determine if an abundant center distribution occurs among ectothermic vertebrates, we are examining range-wide abundance data for over 40 species of amphibians from throughout central and eastern North America. Using breeding call count data from the North American Amphibian Monitoring Program, we are assessing the presence and/or extent of declines in population density as the geographic range edge is approached. Given the tremendous variation in habitat and breeding strategy among our focal species, we are also examining relationships between these factors and adherence to an abundant center distribution. Our results represent some of the most comprehensive data on range-wide variation in abundance among the world's most imperiled vertebrate group, and these data will also allow us to assess the value of citizen science programs in providing abundance data for conservation and management.

Keywords: core and peripheral populations, central-marginal theory, distribution of abundance, macroecology, geographic range edge

29B Geographic range of post-nesting sea turtles from the Yucatan peninsula, Mexico

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The Yucatan Peninsula, Mexico, harbors the largest hawksbill (*Eretmochelys imbricata*) turtle nesting populations, one of the top five most important green (*Chelonia mydas*) turtle nesting populations in the Caribbean, and the only loggerhead (*Caretta caretta*) turtle nesting beaches in Mexico. Since the beginning of sea turtle protection in Mexico, more than 99% of the sea turtle conservation and research efforts had a local and limited geographic approach, focused mainly on individual nesting beaches. During the past decade, sea turtle conservation has gained a wider geographic range scope, and the knowledge of post-nesting sea turtles' spatial dispersion from the peninsula has been a key factor. Since 2006, 24 turtles (12 hawksbills, 10 greens, 2 loggerheads) were tracked by satellite from 15 different locations around the peninsula. Twelve different feeding grounds were identified. Two regional feeding hotspots for hawksbills were identified, harboring 72% of the tracked turtles. The greens clumped at two main hotspots hosting 64% of the tracked turtles. The two loggerheads did not show any hotspot; nevertheless, both reached well-known feeding grounds for this species in the Caribbean and Gulf of Mexico. Regional migratory corridors were also identified at South Gulf of Mexico for green and hawksbill turtles. This wider regional vision for sea turtle conservation linking biological and ecological information for critical habitats (nesting beaches, migratory corridors, and feeding grounds) has come to figure prominently for sea turtle conservation and aiding sea turtle population recovery in Mexico.

Keywords: spatial ecology, migration, hotspots, feeding ground, marine corridors

30B Globalizing conservation efforts helps save species and feed the world

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If the growing needs of humans are to be met, food production must increase. But increasing food production will further compromise biodiversity, once agriculture is the main driver of environmental impacts. Could such human-biodiversity conflicts be mitigated? So far, many solutions have been proposed: reducing food waste, closing yield gaps, and fostering organic agriculture. Moreover, humans want to protect biodiversity by setting aside 17% of terrestrial area for conservation until 2020. Here, we investigate if both agricultural production and biodiversity conservation can be improved by the combination of two strategies: (i) taking agricultural production into consideration, and (ii) integrating countries in a global conservation initiative. We explore strategies to optimize biodiversity conservation benefits and agricultural outputs under three scenarios: decisions are taken globally, regionally, or nationally. We found that both strategies, when applied together, can reduce in 78% the agricultural opportunity costs of implementing protected areas for biodiversity conservation. Further, such strategies can increase in 30% the protection of biodiversity. Consequently, a policy paradigm shift is necessary to help solving the conflict between biodiversity conservation and human needs, in terms of food production. Our results points to a direction in which rigorous science-based policy could inform countries how to think politically about food security and, at the same time, safeguard sites where nature could thrive. Global sustainability can be achieved only by improved global governance that reconciles human development needs with biodiversity conservation.

Keywords: agriculture, conservation conflicts, food production, mammals, systematic conservation planning

31B The significance of integrating genetic patterns of diversity with geographic patterns of suitability

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Low genetic variation can have many evolutionary implications including negative fitness effects, decreased adaptive potential and increased extinction risks for populations. In turn, the role of genetic diversity in natural populations has had a considerable impact on the management of populations experiencing habitat fragmentation, isolation, and high levels of inbreeding. The Core-Periphery (C-P) hypothesis predicts that populations located at the edge of a species range should have lower levels of genetic variation than those at the center of the range. However, most of the research on the C-P hypothesis focuses on geographic distance and not environmental distance. We assess whether genetic diversity varies across a species range in relation to distance from range center or environmental distance based on climatic suitability. We use natural populations of the wood frog (*Lithobates sylvaticus*) and examine 30 populations spanning the entire eastern geographic range from Alabama to Nova Scotia. Twelve polymorphic microsatellites were used to estimate changes in heterozygosity, allelic richness, and population differentiation in populations located in the core (high environmental suitability, mid-range) and edge (low environmental suitability, range margin) of the wood frog's distribution. Core and edge populations showed no significant differences in heterozygosity, allelic richness or population differentiation across the range which might suggest that fluctuating selection pressures are high and genetic variability is being maintained at the periphery to allow for survival at the extremes where habitat suitability is low.

Keywords: biogeography, species' distribution, genetic diversity, environmental suitability, microsatellites

32B Biogeographic patterns of forest fragmentation at global and regional scales

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The effects of habitat fragmentation on biodiversity have been profusely studied. A number of different methods have been proposed to measure fragmentation and, as a consequence, divergent conclusions have been reached regarding both the magnitude and direction of its effects. This is largely due to: (1) Fragmentation is generally measured indirectly, using habitat patches as analysis units, instead of directly quantifying it utilizing landscapes (i.e. constellations of patches) that can be more or less fragmented. (2) There exist multiple indexes to measure fragmentation, which are frequently redundant, correlated and are unable to distinguish between the effects of habitat loss and fragmentation. (3) A lack of a common framework that allows differentiating fragmentation levels, which complicates study comparison. We tackle these issues through the analysis of forest fragmentation at two scales (globally and for the Mediterranean region), exploring in both cases the potential of the Largest Patch Index (LPI) as a synthetic indicator of fragmentation. The results show that LPI is capable of differentiating between greater or lesser fragmented landscapes. We also found that certain combinations of habitat amount and fragmentation do not exist empirically, which has implications in the design of realistic experiments about fragmentation effects. Finally, we found a strong geographic correspondence between forest amount and fragmentation: the most deforested areas are the most fragmented ones. The initiatives to minimize the ongoing large losses of forested areas should also consider the reduction of forest fragmentation levels, both in the Mediterranean and globally.

Keywords: global fragmentation, habitat loss, Largest Patch Index, synthetic fragmentation metric, Global and Mediterranean scales

33B Accounting for geographic variation in species-area relationships improves prediction of plant species richness at the global scale

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The species–area relationship (SAR) is a prominent concept for predicting species richness and biodiversity loss. A key step in defining SARs is to accurately estimate the slope of the relationship but researchers typically apply one global (canonical) slope. We demonstrate that this approach is overly simplistic by investigating how geographically varying determinants of SARs improve species richness estimates of vascular plants at the global scale. We used global species richness data for vascular plants from 1032 geographic units varying in size and shape. As possible determinants of variation in SARs we chose floristic kingdoms and biomes as biogeographical provinces and as surrogates for evolutionary history and energy availability, and land cover as a surrogate for habitat diversity. We found that incorporating variation into SARs improved predictions of global species richness patterns. Moreover, fitting SARs to biomes produced better results than fitting to floristic kingdoms which supports the hypothesis that energy availability complements evolutionary history when generating species richness pattern. Land cover proved equally important as biomes, but the model generated predicted species numbers more accurately at smaller scales. These models explained up to 38% of the species richness variation. Incorporation of second-order interactions of area, land cover and biomes did not improve the predictive ability of the models. We concluded that future models should explicitly consider geographically varying determinants of SAR in order to effectively assess the impact of global land-management scenarios on species richness patterns.

Keywords: biodiversity, vascular plants, biogeography, simultaneous autoregressive model, power law

34B Disease on the road to extinction

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Biodiversity loss and the emergence of novel pathogens have increased interest in understanding the role infectious disease plays in species extinctions worldwide. For species across the world threatened by disease, several critical questions remain. Two of the most important are whether the likelihood of being threatened by disease increases as species move towards extinction and whether other threats (e.g. land use change and invasive species) increase the likelihood that a species will be threatened by disease. To address these questions, we examined 19,378 records of threatened amphibians, birds, and mammals from the 2011 IUCN Red List. Because the Red List does not provide a means of assessing temporal trends in disease to species over time, we tested the null hypothesis that the proportion of species threatened by disease is the same in each Red List status category (Least Concern to Extinct). We also calculated odds ratios to determine whether being threatened by any of the six major threats listed in the Red List increased the likelihood of being threatened by disease. Our findings show that the proportion of species threatened by disease varies between status categories and shows a increase for all taxonomic groups as they become increasingly threatened with extinction. Additionally, our findings show that disease is rarely the sole driver of extinction and is likely to co-occur with other major threats for all taxa. Ultimately, these findings suggest infectious disease may play a larger role in species endangerment in the future as species worldwide become increasingly threatened.

Keywords: species diversity, extinction, disease biogeography

35B Estimating the size of biodiversity building blocks for conservation biogeography

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Community ecology continues to debate the scale of natural communities. This debate translates to biogeographical scales of metacommunities, regional communities, ecoregions, and biomes, which build on local diversity and carry forward a presumed internal integrity and external edge separating them from neighboring systems. What spatial grain best depicts biodiversity? The answer depends on measures used, community traits (e.g., dispersal, range size), and spatial extent. We analyzed beta diversity of winter birds in the contiguous U.S. using Bray-Curtis (abundance-based) and Sorensen (composition-based) indices. We also analyzed species richness. Point counts per person-effort were obtained from eBird.org and aggregated into grids of different size (0.001 to 5 degrees). Spatial extent was standardized to a 10-fold relative neighborhood size (e.g., 0.1 degree grid cell compared to neighbors within 1 degree) using moving window calculations. As expected, mean species richness increased exponentially with grid size. However, mean Bray-Curtis dissimilarity significantly and unimodally peaked with grids of 0.01-0.05 degrees, whereas mean Sorensen dissimilarity fluctuated but peaked at 0.5 degree grids. Winter bird assemblages were best characterized as spatial units ~ 0.01-0.05 degrees in size (i.e., 1-5 km latitude); avian metacommunities and regional communities likely operate at greater scales. Local-scale studies of interactions (e.g., within conifers) of course remain justified, but our results indicate (a) substantially larger scales best represent resulting biodiversity pattern, and (b) efforts to conserve avian wintering grounds should operate at similar scales. Lastly, the convenient, widely-used one degree grid did not capture avian spatial diversity pattern well.

Keywords: assemblage, spatial scale, conservation units, community assembly

36B Pest risk assessment for insect pests in exported temperate tree fruits using ecological niche modeling

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Invasive species are one of the major and most rapidly growing threats to agricultural biosecurity, livelihoods, human and animal health, forestry and biodiversity and result in huge economic losses. Growing trade and transportation along with other elements of globalization have made invasive species an issue of greater concern globally. Temperate fruit flies such as apple maggot (*Rhagoletis pomonella*), and western cherry fruit fly (*Rhagoletis indifferens*), along with Lepidopterian pest codling moth (*Cydia pomonella*) are major quarantine pests in several importing countries where apples and cherries from the United States are shipped. We are using ecological niche models for (1) integrating species-specific phenology data, existing and unpublished occurrence data on apple maggot, codling moth, and western cherry fruit fly for prediction of potential of the establishment and spread of these pests in tropical countries importing tree fruits from the Pacific Northwest of the U.S., and (2) identification of researchable data gaps that may be needed to improve the accuracy of the models and may be used in the development of risk assessments. Our initial results show no risk or very low risk of establishment for the temperate tree fruit pests in several tropical countries (e.g., Indonesia, Taiwan, and Thailand). Our results can provide supporting documentation that can be used in relaxation of the quarantine policies and flexible trade restrictions.

Keywords: agricultural biosecurity, invasive species, Maxent, quarantine pests, western cherry fruit fly

37B Mapping niche overlaps between endemic and exotic fishes over the Mediterranean Sea: a trait-based approach

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Exotic species richness and range overlap between exotic and native species are two commonly used metrics to assess the potential impacts of exotic species on native faunas and floras at large spatial scales. One of the major drawbacks of these metrics is that they do not incorporate information related to ecological and biological similarities between native and exotic species. In the present study, we propose a trait-based approach to assess the potential impacts of exotic species over large spatial scales. We exemplify our approach using the Mediterranean coastal fish fauna as a biological model. Indeed, the Mediterranean Sea is recognized as one of the main hotspots of biological invasions on Earth. For instance, the main event responsible for the massive invasion of exotic fishes in the Mediterranean Sea is the opening of the Suez Canal in 1869 that facilitated unintentional introductions of Red Sea fishes. Specifically, we propose two indices based on biological and ecological traits of endemic and exotic fishes. The first index allows identifying the areas of the Mediterranean Sea where potential ecological interactions between endemic and exotic species are more likely to occur. The second index is species-specific and allows identifying endemic species that display the greatest ecological niche overlap with exotic species as well the greatest range overlap. As the invasion process is dynamic, the proposed indices could be used as indicators in current and future large-scale monitoring programs.

Keywords: exotic species, endemism, ecomorphology, niche overlap, conservation biogeography

38B Spatial thresholds and the diversity of habitat islands

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The application of island biogeography theory in habitat fragmentation research assumes a linear relationship between species richness and fragment area. However, the true relationship in habitat islands is often non-linear and may display one or several break-points, after which species richness precipitously declines. Ascertaining the prevalence of such spatial thresholds, along with efforts to estimate threshold values for guiding land management policy, have been major foci of conservation science in the past twenty years. We conducted a meta-analysis of 80 habitat island data sets in order to compare the performance of traditional species-area relationship (SAR) models with three types of piecewise regression models (continuous, discontinuous, and zero-slope), and thus determine the prevalence of spatial thresholds in fragmented landscapes. Model performance was compared using Akaike's Information Criterion corrected for finite sample size. This methodology was pertinent as the existence of breakpoints was not assumed prior to analysis. The influence of various dataset characteristics on model performance was also tested. For those datasets exhibiting a significant SAR, traditional models performed best. A fifth of significant SAR datasets were best represented by one of the three piecewise regression models. Breakpoint values ranged over two orders of magnitude, highlighting the issue of using individual threshold value to inform

conservation practice. Sample size and the number of smaller islands within a dataset influenced the proportion of significant piecewise relations, indicating the greater performance of traditional models may be the result of a lack of data points around the breakpoint as opposed to any biological significance. Findings were generally consistent among taxonomic groups. Our results highlight the importance of using appropriate statistical techniques when testing for spatial thresholds in fragmented landscapes.

Keywords: fragmentation, habitat destruction, island biogeography theory, model selection, small island effect

39B Testing a land-facet approach for capturing biodiversity in a changing world

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Until recently, conservation planning has largely focused on identifying areas that protect current biodiversity. Although these areas may provide protection for today's biodiversity, they may not provide adequate protection for future biodiversity in rapidly shifting climate landscapes. One strategy for protecting future biodiversity is to protect the landscape diversity that influences biodiversity patterns. Species distributions, communities, ecosystems, and broader biodiversity patterns are influenced by landscape characteristics such as soils, geology, topography, and climate. Although climates will change relatively rapidly over the coming century, these landscape characteristics will not. By protecting diverse landscape types (referred to as land facets), it may be possible to protect areas that will foster a future biotic diversity —albeit different biota than those areas protect today. Although the idea of using landscape diversity as a proxy for biodiversity is not new, it has only recently been applied to conservation problems under changing climate. Thus, the method has not been tested on diverse landscapes, nor do we know how well currently protected areas already protect land facets. Here we address these questions by identifying and mapping land facets across three diverse ecoregions in the Pacific Northwestern United States. We describe the sensitivity of the facets to methodological and data choices, evaluate how well current protected areas protect land facet diversity, use land facets to prioritize areas for conservation, and evaluate how well land facets capture current biodiversity. Additionally, we explore potential methods for testing the robustness of correlations between land facets and biodiversity under shifting climate landscapes.

Keywords: land facets, landscape, biodiversity, conservation, paleobiology

40B Seasonality and host richness predict infection risk for a highly pathogenic amphibian parasite

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Amphibian infections by the trematode parasite *Ribeiroia ondatrae* cause severe malformations including missing, extra, or misshapen limbs. Because malformation severity is strongly correlated with infection intensity, modeling broad-scale predictors of infection intensity facilitates the development of a geographic framework for mitigating disease risk. We used species distribution models (MaxEnt) and generalized least squares regressions to evaluate the relative roles of climate, local environment, and host assemblages on the presence and abundance of *R. ondatrae* using a 10-year, nationwide assessment by the US Fish and Wildlife Service. Using model predictions, we also evaluated how well MaxEnt logistic model output predicted average infection intensity for *R. ondatrae* at 162 sites across the US. Temperature and precipitation seasonality together with host richness were the most informative predictors of parasite occurrence. Sites with high average infection intensities had consistently high MaxEnt model predictions. We discuss the potential utility of presence-only models for predicting disease risk and the implications of our results for amphibian disease.

Keywords: amphibian malformations, disease risk, distributions

41B The impacts of spatial uncertainty associated with species occurrence data on measuring species responses to environmental variables

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In order to identify the ecological processes influencing the spatial distributions of vertebrate species – and reliably predict such distributions – we must account for spatial uncertainty in typical inputs to species distribution models. Species' true responses to environmental conditions may be obscured by locational uncertainty associated with species occurrence data, or by mismatches between this uncertainty and the spatial resolution of gridded environmental data used as predictor variables. While occurrence data are often treated as point locations with (x, y) coordinates, these data do carry spatial uncertainty, the amount of which varies with the method used to determine occurrence locations (e.g. spatially precise GPS units or inexact textual descriptions) and additional processing (e.g. retrospective georeferencing). To understand how ignoring spatial uncertainty affects measurements of species responses to environmental factors, we present three example studies of bird distributions, each at a different spatial grain and extent. These examples combine environmental variables from high-resolution remote sensing data (RS) with occurrence data from recent surveys; medium-resolution RS with telemetry locations; and coarse-resolution RS with occurrence data obtained from global biodiversity portals and assessed for spatial uncertainty. Taxa considered in example studies include a suite of East African species and GPS-tagged oilbirds in northern Venezuela. We argue that spatial uncertainly should be routinely calculated for species occurrence data, incorporated into species distribution model parameters, and considered when interpreting model results.

Keywords: spatial scale, spatial grain, spatial uncertainty, species distributions, East African birds

42B Completeness, grain and biases of the global species point data inventory and its implications for biogeographic research

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An accurate documentation of biodiversity is essential for advancing biogeography and for developing robust conservation strategies. Large quantities of biodiversity point data have become accessible via the Global Biodiversity Information Facility (GBIF). However, these data have inherited taxonomic, geographic, environmental, and temporal biases that hamper their usability. We assessed three vertebrate groups (amphibians, birds, mammals) to quantify and test hypotheses about these biases. Using expert-based range maps as a reference benchmark, we tested for the level of inventory completeness at different spatial grains. At a 100km grain, 42-45% of grid cells have at least one GBIF record. Of these, between 62% (amphibians) and 95% (mammals) have <50% of species richness covered. For grains of 400km and coarser, species richness in North America, Europe, and Australia does appear fairly well-represented in GBIF. Among eight hypotheses regarding sampling bias only the 'proximity-to-research-institutions'-hypothesis received relatively strong support ($r^2 = 0.13\text{-}0.21$). Variation in inventory completeness was best explained by multi-predictor-models including proximity to institutions, travel time from major cities, GDP, protected areas, and latitude ($R^2 = 0.35\text{-}0.44$), highlighting the interplay of multiple mostly socioeconomic factors in shaping our knowledge on species distributions. This study provides the first global test of key hypotheses regarding sampling and mobilization biases in the current global point data record. Our findings highlight the various biases incurred when using available point data for research in ecology, evolution, and conservation. They may help inform new strategies for regional and taxonomic prioritization to most efficiently close existing data and knowledge gaps.

Keywords: Wallacean shortfall, primary biodiversity data, sampling bias, Global Biodiversity Information Facility

43B Furbishing species primary data: a framework to improve biodiversity knowledge in less studied regions

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On-line biodiversity databases (OBD) and museum of natural history collections can be valuable sources of information for less known and studied areas. For these regions with fewer resources for conservation research, OBD can be an inexpensive way to obtain data and guide future studies. Despite the well-known limitations, such as taxonomic, spatial, and/or temporal biases, this type of data can still be used to obtain a picture of biodiversity. Indeed, museum collections are known to be spatially and historically comprehensive enough to address this lack of information. In Mozambique, no recent studies can be found on the overall distribution of its vast biodiversity. Primary biodiversity data of the country's mammal species were compiled in a database. More than 9000 records of 193 mammal species were gathered from the Global Biodiversity Information Facility data portal and from European natural history museum collections. Most of the records had to be georeferenced and taxonomically updated demanding highly time-consuming tasks. Here, we describe the path from data gathering, and cleaning to data analyses, while identifying usual errors and problems added to our solutions to deal with them in a expedite manner. We intend with this paper to present ready-to-use guidelines for similar projects and show the quality and potential of these data to conservation studies.

Keywords: databases, distributions, Mozambique, mammals, GBIF

44B Conservation of crop pollination in oceanic islands: building a model to quantify the pollination delivery in the Canary Islands

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Crop pollination by bees and other animals is an ecosystem service of huge economic value as a large number of crops depends upon pollination of domesticated (e.g. honeybee) as well as wild pollinators (e.g. bumblebee). It is widely accepted that a declining number of bees and other pollinators in recent years will result in a decrease in pollination services which could have major impacts on world food supplies. We have developed an automated method to remotely quantify the pollination delivery at a landscape level. Here, we present a case study in the Canary Islands, Spain. A key question that we addressed is: which areas in the Canary Islands contribute to the supply of the pollination service? We pay special attention to pollination dependent crops (e.g. citrus fruit tree), the ecology of the bees, *Apis mellifera* and *Bombus canariensis*, and their distributions to obtain a comprehensive description of the areas where the pollination service is supplied from. The resulting maps have the potential to identify the relative contribution of land to the provision of pollination services. Thus, this automated approach may help ensure food production and maintaining pollinator habitats in agricultural landscapes.

Keywords: agricultural landscapes, biodiversity, ecosystem services, pollination, species distribution modelling

45B Land-cover changes in- and outside protected areas in China

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Protected areas (PAs) are one of the main tools in the global conservation of biodiversity and ecosystems. This is also the case for China. In 2008 mainland China had 2538 nature reserves covering approximately 15.13 % of the land area. However, only few studies have investigated protected areas´ efficiency in maintaining ecosystems and biodiversity. One way to investigate this is to look at land-cover changes inside the PAs and on the surrounding areas. Surrounding areas can also give an idea of the efficiency of protected areas when they are compared to areas without protection in the same region. We have investigated the following four questions; 1) Have there been any land cover changes inside the PAs? 2) Are any such land cover changes inside the PAs less than in the surrounding areas (areas within xx km from a given PA)? 3) Do land-cover changes inside and outside PAs increase with increasing general human pressures in a region? 4) Does the efficiency of the PAs depend on general human pressures in the region? We use remote sensing data, e.g. MODIS vegetation continuous field to map land-cover changes between 2000-2010 inside the PAs and in the surrounding areas. Furthermore, we link the changes to human pressures in the region, e.g. population growth, populations density, economic growth, infrastructure etc.

Keywords: biodiversity, biogeography, conservation, China, protected areas

46B Endemic fishes of the Cortez biogeographic province (eastern Pacific Ocean)

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The Cortez Province (CP) is located in the transitional warm-temperate/subtropical region and, as a result, the ichthyological component inhabiting the provice is a mixture of elements of different biogeographic affinities. Since the first systematic analysis of the fish fauna of the Gulf of California in the 1960s, 31 new endemic species have been described in the CP. This study constitutes an update of the fish component of the CP, including the most relevant ecological attributes of the species, along with an updated taxonomic list. A comprehensive literature review was made considering current biological knowledge, and taxonomic status of the endemic species from the CP. Those fish species with restricted distribution ranges, falling within the limits of this province, were considered endemic. Additionally, to recognize the dominant ecological attributes of the CP endemic species, the preferential habitat, bathymetric distribution, the reproduction strategy, and the maximum total length were recorded. Seventy-nine endemic species were recognized and grouped in 13 orders, 29 families, and 59 genera. Gobiidae (12), Chaenopsidae (8), and Labrisomidae (7) are the families with the highest species richness, and Sebastes (6 species), the most diverse genus. Forty-five percent of the species are associated with coral and rocky reefs, with 35% distributed within the first 10 m depth layer. The list of endemic species presented in this study is not conclusive, still undescribed species have not been included; detected differences (morphologic and/or genetic) in several species with disjunct populations may increase the diversity of this province.

Keywords: Gulf of California, endemic species, biogeography, Gobiidae

47B Experimental evaluation on the effects of the invasive mud crab *Rhithropanopeus harrisii* Gould (Crustacea, Decapoda) on the native macroalgal and invertebrate assemblage

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The mud crab *Rhithropanopeus harrisii* (Gould) is a native of the North-American coast of the Atlantic where it lives in brackish estuarine waters. In Europe, the mud crab was found for the first time in 1874. In recent years the species suddenly expanded its European distribution area, plausibly associated to a multiple of new introductions and genetic diversification. Currently, the mud crab is observed as north as Pärnu Bay in the Baltic Sea. In an in situ factorial field mesocosm experiment we evaluated the effects of the mud crab on sediment characteristics, local benthic macrophytes and invertebrates. The results indicated that the invasive crab is capable of modifying sediment characteristics (e.g. decrease sediment phaeopigments) and reduce densities of some local macrophyte and invertebrate species including the invasive gammarid amphipod *Gammarus tigrinus*. Providing the fast expansion of its distribution area, high crab density and the lack of such functional trait in the north-eastern Baltic Sea range, this invasion is expected to cause significant repercussions on the structure and functioning of soft and hard bottom benthic macrophyte and invertebrate communities in the near future.

Keywords: expansion range, invasion, ecosystem functioning, field experiment, Baltic Sea

48B Can trait-based analyses of distribution change be generalised to new geographic areas?

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Anthropogenic environmental change is having a major impact on biodiversity. Comparative studies that identify traits that correlate with species distribution change can shed light on the mechanisms driving change. For these comparative studies to be of greater use to conservation it is important to know if predictions from the trait-based models can be generalised to new geographic regions. We tested the ability of trait-based models to predict plant distribution change across seven geographic regions (Flanders and six regions in Britain) that varied in terms of land-cover and species composition. The regional trait-based models gave insights into the main drivers of range change in each region but suffered from low r^2 values. Despite these low r^2 values we found that predictive ability varied between regions and that it was significantly positively correlated to the level of similarity in land cover between regions. This suggests that it may be possible to use trait-based models to predict broad scale changes in species distributions between regions that share similar land cover compositions.

Keywords: comparative analysis, land-use, plants, predictive modeling, range change

49B Spatial correlation between habitat destruction and extinction risk of vertebrates in Brazil

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Habitat loss is the main threat to biodiversity. Brazil, a biodiversity powerhouse, has a comprehensive national system of habitat fragmentation surveillance. However, knowledge on species' conservation status is wanting. We tested the relationship between extinction risk of endemic amphibians, mammals and birds and habitat loss. We assigned species extinction risk drawn from the IUCN Red Lists of threatened species, and the percentage of habitat loss into a presence/absence matrix derived from a grid with a spatial resolution of 1° x 1° latitude x longitude covering all the Brazilian territory. We performed two correlation analyses: the first between the percentage of habitat loss and the maximum extinction risk (a site-based approach in which we controlled for the effects of spatial autocorrelation) and the second between the mean percentage of habitat loss inside the species' range and the species' extinction risk (a species-based approach). We found positive correlations between habitat loss and the maximum extinction risk for birds in the site-based approach, and for mammals in the species-based approach. Our study links biogeographical scale to landscape processes, providing support for the effect of habitat loss on extinction risk. However, the effects appear to be idiosyncratic regarding the taxonomic group evaluated and on the analytical approach applied. Such idiosyncrasy may be related to the low level of knowledge about species' conservation status and landscape use. This sort of assessment would be benefited from knowledge on species' ability to deal with different matrix (non-habitat) types.

Keywords: amphibians, birds, conservation biogeography, mammals, IUCN Red List of threatened species

50B Cryptic invasions of herbivorous insects: Historical demography and impacts

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Distinguishing new invasions from established older invasions or indigenous populations is important, not only for management and trade, but also for understanding and predicting population dynamics and adaptation to a changing environment. Here, we review cryptic invasions of arthropod herbivores in a set of agricultural systems: *Bemisia tabaci* whiteflies "biotypes", in which repeated historical colonizations coincide with periods of human migration; the spider mite *Tetranychus evansi* on solanaceous crops worldwide with populations in Europe and Africa resulting from multiple independent introductions from South America; the olive fly, *Bactrocera oleae*, whose phylogeography suggests Quaternary differentiation between olive subspecies and recolonization of wild and cultivated olives in historical times and more recently; and aphids in the genus *Hyalopterus* (Hemiptera) on plants in the genus *Prunus* (Rosaceae) with divergent lineages structured by specific associations with plum, almond, and peach over broad spatial and temporal scales. Despite the similarity in foraging mode, these studies show that generalizations about the patterns and impacts of cryptic invasions will be difficult. However, data from monitoring, genetic diagnostics, collections, and specimen-level databases, suggest that cryptic invasions are likely common. Further, these studies illustrate the importance of specimen-level data (rather than species) to test hypotheses about the timing and impact of cryptic invasions and to make predictions about future spread and responses to global change.

Keywords: biogeography, collection science, databases, distributions, unique identifiers

51B Spatial homogenization of North American bird communities through

time

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Over the past century anthropogenic climate and land-use change have driven geographic range shifts in disparate plant and animal groups across the globe. Less is known about how this biogeographic reshuffling influences the structure of ecological communities as they re-organize in space. Spatial structure of ecological communities, often measured as beta-diversity, is important for maintaining regional biodiversity. Here I present evidence that beta-diversity of breeding bird communities has decreased in the United States and southern Canada over the past 50 years leading to more spatially homogeneous meta-communities and the possibility of future instability in biodiversity at regional scales. Using data from the North American Breeding Bird Survey (years 1971 to 2011), I quantify beta-diversity as the mean community dissimilarity and its rate of increase across space. I then regress beta-diversity against time, assessing significance of trends using a bootstrap method that preserves spatial and temporal autocorrelation. Two major centers of homogenization (i.e. decreasing beta-diversity) emerge from this analysis. One region runs from the southwest US to the southeastern US seaboard while the other stretches from the northern Rockies to New England. Different mechanisms are likely at play as northern homogenization is coincident with positive temperature anomalies from the past 50 years while southern homogenization is coincident with increased land use intensification and urbanization. Over the past 50 years rarity has also increased across North America. While rarity had no effect on patterns in beta-diversity, increasing rarity inflated gamma-diversity despite decreasing beta-diversity. This mismatch implies that the spatial configuration of bird communities is in flux and current levels of gamma-diversity may not be sustained by current beta-diversity.

Keywords: beta-diversity, breeding birds, global change biology

52B Enhancement of global biodiversity monitoring: an initiative of the group on earth observations and its biodiversity observation network

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Many of the 193 countries, Parties to the Convention on Biological Diversity (CBD), lack sufficient capacity to update their National Biodiversity Strategies and Action Plans. The intergovernmental organization, Group on Earth Observations (GEO), is launching an initiative in support of these countries by following a holistic approach, mobilizing its entire multi-discipline community. Currently, GEO's biodiversity program, i.e. GEO Biodiversity Observation Network (GEO BON), undertakes global activities, such as the development of Essential Biodiversity Variables, the Global Wetlands Observation System *etc*., in support of the CBD Parties. Now, the GEO Secretariat, aiming to support countries in gathering and making systematic use of biodiversity-relevant observations and applying analytical tools to use these observations to detect biodiversity change, goes one step farther. GEO, supported by the CBD Secretariat, launches an initiative that will utilize both the GEO BON's activities focused/applied on the national level and the observations, products, services and capacity building activities of the other GEO programs including land cover, climate change, oceans, agriculture, forests and water. Furthermore, the current national or regional GEO activities, such as AfriGEOSS and regional BONs, are expected to contribute *inter alia* to the engagement of the appropriate stakeholders, and the coordination of regional capacity building, data collection, processing and analysis, and South-South cooperation activities. The biogeography community is expected to be the link between these different communities, such as the land cover and the biodiversity community, and both contribute to the implementation of this initiative and utilize its resources and outputs.

Keywords: traits, national, CBD, GEO, climate change

53B Climatic niche expansion during the Caribbean lionfish invasion

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Under the assumption of climatic niche conservatism, ecological niche models are commonly used to assess extinction risks and range shifts due to global climate change and to estimate invasive threats of non-indigenous species. A notorious example of marine biological invasions is that of the red lionfish, *Pterois volitans*. Native to the Western Pacific, the red lionfish has recently established breeding populations in the southeastern United States and entire Gulf of Mexico and Caribbean in only a decade. The rapid proliferation of an invasive apex predator in an ecosystem already stressed by over-fishing, pollution, and climate change has made the lionfish invasion one of the most significant marine conservation concerns in recent history. Here I test for climatic niche equivalency between native and introduced lionfish populations in order to assess the assumptions underlying ecological niche models and to better understand the factors that will limit the spread and long-term persistence of lionfish in their invasive range. I found that invasive lionfish have expanded their niche along climatic axes related to salinity and temperature and may be limited to further southward expansion to Brazil by a combination of ocean currents and the Amazon freshwater plume. These findings underscore the need for future studies of lionfish physiology, particularly with respect to salinity tolerance, and suggest that ecological niche models may underestimate the capacity of marine species to persist through the next century of climate change.

Keywords: niche conservatism, ecological niche models, species boundaries

54B Interaction of environmental factors that affect patterns of species richness

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To assess the importance of interactions between deterministic factors on diversity, I used experimental and observation data. Experimentally, I created high-energy and low-energy mesocosms stocked with a regional species pool of zooplankton (50 species). I used fourteen small and fourteen large mesocosms with a fully factorial design to better understand how total habitat area affects the importance of energy in aquatic systems. Additionally, I studied environmental heterogeneity by collecting data from a series of ponds within a heavily managed wetland-flowage complex in the Meadow Valley Wildlife Area (MVWA) in the Central Forest Region of Wisconsin. The results from my experiment indicate that larger areas benefit from increased energy, whereas smaller habitats do not. Large, high-energy mesocosms had higher species richness than large, homogenous mesocosms. However, small high and low-energy mesocosms did not differ in species richness. Similar results were observed in the managed wetland ecosystem in Wisconsin. Manipulated environmental heterogeneity was only important in large wetlands, and was not important in small wetland ponds. Additionally, homogenization of wetlands through heavy manipulation, such as dredging, greatly reduced diversity in large wetlands, but had no effect in small wetland ponds. The results from these two studies indicate that managers should focus on creating environmental heterogeneity in large wetland systems, and avoid managing smaller ponds. Additionally, the data suggest that area is the most important mechanism of diversity, because habitat area determines the importance of other mechanisms of diversity.

Keywords: biodiversity, energy, area, species richness relationships

55B The Malabar Pied Hornbill (*Anthracoceros coronatus*) nests near human habitations in highly fragmented landscapes in the Northern Western Ghats, India

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An inherent challenge in conservation biogeography is how to use ecological information gathered at a landscape or regional extent to generate broad-scale conservation schemes. For instance, the availability of nest-sites is critical to the conservation of many species and is usually not captured in biogeographic models. A number of ecological parameters affect nest site selection across species. Here, we present our findings from 26 nests of the Malabar Pied Hornbill, *Anthracoceros coronatus*, in a human-dominated landscape within the Northern Western Ghats of India. Our aim was to determine whether nest tree species, tree size, and distances to habitation and streams affected nest site selection in this species. We found that the Malabar Pied Hornbill seems to prefer nesting closer to human habitation, even though there might be larger trees further away. We hypothesize that these results can be extrapolated to similar areas in the region, as this matrix of protected mixed evergreen forest and agricultural land is seen region-wide. This observation has significant potential conservation implications in such a large, threatened, and ecologically important species. If these findings indeed hold over a larger area, they might also help in the conservation of three other sympatric hornbill species.

Keywords: Konkan, avian conservation

56B Scale dependence of vegetation-environment relationships: a case study on eastern North American trees

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Multiple environmental variables drive spatial variation in plant community composition, but little is known about how the relative influence of different factors varies with spatial scale. In this study, we examined the relative importance of environmental factors as predictors of species and functional trait composition across multiple spatial scales, using a dataset of tree species composition and functional traits in 1500 forest plots in eastern North America. We modeled species and functional trait composition of tree communities at spatial extents ranging from 200-2500 km, and determined the relative amount of variation explained by climatic and edaphic factors. The amount of variation in species composition and functional traits explained by the environment increased with increasing extent, as did the relative importance of climatic factors. Generally, climatic factors were more important than edaphic factors as predictors of species composition and overall functional composition at all but the smallest extents analyzed. The relative importance of climatic vs. edaphic factors and its relationship with extent varied among individual functional traits. These results clearly demonstrate the scale dependence of relationships between environmental factors and tree community structure. Researchers should carefully consider the scale of observation and environmental variation when designing and interpreting studies of vegetation-environment relationships.

Keywords: beta diversity, climate, edaphic, extent, functional traits

57B Keeping conservation aims current: An updated survey of Bahamian bats (Order: Chiroptera)

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As evidence of climate change and anthropogenic effects on biodiversity loss grows, so does the need for current surveys and species descriptions, especially in vulnerable areas. The most recent account of Bahamian bats was published in 1957, describing 11 species. This account included *Mormoops blainvillii*, documented from a single fossil fragment, and *Glossophaga soricina* and *Lonchorhina aurita*, two likely mistaken records known from single specimens. Current natural history databases archive 11 extant species and include sampling from previously unvisited islands. Discrepancies between previous and current information make it difficult to quantify bat diversity in the Bahamas because of taxonomic and locality name changes and limited sampling. An updated description of diversity and distribution of Bahamian bats would provide a reference for museum collections, researchers, and the general public to quickly access summary knowledge. This is especially relevant as interest in Caribbean island biogeography increases due to its high endemism, which is sensitive to contemporary climate change effects. The Bahamas is an extensive archipelago in the Caribbean of approximately 3,000 islands, keys, and islets. Many bats are not well studied on these islands, including *Chilonatalus tumidifrons*, the only endemic species of the Bahamas. Here we distill previous research and voucher data from natural history collections into a descriptive biodiversity and distribution account to serve as a new resource for researchers and museums that may focus future conservation research efforts. We also aim to make this resource easily accessible for public use, encouraging greater common interest in preservation of Caribbean biodiversity.

Keywords: biodiversity, natural history collection, species accounts

58B Lemur species-area relationship in a fragmented landscape: a test of the habitat heterogeneity hypothesis.

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The cause of the species-area relationship has been debated since the relationship was first discovered. One prominent hypothesis used to explain this relationship is the habitat heterogeneity hypothesis, which states that habitat heterogeneity is correlated with area. We tested the habitat heterogeneity hypothesis on the species-area relationship of lemur species in habitat fragments in northwest Madagascar. The fragmented landscape consists of tropical dry deciduous forest surrounded by a savannah matrix. We conducted 1122 surveys of all lemur species in 38 fragments between June and November of 2011. Fragments ranged in size from 0.23-117.7 ha. We found between 0-6 lemurs species within each fragment. There was a significant correlation between lemur species and log fragment area ($R^2=0.83$, $P<0.01$). In each fragment we measured all living tree stems (4042 total stems) over 5cm DBH (diameter at breast height) within 1m of each side the survey transects. The number of stems measured differed considerably, with a minimum of 9 stems in a smaller fragment (0.71 ha) and a maximum of 583 stems in the largest fragment (117.7 ha). We used the standard deviation of stem DBH as a proxy for habitat structural heterogeneity in the fragments, which ranged from 0.66cm-20.82cm. Although we found a clear species-area relationship within the fragmented landscape, we did not find any correlation between habitat heterogeneity and area or species richness. We found no support for habitat heterogeneity as a predictor of lemur species richness in the fragments.

Keywords: richness, biogeography, primates

59B Spatial ecology of the European adder (*Vipera berus*) in commercial forestry plantations

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Little is still known about the factors that influence species distributions across landscapes. One of the difficulties in assessing species distribution patterns in patchy landscapes is that surveying is often limited to presence-absence data, which do not easily explain the processes behind the observed patterns. I employed patch occupancy methods to investigate the spatial ecology of European adders (*Vipera berus*) in the highly spatially structured, dynamic landscape of commercial forestry plantations. Adders were observed to exhibit specific basking site microhabitat selection, however patch occupancy analysis suggested that detection probabilities vary with habitat, but occupancy did not, emphasising the importance of accounting for detection probability in distribution surveys of this species. Potential adder habitat is increasingly being limited due to development, land use change and agricultural intensification. This research suggests that current plantation systems provide a suitable habitat matrix for adders, but that landscape-level management could increase population dispersal, and site-specific management would increase habitat suitability.

Keywords: patch occupancy modelling, distributions, biogeography, forests, plantations

60B New managements of agricultural lands: effects on some bird species

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New management regimes modify agricultural land. Fifteen years ago in eastern Spain orange groves were watered by inundation, and herbaceous plants were removed mechanically. Currently, orange groves are watered using drip irrigation and herbicides eliminate the herbaceous plants. These changes result in the absence of herbaceous plants, because of the restrictions caused by the water drip. We evaluate management of orange groves in Sagunto (eastern Spain) near of Mediterranean Sea shoreline. We have monitored the breeding birds in this region since 1975 using a mixture of techniques including nest searching and mapping. We show the abundance changes of three granivorous species, the serin (*Serinus serinus*), the greenfinch (*Carduelis chloris*) and the European goldfinch (*C. carduelis*), and two species of insectivorous birds the Sardinian warbler (*Sylvia melanocephala*) and the red-necked nightjar (*Caprimulgus ruficollis*). The three granivorous birds showed population declines. The other two species showed increases in the number of breeding pairs, although neither bred during the twenty first years of this study. The decline of granivorous birds can be explained by the decline of herbaceous plants. On the other hand, the increase of driest conditions of orange groves may explain the presence and increase of species that come from warm environments.

Keywords: agricultural intensification, granivorous birds, population, seed, water drip

61B Environmental beliefs and values in Borana Oromo: a focus on narratives

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Human beings and their environments constantly interact, and both are changed by the interactions. In the process of these interactions, humans have developed their own views, values, ideologies and ways of coping with their environments. This human experience, which exists as part of our indigenous knowledge, is mainly exchanged through indigenous communication mechanisms, which include narratives, rituals, folk festivals, plays, puppet shows, folk dances, and songs. While most

African nations now function and communicate within the context of global politics as literate cultures, many of their peoples still live and exist within the paradigm of oral culture. The Borana, who live mainly in southern Ethiopia and northern Kenya, are an Oromo-speaking people. They are estimated to number at least 300,000, about a quarter of whome are in Kenya. The Borana share many features with other pastoral societies in eastern Africa. This study explored dominant environmental beliefs and values of the community as an organized, viable, and dynamic social force basic to the creation and dissemination of environmental messages in Borana community. The researcher used a qualitative approach in the analysis of data gathered through semi-structured interviews, focus group discussions, and extended participant and non-participant observations. The analysis was based on Fairclough's three-dimensional methodological approach of discourse analysis.

62B Biogeographic patterns in Mediterranean-type climates: lessons from invasive acacias

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Management of biological invasions requires a better understanding of the stochastic and human-mediated processes that shape the evolutionary trajectories of introduced species. However, management typically assumes that invasive species are single evolutionary units (i.e. single species), an assumption that may negatively affect the overall success of control and management programmes. Molecular sequence data were used to explore the biogeographic patterns of five tree species in their native Australian and introduced South African ranges. Statistical parsimony showed high intra-specific divergence and within population diversity in the native range, and unstructured but high population level diversity in South Africa. To test if the observed patterns could be generalized across Mediterranean-type ecosystems, we sampled two widely distributed species (*Acacia saligna* and *Paraserianthes lophantha*) across introduced populations in California, the Mediterranean-Basin, and non-native ranges within Australia. Bayesian clustering of microsatellite genotypes show that introduced populations are comprised of an assortment of genetic clusters, and no introduced population is comprised of the same genetic entities. Shared nuclear and chloroplast haplotypes showed that all the known subspecies have been moved around the world. Evidence of intra-specific hybridization and novel genotypes in the introduced range of *A. cyclops*, *A. saligna* and *P. lophantha* raises the question of whether, and how quickly, introduced and native populations should be treated as fundamentally different entities. In all, the observed patterns suggest that intra-specific genetic variation, complex introduction histories and cultivation interact to shape the introduced genetic patterns of commercially important Australian trees.

Keywords: biological invasions, hybridization, management, microsatellites, subspecies

65B Impacts of volcanic activity on bird pollination system in an island ecosystem

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Observation of species interactions during and after volcanic activity provides indispensable opportunities to study how organisms respond to environmental devastation. *Camellia japonica* satisfy the criteria for key plants of forest recovery on Miyake Island, which erupted in 2000, because this species is more resistant to volcanic gases than are other tree species. A small passerine bird, *Zosterops japonica*, is the main pollinator of *C. japonica*. Therefore, we examined the effects of volcanic activity on this plant–pollinator relationship. We also compared the effect of insect herbivores on Niijima Island adjacent to Miyake Island. In areas with low flower density due to volcanic activity and insect damage, *Z. japonica* ranged over larger areas to satisfy their energy demands rather than moving to areas with higher flower density. Genetic differentiation among pollen pools within the mother tree decreased while the rate of unique pollen donors increased as flower densities decreased. Low flower density also raised the efficiency of maternal reproductive success in *C. japonica* (i.e. fruit set rate) on both islands and the genetic diversity of pollen grains adhering to pollinators on Miyake. The results were consistent with previously published data on the movement of *Z. japonica*. Between islands, indirect effects on fruit set rate through the bird pollination system were larger on Miyake, which underwent recent volcanic activity. Overall, our results indicate that compensation mechanisms ensure better reproductive success at sites that are more affected by volcanic activity.

Keywords: *Camellia japonica, Zosterops japonica,* genetic analysis, insect damage, volcanic damage

66B The distribution of breeding colonies of black-headed gull (*Larus ridibundus*) in a recently colonized landscape: the relative influence of lake and scenery characteristics

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Forty years ago the first pairs of the black-headed gull bred in eastern Spain. Ten years later they were found breeding in lakes of central Spain. In the latter region we investigated whether habitat fragmentation influences patch occupancy in this species in an area that includes a large number of wetlands. We selected the 91 out of 193 lakes that were flooded in spring of 2012. In each lake we estimated two groups of variables that describe lake characteristics (chemical: pH and conductivity; bio-physical: size, island number and vegetation variables) and one group that describe the landscape (number of dry or flooded lakes in several radius intervals; distances to several types of potential corridors or food sources). Hierarchical partitioning analyses were conducted using the R "hier.part" package to identify the variables most likely explaining the presence and abundance of this species in our study area. The effect of spatial autocorrelation was controlled by including a quadratic

function of coordinates as a spatial term in all analysis. Our results shown that the probability of gull presence in a lake increases with the presence of islets, the lake surface area, pH, and presence of tamarisks, while it decreases with the presence of other tree species and number of flooded lakes within a radius of 5 km. This last variable is the only significant landscape variable, indicating that lake characteristics are much more important than landscape variables. This result suggests that there are few limitations to dispersal in this landscape. Gull abundance was poorly related to the variables measured.

Keywords: colonization, dispersion, salt lakes, wetlands

67B Building and implementing a global disease outbreak geodatabase

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Since John Snow's study documenting the 1854 Broad Street Cholera Outbreak, spatial and temporal analyses have helped uncover the patterns and processes driving infectious disease outbreaks. To date, however, few studies have analyzed global trends in disease outbreaks. Largely, this is due to a lack of organized geodata documenting the occurrence and impact of many types of diseases. Here we present an automated method (a 'pipeline') to extract textual outbreak records from an online resource (the Global Infectious Diseases Epidemiology Online Network) and organize data into a novel outbreak geodatabase. In addition, we present statistical descriptions of these data: outbreak frequency by taxa, transmission route, and host type since 1980. We also present maps of the global distribution of outbreaks by 5-year increments. By organizing the outbreak data by year and associated longitude and latitude, we are able to analyze the changes in disease biogeography over space and time. Coupled with socio-economic spatial temporal data, we can examine determinants of global outbreak distribution and increase our understanding of global infectious disease outbreaks, including making predictions of future hotspots for infectious disease outbreaks.

68B Trade-offs between native and exotic plants in fecundity and stress-tolerance may facilitate coexistence in local communities

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Trade-offs between native and exotic plants in fecundity and stress tolerance may facilitate coexistence in local communities. However, there has been little empirical work done to determine if these trade-offs exist in communities that have been invaded historically. In this study, we examined whether native and exotic plants exhibit this trade-off in fecundity and stress tolerance in a habitat where native and exotic plants have been coexisting together for nearly two centuries. We found that exotic species exhibited higher seed production and arrival at sites, while native species showed higher viability and tolerance to physical stress. We also determined that the magnitude of this trade-off was roughly symmetrical, such that neither native nor exotic plants consistently had more viable seeds in the seed bank over time. Collectively, these findings may help to provide an important mechanism that may be driving long-term coexistence between native and exotic plants in local communities.

Keywords: conservation; dispersal; ecology; seeds; species invasions

69B A meta-analysis of studies employing presettlement land survey records from Eastern USA, including study of natural, native and Euro-American disturbance

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Presettlement land survey records (PLSRs) in the eastern USA were created by surveyors during Euro-American settlement between the early 1600s and early 1900s. They consist of irregular metes-and-bounds surveys conducted during the colonial period primarily before 1785, and rectangular surveys primarily conducted since then. Metes and bounds surveys used trees and other features to note property boundaries. Rectangular surveys used trees more extensively to note property boundaries, and along survey lines noted vegetation composition and disturbances such as fire and wind. We have found 291 studies published between 1899 and 2011 that have employed PLSRs from the eastern USA, and have compiled information about them to assess how the use of PLSRs has changed over that time. The studies come from 31 eastern states and cover an area equal to 27% of the eastern USA. PLSRs have provided insight into three different types of disturbances: natural, Native, and Euro-American. Historically, studies of PLSRs exhibit the same three stages of knowledge for each of the three types of disturbances: no recognition of that type of disturbance, mention of the possible impact of that disturbance in the Discussion section, and quantification of the frequency or impact of that disturbance. The three most frequently mentioned natural disturbances were fire, disease and wind; the three most frequently mentioned anthropogenic disturbances were logging, farming and pasture. PLSRs have been used to reconstruct the spatial patterns and frequencies of those forms of disturbance, and to assess how much they influenced forest composition.

70B The Biogeography of Pathogen Community Assemblage in the Southeastern United States

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Understanding the variability in community assemblage is enhanced when placed in a geographic context. Pathogen communities rely on the composition of host and vector communities, the immunological state of the host, and the interaction of pathogens with one another; all of which can be better understood from a biogeographic perspective. Feral swine are a ubiquitous invasive mammal in the southeastern United States; their generalist habits allow them to invade multiple habitat types of varying levels of disturbance. We used a state-of-the-art pathogen detection microarray to monitor the presence of >6000 unique viral, bacterial, fungal and protozoan microbes in the blood and feces of 30 feral swine collected across the southeastern United States. We tested 3 central hypotheses: 1) blood-borne and enteric microbes would increase in diversity with decreasing latitude, 2) feral swine in highly disturbed landscapes would have higher pathogen loads than in less disturbed landscapes, 3) pathogen community composition is related to host community composition.

Keywords: biodiversity, disease ecology, feral swine, invasive species, microbial ecology

71B Refugia within refugia – spatial patterns in endemism and cross-taxa genetic divergence are linked to Late Quaternary climate stability in the Iberian Peninsula

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The influence of Pleistocene climatic oscillations on current distributions of genetic and species diversity has long been realized. In Europe, three major refugia in the Mediterranean peninsulas functioned as survival pockets from which northern areas were later colonized. However, growing evidence has revealed complex phylogeographical patterns within these southern regions, suggesting that southern refugia were heterogeneous mosaics of climatic and ecological regions that could host multiple glacial refugia. Historically stable areas or refugia are predicted to enclose higher endemism when compared to unstable regions, as well as genetic signatures of high genetic diversity within and high dissimilarity between refugial populations. Despite these predictions, few studies have provided a direct link between historical climate change and endemism or genetic diversity. Here, we aim to study the patterns of endemism and phylogeographic concordance across animal species in the Iberian Peninsula, one of the most important unglaciated areas in Europe during the Pleistocene, and the extent to which these patterns can be explained in terms of climatic stability within this region. We found that historical climatic stability (notably climatic analogy measures integrating macroclimatic shifts with local spatial topoclimate gradients) was often among the most important predictors of endemic species richness for different taxonomic groups using models that incorporated also descriptions of modern climate conditions. Furthermore, for some taxonomic groups, climatic stability was also significantly correlated with patterns of genetic divergence, and with private haplotypes across species more frequently found in more stable areas.

Keywords*:* Iberian Peninsula, endemism, historical stability, phylogeography

72B Diverging responses of tropical Andean biomes under future climate conditions

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Observations and projections for mountain regions show a strong tendency towards upslope displacement of their biomes under future climate conditions. Because of their climatic and topographic heterogeneity, a more complex response is expected for biodiversity hotspots such as tropical mountain regions. In order to analyze potential changes in the distribution of Tropical Andean biomes, biome distribution models were developed using logistic regressions. These models were then coupled to an ensemble of 8 global climate models to project future distribution of the Andean biomes and their uncertainties. Our results challenge the common believe that climate change will lead to an upslope displacement of biome boundaries in mountain regions. Instead, our models project diverging responses, including downslope expansion for most of the drier biomes, while wetter biomes exhibit, as expected, an upslope displacement of both the upper and the lower boundaries. Despite important losses are projected for several biomes, projections suggest that between 74.8% and 83.1% of the current Tropical Andes will remain stable, depending on the emission scenario and time horizon. Between 3.3% and 7.6% of the study area is projected to change, mostly towards an increase in vertical structure. For the remaining area, there is no

agreement between model projections. However, a significant part of the area expected to change is already affected by land use changes. The inclusion of a comprehensive uncertainty analysis will help to inform conservation strategies in the Tropical Andes, and the methods presented here have the potential to be applied to other tropical mountain regions.

Keywords: biome models, climate change, conservation, uncertainty, vulnerability assessment

73B Thermal physiologies reveal fundamental versus realized niches: A test of the Dobzhansky-MacArthur Hypothesis

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The Dobzhansky-MacArthur hypothesis (DMH) states that biological enemies, such as competitors, predators, and diseases, largely constrain the distribution of species in lowland tropics, whereas abiotic factors, including temperature, constrain the ranges of species at higher elevations and latitudes. We test the DMH using temperature data from thermal tolerances (fundamental niche) and geographic ranges (realized niche) for 40 species of reptiles and 29 amphibians occurring in North America, Europe, Asia, Africa, and oceanic islands. We find that realized niches are smaller than fundamental niches in the tropics, likely due to biotic constraints. In accordance with the DMH, we hypothesize that biological 'enemies' constrain geographic ranges of species in the tropics. In contrast, species at higher latitudes exhibit geographic distributions spanning temperature ranges that are much wider, and typically colder than their physiological tolerance limits. Consistent with the DMH, the realized niche is larger than the fundamental niche at high latitudes and elevations, possibly driving adaptations such as hibernation, torpor, estivation and even freeze-tolerance that allow organisms to persist in environments at temperatures well below their physiological tolerances. These patterns are generally consistent across both elevational and latitudinal gradients and question the usefulness of niche models that rely on abiotic factors.

74B Responses of Chihuahuan desert plants to climate change

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Climate changes have occurred several times throughout the Earth's history; however, the current global warming episode may be occurring at a faster rate. Species may respond to this change by adapting to the new conditions or by shifting their distributions and tracking their niches spatially. Recent studies of projected climate change effects in Mexico concluded that one major spatial foci of serious effects of global warming on biodiversity would be the Chihuahuan Desert. We analyzed if two desert species have tracked their niches during drastic climate change events: 1) in the past (across the Pleistocene–Recent transition), 2) present and 3) future (2020, 2050 years). We used ecological niche modeling to project geographical distributions across these periods, and fieldwork to support our findings. Results show that during the last glaciation the two species were restricted to few sites where environmental conditions were suitable. In the present, we detected evidence of species' responses at the population level, as we found low abundances and recruitment rates in sites where models predicted unsuitable environmental conditions, and recent colonization in new suitable areas for a species with high dispersal rate and successful establishment, but no range expansion for a species with low dispersal capacity. Finally, future projections suggest high risk for the species with current restricted distribution.

Keywords: Global warming, *Larrea tridentata*, population, Pleistocene, Holocene.

75B Ecological dynamics and alternate stable states in the climate system

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Global temperatures are projected to continue to rise by 1.8 to 6.4°C this century in response to continued anthropogenic emissions of greenhouse gases. Determining potential state changes in the climate system is a critical challenge as anthropogenic GHG emissions continue, but the dynamics of the climate system are closely linked to those of the terrestrial biosphere. Terrestrial plants are one of the largest sinks for anthropogenic emissions of CO2 as well as a determinate of earth surface albedo. Forests, for example, absorb about 4 Pg C year-1 of the approximate 7.6 Pg C year-1 released through fossil fuel use and other human industrial activity. Forests are not static entities, however; their ability to sequester carbon is a function of climate, and studies have indicated the potential for declining CO2 absorption with increasing global temperature. Climate change can also drive ecological transitions between forest, savanna, and grassland states through effects on fire regimes and precipitation, as well as through changing atmospheric concentration of CO2. These disparate ecological states, in turn, can have large effects on the climate system through differential carbon sequestration and surface albedo. Understanding the dynamics of the climate system requires models that include ecological processes and the feedbacks between the ecological and climate systems. We develop a dynamical systems model to examine climate-vegetation feedbacks and demonstrate the potential for ecological processes to result in abrupt transitions to alternative stable states in the coupled ecological and climate system.

76B Spatial filtering to reduce the effects of sampling bias on ecological niche models: analyses using the Malagasy mammal *Microgale cowani*

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This study spatially filters occurrence data with the aim of reducing overfitting caused by sampling bias in ecological niche models (ENMs). Presence-background modeling techniques aim to approximate the abiotically suitable habitat of a species by comparing environmental conditions at localities where the species occurs with the overall range of conditions available in the study region. Unfortunately, sampling bias in geographic space leads to localities that may also be biased in environmental space. If so, the model may overfit to that bias. To address this issue, we used MaxEnt, 19 bioclimatic variables, and occurrence records of a Malagasy tenrec, *Microgale cowani*. We modeled using three distinct datasets: unfiltered, spatially filtered, and rarefied unfiltered localities. The unfiltered dataset contained all unique localities. We then spatially filtered that dataset, so that no two localities fell within 10 km of each other. To control for the possible effects of sample size, we also randomly rarefied the unfiltered dataset to match the number of localities of the spatially filtered dataset. To evaluate model performance in predicting spatially independent localities, we then employed k-fold cross-validation with geographic partitions. To quantify overfitting, we calculated the difference between calibration and evaluation AUC (= AUC_{diff}), and used omission rates for two different thresholds. Models made with the filtered dataset showed lower overfitting than the other two suites of models, having both lower omission rates and AUC_{diff}. These results indicate that spatial filtering of occurrence records can allow researchers to produce more accurate models.

77B Avian community composition along an elevation gradient through Yosemite National Park

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My research establishes an avian biogeographic benchmark to the historic Grinnell/Storer cross section of the Sierra Nevada through Yosemite National Park, CA. I surveyed avian community composition in 2004 at twelve sites originally surveyed in 1914-1920 by Joseph Grinnell along an elevation gradient from 86 m to 2,923 m in the high-country of Yosemite NP. Point counts were conducted at eight points along a 1.5 km transect at each site described in Grinnell's field notes. Avian abundance and species richness from modern point counts are compared to historic surveys. The Shannon-Wiener diversity index and the Sorenson's similarity index were compared at each site in the historic and modern surveys. Modern surveys identified 117 species with 26 species exclusive to modern surveys. Of the 115 species identified in the historic surveys, 24 species were not observed in modern times. The combined list yields 143 species. Significant differences in abundance between historic and modern surveys were identified at seven of the twelve sites. Avian diversity was lower in the historical surveys at ten of twelve sites. Diversity in historical surveys ranged from 2.46 at Young Lake to 3.29 at Pleasant Valley. Similarity between surveys at sites ranged from 35% at Tuolumne Meadow to 73% at El Portal, one of 6 sites with >50% similarity. Species turnover is discussed by identifying species exclusive to each time period. My results indicate shifts in avian community composition along the elevation gradient over the approximately 90 year time span.

Keywords: biodiversity, Grinnell-Storer cross section, distributions

78B Predicting the distributions and range shifts of ant species in a warming world

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Understanding the factors that limit the distribution of species and patterns of biodiversity is at the core of ecological and biogeographical research. The complex relationship between environmental conditions and biogeographical distributions often relies on large-scale climatic information and macroecological data from museum records and field guides. Few studies, however, incorporate actual physiological mechanisms and measurements of the studied organisms to understand patterns of diversity and predict the distributions of species in a changing world. In this study, we measured morphological characteristics and trait-based physiological responses (critical thermal limits) of 42 species of ants from 24 sites along a latitudinal gradient from Florida to Maine, USA, spanning approximately 16 degrees latitude, as well as from 32 sites along an elevation gradient (375-1825m) in Great Smoky Mountains National Park, TN, USA. Interestingly, a high degree of intraspecific variation in thermal tolerance occurred across both gradients in several ant species, including one of the most common and ecologically important genera of forest ants in eastern deciduous forests (*Aphaenogaster*). We found that while upper thermal limits declined slightly with increasing elevation and latitude, lower thermal limits showed a much more drastic decline, resulting in populations from high latitudes and elevations having a broader thermal breadth than populations from lower latitudes and elevations. These physiological responses of how different populations respond to variation in temperature, taken with current mean annual temperature and projected climate scenarios, may be integral in estimating how ant communities will be structured in response to ongoing climatic changes.

Keywords: thermal tolerance, physiology, communities, functional traits, climate change

79B Global-scale turnover of terrestrial ecoregions under a future climate

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When setting conservation priorities, the concept of the 'ecoregion' (areas of roughly uniform environments that habour characteristic communities of species) has often proven useful as a basis for planning. Towards this end, the WWF (World Wildlife Fund/World Wide Fund for Nature) have, in partnership with many local and national experts, produced one of the most comprehensive global ecoregion classification initiatives. However, to ensure the success of future conservation efforts, it is important to know how these ecoregions will respond to a changing climate. Unfortunately, due to the nature of the classification data used in this study, standard methods employed in the field of species distribution modelling are not appropriate. We instead investigate the link between the classification of ecoregions and the local climate, whilst accounting for extraneous spatial autocorrelation arising from non-climatic sources, using a hierarchical Bayesian generalisation of the Potts model (originally employed in the field of statistical mechanics to predict particle spin in crystalline lattices). This model was fitted to the existing WWF classification using reversible jump Markov Chain Monte Carlo (rjMCMC) methods, allowing the selection of an ensemble of suitable models: selecting only those climate variables that are relevant to the distribution of each ecoregion and, at the same time, ensuring reasonable parsimony. We demonstrate that despite strong autocorrelative forces ensuring spatial and temporal cohesion in future estimates on the distribution of ecoregions, climate change is likely to induce significant turnover in these ecoregions and cause significant ecological upheaval.

Keywords: Conservation prioritisation, Multinomial autoregression, Landscape classification, Global 200, Biome shifts

80B Distribution of cryptogam diversity and community structure along an elevational gradient in the Canadian Subarctic

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With projected climate change expected to have greatest impact in higher latitudes and altitudes, it is essential that we gain a better understanding of the structure and dynamics of arctic communities in order to predict future change. Phylogenetics has recently emerged as an important tool in this pursuit. Because more closely related species tend to be ecologically more similar, the phylogenetic structure of communities can therefore capture information on their functional and ecological diversity. This research uses phylogenetics, along with traditional measures of diversity, to investigate spatial patterns and turnover in community structure of non-vascular (cryptogam) plants across an elevational gradient in the Subarctic of Canada. Phylogenetic beta-diversity— or the phylogenetic distance between communities—allows us further insight into spatial changes in the functional diversity of communities. The study site lies on an elevational gradient in Western Labrador, transitioning the Boreal forest to the Arctic biome. Diversity and abundance estimates of cryptogams were collected in 88 plots set out over the southern slope of Mount Irony and in situ environmental sensors were placed to document temperature and moisture regimes. Results indicate that cryptogams exhibit differential responses to changes in environmental factors with elevation. Lichen phylogenetic and species diversity increased linearly with altitude ($P<0.001$). In contrast, bryophyte diversity remained relatively constant over elevation. Abiotic factors important in determining distributions differed between lichen and bryophytes. These results suggest that turnover is highly guild-specific, which is a necessary consideration for predicting shifts in community structure with climate change among plant groups.

Keywords: community assembly, community phylogenetics, spatial distributions, altitudinal gradients

81B The distribution of abundance for terrestrial invasive plants: a novel approach for modeling impact risk

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Invasive plants' main impact on ecosystems occurs as a result of competition with native species for resources. Therefore, the level of abundance reached by an invasive plant will partially determine the extent to which a native ecosystem is impacted. When using bioclimatic models to describe the distribution of invasive plants, most studies have used occurrence data to model risk of establishment. This method can approximate the fundamental niche of the species, but overestimates risk of impact on native ecosystems. Many studies have shown that climate change is likely to shift the distribution of invasive plants (i.e., risk of establishment), but none have tested how climate change might affect abundance (i.e., risk of impact). By determining the climate conditions required by an invasive plant to become abundant, it is possible to predict the areas at risk for the greatest impact from invasion. Presence and abundance data were collected for an invasive grass (*Bromus madritensis*) and forb (*Brassica tournefortii*) occurring in the southwest United States. Separate bioclimatic models were created using the presence and abundance data and were then overlaid to determine their relative geographic locations. An ensemble of atmosphere–ocean general circulation models was used to project geographic changes in suitable climate conditions for the presence and abundance of each species under future emission scenarios. This approach has the potential to provide more accurate invasion risk assessments for invasive plants and to contribute to our understanding of the association between areas of abundance and presence under current and future climate conditions.

82B Challenges of predicting species distributions under climate change: the case of the frailejones in the tropical Andes

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The dramatic radiation of the 141+ species of frailejones (subtribe Espeletiinae Cuatrec., Asteraceae) provides a model system to study the effects of climate change on tropical high-elevation ecosystems. Frailejones are locally abundant in the páramos (high altitude grasslands) of Colombia, Venezuela and northern Ecuador and the preservation of this unique ecosystem is tightly linked to these plants' presence and persistence. Like the páramos themselves, which are shrinking rapidly, frailejones are highly threatened by climate change, mining, agriculture and livestock. This project estimated the potential changes in species distributions under different scenarios of climate change. In total, we tested 23 global climate models under three scenarios (A1B, A2A and B2A) for the years 1990 to 2080. Species distribution models were estimated for a total of 133 species, and 12 metrics were measured from predictions. Despite the advantage of modeling species in a distinct and restricted range (i.e. isolated by elevation), various challenges were identified: resolution and accuracy of layers of information; number of occurrences; modeling narrowly distributed species; choosing a global circulation model; measuring the response of species; evaluating the precision of the models; and dealing with computational limitations. Results suggest that most of the species are predicted to experience a reduction in suitable area, with fragmentation and simplification (or extinction) of their populations over time. Species at the extremes of the elevation gradient will suffer the most drastic effects. Overall, an extinction rate of 31-57% is estimated by 2080, with the first extinctions predicted to occur as early as 2020.

Keywords: biogeography, Espeletiinae, extinction, niche modeling, paramos.

83B Expansion and contraction tension zones in western US piñon-juniper woodlands under projected climate change

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Piñon and juniper vegetation types cover >30% of the Colorado Plateau. Two species and one variety of piñon pine (*Pinus monophylla, edulis, monophylla* var. *fallax*) and four species of juniper (*Juniperus osteosperma, monosperma, deppeana, arizonica*) are dominant, and comprise a mosaic of overlapping distributions arranged primarily across a gradient of seasonal precipitation. Individual species have been found to respond uniquely to climate changes, causing shifts in the co-occurrence of species. This is reflected in the differential mortality among species caused by recent droughts, which appear to indicate long-term distribution shifts have already begun. We developed bioclimatic distribution models and applied climate change scenarios to gauge potential shifts in the distributions of individual species and their co-occurrence. The application of climate change scenarios resulted in, for each species / variety, the spatial depiction of currently inhabited areas no longer suitable for regeneration as well as currently uninhabited areas becoming suitable for colonization. Our results suggest individualistic responses of species to climate change will likely cause shifts in their spatial co-occurrence. For example, *J. osteosperma* is predicted move northwest whereas *J. monosperma* is predicted to move northeast resulting in a decrease of co-occurrence. *P. edulis* is predicted to increasingly co-occur with *J. osteosperma* while *P. monophylla* is predicted to decrease or increase depending on the climate change scenario. The character of individual species distributions shifts and their resulting changes in co-occurrence will be largely determined by changes in the summer monsoon rains and in the minimum winter temperatures.

Keywords: piñon-juniper woodlands, climate change, distributions

84B Correlation of plant growth form, diversity and climate

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Plant growth forms are believed to reflect adaptations to different environmental challenges. This is evident in the divergent geographic distribution of different growth forms. A number of underlying controlling factors have been proposed including climatic, edaphic, topographic, disturbance and vegetation-related drivers. Despite their importance, these links are incompletely understood. Here we investigate macroscale growth form-environment links for eight growth forms across the whole New World. Distribution data for 46,695 vascular plant species with 2,496,365 occurrences were extracted from the Botanical Information and Ecology Network (BIEN) database. Proportions of species and occurrences of a given growth form were quantified for each cell in a 100×100 km grid covering the New World. We tested for their links to potential drivers using spatial multiple regression modelling and model averaging. The growth forms showed distinctly different spatial distribution across the New World. Regression analysis revealed that climatic variables were consistently among the most influential variables with annual mean temperature as the most frequent. Correlations with variables were consistent with current hypotheses regarding each growth form. For instance, gymnosperms were negatively correlated with AMT and

positively correlated with temperature seasonality; whereas, broadleaf trees showed the opposite trends demonstrating different environmental links for the two competing growth forms. Plant growth forms showed distinct differences in geographic distribution indicating that the divergent spatial patterns in presence and species richness of plant growth forms reflect their link to different drivers. Climatic variables were important for all growth forms, implying that climate changes are likely to alter spatial patterns.

Keywords*:* biodiversity, biogeography, climate change, habit, model averaging

85B Learning from the past to predict the future: linking palaeophylogeographic models with future climate change risk assessments in Nearctic Chelonians

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Global climate is changing and species must respond by tracking suitable habitat, adapting to the changing conditions, or becoming extinct. To better understand how species will respond to future climate change, we have investigated the historic patterns of response to fluctuating climates of the past 320ka in North American Chelonians. We further modeled the response to future climates of these species using different Intergovernmental Panel on Climate Change (IPCC) scenarios for 2080. Palaeophylogeographic models for the past 320ka reveal different patterns of distributional changes in Nearctic Chelonians, ranging from latitudinal range shifts and range contractions to a complete modeled 'extinction' during glacial maxima. Looking into the future, species distribution models projected on different IPCC climate change scenarios also reveal significant changes in future potential ranges resulting in range shifts. Especially in the South, large areas are facing completely novel climatic conditions from the species' point of view, which might lead to increased environmental stress and even a high extinction risk. In combination of both approaches, this study shows that estimates on extinction risk provided by assessments on prospective climate change have to proceed with caution, since even past climates lead to modeled 'extinctions' in certain species. This might happen for different reasons: 1) relevant processes are acting at much finer scale as typically assessed in macroecological studies, and 2) other parts of the species' fundamental niche which are not represented today become available during changing conditions, keeping the range still viable for the species.

Keywords: niche modeling, global change, palaeophylogeography, biogeography

86B Assessing the predictive ability of ecological niche models using data from the North Slope of Alaska

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One of the most commonly used modeling strategies to predict potential changes in species distribution is the species' ecological niche model. However, this strategy has been widely questioned due to its assumptions and uncertainties. We evaluated the accuracy of this approach by comparing predicted changes in shrub distribution and abundance against observed records of changes in shrub cover across the North Slope of Alaska. We built ecological niche models with shrub presence and abundance records for the year 2000 and environmental data from 1960-1990 for the same region, and then predicted for the 1931-1960 period. A measure of predicted shrub change was obtained by comparing the 1960-1990 models against 1931-1960 projections. Changes were then compared to observed records of increase in shrub cover recorded for the past 50 years using repeat photography. This unique test revealed no correlation between predicted and observed changes, raising important questions regarding the applicability of the models. We discuss limitations of the models and data, and the importance of spatial scale as a key factor to the predictability of species' ecological niche modeling.

Keywords: Species distribution, ecological niche model, shrub, predicted habitat suitability, maximum entropy.

87B Testing species distribution models across space and time: high latitude butterflies and recent warming

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Given the widespread use of species distribution models (SDMs) in global change research, we quantified how reliably SDMs forecasted species distributions under observed climate change. In particular, we tested whether distributional changes at expanding range margins could be predicted accurately and whether the predictive ability of SDMs depended on species characteristics or the inclusion of land cover and soil type variables. Using 10-km butterfly atlas data from two periods, 1992–1999 (t1) and 2002–2009 (t2), with a significant between-period temperature increase, we modelled the effects of climatic warming on butterfly distributions with boosted regression trees (BRTs) and generalized additive models (GAMs). We evaluated the performance of our models first by using the split-sample approach with data from t_1 ("non-independent validation"), and then by comparing model projections based on t_1 with species' observed distributions in t_2 ("independent validation"). We modelled simple SDMs with climate variables only, and compared these to more complex SDMs that included land cover, soil type, or both. Finally, we compared observed and predicted shifts at northern range margins. When forecasting changes at northern range margins, correlations between observed and predicted range shifts were predominantly low. Models that included land cover and soil type variables generally improved model performance while species mobility, flight period and prevalence were negatively related to model accuracy. In conclusion, SDMs can provide useful and relatively accurate predictions for low-mobility species over short (10 year) periods of climate change, but they may fail in predicting range dynamics, especially at the expanding edge.

Keywords: Expanding range margin, land use, Lepidoptera, soil type, species traits.

88B Assessment of influence of climate change on the potential distribution of *Syrmaticus reevesii*

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Global climate change is one of the major threats to biodiversity. Global warming caused by the excess emission of greenhouse gases affects the distribution and physiology of species, and threatens their survival. Thus, predicting and evaluating the consequences of changing climates on species' distributions are important for biodiversity conservation. The

goal of our research was to study the influence of future climates on potential distribution (PD) of Reeves' Pheasant (*Syrmaticus reevesii*), a species endemic to China, using GIS and ecological niche modeling techniques. We built current and future climate layers, and derived bioclimatic variables to use for generating present-day and future potential distributions of Reeves' Pheasant. We evaluated PDs using the area under the curve (AUC) of Receiver Operating Characteristic (ROC) and by comparing present-day PD with the species' historical distribution. Both analyses showed high accuracy for present-day PD. On comparing the difference between current and future PDs, our results indicated that Reeves' Pheasant future PDs would: 1) decrease in extent, 2) shift to higher latitude and higher altitude, 3) have centroids shift northeast, and 4) have gaps in its latitudinal and altitudinal distributions, which may further affect the distribution and dispersal of the species. Additionally, we assessed future changes of PDs in the nature reserves where Reeves Pheasant is known to occur, and provide suggestions for conservation of this species.

89B Adding mechanism to correlative ecological niche models. Operative temperature and the distribution of Iberian lizards

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Ecological Niche Models are tools widely used in macroecology. The most common approach consists of statistically relating species presence with environmental variables to infer an environmental "envelope" for the species. An alternative approach uses a mechanistic understanding of the biophysical processes that allow species to persist under environmental stressors to build models of population dynamics in space and time. Correlative models can be feasibly implemented for a large number of species, but mechanistic models require a deeper understanding of the biophysical processes that govern species distributions and are typically possible for a limited number of species. However, some biophysical processes can be inferred from theory and to compute variables that directly affect organisms. Such variables directly exerting an effect on species distributions can be used to improve the predictions of correlative models typically fitted using surrogate variables. For ectotherms, one of such direct variables is operative temperatures. Here, we use interpolations of operative temperatures across the Iberian Peninsula based on a regional circulation model. We then fit a statistical niche model for several Iberian lizard species using their inferred operative temperature. We compare these results with those of another statistical model fitted using environmental temperatures as estimated from the same regional circulation model. By comparing the results of both projections we evaluate how the addition of biophysical mechanisms changes the influence of the climate variables on the presence of the species.

Keywords: ectotherm, ecological niche model, distribution, mechanism, operative temperature

90B An assessment of coral reef habitat suitability under 21st century climate change scenarios

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A maximum entropy niche model is used to describe coral reef habitat and predict changes to these habitats during the 21st century under two climate change scenarios. Anthropogenic climate change alters the physical and chemical components that comprise the niches of individual species and define oceanographic habitats. Changes in oceanographic habitats can lead to shifts in ecosystem range and distribution, and even species extinction. Coral reefs are valued for their natural beauty and biodiversity, but as climate change alters oceanographic conditions, the geographic range of suitable coral reef habitat is shifting. Of particular importance to corals are increasing sea surface temperatures, which can lead to coral bleaching, and decreasing aragonite saturation state, which compromises the corals' abilities to secrete carbonate skeletons that form reef structures. Further structuring the environment and determining geographical limits of reefs are salinity, photosynthetically active radiation, and current speed. Here we apply a maximum entropy niche model (Maxent) with output from the National Center for Atmospheric Research's Community Earth System Model version 1 (CESM1) to project future coral reef habitat over the next century. Maxent determines habitat goodness of fit for a particular species for each grid cell in the given geographic domain. We illustrate that changes in suitable coral reef habitat varies considerably between the three major ocean basins.

Keywords: climate change, coral reefs, Maxent, niche model

91B Catastrophic vegetation transitions in the Forest-Steppe ecotone in Asia under global climate change

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Vegetation often changes with topography. In the forest-steppe ecotone of northern Mongolia, we observed discontinuous slope aspect-dependent vegetation patterns with larch-forest and grassland on the north and south-facing slopes, respectively. Such vegetation patterns must reflect both physical conditions and human activities, but no theoretical model has succeeded to clarify the mechanisms generating these patterns. One of the critical barriers is the variance in spatial scales, that is, climate conditions are generally observed and modeled with much coarser resolution than human activities, whose distributions are often influenced by topography. To tackle these problems, we developed new models based on field observations in Mongolia. The first is a mathematical dynamics model for the interactions among two plants' biomass and local soil water content (SWC) that limits plant growth, and the second is a hydrological model for the spatial distribution of potential SWC governed by topography of the target region incorporating a strong positive feedback in plant-SWC interaction. By integrating these models we could successfully reconstruct the observed spatial patterns from the topographically estimated potential SWC. This underscores the importance of this feedback process at the topographical scale. Further, we suggest that vegetation might exhibit regime-shift under heavy drought and/or livestock grazing pressure. Using this model, we predicted a gradual vegetation boundary shift at the continental scale due to climate change from catastrophic change at the topographic scale.

Keywords: catastrophic vegetation transition, climate change, topographic scale, positive feedback, mathematical modeling

92B Dietary guild community disaggregation of avian assemblages under climate change

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Ecosystems globally stand to experience significant changes in their community assemblages because of climate change-induced geographic redistributions of species. We explored how climate change projected for the next 100 years may ecologically transform the world's avian assemblages by modelling changes to their dietary guild structure under different species dispersal distances (0 km, 500 km, and 2000 km). For this we selected an individualistic modelling approach (based on integrating many single-species environmental niche models) which captured closely the present dietary structure of avian assemblages when compared to a community modelling approach (which directly models richness or proportion of dietary guilds). We found additionally that most guilds, except frugivores and nectarivores, maintain constant proportions along the richness gradient nowadays. Under climate change, the shorter dispersal would result in smaller changes in proportion of the dietary guilds. Geographically, avian assemblages in Greenland, northern Asia and Africa, and the Arabian Peninsula were projected to undergo the greatest changes in dietary guild make-up, especially under long dispersal. Dietary guilds differed substantially in their patterns of composition, given projected geographic range gains and losses by 2100. We found projected decreases in primary consumers/guilds mainly feeding on plant materials and omnivores to be compensated by projected increases in high-level consumers/guilds mainly feeding on animal materials that comprised the highest proportion of diet contents across the world. Our results highlight impacts on disaggregation of global avian assemblages under climate change.

Keywords: guild assembly, community composition, dispersal, species distributions, climate change

93B An eco-informatics engine for understanding biotic response to global change

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The next generation of predictive models of the biotic response to environmental change must meet the challenge of incorporating the effects of complex interactions among organisms, climate, and their physical and biotic environments. A great variety of data types is required to meet this challenge, including current and past species' distributions, the increasing amount of associated data on their genotypes and phenotypes, and how these have changed in space and time, as well as empirical and modeled data on environmental and climate change. The goal of this project is to develop the informatics infrastructure needed to access, visualize, and analyze these rich data, thus providing the foundation for building the next generation of models of the biotic response to global change. The unique combination of data in Berkeley's Natural History Museums, Field Stations, and faculty labs, our leading role in bioinformatics and the digitizing and serving of organismal and environmental data from web portals, and our world-class community of scholars and students make the unprecedented scale and complexity of the proposed effort possible. The Berkeley Ecoinformatics Engine will innovate with cutting-edge technologies, and once operational online, will enable cross-disciplinary exploration of the rich and disparate data sources required to understand biotic response to global change.

Keywords: biodiversity, climate change, distributions, informatics, niche models, web tools

94B Comparative eco-physiology of cold tolerance-related traits: predicting range expansion in an invasive insect at high latitude

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Physiological tolerance limits are crucial in determining the range limits of species. Invasive species often face environments which dramatically differ in abiotic or biotic characters. To establish themselves and persist, such species must often adjust their life-history and stress-related traits. Understanding how invasive species increase their range can provide important information as to how other species might respond to climate change, since they face similar changes in abiotic conditions as those predicted for large areas in various climate change scenarios. The Colorado potato beetle, *Leptinotarsa decemlineata,* an invasive pest of potato, has expanded its range from ancestral ranges in northern Mexico to very high latitudes in Europe. We show that beetles that invaded northern Europe (60°N) only about 30 years ago are more cold-tolerant than southern counterparts. However, since range expansion has slowed down, further expansion could be constrained by harsh northern conditions. We therefore investigated cold-tolerance in northern European potato beetles and two related Chrysomelid species, with similar overwintering eco-physiology which are found at even higher latitude. Samples were taken from overwintering beetles at different time points and cold tolerance-related physiological traits were studied with large-scale analytical biochemical methods. Preliminary results suggest large species-dependent differences in cold tolerance and underlying physiological traits. The implications of a climate change-related increase in average temperature on the range expansion of the Colorado potato beetle are discussed. We propose that even small increases in average temperature can have a major impact on the range expansion potential of this pest species.

Keywords: overwintering, lipids, metabolism, supercooling point, chrysomelidae

95B A mechanistic analysis of the range expansion of *Lycaena epixanthe* and its implications for species range shifts under climate change

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In the face of climate change, genetic variation may help organisms by increasing species flexibility to adapt. Warmer temperatures are resulting in expansion for many species at the poleward edges of their ranges. Relaxation of individual physiological constraints, such as rising temperatures in previously inhospitable areas, is likely to facilitate range expansions. The bog copper butterfly (*Lycaena epixanthe*) localized to peat bogs of Northeastern North America, has expanded its range northwards by approximately 272 km in 13 years – a rate exponentially higher than average. We investigated variation in morphological and physiological traits to identify mechanisms favouring this rapid expansion. We collected 478 specimens of *L.epixanthe* over a latitudinal gradient (44°- 54° N) ranging from the center to its expanding northern edge during 2011 and 2012. We compared specimen body length, wing surface area, wing loading, mass, and enzyme activity both spatially and temporally. We also compared morphological characteristics to those of the dorcas copper (*Lycaena dorcas*), a species with static populations between 48°- 54° N. Wing surface area and body length had the strongest relationship with latitude, but metabolic activity did not significantly differ across the gradient. Wing morphology was significantly different between pre-1991 and post-2010 specimens, indicating change through time. There appears to be trait convergence between *L.epixanthe* and *L.dorcas*, suggesting that optimal phenotypes may exist in those regions. To our knowledge, this is the first study that has attempted to study physiological patterns on such a large scale in a species that has expanded at an unprecedented rate.

Keywords: Dispersal, macrophysiology, biogeography, adaptation, insect flight

96B Shifting agricultural suitability of banana cultivation in Latin America

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Demand for agricultural crops is projected to increase with human population growth. Compounding this challenge are projected geographically varied shifts in rainfall and temperature associated with global climate change that may alter the future suitability of agricultural zones now productive for specific crops. These shifts in suitability could affect industries of local economic importance as well as potentially increase agricultural development pressure on threatened land cover types and protected areas. Predicting the locations of suitable climate conditions for banana cultivation will assist in food security planning. We investigated geographical shifts in banana cultivation suitability resulting from climate change in the commercial producing counties in Latin America utilizing a species distribution model-based approach. We modeled climatic suitability in the 2060s for conventional and organic banana production, and overlaid projected changes with land cover and protected areas for conventional production, which dominates global trade. Approximately half of conventional sample locations were unsuitable in the 2060s. Areas suitable for conventional cultivation decreased overall, but all countries maintained suitable areas. Some countries, such as Colombia and Honduras experienced large decreases in suitable areas while others, such as Mexico, experienced large increases. Minimal shifts in suitability among land cover categories occurred, but an overall decrease in suitability in protected areas was predicted. With a predicted drier climate, suitable area for organic cultivation nearly doubled These results suggest that areas optimal for commercial banana production will shift with climate change, and industries can use modeling to proactively investigate potential changes in order to better prepare for the future.

Keywords: bananas, agriculture, biogeography, distributions, climate change

97B Applying modelling updating approaches to identify potential conflicts with main roads in the expected geographic adaptation of species to climate change

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This work presents the preliminary results of a project aiming to identify hot spots in the Andalusia (Spain) road network which could hinder the permeability needed by threatened non-volant tetrapod species in their geographic response to climate change. We propose to take advantage of national species distribution models, but update them with variables yielded by climatic models for the regional target area before projecting them to the future. We used the favourability function to model the 20 non-volant tetrapod species, with some degree of threat in Andalusia, under different climate change scenarios (A2 and B2) and the general circulation model GGCM2. We evaluated two different approaches to updating the models obtained for mainland Spain. The first approach was to use the same models for mainland Spain projected only on Andalusia. The second was to use the variables of the national models and to recalibrate them using the presence/ absence data for Andalusia. For all the species and climate scenarios considered in this study the best results according to AUC were obtained using the second updating approach.

Keywords: Andalusia, emission scenarios, favourability function, species distribution model, threatened species

98B Demographically driven distribution models; advantages of using integral projection models to incorporate demography into species distribution models

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Species Distribution Models (SDMs; e.g. Maxent, GARP, GLMs, etc.) are typically used to describe the correlation between occurrence patterns and environmental covariates. Often, these methods are used because species' presence, and sometimes absence, at locations on a landscape are the only available population-level data. While this class of SDMs is useful for exploring spatial occurrence data, they offer limited insights into the underlying population biology that generates these patterns. Here, we show how to use a limited amount of demographic data to produce *demographically driven distribution models* using Integral Projection Models (IPMs) for stage-structured populations. By modeling vital rate functions such as survival, growth, and fecundity, instead of occurrence probability, and combining these functions using IPMS, it is possible to predict more biologically meaningful demographic summaries of population patterns such as population growth rate, life expectancy, or stage (e.g. individual size) distributions. Because vital rate functions are built using regression, they can interpolate across variation in stages and environments to compensate for limited data. To illustrate these principles, we construct demographically driven distribution models for two invasive plants in the northeastern United States by combining data from a variety of sources. We compare these models to SDMs that predict occurrence probability and illustrate inference about the demographic processes that drive differences in habitat suitability. By developing a better understanding of the demographic processes underlying distribution models, we are able to make more meaningful projections of population level patterns under new environmental conditions such as climate change, disturbance, or during invasions.

Keywords: ecological niche model, experimental biogeography, climate change, invasion, vital rates

99B Freshwater fish guild distribution modeling in Neotropical wetlands

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Neotropical freshwater wetlands are highly seasonal pulsating ecosystems. They are threatened by climate change through uncertainty in the distribution of precipitation and temperature variability. Modeling freshwater fish biodiversity distribution in these wetlands is challenging due to the large amount of species, with huge gaps in their distribution record, few locations in most cases, absence of data on environmental conditions related to these occurrences and lack of spatial layers related to habitat variables at all scales, particularly seasonal wetland distribution. We addressed these challenges with a two tiered approach, focusing on Argentine wetlands and fish species of the Parana-Paraguay fluvial corridor. In the first tier we evaluated different modeling algorithms to predict the distribution of wetland classes. We used point samples from streams, lakes and hydric soils digital coverages as wetland targets. Environmental predictors included Bioclim layers, monthly climatic water balance as proxy for river hydrology and wetland seasonality, and SRTM derived terrain variables. Although model performance described by ROC curves was high for all wetland classes and algorithmic approaches, Random Forest was preferred as it provided the spatial predictor importance structure for each wetland class. For the second tier we explored modeling the distribution of ecological guilds instead of single species. We built a database of the fish species of the Parana-Paraguay basin in Argentina, collated data from bibliographic references, GBIF, and unpublished field samples for species occurrences and ecological strategies. We used the spatial predictors of wetland classes as environmental layers to predict guild distributions using both Maxent and Random Forests algorithms. Using this approach we modeled the distribution of physiological, migratory, and breeding guilds covering between 60 and 40% of the species list, depending on the guild, whereas using a species approach, less than 20% would have been covered.

Keywords: guild distribution, Neotropical freshwater fish, Parana–Paraguay corridor, wetland biogeography

100B Geohistorical population dynamics within a marginal sea in East Asia: effects of Pleistocene glacial activities on the genetic divergence and demography of semi-terrestrial arthropods

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Pleistocene climate fluctuations and subsequent changes of sea level influenced genetic divergence and population structure of various living organisms. Genetic diversity of any species within marginal seas may have been greatly impacted by the drastic geological and environmental changes that occurred in their habitats as a result of glacial–interglacial cycling. In order to elucidate any possible phylogeographic pattern and assess relationships among geological factors, genetic divergence and population structures, both phylogenetic and demographic analyses were conducted using partial mitochondrial COI gene sequences from several semi-terrestrial coastal arthropods collected from marginal seas within East Asia, including the Sea of Japan. Results strongly suggested the presence of four allopatric clades in *Tylos granuliferus* (Crustacea), which seem to have diverged along current stream-lines. Demographic reconstruction of the species suggested that recent population expansions within the Japan Sea occurred after a glacial period during the Middle to Late Pleistocene (0.11 Ma). In addition, we performed phylogenetic and demographic analyses in other semi-terrestrial coastal arthropods: *Garypus japonicus* (Chelicerata) and *Eudigraphis takakuwai nigricans* (Myriapoda). These analyses revealed that each species also had an allopatric Japan Sea clade which expanded in the glacial period at the boundary of the Middle to Late Pleistocene (about 0.1 Ma). Such coincidence suggests that several coastal species may share the same geohistorical transitions within marginal seas surrounding the Japanese Archipelago.

Keywords: climate fluctuation,palaeoceanography, phylogeography, Pleistocene glaciation

101B Predicting future climatic suitability for Great Lakes region reptiles using the maximum-entropy approach

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Climate change presents unique challenges to biodiversity policy makers and managers due to potentially significant shifts in the geographic distribution of environmental conditions suitable for population persistence. Reptiles may be especially vulnerable to the effects of climate change because of their thermal dependence and limited dispersal ability. The objectives of this project are to (1) determine the degree to which the distributions of 12 Great Lakes region reptile species of conservation concern are associated with climatic variables, (2) use this information to identify the projected future location of climatically suitable areas, and (3) prioritize species and associated management, research, and policy actions. Ecological niche modeling was performed in Maxent with current climate data from WorldClim and HadCM3 future climate scenarios. Overfitting was minimized by adjusting background area, excluding highly correlated climatic variables, and adjusting regularization parameters to yield approximately monotonic response functions. Extrapolation to climatic conditions not seen within current distributions was excluded. Three representative species, the Queen Snake, Blanding's Turtle, and Kirtland's Snake, all showed diminishing habitat suitability across their current range as time progressed. This diminished suitability typically originated at the southern and western end of the habitat range, and progressed to the north and east. Minor variations appeared between future climate scenarios, but all scenarios showed the same trend of diminishing habitat suitability. By year 2080, 50% or more of current ranges are predicted to be climatically unsuitable for these three species.

Keywords: biogeography, ecological niche model, Maxent, regularization, climate-change

102B A much greener future Greenland? Historical analogs and long-term constraints on the postglacial and future expansion of trees and shrubs across a large arctic island region

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Warming-induced expansion of trees and shrubs into high Arctic tundra areas will have strong impacts on Arctic biodiversity and the functioning of Arctic ecosystems. Greenland harbored a rich boreal shrub and tree flora in the Pliocene, before the Quaternary ice ages, and in warm interglacials during the Pleistocene. Today's Greenland harbors only a small subset of these species. Is current climate or limited postglacial migration the reason? And is Greenland likely to be transformed by a re-invasion of a rich boreal woody flora, similar to the Plio- and early Pleistocene situation, in the 21st Century? We predicted treeline shifts and changes in areas of suitable climate for more than 40 Greenlandic, North American, and European tree and shrub species from the Last Glacial Maximum into the future. About half of the studied North American and European tree and shrub species find potentially suitable areas in Greenland today; this lends support for Greenland's current species pool being strongly shaped by limited migration. Furthermore, we find support for areas of potential tree growth in current tundra vegetation. In combination with observed plantings and growth of trees, these results highlight that the arctic tundra in Greenland currently is lacking trees due to non-equilibrium vegetation dynamics. We conclude that predicted future expansions of trees and shrubs across Greenland will be dependent on the degree to which they are able to disperse across the landscape.

Keywords: migrational lag, non-equilibrium vegetation dynamics, distributions, paleobiology, treeline shifts

103B Potential impacts of climate change on phenology

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Phenology of plant and animal species is sensitive to climatic conditions. In general, spring phenology has advanced while autumn phenology has been delayed in response to recent climate change, although previous studies showed large regional variations in the rates and directions of responses. Here, we evaluate the potential impact of climate change on the phenology of 22 plant and animal species in Japan. We apply random forest models to the long-term phenological observations between 1953 and 2008 at 102 locations throughout Japan and project the phenological responses to 2031-2050 and 2081-2100 under the SRES A1B climate change scenario using four general circulation models (MIROC3, MRI-CGCM2, CSIRO-MK3, and GFDL CM2). Our projections for 2081–2100 were for spring plant phenology to advance by 7.7, 8.0, 12.7 and 14.8 days, and autumn phenology to be delayed by 5.6, 7.8, 10.2 and 14.4 days, under the CSIRO-MK3, MRI-CGCM2, GFDL-CM2 and MIROC3 models, respectively, indicating significant uncertainties in projections. Moreover, there were large regional variations especially for animals. Notably, for some spring-flowering species, such as *Prunus yendoensis* and *Prunus mume*, the flowering was projected to become earlier in northern Japan while progressively becoming later in southern Japan. Delayed flowering of these species is often observed when autumn and winter temperatures are high and the timing of the dormancy break is delayed. Thus, while warming in early spring would advance flowering, further warming could delay flowering when the effects of delays in dormancy break outweigh flowering advances in early spring.

Keywords: phenology model, random forest, uncertainty

104B Climate interpolation of daily maximum temperature: improvements for the production of climate datasets

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Studies in global environmental changes such as tracking of shifts in species ranges and climatic changes benefit greatly from the existence of long-term climate datasets at fine spatial resolution and high temporal frequency. In this research, we use meteorological stations and land surface temperature (LST) from the MODIS sensor to explore novel ways of interpolating daily maximum temperature at a one kilometer resolution in the state of Oregon, USA. We compared interpolated surfaces produced using three single time-scale methods including Kriging, Geographically Weighted Regression (GWR) and Generalized Additive Models (GAM) as well as two multi-scale methods: Climatologically Aided Interpolation (CAI) and Fusion of Satellites Station (FSS). Results indicate that multi-time scale methods (CAI and FSS) have on average similar root mean square errors (RMSE) and mean absolute error (MAE) values, and that they outperform single time-scale method (Kriging, GWR and GAM). Examination of spatial patterns demonstrates that CAI produces overly smooth surfaces in contrast to FSS which exhibits spatial details related to the physiography and topography of the study area. In particular, we found that FSS captures landscape features related to variations in temperature from land cover (forest, crop, shrub areas) as well as elevation. Results indicate that MAE and RMSE metrics fail to differentiate between CAI and FSS interpolation methods, and that a denser climate station network may be necessary. Results suggest, however, that the inclusion of satellite observations provides spatial information not contained in the station network, thereby providing a means to improve future interpolated products.

Keywords: Earth observations, interpolation accuracy, satellite remote sensing, spline, weather stations

105B The grass ceiling: recruitment limitation above timberline may limit tropical montane cloud forest's ability to adapt to global climate change

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As global temperatures rise, climatic conditions suitable to tropical montane plant species will be displaced towards higher elevations. In the Andes, plants will need to shift their distributions upslope past timberline into currently unforested grasslands (puna or páramo) in order to remain within their thermal niches. This expansion of cloudforest will only be possible if temperature is the most important factor determining the location of timberline, as is widely hypothesized. We investigated the predicted expansion of forest across current timberline with warming, as well as the effects of elevated UV radiation above timberline, in Manu National Park, Peru. We translocated 649 seedlings of a common timberline tree species, into the puna under 5 different experimental treatments, 1) control, 2) open puna, 3) warming, 4) shading, 5) warming + shading. Warming did not have a significant effect on seedling survival (19% survival) when compared to controls (40%) but did significantly increase seedling survival when compared to seedlings transplanted into the puna at ambient temperatures (7%; G test, $p = 0.02$). Both shading and shading + warming treatments had a significant positive effect on seedling survival (15 and 46% survival respectively) when compared to seedlings that were transplanted to the open puna without shade (7%, G test $p < 0.01$). These findings suggest that intense UV radiation, in conjunction with cold temperatures, may be preventing recruitment of tree species in the puna. Therefore, forest may not be able to expand upslope in the future since radiation will not change concomitantly with temperatures.

Keywords: translocation experiment, puna, forest expansion, shading, UV radiation

106B Making the most of mechanistic models

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Mechanistic models of species distributions have been subjected to increased testing, but recent comparisons with correlative approaches have not shown their putative benefits, which include strengthened inference due to a priori predictions and the ability to identify evolutionary dynamics. Through a new implementation of a butterfly distribution model focused on the sachem skipper (Atalopedes campestris) subjected to past comparisons, we show these benefits by using abundance data derived from a large-scale citizen-science monitoring program. Abundance is a more amenable metric to a model that predicts relative performance under differing conditions. We show that abundances have a positive relationship to predicted growth rates, but only in the cooler parts of this butterfly's range, suggesting an unidentified mortality source in warmer regions. We also identified two populations that may be experiencing local adaptation and suggest how this could be tested. Finally, we show how matching the year ranges of the environmental to distributional data provides a more robust test and suggests this species may not be in equilibrium with the recent climate.

Keywords: species distribution model, climate, butterfly, citizen science

107B Comparing past and future changes in European beech distribution: the effects of climate, dispersal, and land-use

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Many distribution models have been developed to predict species distribution shifts in response to climate change. One of the key questions about the shift of species distributions over time remains: Will species be able to track their future climate optimum? Process-based species distribution models have attempted to address this question for large spatial and temporal scales, but dispersal mechanisms in many process-based models are not explicitly simulated. In this study we investigated how the distribution of European beech (*Fagus sylvatica*) shifts from 12000 years ago to the end of the 21st C considering both plant trait responses to climate change and the dispersal abilities of the species. We used a process-based species distribution model (Phenofit) coupled with a new kind of phenomenological dispersal model based on the Gibbs point pattern process, both of which have been parameterized using species-specific modern ecological data. Our results show that while the progression of the northeastern boundary of past European beech distribution was entirely controlled by climate, particularly by the ability of beech to survive drought, dispersal controlled the progression of the northwestern boundary. However, under projected future conditions, interannual climate variability and landscape fragmentation may prevent European beech from colonizing its future potential habitat.

108B Large-scale current and future latitudinal gradients in stream macroinvertebrates richness across North America

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Understanding broad-scale biodiversity patterns provides a baseline against which to measure the impacts of climate change and as a prerequisite for the preservation of biodiversity. However, lack of standardized surveys along latitudinal gradients often yields chaos patterns. To overcome such limitations, we used predictions of species distributional ranges by applying Bioclimatic Envelope Models (BEMs). We analyzed patterns of freshwater aquatic insects genus richness for 191 genera belonging to Ephemeroptera, Plecoptera and Trichoptera (EPT) taxa. These orders were selected because trends in EPT richness are often strongly correlated with trends in overall richness. We first estimated the current potential geographic distribution by identifying the suitable habitat area in the region by means of consensus projections of six algorithms as implemented in the BIOMOD-package in R. We then generated richness patterns by overlaying predicted distributions for all genera. Model outputs coorelated well with empirically observed patterns. Different orders showed different richness peak patterns. Ephemeroptera richness showed a plateau of higher richness between 40° N and 48° N latitude. Plecoptera genera richness showed three peaks at 33°, 45° & 55°N with highest at 45°N latitude. Trichoptera genera richness was highest at 47° N latitude. We then used the current distribution to explore potential changes in biodiversity under the A2a and B2a IPCC emission scenarios for the year 2080 and determined average distributional shifts for the taxa. Our results also show how BEMs can be applied to explore broad patterns of freshwater biodiversity for taxa for which limited distributional data are available.

Keywords: Biodiversity, Bioclimatic Envelope Models, Biogeography, Climate change, Freshwater

109B Geographical patterns of community-based tree species richness in Chinese mountain forests: the effects of contemporary climate versus regional history

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The relationship between climate/productivity and historical/regional contingency and their rules on geographical patterns of species richness (GPSR) are still unresolved. Based on data from 1,494 plots of forests on 63 mountains across China, we document the GPSR for community-level tree species at the sub-continental scale. Regression tree and GLMs were used to explore the discreteness and gradient of species richness distribution, and to estimate the correlations of climate, historical floristic region, and local habitat with species richness. The collinearity between climatic variables and region were further disentangled; and the spatial autocorrelation in data was analyzed with Moran's I correlogram. Overall, 75% of variation in community-based tree species richness was accounted for by all variables included, about 66.5%, 64.5% and 27.9% by climate, region, and local habitat respectively. The explanatory power varied for different species groups. Ambient temperature was more important for tree species richness pattern than other climatic variables. Spatial autocorrelation in species richness pattern and could be accounted for mainly by the pattern of climate. The concordance between alpha diversity of tree species, historical flora and contemporary climate suggests the climate/ productivity and historical/regional contingency explanations contribute to the GPSR in a complimentary manner by providing continuous versus discrete perspectives, and focusing on different spatiotemporal scales. Our results provided an unique evidence to the link of climate effects on species richness across scales.

Keywords: floristic region, continuous and discrete perspectives, spatial autocorrelation

110B Prediction of migratory networks from climate change velocity

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Climate change velocity (CCV) is the speed and direction which a species would have to move to remain in its preferred climate. To date CCV has been calculated assuming a "hydrological" model in which species move in the direction of the steepest "downhill" gradient (direction in which velocity is the least). Although this simplification predicts the most likely direction of migration, it does not predict all potential routes of successful dispersal. It can also predict that species move in less-favorable directions or not at all, even when favorable habitat exists nearby. Here I extend the calculation of CCV to account for multidirectional movements and use it to predict the most likely routes of migration for threatened plants of the North American Central Highlands. Unlike the unidirectional flow predicted by "hydrological" CCV, multidirectional CCV predicts reticulated networks of migration. Multidirectional CCV can be used to identify chokepoints, dead ends, thoroughfares of migration in response to climate change.

Keywords: climate change, migration, climate change velocity, migratory networks

111B Including seed dispersal in a dynamic vegetation-climate model

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Predicting the migration of vegetation in response to climate change is often done with a vegetation-climate model; however, the lack of seed dispersal in these models is a common criticism. Previous efforts to incorporate seed dispersal limitations have occurred exclusively in bioclimatic envelope models. I present a mechanistic representation of long distance seed dispersal that is fully integrated into a dynamic vegetation-climate model (LPJ-GUESS). This is the first time all the steps required for simulating plant migration (i.e. seed production, dispersal, establishment, growth and reproductive maturity) have been included in a vegetation-climate model. The new model (LPJ-DISP) was able to simulate the migration of various tree species following climate warming. Simulated rates for *Acer* and *Pinus* matched closely with reconstructed rates based on genetics and pollen; however, migration for several other species (i.e. *Tsuga*, *Fagus*, *Picea*) was considerably slower than paleo estimates. To reconcile the differences, either a greater proportion of seeds are long distance dispersers or there are undetected northerly refugia populations. I demonstrate how northerly refugia populations can be included in LPJ-DISP, to

determine their impact on perceived migration rates and to improve our understanding of how rapid plant migration was achieved in the past. Improving the representation of seed dispersal in vegetation-climate models gives us more confidence in the quality of future climate change predictions.

Keywords: migration, long distance seed dispersal, simulation modelling, climate change

112B Predicting population persistence: can blue mussels redistribute poleward under climate change?

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As the climate warms, those species that cannot tolerate, acclimate to, or adapt to the changing conditions will only persist if they undergo range shifts. Redistribution may be particularly difficult for species that disperse in currents flowing in a direction opposite likely climate shifts. In the Gulf of Maine, the dominant Labrador Current flows southward, potentially slowing or preventing northward range shifts of species vulnerable to increasing temperatures. The blue mussel, *Mytilus edulis*, has recently experienced a warming-related range contraction in the southeastern U.S., and there is some indication that similar population declines are occurring further north. Thus, blue mussels may be especially vulnerable to warming, and understanding dispersal patterns is crucial given the relatively long planktonic larval period (>1 month) of the species. To determine whether blue mussels are able to disperse poleward in this advective system, we used trace element geochemistry to assess the connectivity patterns of seven blue mussel populations between Cape Cod, Massachusetts and northern Maine. By comparing the trace element composition of larval shells to that of juvenile shell edges (produced at the known collection sites), we predicted the natal origin of each mussel recruit. We found that although the majority of recruiting mussels either originated from northern sources or self-recruited within their natal region, poleward dispersal was possible and could facilitate northward range shifts of this species. Future studies are needed to determine recent population trajectories of blue mussels in the Gulf of Maine and to identify the most important sources of dispersive propagules.

Keywords: climate change, dispersal, marine, population connectivity, range shift

113B Projected response to climate change of waterbirds in the Prairie Pothole region, USA

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The Prairie Pothole Region (PPR) of the north-central U.S. and south-central Canada contains millions of small prairie wetlands that provide critical habitat to many migrating and breeding waterbirds. Due to their small size and the relatively dry climate of the region, these wetlands are considered to be at high risk for negative climate change effects as temperatures increase. To look at the potential effects of climate change on breeding waterbirds, we predicted current and future distributions using species distribution models (SDMs). We created regional-scale SDMs for the U.S. PPR using Breeding Bird Survey occurrence records and wetland, upland, and climate predictors. For each species, we predicted current distribution based on climate records for 1981-2000 and projected future distributions to future climate scenarios for 2040-2049. Range reductions were projected for almost all species. Individual species assessments varied widely but appeared related to habitat associations. Thus, targeted wetland management, easements, and restoration may ameliorate the future effects of climate change on wetland birds.

Keywords: bioclimatic species distribution models

114B Can demographic variability influence species responses to climate change?

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Organisms are under pressure to shift ranges under projected climatic changes. These range shifts are typically predicted by niche models, which predict species susceptibility to climate based solely on future habitat suitability. In order to include more realism into these models, we combined a niche model with a spatially-explicit stochastic matrix model for the monocarpic thistle *Carlina vulgaris* across northern Europe. We first developed a life history model with average fecundity and survival rates, and used a niche model to predict the change in habitat suitability through time. A comparison of the expected minimum abundance under stable and changing climate provided an assessment of the species vulnerability to climate change. We then varied the matrix values based upon demographic rates of local populations that were translocated to regions with different climates. The aim of the study was to provide a fuller understanding of species responses to climatic change by considering potential changes in demographic rates in conjunction with future suitable habitat. The following questions were addressed by the study: 1. How does *Carlina vulgaris* respond to projected changes in habitat suitability due to climate change? 2. How does information on between-population variation in vital rates affect predictions of the response of *Carlina vulgaris* to climate change? 3. Does intra-specific variation offset or exacerbate the effects of changes in habitat suitability on population viability? The results predict that *C. vulgaris* will be negatively impacted by climate change throughout much of its range, and that demographic variability will do little to mitigate this.

Keywords: SDMs, demography, climate

115B Preliminary analysis of a 35-year phenology data set from Cincinnati Ohio

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Weekly records of birds and wildflowers were collected from 1956 through 1990 on a small wooded residential property in a suburb of Cincinnati Ohio. Data include first arrival date for migrating birds and first bloom date for wildflowers. Data are analyzed to examine the presence and absence of changes over time, the relationship between bird and wildflower phenology in a single location, and the relationship of both bird and wildflower phenology to regional climate variables. Where possible, these data are compared with other data sets from the Cincinnati area. Bird and wildflower data are also placed in the context of other habitat data from the same property, including a tree census showing local forest succession. The importance of habitat fragments in residential areas is discussed.

Keywords: bird migration, first flowering, climate change, habitat fragments, citizen science

116B The relationship between area of elevation zones, species pool and alpha diversity along elevation gradients

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The relationship between area and species richness is well established in biogeography, and includes richness patterns along elevation gradients. Lomolino introduced the concept of elevational gamma diversity; the total richness of an entire elevation zone in given mountain range. This represents the species pool in a given elevation zone and may influence plot richness, i.e. alpha diversity. Rosenzweig termed this indirect influence of area on plot species richness an echo effect, and it has been verified on several mountain areas. On most mountains areadeclines monotonically with an increase in elevation, whereas species richness has a unimodal response to elevation. Thus the indirect effect of area on species pool and plot richness may be obscured at lower elevation. We tested the relationships between area, species pool (gamma diversity), and plot richness on three datasets from the Himalaya: (i) subtropical: 100-1500 m asl, (ii) warm temperate 1000-1900 m asl, and (iii) warm to cool temperate – and subalpine zones 2000-4000 m asl. There were strong and significant positive correlations between area, species pool, and plot richness from 2-4000 m asl, but there were no positive correlations between area and local plot richness in the two datasets below 2000 m asl; one had positive and the other negative correlations between species pool and plot richness. The strong echo effect at higher elevations is caused by both spatial and temporal dimensions. The species pool declines because of a simultaneously decreasing spatial extension and length of growing season above the subtropical zone.

117B Comparing climate and land use change scenario predictions of the future range of an invasive species

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Climate change and land use change threaten biodiversity and have a major influence on species distributions. While many species are negatively affected by these drivers of change, invasive species are likely to thrive in ecosystems disturbed by urbanization and climate change due to their ability to capitalize on marginal habitats. We model mute swan (*Cygnus olor*) distribution in its non-native range of Ontario (Canada) using a generalized linear model and MaxEnt. We then predict mute swan distribution in 2050 utilizing ensemble forecasting of different scenarios of climate change and land use change. The magnitude of range expansion predicted by climate change and land use change scenarios significantly differ. As urban areas expand, the probability of mute swan occupancy of these areas also increases. However, this is a relatively localized function whereby the changes in location are only noticeable in the direct vicinity of current urban areas. In comparison, ensemble forecasting of climate change scenarios predict a significant increase in the number of sites with suitable habitat for mute swans. Both generalized linear models and MaxEnt indicate a range expansion of the mute swan northwards by 2050. This has significant implications for invasive species management as efforts should focus on preparing management strategies for mute swans in areas that are currently outside of its range and these strategies should specifically focus on urban areas at the northern range limits of this species.

Keywords*:* MaxEnt, range expansion, species distribution models, urbanization

118B Forest climate requirements change through species life history

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Biogeographic responses of plant species to climate change are determined by the requirements of juveniles, which can limit spread to new environments. By contrast, most models of climate response are calibrated to adults, which may not reflect the climate that determined their original establishment. Despite a large literature showing environmental requirements change through life history for animals, there is little direct evidence from plants that could provide insight on its consequences for climate-mediated migration potential. Using USDA Forest Service's Forest Inventory and Analysis data, we built a species distribution model to jointly quantify juvenile and adult trees' abundance distributions in relationship with the two most commonly used climate variables - temperature and precipitation. By comparing the differences between juvenile and adult response surfaces, we found that most species have higher temperature optima in adults than juveniles, and adults have narrower breadths than juveniles in their abundance-climate relationships. This pattern is consistent with the recruitment filtering hypothesis, in which seeds are often dispersed to more sites than are suitable for establishment, as adults may experience a range of abiotic and biotic limiting factors in their development. We demonstrate for a large number of species across the eastern United States how climate calibrations of both adults and juveniles are impacted by climate change and the emerging role of new competitive environments.

Keywords: abundance-climate relationship, biogeography, Forest Inventory and Analysis, species distribution model, tree migration

121B Quantifying Quaternary climate change in the Tropical Andes using non-biting midges (Chironomidae)

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Palaeoclimate records are critical to determining past climate change magnitude and impact upon the environment. However long-term (>1,000 year) quantitative records from the tropical Andes are scarce due to a low density of study sites and the lack of application of palaeoclimate proxies. One such unused palaeoclimate proxy in the Tropical Andes is Chironomidae (non-biting midges). The method has been successfully used to reconstruct temperature elsewhere in the world.Chironomidae is a family of two-winged aquatic insects of the order Diptera (midges). They occur across a range of habitats, are globally distributed and are one of the most diverse families within aquatic ecosystems. The modern distribution is predominantly driven by summer air temperature and the head capsules of chironomid larvae are well preserved in lake sediments. Consequently, Chironomidae fossils have been used as palaeoclimate proxies extensively throughout the Northern Hemisphere, producing low error estimates of summer air temperature. This project aims to develop the first modern environmental calibration set in order to understand the main drivers of chironomid species distribution across the tropical Andes. Using surface sediments from c. 80 lakes from Bolivia to Columbia (20°S - 5°N) across a broad altitudinal range (100-4000 m.a.s.l), we have begun to characterise the Andean chironomid fauna and determine the influence of key environmental variables: temperature, pH, water depth and salinity. This information will be used to formulate a chironomid-based inference model which will be applied to fossil chironomid sequences from the Andes to reconstruct past climate conditions.

Keywords: South America, Palaeoclimate, Transfer function, temperature, limnology

122B Building up the biota in novel environments: insights using the fossil record of epeiric seas

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Throughout the Phanerozoic, times of rising sea level were often accompanied by the development of shallow seas on the continents. These epeiric seas formed relatively rapidly in geologic time and differed physically from open marine habitats, with shallower depths and altered salinity, temperature, and circulation. The build-up of diversity within these new habitats must result from one or more of the following processes: uninhibited dispersal of open marine taxa, limited dispersal with ecological filtering of open marine taxa, and one or more rounds of *in situ* speciation. The paleontological record allows discrimination between these processes and additionally chronicles any accompanying anagenesis. Despite the extensive representation of epeiric seas in the fossil record, little has been done to characterize and determine the source of epeiric biotas. My focus is on ammonites in the Late Cretaceous, characterized by high sea levels and inland flooding, including creation of a seaway across North America between the Arctic Ocean and the Caribbean Sea. Ammonites are an ideal study group because they are fast evolving, abundant and wellpreserved – features that allow for fine temporal and spatial control. Using geographic and temporal distributions and body size data for over 500 species of ammonite, I present spatial patterns in diversity and ecology of Cretaceous ammonites across epeiric and non-epeiric habitats to determine the relative importance of the various processes that build diversity in novel environments.

Keywords: biogeography, Cretaceous, marine ecosystem, paleobiology

123B Giant goblins on a sunken island? Biogeography of the spider family Orsolobidae

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The islands that made up Gondwana have provided some of the most striking examples of the role of ancient vicariance in shaping biodiversity. However, recent arguments point to a much larger role of recent dispersal events, with some suggesting that islands such as New Zealand, were “drowned” in the Oligocene. Here, we address the role of vicariance versus dispersal in the biogeography of the Gondwanan spider family Orsolobidae, which has its greatest diversity in New Zealand. We use a dataset of 6 genes, protein coding and ribosomal, mitochondrial and nuclear, from representatives of more than half Orsolobid genera and numerous outgroups. We present a dated phylogeny using maximum likelihood and Bayesian methods. We discuss the implications of our results for the vicariance vs. dispersal hypotheses for the distribution of this spider family, as well as for the idea that New Zealand was “drowned” during the middle Tertiary.

Keywords: Godwanan distribution, “drowned” New Zealand hypothesis, molecular phylogenetics

124B Oregon’s orphan redwood: A potential late-Holocene disjunction of *Sequoia sempervirens* 250 km north of its extant distribution

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A large *Sequoia* stump occurring upright on an Oregon beach, 257 km from the northern limit of its native distribution, may be a remnant of an extinct disjunct population or it may be the result of vertical emplacement of a drift log. Holocene tree stumps *in situ* in paleosols commonly emerge on the shore platform as a result of a complex history of subsidence, dune activity, and erosion. An historical account reported organic soils associated with the stump during the late 1800s; such soils are normally quickly removed by wave action after exposure. We used several methods to corroborate this account. The stump’s *in situ* origin is supported by 1) a radiocarbon age indicating a death date between 1820 and 1720 years ago, coeval with other paleosols and *in situ* stumps, 2) its height and upright position, which are only matched by other *in situ* stumps, and 3) a photograph from 1912 showing uneroded wood inconsistent with a sea-drift history. In addition, paleoclimate data suggest atmospheric circulation patterns during the late Holocene that would have ameliorated freezing injury at *Sequoia’s* northern limit. However, the sparse paleocological record is insufficient to corroborate an *in situ* origin. The only support for a sea-drift origin is that its age slightly predates a known tsunami that may have emplaced the stump. The balance of evidence suggests that the *Sequoia* stump is a remnant of an extinct late-Holocene disjunct population. This suggests a much more dynamic biogeographic history of *Sequoia* than previously understood.

Keywords: Cascadia; driftwood; late-Holocene; redwood; subduction zone earthquakes

125B The effects of the Late Quaternary glacial-interglacial cycles on Anatolian ground squirrels: range expansion during the glacial periods?

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In this study, the main aim was to understand how Anatolian ground squirrels, *Spermophilus xanthoprymnus* (Bennett, 1835), have responded to global climate changes through the Late Quaternary glacial-interglacial cycles. For this, I used ecological niche modelling, together with molecular phylogeography. Using species occurrence data compiled from field observations and relevant sources and the maximum entropy machine learning algorithm in MAXENT software, I developed an ecological niche model to predict the potential geographic distribution of *S. xanthoprymnus* under reconstructed past (the last interglacial, ~ 130 000 to 116 000 years ago and the last glacial maximum, 21 000 years ago) and present (1950 to 2000) bioclimatic conditions. In addition, using cytochrome *b* mitochondrial DNA sequences deposited in GenBank and the Bayesian skyline plot in BEAST software, I further assessed demographic events (population fluctuations) over the history of Anatolian ground squirrels. Combined ecological niche modelling and molecular phylogeography revealed that *S. xanthoprymnus*, itself also a temperate (mid-latitude) species, has responded to global climate changes through the Late Quaternary glacial-interglacial cycles in a fashion converse to that of most temperate (mid-latitude) species, that is, its range expanded rather than contracted during the glacial periods and contracted rather than expanded during the interglacial periods. In other words, Anatolian ground squirrels have been in refugia during the interglacial periods, suggesting that the classical paradigm of glacial range contraction and interglacial range expansion for temperate species may not be as general as previously thought.

Keywords: ecological niche modelling, global climate changes, last glacial maximum, last interglacial, molecular phylogeography

126B Climate and vegetation in a putative Pleistocene refugium in northern Idaho inferred from a 200,000-year sediment record

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The interior mesic forests of northern Idaho's Rocky Mountains are unique because they support more than 100 vascular plant species disjunct from their main distribution along the Pacific Northwest coast. The uplift of the Cascade Mountains during the Miocene led to the development of a disjunct interior mesic climate in the northern Rocky Mountains. The interior mesic climate is separated from the coastal mesic climate due to the rain shadow that developed from this orogeny. It is unclear how and when the associated disjunctions within the interior mesic climate were established. Specifically, it is unclear whether most species with an inland disjunction, including *Thuja,* survived the glacial periods of the Pleistocene in their present locations or whether they more recently dispersed from coastal areas. Recent phylogeography and modern distribution studies suggest that a mesic refugium may have existed in deep river canyons of northern Idaho. A ca. 200,000 year sediment record was recovered from Star Meadows, a paleomeander of the Lochsa River, located within the proposed refugium. Pollen recovered from this sediment record provides evidence for changes in forest composition that occurred in conjunction with changing climatic conditions since the pre-Illinoian A (MIS 7a) interglacial. Preliminary results from pollen analysis indicate the forest composition during previous interglacials was very different than the mesic-adapted vegetation of the current interglacial. A late-Holocene arrival of *Thuja* to the region suggests a recent dispersal from coastal areas. This sediment record is indispensible in our understanding of Pleistocene climates in western North America.

Keywords: Pleistocene, fossils, paleoecology, pollen, Idaho

127B Using the Quaternary fossil record to understand the spatiotemporal richness of Caribbean lizard communities

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Without temporal data, we are forced to reconstruct historic processes by the investigation of 'snapshots' of present patterns of biological diversity. Use of fossil data permit 'moving pictures' of diversity through time, and the revolutions of paleogenetics now permit us to unambiguously determine which species were where through millennia. An understanding of historic biogeographic patterns will help define phenomena such as vicariance and dispersal in the establishment of biodiversity. The Caribbean herpetofauna provide a wealth of replicate tests of vicariance and dispersal for many species across many islands. Lizards of several genera, including the iconic *Anolis*, are richly diverse, are adapted to a broad variety of habitats, are widely distributed across the archipelago, and occupy islands of every substrate and size. Here, we examine paleontological data from Anguilla, an island whose fauna is derived from the Anguillan bank, a significantly larger oceanic island that has been fragmented since the Late Pleistocene. While statistical analyses, morphometric identifications, and preliminary ancient DNA data reveal a rich paleocommunity, we found no evidence of *Anolis pogus*, a species thought to be extirpated from present-day Anguilla. These data suggest that the range of *Anolis pogus* was more limited in the past than previously thought. We believe that additional paleontological excavations, specifically in the Lesser Antilles, are required to understand fully the spatiotemporal species richness of lizards in the Caribbean.

Keywords: *island biogeography, paleobiology, paleogenetics,*

128B New insights into the evolutionary histories behind the Irano-Turanian and the Mediterranean floristic regions and their interactions: spatial and temporal patterns from a xerophyte (citrus family: *Haplophyllum*)

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The Irano-Tranian (I-T) floristic region is characterized by a high number of endemic genera and species. Despite its potential role as a source of xerophytic species for neighboring regions (*i.e.* Mediterranean region), the I-T region remains poorly studied. The aim of this study is to test various biogeographic scenarios, *i.e.* to investigate if the I-T region has been a potential source for the colonization of the Mediterranean region. We thus focused on *Haplophyllum* (citrus family), which is used to characterize the I-T region. Due to the fact that *Haplophyllum* contains species present in the Mediterranean region, it can be used to explore the biogeographic links between the two floristic regions. We performed molecular dating and ancestral range reconstructions analyses to investigate the extent to which past geological and climatic events of the regions explain the current distribution of the genus. Our results strongly suggest that *Haplophyllum* originated in the Central Asian part of the I-T region in the early Eocene and started to diversify within this region in the early Oligocene. At the latter epoch, the Tethys sea vanished and the Paratethys and the Mediterranean seas arose. *Haplophyllum* subsequently migrated to the Mediterranean basin in the middle Miocene during the Paratethys salinity crisis. Our study shows that the I-T floristic region can be a "donor" of xerophytic species to the "recipient" neighboring regions. The I-T floristic region thus requires serious conservation strategies by the governments of the countries that have the privilege to host its major evolutionary and biodiversity centers.

Keywords: Irano-Turanian, Mediterranean, floristic region, xerophytic, *Haplophyllum*

129B Founder-event speciation in BioGeoBEARS package dramatically improves likelihoods and alters parameter inference in Dispersal-Extinction-Cladogenesis (DEC) analyses

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Probabilistic modeling of geographic range evolution was a major advance in historical biogeography, making biogeographical problems accessible to model-based maximum likelihood (ML) and Bayesian methodologies. The most popular model is Dispersal-Extinction-Cladogenesis (DEC), implemented in the software LAGRANGE (Ree & Smith 2008). Standard DEC is a model with two free parameters specifying the rate of "dispersal" (range expansion) and "extinction" (range contraction). However, while dispersal and extinction rates are free parameters, the cladogenesis model is fixed, such that the geographic range of the ancestral lineage is inherited by the two daughter lineages through a variety of scenarios fixed to have equal probability. This fixed nature of the cladogenesis model means that it has been indiscriminately applied in all DEC analyses, and has not been subjected to any inference or formal model testing. I re-implement DEC in my R package BioGeoBEARS, which exactly reproduces LAGRANGE 2-parameter inferences and likelihoods. However, BioGeoBEARS also allows additional parameters controlling the probability of new cladogenesis models, such as "founder-event speciation", in which one daughter jumps to an area completely outside the ancestral range. The effects are dramatic in several test datasets. For example, for Hawaiian *Psychotria*, the original test clade for LAGRANGE, addition of founder-event speciation to a geographically unconstrained analysis improves the log-likelihood from -34.5 to -20.9, and the ML inferences for dispersal and extinction rates are moved to zero. The 3-parameter model is 300490 times more probable in terms of relative AIC weight. Thus, careful consideration of cladogenesis models in historical biogeography is recommended.

Keywords: cladogenesis, historical biogeography, LAGRANGE, model-testing, speciation

130B (Paleo-)Biogeography of *Polylepis* spp. woodlands in the Ecuadorian Andes (South America)

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Polylepis is the highest-growing tree genus in the world, forming woodland patches up to 4000 m elevation from Venezuela to Chile. The present distribution pattern of these woodlands has been attributed to deforestation, fires, and past climate change. In addition, estimates of past woodland extent vary widely, from near-continuous woodland belts to the long-term persistence of interconnected patches. Here, we present a compilation of published fossil pollen records from the Ecuadorian Andes, using this information to draw inferences about the paleo-biogeography and dynamics of *Polylepis* woodlands.

Among more than 20 records reviewed, only 6 sequences included information about the past trends of *Polylepis* distribution and its relationships with the environment. These studies show that the establishment of *Polylepis* woodlands has been asynchronous since the Last Glacial Maximum (LGM, c. 21500 yr ago), and that the maximum local abundances of this genus were attained at different time periods, under different climatic conditions, and coeval or not to the presence of fires. Instead, local area features (e.g., slope, edaphic conditions) and micro-climate conditions seem to have played a major role. None of the studies support the hypothesis of a continuous cover of these woodlands in the past. In addition, Andean records from outside Ecuador have been added to infer a common pattern. The ecological, socio-cultural and economic value of *Polylepis* makes mandatory more paleoecological research into the main drivers involved in its abundance changes.

Keywords: climate, edaphic conditions, fires, paleoecolgy

131B Comparing climatic and biotic velocities for woody taxa distributions over the last 16,000 years in eastern North America

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We estimated the latitudinal velocity (km/decade) of the northern and southern boundaries of core distributions for 30 woody taxa over the last 16,000 years (16ka) using networks of fossil pollen records and compared these to climate velocities estimated from CCSM3 simulations. Biotic velocities were faster during periods of rapid climatic change (16-to-10ka: -0.6 to 3km/decade) than times of climatic stability (10-to-0ka: -0.6 to 2km/decade), with a consistent northward movement of the core distributions northern and southern boundaries. Northward Biotic velocities were faster for northern boundaries than for southern boundaries, resulting in expanding distributions for 35 to 86% of taxa. For individual time periods, the association between biotic and climatic velocity was qualitatively but not quantitatively significant across taxa. These results support the MacArthur hypothesis that poleward populations are climate-limited distributions, particularly for northern populations, and that climate change paced the rates of biotic velocity and within-range shifts in population abundances. A similar sensitivity and pacing is expected during 21st-century climate change.

Keywords: Biotic velocity, climate change, climate velocity, Holocene, paleoecology, Pleistocene, pollen, Quaternary, species distributions

132B The palaeobiogeographical history of the Western Mediterranean before the Quaternary: decoding biotic evidence

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Because of its high level of biodiversity and rate of regional endemism in both the present and past, the Mediterranean Basin is a hotspot for biogeographical studies. Mediterranean geology has been shaped by the interplay between the African and European plates along with smaller intervening microplates. The evolution of the Western Mediterranean Basin started about 30 Ma due to migration of orogenic belts and widespread extensional tectonics of back-arc basins. This complex geological history caused repeated isolations/connections of insular and mainland territories that led to a peculiar biogeographical history of the main insular realms (Balearic, Sardinia and Sicily islands, Tusco-Sardinia, and Abruzzi–Apulia palaeobioprovinces). Although few African lineages have been claimed to be present in Sardinia, most of Balearic, Tusco-Sardinian and Abruzzi–Apulian settlers had a European origin, while Sicily, an island since the Late Pliocene, and Southern Calabria were parts of a mainland, extending at the northern border of the African plate. The patterns of faunal evolution mainly depend on palaeogeographical control, resulting from the interaction of geodynamic events and marked sea level fluctuations, e.g. at the time of the Messinian Salinity Crisis. Reconstructing timing, modes and "routes" of dispersal is a challenging task. Alternating connections with the Paratethys played a prominent role in the distribution of non-marine and marine molluscs. Insights from plants suggest that part of the modern genetic structure of Mediterranean populations may be traced back to the Tertiary history of taxa, which could help in delineating pre-Quaternary palaeobiogeographic scenarios.

133B Body size and geographic distribution of the extinct shark Megalodon (*Carcharcoles megalodon*)

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Carcharocles megalodon is the biggest shark that ever existed. It lived from 18 to 2 million years ago. The reasons of its extinction are still unknown. Fossils of *C. megalodon* are found worldwide, including the Gatun Formation of Panama. Based on the high frequency of juveniles, we proposed that the Gatun Formation was a nursery habitat for this species. Ontogeny is difficult to assess in the fossil record; therefore, to be able to separate adults from juveniles, we developed a series of teeth comparisons using collections from different time periods. We found that size of *C. megalodon* does not change over geologic time. This is surprising because it is widely stated in the literature that there is a tendency in some animals to become larger through time. We want to test the hypothesis that, contrary to a gradual increase in size, *C. megalodon* exhibits stasis. Accordingly, measurement comparisons of fossil collections from different ages around the world will be made. Additionally, all occurrences will be mapped using the paleobiology database. This will allow determination of patterns in global distribution over time. Furthermore, the identification of the relationships between body size and geographic distribution will enhance the understanding of the extinction of this shark. It is important to know what could lead to the extinction *C. megalodon* because it was an apex predator. The removal of apex predators has catastrophic effects in all trophic levels. Knowing why *C. megalodon* became extinct will provide critical information for the conservation of modern sharks.

Keywords: conservation paleobiology, extinction, gigantism, paleoecology, paleobiogeography

134B Studies on temporal and spatial changes of forest in Shanxi

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Areal coverage of Shanxi forest formations in both 1984 and 2005 were calculated in ArcGIS from map and attribution data. Successional and other changes, and changes in coverage and distribution of the forest formations were studied with overlay analysis methods. Forest is spatially concentrated in southwest Shanxi and dispersed in other parts of the province. Much increase of forest was observed in northwest Shanxi, which was formerly steppe; the reason was a government policy of planting many trees in order to protect the environment. The area and range of *Pinus tabulaeformis* forest was greatest across all forest formations, andincreased and extended into northeast Shanxi, which was formerly scrub. Of the other forest formations, areas of *Quercus liaotungensis* forest, *Populus simonii* forest and *Populus davidiana*/*Betula platyphylla* forest were biggest; the first two of these increased, but the last one decreased, over the 21 years. *Quercus liaotungensis* and *Populus simonii* were planted into scrub and herbaceous vegetation respectively, causing the increases. *Populus davidiana*/ *Betula platyphylla* forest decrease both because of human-caused conversion to scrub and because *Pinus tabulaeformis* was planted into it and became dominant.

Keywords: change, distributions, formations of forest, time

135B Untangling the climatic signal of the hemlock decline (*Tsuga canadensis*): a species distribution modelling approach

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The mid-Holocene hemlock decline is one of the most intensively studied palaeoecological events. Marked by a steep decline in pollen percentages across North America ca. 5,500 years ago, the hemlock decline occurred in less than a century, and in some places in even less than a decade. Whilst one study concluded that a pest or pathogen outbreak was the most likely explanation, several others have raised the possibility that droughts played an important role. If so, the hemlock decline may be an important ancient counterpart to the drought-and pest-induced tree mortality events that are becoming increasingly widespread. This study uses a suite of species distribution models (SDMs) to predict the distribution of hemlock at three time intervals (6 ka, 4 ka, and 0 ka) over the Holocene. Pollen data from sites across its contemporary range are calibrated against palaeoclimate data from a Global Climate Model (GCM) at approximately 1° resolution. The parameters from the 6 ka model are used to predict the hemlock range at 4 ka, and at 0 ka using the equivalent GCM output. This process is repeated for each of the models at each of the timesteps involved. Pollen distributions from the equivalent time steps are then used to test model performance. The study then investigates two research questions; i) Can the 6 ka and 0 ka species distribution models be used to predict hemlock distribution at 4 ka, at a time when abundance is known to have been low? ii) is niche conservatism between time periods observed?

Keywords: hemlock decline, palaeoecology, species distribution modeling, climate change, fundamental niche

136B Biogeographic anomalies in the species richness of Chilean forests: incorporating evolution into a climatic-historic scenario

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Broad-scale richness gradients are closely associated with temperature and water availability. However, historical and evolutionary processes must also contribute to current diversity patterns. In this paper we focus on the potential influences of Pleistocene glaciation and niche conservatism on the tree diversity gradient in Chile. We also quantify the primary climatic correlates. Tree species richness is greatest at mid-latitudes, particularly in the Andes and coastal ranges, and decreases abruptly to the south and north. Regression tree analysis identified annual precipitation and annual temperature as the probable primary drivers of this pattern. Ice cover during the Last Glacial Maximum was also identified as an “important” variable, but the contemporary and historical predictors are strongly collinear. Geographically weighted regression also indicated that the relationship between richness and environmental variables is non-stationary: the relationship between tree richness and precipitation is stronger in north-central Chile; whereas tree richness and temperature is most strongly associated in south-central Chile. By assigning each species the age of the family to which it belongs and averaging all species in each geographical unit, we also found that species from the oldest families are distributed mainly in mid to high latitudes, and species from younger families are distributed mainly at lower latitudes. This pattern is closely associated with annual precipitation. Thus, the ecological component of tree richness follows contemporary climatic gradients of both energy and water, but aridification of the Atacama Desert was an important driver over evolutionary time. The influence of recent Pleistocene glaciation remains unresolved but cannot be discounted.

Keywords: Climate–richness relationships, diversity gradients, Pleistocene glaciations, tropical conservatism hypothesis

137B Forest distribution on mountains in the dryland of China: modern and historical points of view

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Marginal forests in dryland environments are very sensitive to climate change. We systematically studied forest distribution on mountains in the dryland of China, including Mt. Dahaituo, Mt. Xiaowutai, Mt. Liupan where the forest-steppe ecotone is located and Mt. Qilian with forest-steppe transitional vegetation as a vertical belt. Local observations showed that forest distribution was determined by slope (gradient, aspect) and soil (thickness). A model simulation indicated that a minimum soil thickness of 70 cm on shady slopes can provide sufficient soil water for forest distribution. Based on palaeoecological works in previous studies, the history of soil erosion and vegetation development was reconstructed. Sediment grain size showed that soil erosion in the forest-steppe ecotone had become strong with climatic drying between 5 and 2 ka BP. During this period, forest vegetation was still dominated this region, but deciduous forests were replaced by conifers (pine). It is likely that low forest cover of pine forest had enhanced soil erosion. During the last 2000 years, human logging of forests has led to decreased forest cover, but expansion of shrubs has prevented soil erosion. We predict that reduction in vegetation cover under climatic drying will accelerate forest retreat in this region. If the final loss of forests is followed by substantial soil erosion in this region as modeled, redistribution of forests will become even more difficult. Our results imply that forest management in this region should focus on preventing soil erosion.

Keywords: soil erosion, Holocene, climate drying, forest redistribution

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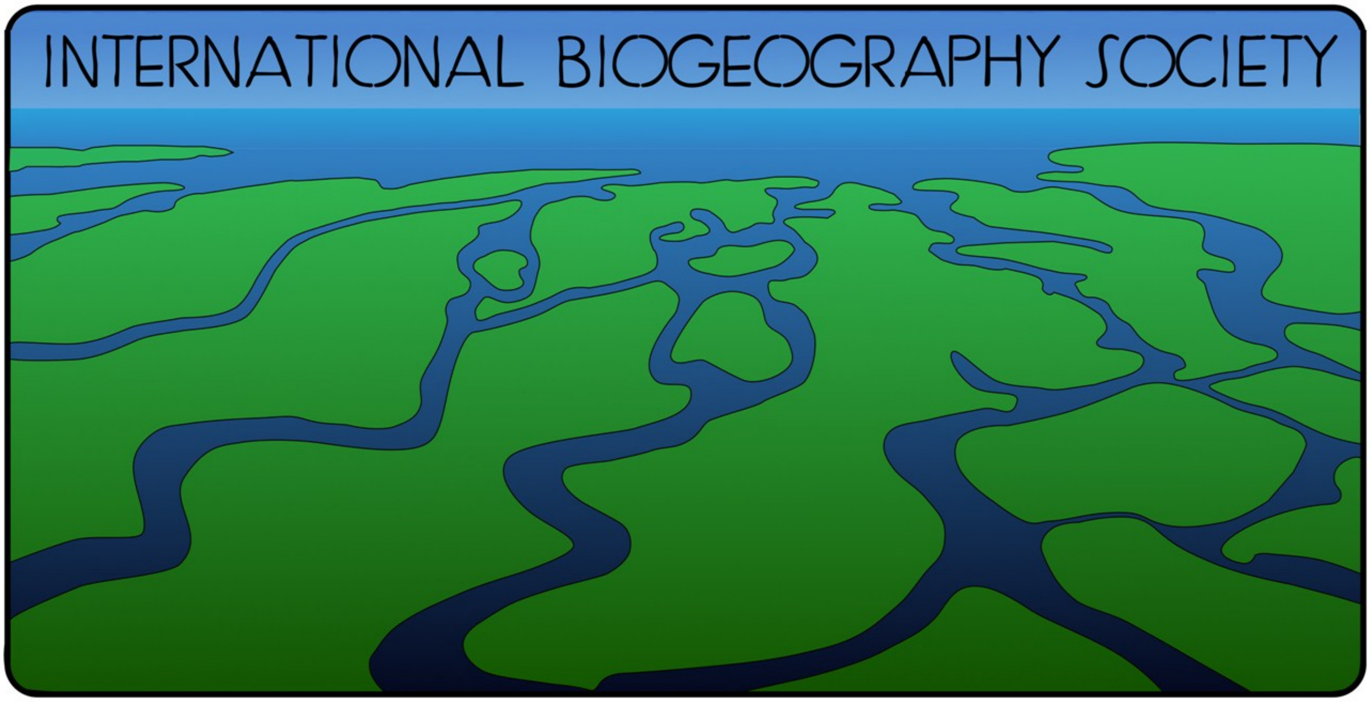

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