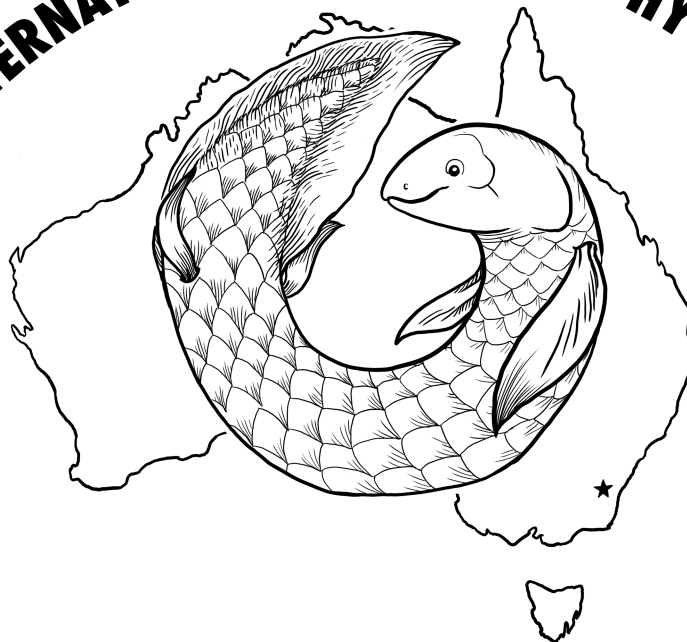


INTERNATIONAL BIOGEOGRAPHY SOCIETY



**EARLY CAREER CONFERENCE
CANBERRA 2014**

Australian National University

7-11 January, 2014

Conference Program
&
Presentation Abstracts

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ANU Commons, Rimmer Street, Corner Barry Drive and Marcus Clarke Street, Acton
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Workshops

January 7, 2014

Introduction to species distribution modelling

Presenters: Jane Elith (University of Melbourne), Yung En Chee (University of Melbourne), Dan Warren (ANU)

Modelling compositional turnover using generalised dissimilarity modelling

Presenters: Dan Rosauer (ANU) and Karel Mokany (CSIRO Ecosystem Sciences)

An Introduction to R for beginners

Presenter: Rob Lanfear (ANU)

Free your mind: Model comparison and model testing in historical biogeography with the R package 'BioGeoBEARS'

Presenter: Nick Matzke (UC Berkeley)

Species distribution across time and space

January 8, 2014

| Time | Presenter's Name | Title of Presentation |
|--------------------|--------------------------------|---|
| 08:50-09:00 | Conference Opening | |
| 09:00-09:30 | Michael Kearney | Keynote: The Thermodynamic Niche – physiologically based models of climatic constraints on animals |
| 09:30-09:45 | Matthew Van Dam | Natural History Matters in Climate Niche Modeling |
| 09:45-10:00 | Michael B Ashcroft | Topoclimatic grids of extreme temperatures explain the distribution of the endangered brush-tailed rock-wallaby (<i>Petrogale penicillata</i>) |
| 10:00-10:15 | David Nogués-Bravo | Niche Evolution of Modern Humans During the Late Pleistocene |
| 10:15-10:30 | Valeria Di Cola | Ecological and evolutionary drivers of the environmental niche of Neotropical snakes |
| 10:30-10:45 | Robert Koch | Modeling Caatinga plant species in a semi-arid area of northeast Brazil with MaxEnt |
| 10:45-11:00 | Jesper Sonne | Hotspots of range-restricted species is tightly linked to climate and specialization in plant-hummingbird networks across the New World |
| 11:00-11:30 | Coffee break | |
| 11:30-11:45 | Mariana Munguía | Selecting Indicator Traits for monitoring Landscape degradation of Mammals in Mexico |
| 11:45-12:00 | Morgane Barbet-Massin | Species distribution modeling: choosing relevant climate predictors for better accuracy? |
| 12:00-12:15 | Sara Pinzon-Navarro | Can Acacia distribution predict the distribution of their seed feeding weevil? |
| 12:15-12:30 | Diego R. Barneche | Scaling metabolism from individuals to reef-fish communities at the global scale |
| 12:30-12:45 | Osmar Luiz | Adult and larval traits as determinants of geographic range size among tropical reef fishes |
| 12:45-13:00 | Alicia Sutton | Drivers of krill zoogeography in the Indian Ocean: the implications of poleward flowing boundary currents |
| 13:00-14:00 | Lunch | |
| 14:00-14:15 | Jan Laurens Geffert | Known unknowns: Correcting for sampling bias in marine species distribution models |
| 14:15-14:30 | Dan L. Warren | Incorporating evolutionary history into niche and distribution modeling |
| 14:30-14:45 | William Godsoe | Information on biotic interactions improves transferability of distribution models |
| 14:45-15:00 | Sabela Lois | Integrating parasite-host interactions in distribution and abundance models to understand spatial patterns and to address conservation of an endangered freshwater mussel and its hosts |
| 15:00-15:15 | Paulo Henrique Chaves Cordeiro | Modelling the distribution of <i>Formicivora serrana</i> complex (Aves:Passeriformes) in southeastern brazilian Atlantic Forest during the Late Quaternary |
| 15:15-15:30 | Jessica A. Oswald | Biogeography and extinction of New World passerines: evidence from Pleistocene fossils |
| 15:30-15:45 | Malte Semmler | Uncovering determining factors for Holocene vegetation pattern in central Europe |

Species distribution across time and space
January 8, 2014

| Time | Presenter's Name | Title of Presentation |
|--------------------|--------------------------------|---|
| 15:45-16:00 | Spyros Theodoridis | Integrating paleodistribution modeling and next generation statistical phylogeography to explain the effects of Quaternary climatic oscillations in alpine-arctic plants |
| 16:00-16:30 | Coffee break | |
| 16:30-17:00 | Catherine Graham | Keynote: Comparing taxonomic, phylogenetic and functional dimensions of diversity in Andean Hummingbirds |
| | Lightning Talks session | |
| 17:00-17:05 | Anders Bryn | Splitting of mosaic vegetation type polygons using maximum entropy modelling |
| 17:05-17:10 | Anna L. Carter | Modelled thermal environment informs sex ratio predictions in New Zealand tuatara |
| 17:10-17:15 | Fabio Avila | Finding biogeographic patterns in Neotropical species of Macadamieae and Gevuiniinae (Proteaceae) |
| 17:15-17:20 | Wun Ho | A framework for understanding niche dynamics of invasive species through reciprocal distribution modeling |
| 17:20-17:25 | Hanieh Saeedi | Global biodiversity and biogeography of razor clams |
| 17:25-17:30 | Anders K Wollan | Scale-dependence of vascular plant distributional patterns: a multi-scale study |
| 17:30-17:35 | Marwa Halmy | Modeling the distribution of plant communities of Moghra Oasis |
| 17:40-18:40 | Poster session | |
| | Jorge Ari Noriega | 24 years since the arrival of the invasive dung beetle <i>Digitonthophagus gazella</i> (Coleoptera: Scarabaeidae) to South America: dispersion process and population effects on native species |
| | Yasmin Hageer | Prediction of the distribution of arid shrublands in Australia as a function of climate |
| | Buntarou Kusumoto | Plant diversity hotspot as a historical product under imminent threats |
| | Mora Franz | A methodology to estimate Extinction Debt for Mammals in a Fragmented landscape of Mexico |
| | Ana Catarina Silva | Ecological niche modelling and phylogeography of two sister species with different thermal ranges |
| | Constantino González-Salazar | Estimating trophic complexity of predator-prey interactions in a fragmented landscape using complex network and species distribution models |
| | Andreas Schweiger | Monitoring of helocrenic forest springs as a solution to the riddle of regional-scale climate change effects |

Advances in phylogenetic methods for biogeography January 9, 2014

| Time | Presenter's Name | Title of Presentation |
|--------------------|-------------------------|---|
| 09:00-09:30 | Craig Moritz | Keynote: Phylogenomics at the tips - improving knowledge of diversity and understanding of its evolutionary dynamics |
| 09:30-09:45 | Emmanuel F.A. Toussaint | Unveiling the Diversification Dynamics of Australasian Predaceous Diving Beetles in the Cenozoic |
| 09:45-10:00 | Mericien Venzon | Not so hot spots? High speciation rates do not explain reef fish species richness in the Coral Triangle or other marine hotspots |
| 10:00-10:15 | Julie Ardley | Do rhizobia have biogeography? |
| 10:15-10:30 | Peter F. Cowman | Vicariance across major marine biogeographic barriers: temporal concordance and the relative intensity of hard versus soft barriers |
| 10:30-10:45 | Hannah L. Owens | Incorporating Phylogenetics and Ecological Niche Modeling for Biogeographic Analysis |
| 10:45-11:00 | Mitzy Pepper | Ancient rocks and drainages divide recent gecko species in Australia's arid zone |
| 11:00-11:30 | Coffee break | |
| 11:30-11:45 | Robert M. Kooyman | Landscape patterns in rainforest phylogenetic and functional signals: the biogeography of isolation and continental distributions |
| 11:45-12:00 | Tyrone Lavery | <i>Hippo</i> -critical bats: genetics contradict morphology in the identification of Solomon Island <i>Hipposideros</i> species |
| 12:00-12:15 | Andreia Miraldo | Competitive Release Leads to Range Expansion and Rampant Speciation in Malagasy Dung Beetles |
| 12:15-12:30 | Jahnavi Joshi | Did southern Western Ghats of peninsular India serve as refugia for its endemic biota during the Cretaceous volcanism? |
| 12:30-12:45 | Kate Hodges | The biogeography of hybridisation in east Australian long necked turtles |
| 12:45-13:00 | Xia Hua | Tracking the formation of a species assemblage over time: phylogenetic reconstruction of patterns of colonisation and speciation |
| 13:00-14:15 | Lunch | |
| 14:15-14:30 | Nicholas J. Matzke | Model selection reveals differences in cladogenesis processes operating in island versus continental clades |
| 14:30-14:45 | Sally Potter | Applying exon capture to study biogeographical processes shaping the diversity of the Australian monsoonal tropics. |
| 14:45-15:00 | Danilo Harms | Vicariance and the origins of diversity in arachnids – a case study from ancient pseudoscorpions |
| 15:00-15:15 | Peter Unmack | Using GIS to predict how changes in sea level potentially influence phylogeographic patterns in freshwater and coastal marine fishes |
| 15:15-15:30 | Alexander T. Xue | Population structure, demographic history, and signatures of selection among transposable elements in <i>Anolis carolinensis</i> |
| 15:30-15:45 | Fabricius Domingos | Phylogeography of a Cerrado endemic gecko: Using Species Distribution Modelling, Next-Generation Sequencing and morphology to disentangle complex phylogeographic scenarios |

Advances in phylogenetic methods for biogeography

January 9, 2014

| Time | Presenter's Name | Title of Presentation |
|--------------------|--|--|
| 15:45-16:00 | Eleanor Dormontt | How can biogeography inform on DNA timber tracking? |
| 16:00-16:30 | Coffee break | |
| 16:30-17:00 | Hélène Morlon | Keynote: Phylogenetic approaches for understanding how species are distributed in space and time |
| | Lightning Talks session | |
| 17:00-17:05 | Juan-Carlos Garcia-R | Phylogeographic analysis of the supertramp swampphen <i>Porphyrio porphyrio</i> (Aves: Rallidae): diversification and gene flow with emphasis on the Indo-Pacific region |
| 17:05-17:10 | Heidi Nistelberger | Comparative phylogeography of three, banded iron formation endemics from semi-arid Western Australia |
| 17:10-17:15 | David Duchene | Phylogenies reveal equilibrium processes along the latitudinal diversity gradient |
| 17:15-17:20 | Elisa Diana Ruiz Ramos | Does the 'island rule' apply for birds? An analysis of morphological variation between insular and mainland birds from the Australian, New Zealand and Antarctic region |
| 17:20-17:25 | Andrew Mather | Contrasting phylogeographic patterns of two co-distributed Australian freshwater rainbowfish |
| 17:25-17:30 | Jude Keyse | Patterns and predictors of genetic diversity within Indo-Pacific marine fauna. |
| 17:30-17:35 | Xiaolei Huang | Deciphering the disjunct biogeographical patterns of Mindarinae: ancestral in East Asia but recently radiated in North America |
| 17:40-18:40 | Poster session | |
| | Chandravilashini Shantha Hettiarachchi | Biogeography and Biodiversity of Sri Lanka |
| | Peter F Cowman | Coral reef fishes: the origins of biodiversity hotspots and biogeographic patterns |
| | Miyagi Yuuta | Identifying the relative importance of historical and ecological factors on global biodiversity pattern of Scleractinia corals |
| | Gabrielle Openshaw | Plans for Phylogeographic Analysis of a Widespread Australian Lizard |
| | C. Haris Saslis-Lagoudakis | Divergent lineages overlap in geographic ranges and climatic preferences in a biodiversity hotspot |
| | Cheng-Min Shi | Genetic legacy of Quaternary climate changes in temperate East Asia: insights from the phylogeography of Chinese scorpion, <i>Mesobuthus martensii</i> |
| | Mericien Venzon | Harnessing the Power of High-Throughput: Using Targeted Enrichment of DNA Ultraconserved Elements for the Phylogenomic Analysis of Coral Reef Fishes |
| | Luis Darcy Verde Arregoitia | Diversification, extinction and global conservation status of lagomorphs |

Biodiversity turnover across spatial scales

January 10, 2014

| Time | Presenter's Name | Title of Presentation |
|--------------------|--|--|
| 09:00-09:30 | Simon Ferrier | Keynote: Modelling compositional turnover for biodiversity conservation assessment |
| 09:30-09:45 | Leticia Margarita Ochoa Ochoa | Patterns of diversity differentiation (beta-diversity) and environmental heterogeneity |
| 09:45-10:00 | Hugh Burley | Beta diversity and ecosystem processes: a macroecological perspective |
| 10:00-10:15 | Andrew Letten | Tracking community stability through time: a phylogenetic and functional perspective |
| 10:15-10:30 | Giovanni Di Virgilio | Environmental predictors of reptile species turnover and endemism vary among local, regional and national scales, an example from New Zealand |
| 10:30-10:45 | Carlos. E. Gonzalez-Orozco | Environmental drivers of turnover define Australian phytogeographical regions |
| 10:45-11:00 | Dan F. Rosauer | Modelling phylogenetic beta diversity for conservation gap analysis |
| 11:00-11:30 | Coffee break | |
| 11:30-11:45 | Karel Mokany | The importance of dispersal for tropical forest biodiversity under climate change |
| 11:45-12:00 | Shawn W. Laffan | Measures of species and phylogenetic turnover weighted by range-restriction |
| 12:00-12:15 | Ivis Chan | Incorporating beta diversity into estimates of tree species loss in the Mesoamerican region |
| 12:15-12:30 | Thomas Davis | Changes in phylogenetic structure of a bird community along an elevational gradient, in Eastern NSW |
| 12:30-12:45 | Murilo S. Dias | Influence of past sea-level changes on global-scale patterns of freshwater fish beta diversity |
| 12:45-13:00 | Skipton N.C. Woolley | Turnover of deep-sea brittle stars (Ophiuroidea) across Australia, New Zealand and Antarctica |
| 13:00-14:15 | Lunch | |
| 14:15-14:30 | Cristiano Nogueira | Endemism, vicariance and distribution patterns of Cerrado herpetofauna (Brazil) |
| 14:30-14:45 | Anna W. McCallum | Towards a global biogeography of the deep seafloor using distributional data of squat lobsters |
| 14:45-15:00 | Lisa Pope | Marine genetic diversity and connectivity around Australia: a synthesis |
| 15:00-15:15 | Joanna Bugar | The value of ecology in conservation biogeography – elucidating bat community assembly patterns across a restored landscape in south-western Australia |
| 15:15-15:30 | Alejandro Ordonez | Climatic legacies in European plant functional diversity geographical patterns |
| 15:30-15:45 | Ceridwen Fraser | The race for new space: density-blocking masks dispersal and shapes biodiversity patterns |
| 15:45-16:00 | Jan O. Engler | Exploring moving range edges in parapatric distributed passerines: From climate, genes and biotic interactions |
| 16:00-16:30 | Coffee break | |
| 16:30-17:00 | Matthew Fitzpatrick | Keynote: Using community-level models to map current and future spatial patterns of adaptive genetic variation |
| 17:00-17:20 | Matthew Iacchei (Thesis Prize Winner) | Population genetic and phylogenetic insights into the phyllosomal odyssey |
| 17:20-17:30 | Wrap up - Prize giving | |

Keynotes presentations

Abstracts

The Thermodynamic Niche – physiologically based models of climatic constraints on animals

Michael Kearney

Department of Zoology, University of Melbourne

Climate influences the distribution and abundance of terrestrial animals in a rich variety of ways. Most directly, however, it imposes thermodynamic constraints on heat, water and nutritional balances. The sum of these constraints can be thought of as defining the 'thermodynamic niche'. I will discuss how the thermodynamic niche can be characterized using integrated models of the biophysics of animals and their microclimates, together with metabolic theory. I will show how the models can be coupled to weather and climate databases to predict constraints on animal survival, behaviour, phenology, growth, development and reproduction, and ultimately distribution limits.

Comparing taxonomic, phylogenetic and functional dimensions of diversity in Andean Hummingbirds

Catherine Graham¹, Ben Weinstein¹, Juan Parra²

¹*Department of Ecology and Evolution, Stony Brook University, Stony Brook, USA*

²*Department of Biology, University of Antioquia, Medellin, Colombia*

Different dimensions of diversity – such as taxonomic, phylogenetic and trait – alone or in combination can provide unique insights into the mechanisms that underlie current diversity. Simultaneous comparison of these dimensions may uncover the mechanisms, such as geographic isolation, environmental filtering, trait conservatism and convergent adaptation, which maintain and generate biodiversity. We explore the insights yielded by simultaneous comparison of dimensions for uncovering the mechanisms underlying patterns of betadiversity and for forecasting how assemblages might change with climate change. We focus largely on Andean hummingbirds. While we provide insight into the mechanisms governing biodiversity patterns in hummingbird assemblages of Northern South America, our framework is broadly applicable to other taxonomic groups.

Phylogenomics at the tips - improving knowledge of diversity and understanding of its evolutionary dynamics

Craig Moritz

Research School of Biology, Australian National University

Much of our current knowledge of diversity, biogeography and underlying processes of speciation and macroevolution starts with traditionally recognised morpho-species as units of analysis. Yet, for many taxa, multi-locus genetic analyses are revealing high levels of eco-morphological cryptic divergence, or species boundaries that are misconstrued because of parallel evolution of supposed diagnostic traits. As we scale-up from single-locus barcoding to a few independent loci, and with new next-gen sequencing tools to 100's or 1000's of loci, phylogenomic approaches to delineating evolutionary lineages and inferring their divergence history are becoming increasingly robust. Yet, it remains crucial to integrate phenotypic analyses with genome-lead discovery of lineage and phylogenetic diversity. Incorporating both sources of evidence suggests a stronger role for eco-morphologically cryptic speciation, reveals new hotspots of endemism, and could well affect interpretations of macroevolutionary dynamics.

Phylogenetic approaches for understanding how species are distributed in space and time

Hélène Morlon

CMAP, Ecole Polytechnique, Paris

The patterns of species distribution across geographical areas can be explained by past and current speciation, extinction and dispersal events, themselves influenced by various ecological and evolutionary processes. Estimating rates of diversification, and understanding how and why they vary over evolutionary time, geographical space, and species groups, is thus central to biogeographical studies. Phylogenetic approaches are critical for making such inferences, especially in groups or regions lacking fossil data. I will illustrate how phylogenies, coupled with models of cladogenesis, current species distribution data, macroecological patterns, and paleoenvironmental data, can be used to address long-lasting questions in biogeography, such as understanding the latitudinal gradient in species richness and how major environmental changes shaped the patterns of diversity that we observe today.

Modelling compositional turnover for biodiversity conservation assessment

Simon Ferrier¹, Kristen J Williams, Thomas D Harwood, Karel Mokany, Dan Rosauer²

¹*CSIRO Ecosystem Sciences, Australia, simon.ferrier@csiro.au*

²*Australian National University, Australia*

Interest in using modelling of spatial turnover in biological composition to inform conservation assessment and planning has grown rapidly over the past 10 years. Techniques such as generalised dissimilarity modelling (GDM) offer a cost-effective means of characterising, and mapping, compositional turnover across extensive regions by linking location records for large numbers of species to remotely derived environmental surfaces. Space-for-time substitution of predictions from these models is also being used increasingly to project potential impacts of climate and land-use change on biodiversity. In this talk I will provide an overview of the many different ways in which compositional-turnover modelling across space and time is now contributing to conservation assessment activities at regional, continental and global scales – including assessments of the representativeness of protected areas, the location of potential climate-change refugia, and the implications of alternative socio-economic pathways. I will then explore a number of emerging directions in compositional-turnover modelling including the incorporation of phylogenetic and metagenomic data, the integration of dynamic ecological processes into model-based projections of biodiversity change, and the use of paleo-ecological data to evaluate predictive performance.

Using community-level models to map current and future spatial patterns of adaptive genetic variation

Matthew C. Fitzpatrick¹, Stephen R. Keller¹

¹*University of Maryland Center for Environmental Science, Appalachian Laboratory, USA, mfitzpatrick@umces.edu*

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 – now and in the future. Similar challenges confront analyses of compositional turnover in diverse assemblages of species, some of which are rarely recorded. In this study, we explore how these challenges can be addressed using “community-level” modeling techniques 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 fish, trees, and humans as case studies, we demonstrate that novel application of community-level modeling methods offer unique strengths for exploring and mapping adaptive genomic variation that are complementary to or improve upon the currently available techniques in landscape genetics.

Species distribution across time and space

January 8, 2014

Abstracts

Natural History Matters in Climate Niche Modeling

Matthew H. Van Dam¹, Andrew J. Rominger², Michael S. Brewer³

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We explore how partitioning climate data by day influences niche model predictions, as estimated by the MaxEnt machine learning algorithm, of taxa with constrained phenologies. We compare the results with WorldClim data that is partitioned by month to examine what effect using more precise data has on species distribution models. We also compare two different taxa (*Rhaphiomidas* flies & *Trigonoscutea* weevils) that have different life history strategies for dealing with climate change. We examine how phylogenetic signal in both their life history traits and climate tolerances can tell us about how they adapt to different climates. Quantitative information about adaptation can be used to better inform projected range shifts and local extirpations.

Keywords: biogeography, phylogenetic signal, adaptation, climate change

Topoclimatic grids of extreme temperatures explain the distribution of the endangered brush-tailed rock-wallaby (*Petrogale penicillata*)

Michael B Ashcroft^{1,2}, Mike Cavanagh³, Mark D B Eldridge¹, John R Gollan^{1,4}

¹Australian Museum, Australia, Mick.Ashcroft@austmus.gov.au

²Australian Wetlands, Rivers and Landscapes Centre, UNSW, Australia

³NSW Office of Environment and Heritage, Australia

⁴University of Technology Sydney, Australia

Ecologists often estimate fine-scale climate based largely on elevation. This may be appropriate for mild conditions or long-term averages, but extremes are determined more by factors such as cold air drainage, canopy cover, and topographic exposure to winds and radiation. We used brush-tailed rock-wallabies (BTRW) in the Hunter Valley, NSW, Australia, to test whether innovative topoclimatic grids of extreme temperatures were a good predictor of regional-scale species distributions. We modeled all observations as well as known colonies using topoclimatic, macroclimatic, topographic and habitat factors. We employed a randomisation procedure to reduce clustering of records and divide the data into ten different training and test datasets. Models were assessed using AIC, AUC, and the consistency of response curves. We

compared multiple univariate and multivariate models to examine the evidence that environmental factors consistently influenced the distribution of BTRW. The environmental factors that were strongest at explaining the distribution of BTRW were the topoclimatic estimate of extreme cold, the annual precipitation, and the amount of cleared land within 1600 m. BTRW colonies occurred where minimum temperatures were high, rainfall was low, and there was little cleared land in the surrounding area. These locations were often local topographic maxima that were not susceptible to cold air drainage, and this effect was not detected using elevation or macroclimatic variables directly. We concluded that accurate topoclimatic maps are an important aspect of modelling regional species distributions. Ecologists should place more emphasis on the derivation and accuracy of fine-scale climate grids, not just the resolution.

Keywords: climate refuges, cold tolerance, ecological niche model, predictor selection, regional scale.

Niche Evolution of Modern Humans During the Late Pleistocene

Konstantinos Giampoudakis¹, Katharine Ann Marske¹, Andrew Ugan², Joy Singerayer³, Carsten Rahbek¹, [David Nogués-Bravo¹](mailto:k.giab@hotmail.com)

¹*Center for Macroecology, Evolution and Climate. Natural History Museum of Denmark. University of Copenhagen. k.giab@hotmail.com;*

²*Dept. of Anthropology, University of Utah, USA*

³*Dept. of Meteorology, University of Reading, UK*

New insights about the geographical spread of modern humans across the planet under Pleistocene climatic changes have been recently provided by population genetics and diffusion approaches. Yet, the evolution of the climatic niche of humans meanwhile migrating, the modes of migration and the role of climatic forcing and cultural-technological developments on modern human niche evolution remains to be explored. Here, we take a different approach that unifies macroecological and community ecology models, the archeological record and palaeoclimatic simulations. We show that the climatic niche of central and north Eurasian populations during the last 50,000 years was evolving fast during the MIS3 and reached stability during the MIS2. These results suggest two different modes of human migration: niche evolution to adapt and colonize new climatic conditions during MIS3, and niche stasis but geographical tracking during MIS2. Also, both climatic forcing and cultural and technological advancements drove niche human evolution. Our framework, which complements both population genetic and diffusion approaches, provides accurate reconstruction of human spatiotemporal niche dynamics and can be applied to other *Homo* species across the planet.

Keywords: *Homo Sapiens sapiens*, migrations, adaptation, dispersal, climate change

Ecological and evolutionary drivers of the environmental niche of Neotropical snakes

Valeria Di Cola¹, Antoine Guisan², Margarita Chiaraviglio³

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²*Department of Ecology & Evolution (DEE) and Institute of Earth Sciences - University of Lausanne, Switzerland.*

³*Lab. de Biología del Comportamiento, IDEA - CONICET - Universidad Nacional de Córdoba, Argentina.*

Phylogenetic-based comparisons between life history traits and environmental niche offer a powerful approach to identify biogeographical patterns. Within the order Squamata, viviparity has evolved several times independently and it has been suggested that viviparity may have prevented snakes from the negative impacts of cooling climates. Furthermore, body size influences many aspects of snakes' life history and interactions with their environment. Squamates thus provide an ideal system for investigating the relationship between life history traits and the niche. Here we test the assumption that snakes' environmental niche is influenced by their life history traits, and thus, that species that share life history traits should be similar in their environmental requirements regardless of phylogenetic history. We considered 40 South American snake species of the Boidae, Colubridae, Elapidae and Viperidae Families and evaluated their habitat requirements using species distribution modelling. We found that snakes with larger body size occupy warmer and more humid environments. Colubrid snakes show a phylogenetic association with body size and vegetation productivity. Viviparous Colubrids have smaller body size and occupy areas with lower vegetation productivity. Boidae species show no phylogenetic signal in life history traits nor environmental requirements. We conclude that niche divergence and conservatism are processes that operate differently according to the phylogenetic scale considered. Nevertheless, the combination of species distribution models, environmental data and phylogenetic information allows us to better define the time scales at which niche evolution occur.

Keywords: serpents, viviparity, body size, SDM, phylogenetic comparisons.

Modeling Caatinga plant species in a semi-arid area of northeast Brazil with MaxEnt

Robert Koch¹, Birgit Kleinschmit¹

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Anthropogenic interferences initiate impacts to ecosystems resulting in environmental problems such as loss of biodiversity. Our scientific focus is on impacts of land use and climate change on key plant species in the semi-arid area of northeast Brazil. The study area is located in the entire Sao Francisco River watershed (northeast Brazil), has a size of ca. 670.000 km² and contains the three biogeographic regions Caatinga, Cerrado, and Mata Atlantica. In our research

we focus on the Caatinga biome, classified as a seasonally dry tropical forest, which was already affected by severe drought periods in the last decades. As the Caatinga biome is poorly researched, we are dealing with imperfect data conditions (few presence-only data). Therefore, we decided to use a maximum entropy approach for modeling plant species distributions. For a general understanding of the spatial conditions in the floristic system we model the distributions of 10 key plant species that provide several ecosystem services in that region. Due to its valid results despite imperfect data we use MaxEnt at a high spatial resolution (30-arc-sec) at a regional level (670.000 km²) with 12 selected environmental parameters (climate, soil, topography). To gain convenient maps for detecting priority areas and to support conservation planning we derive the relative species richness for the entire watershed. Furthermore, several future land use and climate change scenarios will be integrated into the model to assess the consequence of environmental change on species distribution and on selected ecosystem services.

Keywords: biodiversity, species distribution modeling, dry tropical forest, small sample size, land use change

Hotspots of range-restricted species is tightly linked to climate and specialization in plant-hummingbird networks across the New World

Jesper Sonne¹, Carsten Rahbek¹, Bo Dalsgaard¹

¹ *Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark, University of Copenhagen, Denmark, hzc973@alumni.ku.dk*

Quaternary spatio-temporal climate stability is thought to facilitate high degree of endemism and high biotic specialization. Although a link between endemism and biotic specialization is often expected, the idea lack support from empirical evidence. Using data for 54 plant-hummingbird mutualistic networks distributed across the New World, we here demonstrate a strong relationship between community-level biotic specialization and endemism measured as the proportion of range-restricted hummingbird species. Although degree of endemism was also associated with measurements of contemporary and Quaternary climate stability, biotic specialization still explained a considerable amount of unique variation in partial regression analyses. The results are in accordance with the hypothesized interrelatedness of biotic specialization and hotspots of range-restricted species, and although this partly illustrates the link of these to contemporary and Quaternary climate, it also indicates the unique effect of a shared evolutionary history of coexistent species. Our study emphasizes the role of biotic interactions in shaping range-size distributions.

Keywords: endemism, specialization, mutualistic networks, contemporary climate, Quaternary climate stability

Selecting Indicator Traits for monitoring Landscape degradation of Mammals in Mexico

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As a result of human population growth and a high rate of infrastructure development, natural landscape of Mexico has a high degree of environmental degradation. Land use changes have caused degradation of ecosystems, and indicators for detecting and monitoring impacts are needed. We use a three table ordination method (RQL analysis) to identify species traits in mammals indicating environmental degradation. RQL analysis has the advantage of linking species traits directly to environmental attributes, hence detecting the major ecological impacts of habitat degradation. Mammals and environmental data were sampled nationwide in 2761 localities (from 1970-2013), including geographic records of 369 species of mammals, from the Sistema Nacional de Información sobre Biodiversidad (CONABIO). Twelve environmental variables (including geophysical and land use impacts) were generated using GIS. Three types of traits were evaluated: locomotion, trophic habit and body size. We identified a gradient associated with mammals, mostly determined by road distance and human settlement index, where low index values represented sites with high ecological integrity. Species traits associated with low human impact were arboreal locomotion type, frugivore-hervivore, and body size above 10 kg. In contrast, fossorial locomotion type and grassers are common in sites highly impacted. Similar results were found when the analyses included only species at some status of risk. Environmental-traits relationships could establish the basis for making predictions about changes in biological and functional diversity in response to land use changes. It is necessary to conduct specific analyses to identify local scale traits in order to improve the monitoring system.

Keywords: trophic groups, land use change, conservation biogeography, habitat lost, degradation

Species distribution modeling: choosing relevant climate predictors for better accuracy?

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Species distribution models (SDMs) relate species presence / absence data to environmental variables based on statistically or theoretically derived response surfaces. The crucial step of selecting the most relevant variables has received little attention compared to the choice of the modeling, despite being an important source of uncertainty. Here, using the North American

Breeding Bird Survey data for 331 species, we assessed which climate predictors (among 22 commonly used predictors) provided the most accurate SDMs (using both spatial and temporal evaluation) for bird distribution in the US while controlling for co-linearity among predictors. Three temperature related variables (annual PET, the mean annual temperature, and GDD) were significantly more relevant. As for the precipitation variables, the use of the annual precipitation clearly led to more accurate results than any other precipitation variable. Interestingly, yearly based predictors produced more accurate distributions than seasonal predictors, even though most of the species considered in this study are migratory. Another interesting result is that the moisture index (ratio of annual precipitation over PET) appeared to be at least as important as annual precipitation, although it is only rarely considered as a predictor in SDMs. Both spatial and temporal (over 40 years) evaluation provided highly similar results. The importance of such results is twofold: by identifying the most relevant predictors of species distributions at large spatial scale, we can extrapolate that these predictors are more likely to be ecologically meaningful, which should allow to better predict the potential impact of climate change on bird distributions.

Keywords: WorldClim, GAM, GLM, FDA, BRT, ANN, RF

Can *Acacia* distribution predict the distribution of their seed feeding weevil?

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The native Australian genus *Melanterius* (Coleoptera: Curculionoidea) is of great importance given their use as biocontrol agent. *Melanterius* is a large group of seed-feeding weevils closely associated with Australian Acacias. More than 90 species of *Melanterius* are hitherto described, though many species remain unknown and few records of their host species and distribution are available. Australia has more than 1000 *Acacia* species of which the Botrycephalae Section (approx. 46 species) is of great importance as it includes species invasive in Africa. Distribution information of Acacias will be used to estimate the weevil distribution and compared with results found from intensive sampling of both, Acacias and Weevils in the last few years. This information will also provide insights in the specificity of the weevils to try to delimit further species for use in biological control.

Keywords: Weevils, host-plant interactions, distribution estimates, host-specificity.

Scaling metabolism from individuals to reef-fish communities at the global scale

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Fishes contribute substantially to energy and nutrient flux in reef ecosystems, but quantifying these roles is challenging. Here we formulate and test predictions that link individual fish to reef-community structure and ecosystem function based on metabolic rate. To do so, we first analyse the largest compilation of fish metabolic-rate data available and find support for predictions of metabolic theory regarding the exponential temperature scaling (activation energy of ~ 0.65 eV) and 0.75-power body-size scaling of metabolic rate, but only when averaged across family-level variation. We then use a novel Bayesian approach to synthesize these scaling relationships with a global compilation of reef-fish community data in order to first 'size correct' community biomass and then quantify community structure and respiratory flux. The community-level analysis yields two key findings. First, size-corrected biomass is generally higher for herbivores than piscivores and omnivores, consistent with energy losses between trophic levels, but highest for carnivores, indicating substantial energy subsidies to this group from invertebrates and zooplankton. Second, respiratory fluxes of reef-fish communities increase ~ 3.3 -fold from subtropical to tropical sites (22-28°C), indicating that their absolute contributions to energy and nutrient fluxes in reef ecosystems is greatest at the warmest sites. Our study demonstrates how individual- and community-level data and analysis can be synthesized to identify important global-scale trends in ecosystem dynamics.

Keywords: allometry, climate change, ecosystem function, coral reef, metabolic theory of ecology

Adult and larval traits as determinants of geographic range size among tropical reef fishes

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Geographic range size is a fundamental biogeographic variable that, among other effects, strongly influences a species susceptibility to extinction. Because most marine organisms disperse via ocean currents as larvae, it is often assumed that pelagic larval duration (PLD) affects species dispersal, determining their geographic range sizes. Empirical tests of this hypothesis have yielded mixed results, and alternative hypotheses have rarely been considered. Here we assess the influence of adult and larval life-history traits on geographic range size among reef fishes, using data on 590 species in 47 families from all three tropical oceans, the largest compilation of such data to date for any marine group. The analysis controls for the non-independence of shared traits among related species and regional limits on range-size by using linear mixed-effects modeling (LMM). Our analysis indicates that three adult traits—body size, schooling behaviour and nocturnal activity—are equal or better predictors of range size than PLD. All three of the positive adult-traits correlates of range size may influence range expansion by enhancing the establishment of new populations, and hence may affect geographic responses of reef fishes to climate change. Predictions of poleward range shifts by marine species in response to sea warming have been based on their thermo-physiological tolerance. However, other life-history traits, such as those identified here, may constrain range extension and thereby influence extinction risk.

Keywords: Marine Dispersal, Pelagic Larvae, Mixed-Effect Models, Body Size, Schooling.

Drivers of krill zoogeography in the Indian Ocean: the implications of poleward flowing boundary currents

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With 86 species known worldwide, krill (Euphausiacea) are widespread in all oceans and are an important link in marine food webs. In the Indian Ocean, the first basin-wide investigation of krill zoogeography was conducted during the International Indian Ocean Expedition (1962-65). Subsequent plankton and micro-nekton studies, conducted in the Indian Ocean over the past five decades, have been collated in a Geographical Information System to produce a species richness map of the 66 krill species occurring throughout the Indian Ocean. Species richness was greatest around the tropical and subtropical latitudes, with a decline towards more temperate zones. This latitudinal trend has also been observed for krill in the Pacific Ocean (80 species) and Atlantic Ocean (54 species). One of the features that makes the Indian Ocean unique is the unusual presence of two poleward flowing boundary currents, the Agulhas Current in the south-west and the Leeuwin Current in the south-east. Both currents seem to drive the southward dispersal of species to create species rich regions along their respective coastlines, a pattern that has been observed for other tropical marine fauna such as Indo-Pacific fishes. Through the availability of satellite imagery and Argo float data, trends in krill zoogeography can be correlated with broad scale environmental factors to establish basin wide relationships within the Indian Ocean. Factors such as sea temperature, chlorophyll *a*, latitude and depth are being investigated for their potential influence on krill zoogeography.

Keywords: Leeuwin Current, zoogeography, krill, environmental drivers

Known unknowns: Correcting for sampling bias in marine species distribution models

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Species distribution models (SDMs) have long been popular in the terrestrial realm and are now increasingly applied to marine species. On large spatial scales, presence only models using “big data” from GBIF and OBIS are amongst the most widely used approaches. These presence only data however are highly biased, both spatially and environmentally. Most records stem from the coast, the continental shelves and the northern hemisphere. This violates one of the central assumptions of such SDMs that require equal sampling intensity throughout the study area. An approach to overcome this limitation is the target-group background approach, which selects background data for model calibration according to documented species richness of the respective group, assuming that observed richness is an indicator of sampling bias. Yet, in

marine systems, sampling bias coincides with actual higher diversity and abundance in coastal and shallow waters. Occurrence record density and documented species richness therefore represent a confusing mixture of sampling artifacts and real ecological patterns. Rarefaction accumulation curves of species records provide an indicator of actual sampling effort and intensity, disentangling macroecological patterns and data artifacts. Together with the target background approach, this measure can significantly increase model performance for presence-only SDMs in spatially and environmentally biased sampling situations. Here, this approach is applied to Elasmobranchii (sharks, rays and skates) using OBIS presence only data. Resulting maps are compared to IUCN range maps and fisheries data for verification.

Keywords: marine, sharks, environmental niche model, presence only, taxonomic completeness

Incorporating evolutionary history into niche and distribution modeling

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Niche models (alternatively species distribution models) typically use presence-only data for a species in conjunction with fine-scale geographic coverages of ecologically relevant predictor variables in order to construct a mathematical model of the species' biological tolerances or preferences. These models are used across evolution, ecology, and conservation biology to estimate species' environmental niches and potential geographic distributions. However, recent empirical results indicate that rates of evolution of the environmental niche can range from extremely slow, so that closely related species are effectively environmentally interchangeable, to very fast, so that significant differences in environmental associations are seen between lineages within a single species. Given these insights, it is reasonable to question whether the a priori assumption that the species is the appropriate taxonomic scale for modeling is always justified. We demonstrate new methods based on model selection that address this issue. These methods allow the data to determine the appropriate groupings of species for model construction. The methods allow us to leverage greater sample sizes and sampling of geographic and environmental space where appropriate, thus allowing us to construct better, more reliable models of the ecological niche.

Keywords: biodiversity, biogeography, distributions, phylogeography, conservation

Information on biotic interactions improves transferability of distribution models

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Predicting changes in species' distributions is a crucial problem in ecology, with leading methods assuming that a species' distribution reflects its climatic requirements. Empirical support for this approach relies on our ability to use observations of a species' distribution in one region to predict its range in other regions (model transferability). Here, we contradict this inference by showing how competition among different species (biotic interactions) produce model transferability. We show that biotic interactions shape range margins through several previously unrecognized mechanisms, that for some mechanisms, small changes in species' interactions dramatically shift range margins and that model transferability can arise from a tradeoff among mechanisms. Our work indicates that information on biotic interactions will improve predictions of species' range margins when species interactions differ markedly from one region to another, or when range margins are sensitive to small changes in species' interactions.

Keywords: biodiversity, biogeography, distributions, species interactions, model transferability.

Integrating parasite-host interactions in distribution and abundance models to understand spatial patterns and to address conservation of an endangered freshwater mussel and its hosts.

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Understanding biotic interactions between species is a key challenge to prevent biodiversity loss, but their role in shaping spatial patterns is largely unexplored. Our main objective is to include biotic interactions when modeling distribution and abundance of the most endangered and widespread freshwater mussel species. We present an analysis across fifty-four river systems and 23 basins in southern Europe, Spain. Maximum entropy modelling was used to account for biotic interactions related to host species and abiotic factors when predicting species distribution. Path analysis was implemented for determination of direct and indirect effects of abiotic and biotic factors on abundance and to identify broad scale patterns in biotic interactions. Using 435 records and 13 predictors in maximum entropy modelling showed that host fish distributions and abundances influence the distribution of the freshwater pearl mussel (*Margaritifera margaritifera*). Path analyses identified discontinuity in biotic interactions affecting spatial patterns of mussel abundance. Results clearly showed an important biophysical linkage of the mussel with its migratory host fish. Accounting for biotic interactions at a broad

scale between *M. margaritifera* and its hosts shows that coextinction is a primary conservation concern in fragmented ecosystems. Dams and impacts that fragment habitats, extirpate fish hosts or otherwise interfere with interactions in the parasite-host system are a major threat for extinction of freshwater mussels. Inclusion of biotic interactions in species distribution models will help to plan better habitat protection, allocate reserves to facilitate biotic interactions, and to improve conservation strategies for the most widespread and endangered animals in freshwater.

Keywords: biotic interactions, macroecology, coextinction, unionoids, habitat fragmentation, connectivity, river ecosystems.

Modelling the distribution of *Formicivora serrana* complex (Aves:Passeriformes) in southeastern brazilian Atlantic Forest during the Late Quaternary

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The *Formicivora serrana* complex is endemic of Atlantic Forest and restricted at semi-deciduous formations in southeastern Brazil. There are three known forms: *F. s. serrana* which occurs inland up to 1500m; followed by *F. s. interposita* that inhabits the Paraíba-do-Sul valley (500-700m); and *F. s. littoralis* confined at the costal lowland formation (restinga) and a few offshore islands. The aim of this study is to investigate the complex geographical distribution dynamics after the last glacial maximum (LGM). Based on 60 occurrence records and 19 WorldClim bioclimatic predictors, a species distribution modeling (SDM) was used to produce both present and past potential ranges (MaxEnt 3.3.3). A geographic information system (GIS) helped processing and analyzing the distribution maps (ArcMap 9.3). Models pointed out that inland groups (*F. s. serrana* and *F. s. interposita*) have the same bioclimatic predictors: Bio4 (temperature sazonality) and Bio19 (precipitation of coldest quarter). The outputs show that their distributions remained similar after the last Quaternary climatic changes. In the other hand, *F. s. littoralis* models indicated as major predictors: Bio2 (mean diurnal range), Bio6 (minimum temperature of coldest month) and Bio12 (annual precipitation). The models predicted suitable areas over continental slope, by that time exposed due to LGM marine regression. In this case, there is no overlapping between present and past geographic ranges, suggesting a recent distributional shift. This pattern can explain nowadays isolation on restingas and the relictual occurrence in offshore islands. Phylogeographical and molecular studies may enlighten the evolution of complex.

Keywords: bioclimatic predictors, historical biogeography, geographic distribution

Biogeography and extinction of New World passerines: evidence from Pleistocene fossils

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In the Americas climate change from the last glacial-to-interglacial transition and overhunting by humans ca. 12,000 years ago have been implicated in the extinction of as many as 50 genera of large mammals (megafauna). The megafaunal extinctions undoubtedly triggered trophic cascades with broad-ranging implications for New World plant and animal communities. We are just beginning to understand how the distribution and diversity of songbirds (Passeriformes) were affected. Based on our fossil identifications, it seems that songbirds suffered substantial extinction and range contraction at the end of the Pleistocene. This pattern is most evident in the family Icteridae (blackbirds), exemplified by the extinct species *Euphagus magnirostris* first discovered in California and identified by us at two South American fossil sites > 5,000 km away. While the precise causes of extinction may not be directly measurable, it is clear that passerine birds, even ones that had very large ranges, were affected by similar factors that led to the demise of so many other species once dominant during the Pleistocene. Songbird diversity was even higher in the Neotropics in the geologically recent past than it is today.

Keywords: Neotropical biodiversity, Birds, Climate change, Range shifts

Uncovering determining factors for Holocene vegetation pattern in central Europe

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Pollen diagrams represent the most extensively available proxy for past plant cover. The numerical values for many of these datasets are stored in databases, which for Europe is mainly the European Pollen Database (EPD). Analysing past spatial vegetation pattern from pollen diagrams is hampered by their uneven distribution in space, requiring spatial interpolations. For this purpose, maps of pollen abundances of major European species were constructed in 500-year steps for central Europe where site density is high. In addition to data from the EPD and the Czech pollen database (PALYN CZ) we collected further pollen diagrams through personal contact to other scientist. We also digitized diagrams from publications where the original data could not be accessed. The results show changes in distribution and abundance of major species across central Europe based on 410 pollen diagrams. To take account of elevation as an important determining factor for species distribution and abundance we used a tricubic interpolation method to interpolate between the uneven distributed data points. The resulting

maps are used to explore shifts in the distribution and abundance of species and compare them to climate gradients. These analyses indicate that some spatial gradients in abundance are stable through time and can be linked to climate gradients such as continentality (distance to the sea). The continentality gradient is most pronounced in the distribution of *Pinus* and *Quercus* which show positive and negative affinities, respectively. However, this gradient only establishes around 10,000 B.P. The elevation gradient of species abundance strengthens with increasing warming in the later part of the Holocene and increasing human land use. Overall, the results provide insights into determining factors for past distribution and abundance gradients and a reference for data model comparisons.

Keywords: distributions, paleoecology, past vegetation change, vegetation maps, distribution models

Integrating paleodistribution modeling and next generation statistical phylogeography to explain the effects of Quaternary climatic oscillations in alpine-arctic plants

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The role of Quaternary climatic oscillations in shaping the distribution of organisms has long been discussed by biogeographers. Recent advances both in Species Distribution Modeling (SDM) and molecular phylogeographical analyses now allow us to reconstruct past distributions and infer demographic events of populations by combining the fields of macroecology and phylogeography. Here, we use a comprehensive occurrence record of the alpine-arctic plant *Primula farinosa*, ensemble SDMs and high-resolution paleoclimatic layers to reconstruct the distribution of this species during the last 72ky in 1-4 ky time intervals. We identify expansion and contraction events and refugia where *P. farinosa* may have persisted through the glacial cycles. Based on the results of paleodistribution modeling we formulate alternative biogeographical hypotheses to explain the current disjunct distribution of the species. We collect genome-wide genetic data from 70 populations sampled across the Eurasian range of *P. farinosa* via next-generation sequencing (NGS) platforms to explicitly test the biogeographical hypotheses. Using allele frequencies we generate coalescent simulations and test for alternative scenarios of population splits and mixtures in multiple populations. By combining genomic and ecological data, we elucidate the complex evolutionary history of alpine/arctic species in response to the Quaternary climatic oscillations and inform conservation strategies in the face of climate change.

Keywords: Species Distribution Modeling, Last Glacial Maximum, European refugia, Isolation, Migration

Lightning Talks

(Poster 1)

Splitting of mosaic vegetation type polygons using maximum entropy modelling

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Many areas around the world have been mapped using predefined vegetation types for different spatial scales. These maps frequently include larger polygons with mosaic signatures, i.e. delineated areas containing two or more vegetation types in each polygon. These mosaic polygons pose management challenges, mainly because they lack the spatially explicit information of where the different vegetation types are found within the given area. In this study we propose a method for splitting of mosaic polygons into smaller entities with unmixed vegetation types, thereby increasing the spatial precision and resolution of these maps. The following spatial datasets covering 47.5 km² of Thingvellir National Park (Iceland) were selected: a vegetation map (1:15 000), a digital elevation model (DEM: 5m x 5m), RapidEye satellite images, and ten spatial variables derived from the DEM. Four vegetation types which frequently appear as mosaics in the Thingvellir vegetation map were tested. We used three methods to distribute different densities of presence-only points: random, grid-based and polygon centroid. The training points were only allowed within unmixed vegetation type polygons. We then used maximum entropy modelling, including presence-only points and explanatory variables, to split the mosaic polygons. Preliminary results indicate that the study design and methods implemented perform well in separating the tested mosaic vegetation types. The modelling performance will also be tested with independently sampled presence-absence data. The results are discussed with respect to presence-only point distribution, explanatory variables and spatial challenges related to distribution modelling of vegetation types.

Keywords: distribution modelling, explanatory variables, spatial scale, presence-only point distribution

(Poster 3)

Modelled thermal environment informs sex ratio predictions in New Zealand tuataraAnna L. Carter¹, Nicola J. Mitchell², Michael R. Kearney³, Stephen Hartley¹, & Nicola J. Nelson¹¹*Victoria University of Wellington, New Zealand, anna.carter@vuw.ac.nz*²*University of Western Australia, Australia*³*University of Melbourne, Australia*

Species distribution and niche models are being used increasingly for examining population viability and predicting range shifts within the context of modern climate change. Climate envelopes and other commonly used correlative methods are of limited use if the primary conservation concern is not the availability of suitable or sufficient habitat. In species with temperature-dependent sex determination (TSD), environmental variation with minimal detectable effect on the distribution or health of adults may dramatically skew offspring sex ratios, eventually endangering population viability. Predicting offspring sex ratios requires high-resolution (i.e., nest microsite), mechanistic predictions of incubation temperatures. We used an R-implemented microclimate model to generate soil temperatures for multiple hypothetical climate scenarios, informed by in-situ observations of nesting behaviour in a population of tuatara, a long-lived reptile with TSD. We then used a biophysical model of embryonic development to predict current and future offspring sex ratios. In particular, interactions between female nest site selection behaviour and the changing vegetation profile of our study location highlighted (1) the effects of previously un-quantified behavioural patterns on incubation temperatures and (2) the extent to which relatively small habitat changes can potentially influence offspring sex ratios in TSD species, even under maximum hypothetical warming scenarios.

Keywords: temperature-dependent sex determination, remote sensing, mechanistic climate modelling

(Poster 5)

Finding biogeographic patterns in species Macadamieae and Gevuininae (Proteaceae)Fabio Avila¹, Favio González²¹*National University of Colombia and District University Francisco José de Caldas, Colombia, faaavilaca@unal.edu.co*²*National University of Colombia, Colombia*

Proteaceae have been widely studied as an excellent group to understand Austral Biogeography, nevertheless some extant genera (*Panopsis* and *Roupala*) have reached Central American and Mexico areas, which are not properly austral areas. According with estimated divergence times in the family is suggested that disjunction patterns are related with transoceanic dispersal and vicariance. We found special interest in the biogeographic patterns along the Grevilleoideae subfamily, but even more in species of newly circumscribed Macadamieae. In this sense, we

have added new terminals to the current proposed relationships based on morphology within the tribe and defined current areas of distribution for each species. So, we found potential paralogy of areas between area relationships of Macadamiinae (*Panopsis-Nothorites-Brabejum*) and Roupaliinae (*Roupala-Orites-Banksia*) in the relationship Tropical America-Oceania and Australia-Africa. In addition, we tried to find the distribution patterns of *Panopsis*' species in order to track if Central American terminals belonged to one clade. We wonder about when Central American *Panopsis* cross the biogeographic barrier of Isthmus of Panama and which other barriers were frequent in distribution of Neotropical Proteaceae.

Keywords: austral, biogeographic barriers, biogeography, Central America, endemism.

(Poster 7)

A framework for understanding niche dynamics of invasive species through reciprocal distribution modeling

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Correlative species distribution models are often used to predict a species' potential distribution in invasive risk modeling. However, when there is dissonance between projected and realised distributions, it is not clear whether there is a niche shift in the adventive population, or whether this difference arises from the formation or decoupling of dispersive constraints, or from sampling bias. We suggest that reciprocal distribution models (RDMs), which predict a species' adventive range from its native range, and vice versa, can be extended to a new framework that differentiates niche shifts from changes in biotic associations and sampling artefacts. We use species from the geophytic family Iridaceae to test our framework, by studying changes in plant-pollinator and plant-herbivore interactions, following introduction to Australia from the Cape Region in South Africa. This is underpinned with molecular work on their population genetic structure. Concurrently, we are exploring ecological niche models across both continents using MaxEnt. Finally, we hope to contrast the species' genetic diversity and structure against RDM results, to explain distribution patterns in Australia. In particular, the sexual-aseexual congeners *Watsonia meriana* var. *meriana* and *W. meriana* var. *bulbillifera*, with reversed distribution patterns between native and introduced ranges (*W. meriana* var. *meriana* is more widespread in the Cape Region, but *W. meriana* var. *bulbillifera* is the more prevalent in Australia) present a phylogenetically-independent insight into ecological and niche processes governing invasive and natural species distribution patterns.

(Poster 9)

Global biodiversity and biogeography of razor clamsHanieh Saeedi¹, Mark J Costello², Todd Dennis²¹ Leigh Marine Laboratory, University of Auckland, New Zealand, hanieh.saeedi@gmail.com² Leigh Marine Laboratory, University of Auckland, New Zealand³ School of Biological Sciences, University of Auckland, New Zealand

Razor clams (Solenidae and Pharidae) are deep-burrowing bivalves that inhabit intertidal and shallow sub-tidal soft-bottom sediments of tropical and sub-tropical areas. Here we used combined data published in the literature and open-access databases including the Global Biodiversity Information Facility (GBIF), the Ocean Biogeographic Information System (OBIS), and museums' geographical distribution records to map the global geographic distribution of Solenidae species. Species nomenclature and synonyms were reconciled using the World Register of Marine Species (WoRMS). Environmental data were obtained at a spatial resolution of 0.083° from Bio-Oracle. We applied a species distribution modeling program 'Maximum Entropy' (Maxent) to predict suitable habitats for Solenidae species. The geographic distribution of species in 5° latitudinal bands showed a distinct bimodal pattern, and global patterns of richness decreased from the equator to the poles. Eastern and southern parts of Asia exhibited the greatest diversity; there were no distribution records for this family in Antarctica and some large oceanic islands such as New Zealand. Model outputs indicated the majority of suitable Solenidae habitats are likely to occur in the shallow waters of the Indo-Pacific area and the North Atlantic Ocean. The most important environmental factors in determining Solenidae habitat suitability were depth, chlorophyll A concentration, calcite concentration, and sea surface temperature. Knowledge of the biogeographical patterns of Solenidae on a global scale will help identify factors such as geological and climatological phenomena that are known to influence the diversity patterns of ecologically and environmentally important marine organisms such as razor clams.

Keywords: distributions, modeling, Maxent, environmental variables, Solenidae

(Poster 11)

Scale-dependence of vascular plant distributional patterns: a multi-scale studyAnders K Wollan¹, Vegar Bakkestuen², Rune Halvorsen²¹Natural History Museum, University of Oslo, Norway, anders.wollan@nhm.uio.no²Natural History Museum, University of Oslo, Norway

Patterns of variation in vascular plant distributions at different spatial scales were studied with the purpose of identifying factors (plant traits and environmental gradients) that may explain such patterns. Our data (collected during 9 months of intensive field work) were obtained from five plots, 1024 × 1024 m each, situated in different ecosystems and spread out over Norway. In each plot, presence or absence of 43 selected species were recorded in seven nested plots of standard size, each with 256 subplots, i.e., with a 1:16 linear relationship between grain and

extent. Thus, the five top-level plots were divided into 64-m subplots, of which two were taken as plots on the next nesting level and divided into 4-m subplots, of which four were taken as plots on the lowermost nesting level (divided into 25-cm subplots). Environmental information was obtained for each plot by recording variables in the field and by use of proxies obtained from detailed mapping of nature types, using a gradient-based typification system. Vascular plants species were selected to represent variation in traits such as environmental tolerance (generalist to specialist species) and local abundance (common to rare species), as accounted for by categories of the CURS (core-urban-rural-satellite) species model. Preliminary results show considerable variation in prevalence (subplot frequency) between species and within species, among plots and spatial scales. The tendency for single species to obtain high prevalence increased towards finer scales. The results are discussed with respect to species properties, environmental variation and models for spatial distributions of species.

Keywords: Beta diversity, ecological processes, environmental variation, spatial scale

(Poster 13)

Modeling the distribution of plant communities of Moghra Oasis

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Moghra oasis is one of the oases and depressions that characterize the Western Desert of Egypt. It is recognized as a valuable Egyptian inland wetland area serving as resting station for migratory birds. It is also considered important to the local communities inhabiting the northern coast because they use it as an alternative rangeland during the dry season. However, the study of the oasis vegetation was overlooked. The current study thought to identify the plant communities in the oasis and provide predictive model of their spatial distribution. Both the multidimensional scaling approach and the agglomerative hierarchical clustering technique were applied to vegetation data collected from the oasis to help identify the plant communities dominating the oasis. Six major plant communities were identified in the oasis. An ensemble modeling approach was applied to spectral data derived from satellite imagery and land-surface parameters of the oasis to predict the distribution of the identified plant communities. The predictive model was then used to produce a predictive map of the plant communities distribution. The map would provide guidance for any future conservation measures or management plans for the oasis.

Keywords: Modeling, plant communities, distributions, Moghra Oasis, Egypt

Advances in phylogenetic methods for biogeography

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Abstracts

Unveiling the Diversification Dynamics of Australasian Predaceous Diving Beetles in the Cenozoic

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During the Miocene, Australia experienced a major climatic and ecological turnover that still escalates today. Flourishing tropical ecosystems from the Oligocene were progressively restricted to the coasts and replaced by more arid-adapted communities. While the role of the Miocenic desertification has been investigated in terrestrial organism diversification patterns, the response of freshwater clades remains poorly investigated. To gain insights into the diversification processes of a freshwater radiation, we studied the evolutionary history of the Australasian predaceous diving beetles of the tribe Hydroporini. Robust and well-resolved molecular phylogenies indicated a late Oligocene origin of Hydroporini with an important period of diversification in the Miocene. Biogeographic analyses showed an origin in the East Coast of Australia, and a dynamic biogeographic scenario implying dispersal events. The group successfully colonized the tropical coastal regions carved by a rampant desertification, and colonized groundwater ecosystems in Central Australia. Diversification rate analyses suggest that aridification of Australia has not only triggered an extraordinary radiation resulting in a striking boost of species accumulation explained by constant diversification rate until the early Pliocene, but also contributed to a major wave of extinctions since the late Pliocene, probably attributable to on-going aridity and range contractions. When comparing subterranean and epigeal genera, we also unveiled different diversification processes explaining their current diversity pattern. As a result, this Australasian radiation has been promoted by climatic shifts likely opening new ecological opportunities, and as continental Australia carried on drying, the aridification that once favored thriving, started to trigger the wane of the tribe.

Keywords: Adaptive radiation; Dytiscidae; Pleistocene extinction; freshwater biota; ground water organisms.

Not so hot spots? High speciation rates do not explain reef fish species richness in the Coral Triangle or other marine hotspots

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Amongst all marine habitats, coral reefs have historically been recognized as areas of highly concentrated diversity, with a maximum amount of fish diversity occurring in the Indo-Australian Archipelago (IAA)—a collection of tens of thousands of islands recognized for its diverse biotas and high numbers of endemic species. In the last decade the IAA has been recognized as an important engine of marine fish biodiversity through three possible mechanisms: the IAA as a center of origin, a center of refuge or survival, and as a center of accumulation. More recently, a dynamic role for the IAA has been suggested with the region acting during different geologic intervals as a center of origin or refuge. We tested these hypotheses using a suite of comparative phylogenetic methods across eight major lineages of reef fishes. Contrary to the center of origin hypothesis, we find little evidence for exceptional speciation rates within the IAA. Similarly, we found no evidence for time-dependence of diversification rates for most families. Analysis of diversification rates across additional marine hotspots also showed that speciation rates within these regions are not exceptionally rapid. Elevated rates of dispersal into the IAA detected across all families support the center of accumulation hypothesis, and suggest that the connectivity between regions is the main factor driving extant global biodiversity patterns.

Keywords: Indo-Australian Archipelago, biodiversity hotspot, Diversitree, BAMM, GIS

Do rhizobia have biogeography?

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The rhizobia-legume symbiosis is a highly important source of nitrogen (N) in both natural and agricultural systems. Nodulated legumes are found in nearly all terrestrial and even some aquatic ecosystems. Rhizobial microsymbionts are phylogenetically and genetically diverse. Their symbiotic ability is conferred by a group of approximately 400 genes, which enable nodulation and N₂-fixation with the legume host and can be acquired by horizontal gene transfer. While certain rhizobial species are known to be specifically associated with particular legume hosts, recent studies also provide evidence of emerging trends in rhizobial biogeography, in which edaphic and climatic factors strongly influence rhizobial distribution patterns. Research at the Centre for *Rhizobium* Studies (CRS) has shown that an understanding

of these distribution patterns is critical in assessing the suitability of novel legumes and their associated rhizobia for introduction into agricultural systems. Rhizobial biogeography also appears to play a role in determining which species of microsymbionts are nodule occupants of several invasive legume weeds. We present here an overview of the adaptation of different rhizobial species and genera to specific environments, with case studies of species of *Burkholderia* and *Sinorhizobium* (*Ensifer*). The sequenced genomes of more than 142 strains of rhizobia from 9 different genera are now available, largely through joint ventures between the CRS, the DoE Joint Genome Institute (JGI) and an international consortium of scientists (<http://genome.jgi.doe.gov/programs/bacteria-archaea/GEBA-RNB.jsf>). These can be used to determine connections between rhizobial genetic backgrounds and patterns of biogeographic distribution.

Keywords: rhizobia, edaphic factors, biomes, symbiosis

Vicariance across major marine biogeographic barriers: temporal concordance and the relative intensity of hard versus soft barriers

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The marine tropics contain five major biogeographic regions (East Pacific, Atlantic, Indian Ocean, Indo-Australian Archipelago (IAA) and Central Pacific). These regions are separated by both hard and soft barriers. Reconstructing ancestral vicariance, we evaluate the extent of temporal concordance in vicariance events across three major barriers (Terminal Tethyan Event (TTE), Isthmus of Panama (IOP), East Pacific Barrier, EPB) and two incomplete barriers (either side of the IAA) for the Labridae, Pomacentridae and Chaetodontidae. We found a marked lack of temporal congruence within and among the three fish families in vicariance events associated with the EPB, TTE and IOP. Vicariance across hard barriers separating the Atlantic and Indo-Pacific (TTE, IOP) is temporally diffuse, with many vicariance events preceding barrier formation. In marked contrast, soft barriers either side of the IAA hotspot support tightly concordant vicariance events (2.5 Myr on Indian Ocean side; 6 Myr on Central Pacific side). Temporal concordance in vicariance points to large-scale temporally restricted gene flow during the Late Miocene and Pliocene. Despite different and often complex histories, both hard and soft barriers have comparably strong effects on the evolution of coral reef taxa.

Keywords: coral reef fishes, phylogeny, Lagrange, DEC model, ancestral biogeography

Incorporating Phylogenetics and Ecological Niche Modeling for Biogeographic Analysis

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Fishes of the subfamily Gadinae are distributed throughout the Arctic, northern Pacific and Atlantic Oceans, and Mediterranean Sea, occupying ecological niches ranging from the temperate benthos of the continental shelf to the edges of Arctic sea ice. The biogeographic history of crown Gadinae has been the subject of much debate. Past researchers have investigated two essential scenarios: (1) a widespread Arctic ancestor served as an intermediate bridge between the Pacific and Atlantic temperate lineages, or (2) Arctic-distributed lineages resulted from a single dispersal event from temperate waters. However, traditional methods for determining the clade's biogeographic history may be inappropriate, as Pleistocene climate cycles led to dramatic changes in distribution of arctic and temperate oceans. Instead, this study combines ecological niche modeling with phylogenetic character analysis to test several hypotheses of evolutionary history of ecological niche independent of geographic distribution. Occurrence data from the Global Biodiversity Information Facility database and several museums, in combination with environmental data from NOAA's World Ocean Atlas 2009 were used to generate ecological niche models using Maxent. For each species, the resulting distributions were used to calculate predicted niche occupancy (PNO) profiles, a measure of where a species can be found in multimodal ecological parameter space. A phylogenetic tree was developed for Gadinae using mitochondrial and nuclear DNA sequences. PNOs were then plotted as characters onto the tree to demonstrate how niche occupancy among gadine lineages has evolved. The results of this study, while equivocal, suggest that the crown clade of gadine originated in temperate oceans.

Keywords: biogeography, distributions, fish, ancestral state reconstruction, ecological niche modeling

Ancient rocks and drainages divide recent gecko species in Australia's arid zone

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Deserts and other arid zones remain among the least studied biomes on Earth. Emerging genetic patterns of arid distributed biota suggest a strong link between diversification history and both the onset of Miocene aridification as well as recent cycles of severe aridification. The influence of landscape evolution and underlying geology also is becoming increasingly clear, as the geographic distribution of genetic lineages often is correlated to distinct geological and landscape discontinuities. We explore these patterns using detailed genetic studies of arid zone gecko lizards. In a number of saxicolous geckos, deep phylogenetic structure appears to correlate to the onset of aridification across Australia, and is suggestive of persistence over long time periods in disjunct, mesic "refuges" such as the mountain systems of the Pilbara,

Kimberley, and Central Australia. In stark contrast, genetic diversity in true desert geckos is extremely shallow, seemingly “erased” during the punctuated arid cycles of the Pleistocene. The distribution of these lineages across what is now relatively homogeneous sand deserts may relate to a topographic divide between the western uplands and eastern lowlands, with species’ distributions limited by major drainage divisions. Finally, geological complexity in the Pilbara region has had a profound effect on the evolution and diversification of biota, where diversity of both subterranean invertebrates and gecko lizards is amongst the highest in the world. Understanding the biogeography of the Pilbara and how genetic diversity is partitioned across the ancient and heterogeneous landscape is crucial in the face of rapidly expanding economic and developmental pressures.

Keywords: biodiversity, biogeography, phylogeography, phylogeny, aridification

Landscape patterns in rainforest phylogenetic and functional signals: the biogeography of isolation and continental distributions

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We identified patterns of change in landscape connectivity, diversity, concentrations of evolutionary history, and assembly of Australian rainforests using the distribution records of all known rainforest woody species in Australia across their full continental extent. These were analysed using measures of species richness, phylogenetic diversity (PD), phylogenetic endemism (PE), phylogenetic structure (net relatedness index; NRI), and functional trait diversity. Phylogenetic structure was assessed using both continental and regional species pools. The PE analyses identified four main areas of substantially restricted phylogenetic diversity, including parts of Cape York, Wet Tropics, Border Ranges, and Tasmania. The continental pool NRI results showed evenness (species less related than expected by chance) in contiguous groups of grid cells in coastally aligned areas of species rich tropical and subtropical rainforest, and in low diversity moist forest areas in the south-east of the Great Dividing Range and in Tasmania. Monsoon and drier vine forests, and moist forests inland from upland refugia showed phylogenetic clustering, reflecting lower diversity and more relatedness. Signals for evenness in Tasmania and clustering in northern monsoon forests weakened in analyses using regional species pools. For climbing plants, values for NRI by grid cell showed strong spatial structuring, with high diversity and PE concentrated in moist tropical and subtropical regions. Functional traits showed strong latitudinal patterns for seed dry mass and leaf size but measures of total trait variance relative to species richness among a larger set of traits showed a range of patterns.

Keywords: functional and phylogenetic diversity, biogeography, distributions, rainforest, Australia

Hippo-critical bats: genetics contradict morphology in the identification of Solomon Island *Hipposideros* species

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Islands are extremely useful for formulating and testing theories of speciation. Studies of insular fauna have built support for the role of geographic isolation in speciation. The dominance of phylogenetics for delineation of species has augmented this theory and provided examples of cryptic species that are geographically separated, morphologically indistinct, but genetically divergent. Examples of the opposite scenario, where speciation is driven by ecology, and where morphological speciation is complete with minimal genetic differentiation, are far less common and difficult to demonstrate. Such cases have great potential to provide insight into the nature of speciation and species concepts. We examined the taxonomic and evolutionary relationships between an ancestral species, and two derived species (one sympatric and one allopatric) of *Hipposideros* leaf-nosed bats in the Solomon Islands. We used genetic sequencing, microsatellites, and morphological and ecological data to assess the relationships between *Hipposideros diadema*, *H. dinops* and *H. demissus*. All three forms were easily separated by their morphology; their echolocation calls differed; and syntopic populations were reproductively isolated. These considerations support their recognition as ‘morpho-species’. However, our use of two mitochondrial and three nuclear markers revealed that all three morpho-species were a single genetic species. We suggest ‘*H. dinops*’ is an example of a *genetically cryptic biological species* that contradicts the Genetic Species Concept. We postulate that this speciation has been rapid and successful because of the close links between body size, echolocation frequency and prey selection in *Hipposideros* bats.

Keywords: Genetic Species Concept, isolation by ecology, leaf-nosed bat, speciation.

Competitive Release Leads to Range Expansion and Rampant Speciation in Malagasy Dung Beetles

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Competition is often considered to promote ecological diversification during evolutionary radiations, which would allow more species to coexist. At large spatial scales, species may coexist by having allopatric distributions, which raises the question about the role of range expansion in the proliferation of species during radiations. Dung beetles form highly competitive communities and therefore are likely to show patterns of diversification consistent with the diversity-dependent model of radiation, whereby the progressive filling of ecological

space, characterized by an initial rapid accumulation of lineages, is followed by a slowdown in net diversification rate. In such cases, further diversification will only be possible following a “key innovation”, which would decouple the rate of diversification in the “innovative” lineage from that in the main radiation. Here, we integrate a well-sampled (50 out of 74 species) and timed phylogeny of *Nanos* and *Apotolamprus* dung beetles (Canthonini) in Madagascar with data on species’ geographical ranges, abundances, and body sizes. There is an overall decline in lineage accumulation through time since the colonization of northern Madagascar in mid Miocene (24 to 13 Ma). A clade of 24 extant *Nanos* species (clade L) originating 6.0 Ma exhibits a secondary increase in speciation rate, which is associated with a significant increase in body size and strikingly allopatric distributions of the species. Large body size typically confers a competitive advantage in dung beetles, which is here reflected by strong numerical dominance of clade L species in local communities. We suggest that the ‘key innovation’ of large body size has allowed range expansion due to competitive release, which has created extensive opportunities for allopatric speciation and differentiation along environmental gradients. Most theories to explain diversification patterns in Madagascar rely on allopatric modes of speciation, but they fail to explain how ancestral species became widespread in the first place. The mechanism proposed here, involving range expansion following competitive release, may have operated in other Malagasy taxa with large numbers of species with small geographic ranges.

Keywords: microendemism, species-turnover, key-innovation, diversification, body-size

Did southern Western Ghats of peninsular India serve as refugia for its endemic biota during the Cretaceous volcanism?

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The Western Ghats (WG) of peninsular India, a global biodiversity hotspot, has experienced complex geological history being a part of Gondwana landmass. The species richness and endemism is not distributed uniformly across the WG, southern parts of it being extremely diverse with high endemism as compared to the central and northern parts of WG. Largely, studies have looked at the role of ecological processes, although, given the complex geological history, historical factors could have played a significant role in governing distribution of the WG biota. In this study we explore historical biogeography, particularly of the wet evergreen forest species of the WG, three explicit biogeographical scenarios with specific phylogenetic predictions 1) southern Western Ghats was a refuge during the Cretaceous volcanism, 2) phylogenetic breaks in the phylogeny would correspond to geographic breaks 3) local climatic adaptations leading to species assemblage formation. These hypotheses were tested on the centipede genus *Digitipes* from the WG which is known to be an ancient, endemic and monophyletic group. Two of the higher level dispersals were from the southern WG to the central and northern WG independently in the Early Palaeocene, after the Cretaceous Volcanism. Moreover, species level diversifications were in Eocene- Miocene, post-volcanic

periods, central and northern WG species were nested within southern WG, suggesting that southern WG was indeed a refuge for *Digitipes* species during Cretaceous volcanism. Furthermore, it suggests the explanation for diversity patterns seen in the WG, particularly for taxa where the southern WG are more diverse than the central and northern WG.

Keywords: historical biogeography, phylogeny, centipedes

The biogeography of hybridisation in east Australian long necked turtles

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Contrasting biogeographic patterns obtained from mitochondrial and nuclear DNA can inform drivers of discordance, and highlight population level responses to past landscape change. We examine the phylogeographic structure of two sympatric species of freshwater turtle in Australia's inland Murray-Darling Basin and coastal south east Queensland. We find extensive discordance between mitochondrial and nuclear gene trees and concomitant differences in the geographic distribution of genetic structure. The nuclear gene tree recovers reciprocal monophyly, supports ancient divergence in the mid Miocene, and shows no phylogeographic structure within the range of each species. Conversely, the two species share mitochondrial haplotypes on three occasions and occur together in polyphyly over two major haplogroups, with one encompassing a third long-necked turtle species. Haplogroup distributions are closely tied to freshwater biogeographic regions and have a complex geographic arrangement. Haplogroups are broadly sympatric yet populations of the same species within in each haplogroup are not. We used fossil-calibrated Bayesian dating analyses and coalescent isolation with migration models to identify multiple cases of introgressive hybridisation and Plio/Pleistocene mitochondrial gene capture. Gene flow was unidirectional, and species palaeo-distribution modelling suggests directionality was likely from the established species towards the coloniser. We interpret these results with reference to the demographic and biogeographic arena presented by Plio/Pleistocene aridification and conclude that disparities in species effective population size facilitated introgression during population contraction to habitat isolates.

Keywords: phylogeography, mito-nuclear discordance, introgression, palaeo-distribution modelling.

Tracking the formation of a species assemblage over time: phylogenetic reconstruction of patterns of colonisation and speciation

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Studies of temporal patterns in the formation of species assemblages have generally focused on taxa with a rich, continuous fossil record, or on extant species in islands of habitat with known histories. Given the growing availability of molecular and phylogenetic information for ever-increasing numbers of species, we should be able to extend the phyloinformatic approach to macroecology and macroevolution to a wider range of species assemblages. Here, we suggest some methods for estimating the timing of addition of species to assemblages which may prove useful. We show how whole-assemblage phylogenies estimated from publicly available data can be used to describe temporal patterns of the addition of species to assemblages, through both colonization and *in situ* speciation. The advantages of this approach is that it accounts for uncertainty in phylogenetic estimation and for uncertainty in deriving dates of biological events from nodes and branch lengths, it explicitly models sampling bias associated with detecting more recent speciation or colonization events, and it formally considers patterns of colonization and speciation within a hypothesis testing framework. We road test this approach on two data sets, New Zealand passerines and Madagascar squamates.

Keywords: Species assemblage, phylogeny, colonisation, speciation

Model selection reveals differences in cladogenesis processes operating in island versus continental clades

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Historical biogeography has been plagued with unresolved debates over issues such as dispersal versus vicariance. To address this issue, likelihood versions of the LAGRANGE DEC, DIVA, and BayArea cladogenesis models were implemented in the R package BioGeoBEARS, along with “+J” versions of these models which include founder-event speciation. These six models were run on 63 clades/constraints combinations, sampling both island and non-island clades. Models were compared using the likelihood-ratio test and AICc model weights. Almost all analyses, including continental clades, strongly favored the “+J” models over the models without founder-event speciation. However, founder-event speciation was measurably less frequent in non-island analyses, being 2-4 times weaker than in analyses of island clades. Only one clade was found (“Taygetis clade” butterflies from the Neotropics) which favored the DEC model over all others. The main conclusion is that formal model selection procedures can be applied in phylogenetic inferences of historical biogeography, and the relative importance of

different processes can be measured. These techniques have great potential for strengthening quantitative inference in historical biogeography.

Keywords: founder-event speciation, historical biogeography, LAGRANGE, BioGeoBEARS, phylogenetics

Applying exon capture to study biogeographical processes shaping the diversity of the Australian monsoonal tropics.

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Our understanding of the biogeographical processes shaping the biodiversity across the monsoonal tropics of northern Australia is currently limited. Recent phylogeographic studies highlight that current taxonomy underrepresents the true biodiversity of taxa across the region. Development of next generation sequencing methods have allowed methods to better understand patterns and processes shaping the evolution of taxa. We applied exon capture hybridisation methods to a widespread and low dispersal skink, *Carlia amax*, another taxon that has signaled the presence of more fine-scale genetic structure across its distribution. Mitochondrial sequences reveal deep divergent lineages broadly across northern Australia. The exon capture results suggest deeper structure within the Kimberley region of the northwest compared to the mtDNA, highlighting the power associated with large datasets. When assessed in conjunction with additional sympatric *Carlia* species and other taxa we are able to piece together the biogeographical patterns and the processes that have shaped the distribution of diversity in northern Australia.

Keywords: next generation sequencing, phylogeography, monsoonal tropics, Australia

Vicariance and the origins of diversity in arachnids – a case study from ancient pseudoscorpions.

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Globally distributed lineages may show one of two patterns of relatedness: relationships strictly follow vicariance predicted by continental drift or, dispersal following drift generates unpredictable patterns of relatedness. Pseudoscorpions are globally distributed and allow tests of the relative importance of these two biogeographic models. I analysed relationships in the

ancient family Pseudotyrannochthoniidae using five genes – a total of 7000 base pairs. Bayesian, likelihood and parsimony approaches were used to infer phylogenetic trees and the age of divergence dates was estimated using BEAST. Northern and southern hemisphere faunas form two independent monophyletic lineages consistent with the break-up of Pangaea into northern (Laurasia) and southern (Gondwana) landmasses some 180 mya. Eastern Palaeartic and western North America faunas show strong phylogenetic affinities, highlighting an ancient trans-Beringian distribution predating the Paleogene. The Southern hemisphere has 1) an eastern-Gondwanan clade comprising species from Madagascar, eastern South Africa and Sri Lanka, and 2) a southern Gondwanan clade comprising species from Australia, Chile and the Cape Provinces in South Africa. The fauna of Australia is paraphyletic with respect to Chile and this pattern is ancient, reflecting a former connection via Antarctica. The South African fauna is polyphyletic and includes lineages from both eastern and southern Gondwana. Several landmasses have seen extensive *in-situ* speciation events, resulting in high numbers of endemic species and highly interesting intra-continental distribution patterns reflecting vicariance since the mid-Tertiary. These patterns are highlighted by the Australian fauna, a continent with recent dramatic climatic change, resulting in aridification and contraction of its original mesic biomes.

Keywords: biogeography, continental drift, invertebrates, phylogeography, refugia.

Using GIS to predict how changes in sea level potentially influence phylogeographic patterns in freshwater and coastal marine fishes

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Most research within phylogeography has concentrated on first identifying a biogeographic pattern from their phylogenetic results and then explaining this pattern due to some earth history event. My goal is to shift the focus in the opposite direction. That is, to map relevant aspects of earth history across the landscape and then see how consistent these earth history patterns are relative to the phylogenetic data. If these aspects of earth history are important in determining biogeographic patterns then phylogeographic patterns should be fairly consistent with them. If the patterns are not consistent then it suggests that we need to find alternative explanations for the observed phylogeographic patterns and that the earth history factors are not strong forces with broad impact. Here I present two examples using different aspects of continental shelf width to predict phylogeographic patterns. The first quantifies the relative degree and difficulty of movement of obligate freshwater organisms between drainage basins via low sea level connections. The second aspect of this research is to quantify potential habitat for coastal marine fishes at different sea level heights to contrast potential changes in population size since the last low sea level stand. Using GIS I have developed datasets that allow researchers to visualize and quantify continental shelf width for any region of the world. I provide some examples that demonstrate the utility of this approach.

Population structure, demographic history, and signatures of selection among transposable elements in *Anolis carolinensis*

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It is crucial to understand the biogeographic and demographic history when estimating and characterizing the amount of natural selection at the genetic level. This study focuses on the population genetics/phylogeography of *Anolis carolinensis* in order to understand how natural selection may have shaped the genomic architecture of Long Interspersed Nuclear Elements (*LINE*) retrotransposons in this model reptile organism. Nearly 50 individuals were collected from 30 sampling sites in the Southeastern United States and approximately 500 loci, each over 500 base pairs, were gathered using anchored hybrid enrichment probes. After inferring population structure, we tested competing demographic models, including one, two, and three population models, various scenarios of post-divergence admixture, and population growth and compression trajectories. The population history will subsequently be used as a neutral background to scan for selection among approximately 70 *LINE*s and similar transposon markers. Reptile genomes contain an extraordinary diversity of active *LINE* families, and this study will determine a geographic component of *LINE*s, a first study of its kind.

Keywords: anole, *LINE*, phylogeography, genomic architecture

Phylogeography of a Cerrado endemic gecko: Using Species Distribution Modelling, Next-Generation Sequencing and morphology to disentangle complex phylogeographic scenarios

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Cerrado, the Brazilian Savanna, is the second largest biome of South America and one of the world's formally recognized 25 biodiversity hotspots. The squamate levels of endemism are higher than that of any other vertebrate group in this biome, with 42% of the Cerrado lizard species being endemic. Recent studies suggest a major role of ancient vicariant processes in shaping the biogeographic history of the region. However, there is still great debate considering the evolutionary origins and diversification patterns of the Cerrado herpetofauna. We used Species Distribution Modelling (past and present), morphological data, Sanger-sequencing and Next-Generation Sequencing to investigate the phylogeographic history of a Cerrado endemic

gecko, *Gymnodactylus amarali*. Using a hypotheses testing framework that combined paleoclimatic models and coalescent-based methods we could retrieve evolutionary patterns consistent with the geological history of the Cerrado. Results indicate a number of divergent clades within the species that possibly relate to cryptic speciation. Moreover, phylogeographic patterns appear linked to the tectonic uplift of the Central Brazilian Plateau, with deeply divergent groups found in disconnected plateaus and shallower divergences in the valleys. This study is part of an ongoing comparative phylogeography project that includes other two widely distributed endemic Cerrado lizards.

Keywords: *Gymnodactylus*, Squamata, Cryptic Species, Continent-Wide Phylogeography.

How can biogeography inform on DNA timber tracking?

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Technology has now reached the point where DNA fingerprinting can be used to independently verify declared sources of timber. Illegal logging is a scourge on global efforts to protect natural forests and the wealth of biodiversity they contain. Methods supporting robust supply chains and provision of non-falsifiable assurances of legality are therefore critical tools in the fight against deforestation and mass extinction. Current capabilities allow tracking of individual logs and verification of species. More exciting (yet more difficult) is the identification of source by ascertaining the statistical likelihood of a log originating from a particular population. With the right background knowledge, DNA timber tracking can confirm a legal declaration, or refute it, and potentially point to genuine geographic origin. As molecular techniques mature and more governments introduce legislation requiring robust due diligence on the part of importers, the need for extensive timber reference databases grows. The question then becomes, how do we best approach developing these databases? Much like for human DNA reference databases, the answer lies in biogeography. It's impossible to sample all individuals; instead we look for representatives from distinct groups based on our understanding of population structure, historical movements and shared ancestry. How do we do this with trees? What is the essential background knowledge? In the absence of detailed phylogeographical information, where should we start? Are there proxies we can use to inform our sampling strategy? Timber tracking is multidisciplinary endeavor... it's time to get the biogeographers involved.

Keywords: distributions, phylogeography

Lightning talks

(Poster 2)

Phylogeographic analysis of the supertramp swamphen *Porphyrio porphyrio* (Aves: Rallidae): diversification and gene flow with emphasis on the Indo-Pacific region

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The family Rallidae (Aves: Gruiformes) show lineages with high rates of historical diversification across insular landscapes with some species that are common to many islands, but also contains many island endemics (e.g. *Porphyrio*, *Gallirallus*, *Gallinula*). These lineages may exemplify the influence of directional asymmetry in colonization or the efficiency of natural selection overriding gene flow. Explanations may be sensitive to diversification rate; gradual break down in gene flow, or rapid species radiation following a wave of dispersal. The purple swamphen (*Porphyrio porphyrio*) has an extensive range from Africa and the Mediterranean east to the Pacific with many morphological variants that have been classified into ~13 subspecies or species. *Porphyrio porphyrio* is considered to be a reluctant flier but has nevertheless succeeded in reaching many oceanic islands, founding many distinct insular populations throughout the Indian and western Pacific Ocean. It has colonised New Zealand at least three times resulting in speciation of the large flightless herbivores *Porphyrio mantelli* and *P. hochstetteri*. We use mitochondrial and nuclear DNA sequences from the seven known species in *Porphyrio* and most of the *Porphyrio porphyrio* subspecies. We also sampled populations in New Zealand, Australia and Indonesia separated by >1500 km of sea, which provided an array of environmental heterogeneity to explore gene flow at different spatial scales. Our study uses phylogenetics and population genetics to reconstruct relationships and understand how is operating and affecting the influx of gene migration in the purple swamphen. Implications of analysis to date will be discussed.

Keywords: colonisation, evolution, phylogeography, Rallidae, speciation

(Poster 4)

Comparative phylogeography of three, banded iron formation endemics from semi-arid Western Australia

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The Yilgarn region of Western Australia is a geologically stable and ancient landscape comprised of multiple banded iron formations (BIFs) that behave as terrestrial islands within an otherwise flat, semi-arid landscape and are characterised by high species richness and endemism. Regional endemics, which are found on multiple BIFs but not the intervening landscape, provide an ideal context for phylogeographic analysis to examine patterns of genetic variation at both spatial and temporal scales. I present results from three species, a Spirostreptid millipede and two proteaceous plant species where cytoplasmic and nuclear DNA markers point to complex evolutionary histories that are characterized by long-term isolation of BIF populations, with little connectivity via migration or gene flow. Temporal patterns show isolation of populations during the Pleistocene, highlighting the importance of climatic fluctuations during this period in driving species diversification and differentiation within this landscape. The patterns revealed emphasize the need to conserve BIF populations owing to their unique, genetically differentiated nature.

Keywords: terrestrial islands, Pleistocene, short-range endemism, biogeography, Western Australia

(Poster 6)

Phylogenies reveal equilibrium processes along the latitudinal diversity gradient

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The latitudinal diversity gradient describes a decline in species diversity with increasing latitude, but the factors responsible for this prominent biological pattern remain unknown. Three major explanations have been proposed: tropical regions offer more ecological space for diversification, tropical regions are older, or tropical clades diversify more quickly. Although constant rates of diversification are often assumed when testing explanations for the latitudinal diversity gradient, a growing body of evidence suggests ecological processes can slow the diversification of a clade. In this study we present evidence for a latitudinal gradient in diversification rate slowdown in a large number of family-level phylogenies of mammals and birds. We did not find a latitudinal bias in diversification rate, so evidence for this hypothesis remains inconclusive. These results support a scenario in which tropical regions contain more ecological space for diversification. This suggests a significant role for equilibrium mechanisms

in shaping the latitudinal diversity gradient, contrasting with the focus of the majority of recent studies on non-equilibrium mechanisms.

Keywords: latitudinal diversity gradient, diversification rate slowdown, ecological limits, bird richness gradients, mammal richness gradients

(Poster 8)

Does the ‘island rule’ apply for birds? An analysis of morphological variation between insular and mainland birds from the Australian, New Zealand and Antarctic region

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The ‘island rule’ states that in islands, big animals become smaller and small animals become bigger. These morphological shifts have been generalized for all vertebrates as a strategy to better exploit limited resources in constrained areas with less interspecific competition and predation pressures. In the case of birds, most of the studies that validate this rule have focused on passerines, leading into a discussion on whether it applies to other orders or not. Another notorious insular morphological shift associated to the ‘island rule’ is greater sexual divergence in comparison to mainland counterparts. For birds, this insular strategy has been translated into a larger bill size variation influenced by the physical characteristics of each island. However, this remarkable sexual dimorphism has only been studied on California song sparrows, leaving into question its presence in other bird species and regions. This study aims to test the validity of the ‘island rule’ for many orders of the Australian, New Zealand and Antarctic region. In order to do so, I will compare and analyze existing morphological measurements for insular and mainland species occurring in the region, linking them with abiotic characteristics of each island. Significant differences in morphology between insular and mainland closely-related species are expected, validating this rule for different avian orders of the region. Moreover, a greater bill size variation between sexes in islands as well as relationships between some abiotic insular features and body size variation are predicted. The obtained information will help towards the conservation of this region’s unique avifauna.

Keywords: island biogeography, island ecology

(Poster 10)

Contrasting phylogeographic patterns of two co-distributed Australian freshwater rainbowfishAndrew Mather¹, Cynthia Riginos¹¹*The University of Queensland, Australia, a.mather@uq.edu.au*

Diversity in Australia's freshwater fish fauna is relatively depauperate when compared to other landmasses. However the family Melanotaeniidae, and the genus *Melanotaenia* is one of Australia's most widespread and speciose groups of freshwater fishes. This study uses two co-distributed *Melanotaenia* species to test the hypothesis that a widespread habitat generalist will have lower levels of genetic diversity and population structure than a closely related habitat specialist. We use mitochondrial and nuclear sequence data to investigate patterns of genetic diversity in *M. splendida* and *M. trifasciata* and to determine how differences in habitat preference and historical changes in drainage boundaries have affected patterns of connectivity and isolation. *Melanotaenia splendida*, a widespread species found in the vast majority of freshwater habitats in northern Australia, shows low levels of genetic diversity, and very little population structure across its entire range, with major genetic clades matching already described subspecies. Conversely, *M. trifasciata*, having a greatly contracted distribution to the northernmost rivers of Queensland and the Northern Territory and habitat preference to faster flowing, highly oxygenated upland streams, shows extremely high levels of population structure, with up to four genetically distinct clades found in Queensland alone. These results suggest that, although these species are co-distributed they appear to have experienced different evolutionary histories, with differences in habitat preference within waterways resulting in contrasting genetic patterns.

Keywords: biodiversity, biogeography, phylogeography

(Poster 12)

Patterns and predictors of genetic diversity within Indo-Pacific marine faunaJude Keyse¹, Cynthia Riginos¹, Eric A Trembl², Jonathan R Rhodes¹¹*The University of Queensland, Australia, judith.keyse@uqconnect.edu.au*²*The University of Melbourne, Australia*

The pattern of decreasing species richness of tropical marine taxa with distance from the Coral Triangle is well known and supported by data from numerous studies. A concordant pattern has been suggested in genetic diversity, with support from a few taxa, however this concordance has not been explicitly tested. In fact, little is known of the patterns and drivers of genetic diversity in the region, despite this level of diversity having important implications for the understanding of the evolutionary history and sustainable future of marine species. Genetic diversity data is often published in studies of the phylogeography or population genetics of a single or few species. These 'free' data can be used to answer questions on a larger scale than

the scale of their constituent parts, yet use of these data carries certain caveats. Data mining involves extensive searching and data entry, and the disparate sampling strategies of original studies result in patchy coverage. However, this technique allows synthetic approaches to answering some of the 'big questions' in marine biogeography. This research uses a literature search to collate studies reporting genetic diversity data for marine fauna in the tropical Indo-Pacific. We combine genetic diversity data from 108 species with species richness data for reef fishes and publicly-available spatial environmental data to consider which factors are associated with peaks of genetic diversity in the region.

Keywords: biodiversity, Indo-Pacific, synthesis, marine, macro-ecology

(Poster 14)

Deciphering the disjunct biogeographical patterns of Mindarinae: ancestral in East Asia but recently radiated in North America

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Mindaridae (Insecta: Aphididae) has disjunct distribution patterns at global and regional scales, high host plant specificity as well as reliable fossil records, which make this phytophagous insect group a good system to investigate important hypotheses in biogeography and evolutionary biology. Based on global sampling and molecular data from mitochondrial, nuclear and *Buchnera* (primary endosymbiont of aphids) genomes, with integration of biological and fossil data, we reconstructed the phylogenetic framework of Mindaridae, estimated divergence times for major clades, and investigated key issues such as the evolution of disjunct distribution patterns and species diversification driven by host plants. The major conclusions include: 1) several cryptic species have been revealed; 2) *Mindarus keteleerifoliae* in southwest mountains in China is the most ancestral species among all extant Mindaridae species; 3) a species complex in North America resulted from rapid radiations; 4) the disjunct distribution patterns have been jointly determined by relatively old and recent geological events; 4) host plant specialization and geographical factors have effected on species differentiation in Mindaridae.

Keywords: aphid, divergence time, host plant, phylogeny, speciation

Biodiversity turnover across spatial scales

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Abstracts

Patterns of diversity differentiation (beta-diversity) and environmental heterogeneity

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Since its inception beta-diversity has been a debated term. Recently, there has been a renewed interest in comparing the relationships between diversity measures whereas attempts to explore their different 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, and with environmental heterogeneity. We divided the metrics in two sets: pool-dependent and pool-independent. We used data from distribution maps of the IUCN for amphibians (6,188 species), mammals (5,276 species) and reptiles (2,357 species), and from Birdlife international for birds including more than 10,000 thousand species. To test the differences in the spatial patterns, we calculated the metrics by overlying a grid of 100 squares kilometers for all emerged land excluding the Antarctica (using the equal-area Berhmann's projection). Patterns were expected to vary among taxonomic groups, and so their relationships with environmental heterogeneity. Nevertheless, relationships among metrics and environmental heterogeneity varied greatly among groups.

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

Beta diversity and ecosystem processes: a macroecological perspective

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Biological diversity has long been thought to exert strong influences over ecosystem processes. Research into diversity-process relationships has linked higher diversity to stability of temporal processes, highlighted the role of functional traits and suggested that diversity effects increase with spatiotemporal extent. However, most work has focused on biological variation at single locations (α -diversity) in an essentially aspatial manner. The same concepts of diversity providing 'insurance' and 'resilience' against environmental fluctuations such as climate change can be equally applied at the metacommunity scale, using explicit spatiotemporal approaches. This requires a framework for integrating metacommunity dynamics with site-level effects to guide hypothesis testing. The 'insurance' effects of diversity have been attributed to spatiotemporally interacting communities across heterogeneous regions, facilitated by mechanisms such as response diversity, dispersal and connectivity. These mechanisms are inherently related to the biological variation *between* locations across regions (β -diversity). We present an ecological framework whereby local and regional β -diversity configurations provide feedback mechanisms, influencing local and regional ecosystem processes through functional 'effect' and 'response' traits. Macroecological analyses of β -process relationships face several key challenges. Principally, the influence of β -diversity should be separated from environmental variables, and spatiotemporal resolutions should correspond to the focal processes and ecological contexts. The framework outlined here aims to guide a generalised research program into macroecological β -process relationships, combining observational data with recent advances in spatial analyses, empirical modelling and spatiotemporal remote sensing.

Keywords: Insurance hypothesis, metacommunity, functional traits, spatial analysis, environmental change.

Tracking community stability through time: a phylogenetic and functional perspective

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Given limited scope for experimental manipulation in natural systems, a common approach in community ecology is to infer underlying processes from observed patterns. Inferring processes from patterns is of course non-trivial, relying as it necessarily does on a raft of soft assumptions about how the components of communities (i.e. species) respond to each other and their environment. This *modus operandi* is nowhere more apparent than in the phylogenetic and

trait-based approaches that have become increasingly popular in recent years. One potentially confounding factor of these approaches that has received comparatively little attention is the role of temporal change in the dominance of different processes and how this might affect observed patterns. Indeed, the vast majority of studies published to date have comprised 'static' analyses where assembly processes are inferred from patterns observed at a single snapshot in time. We investigated temporal stability in the phylogenetic and functional community structure of herbaceous vegetation over a 20 year period in a fire-dominated heathland. Contrary to expectations (and theory), phylogenetic community structure was relatively stable over time, with plots typically comprising species more closely related than expected by chance (phylogenetically clustered) throughout succession. However, early data exploration indicates that the apparent stability of phylogenetic community structure may be masking significant temporal turnover in both taxonomic and functional community composition. These provisional results not only highlight the importance of accounting for temporal instability in phylogenetic and functional community structure, but also strengthen the case for a multi-metric approach to studies of community assembly.

Keywords: community phylogenetics, beta diversity, stability

Environmental predictors of reptile species turnover and endemism vary among local, regional and national scales, an example from New Zealand

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To quantify reptile species turnover and endemism in New Zealand and assess whether these patterns correspond to the country's main biogeographic regions, which delineate areas of varying diversity and endemism. To quantify the associated turnover in environmental variables to assess how their influence on reptile distributions varies across different spatial extents and geographic locations. Directional variation in reptile turnover, endemism and spatial turnover in topography, climate and surface geology was measured using directional moving window analyses, rotated through 360°. These were applied to georeferenced reptile occurrences and environmental variables. Reptile turnover and endemism were correlated with environmental turnover surfaces at a national extent and also with these variables stratified into regional and local extents. A greater proportion of the variation in reptile turnover and endemism is explained once biotic and environmental patterns are analysed at local extents. In the upper North Island, associations between reptile and environmental turnover are predominantly positive, whereas they are negative in all other regions. Zones of low turnover comprise <11% of New Zealand, yet diverse reptile communities (72 species) comprising >50% of observations occur in these zones. High turnover zones are sparsely populated. Low turnover areas occur throughout New Zealand, both in regions regarded as high diversity or historical

glacial refugia, and also in regions regarded as biologically depauperate. The effects of environmental turnover on reptile distributions are most apparent when analysed at local scales. Biophysical relationships varied in different locations, such that relationships in one region are not predictive of relationships in another area.

Keywords: Biogeographic regionalisation, climate, endemism, New Zealand, reptiles, scale invariance, spatial turnover

Environmental drivers of turnover define Australian phytogeographical regions

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The definition of biogeographical regions is fundamental for understanding the distribution of biodiversity. The characteristics and terms used to define areas in biogeography are not always used consistently. Our phytogeographical regions of Australia were defined using quantitative analyses of species turnover, the rate of change in species composition between sites, calculated as Simpson's beta. Eleven environmental variables were used to analyze the environmental correlates of species turnover. Non-metric multidimensional scaling (NMDS) of the Simpson's beta (β_{sim}), ANOVA, Getis-Ord G_i^* hotspot spatial statistics were used to investigate the environmental drivers at the continental level and for each of the phytogeographical regions. We identified six major phytogeographical regions for Australia: Euronotian, Eremaean North, Eremaean South, Central-Eastern, South-Eastern, and South-Western. Here, we present a summary of the key environmental drivers that define such phytogeographical regions. We demonstrate how regions of geospatial turnover are defined by patterns of climate. We also found that some of the major flora groups such as *Acacia* and eucalypts have strong association to soil chemistry. As a result, the environmental drivers of phyto-regions of species turnover are broadly consistent with the continental patterns of summer and winter rainfall below and above the Tropic of Capricorn. Interestingly, there is also correlation to historical factors such as soil and landscape properties.

Keywords: Australia, biomes, environmental drivers, regionalization, species turnover β_{sim}

Modelling phylogenetic beta diversity for conservation gap analysis

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Mapping the distribution of elements of biodiversity is essential to understanding macro-evolutionary processes as well as to any planned approach for allocating resources to conservation. Rather than mapping the distribution of each individual species, recent approaches such as generalised dissimilarity modelling (GDM) use environmental data to model an emergent property of biodiversity: compositional turnover or beta diversity. A recent extension of these techniques, phylogenetic generalised dissimilarity modelling (phylo-GDM), brings together community composition, environment and phylogenetic data to create a spatial model of phylogenetic relatedness. The benefits of considering phylogenetic diversity in conservation planning have long been established, but such approaches are rarely implemented on a large scale. Here we apply phylo-GDM to model phylogenetic turnover in frog composition along Australia's east coast, the most diverse area for Australian frogs, with strong environmental gradients influenced by latitude, topography and proximity oceans. We use the resulting model, which predicts the compositional turnover between sites along these gradients, to estimate how well the existing reserve system represents frog phylogenetic diversity, and to identify areas where the underrepresentation is most severe. With the increasing quality and availability of phylogenetic data, we believe that this approach to assessing conservation status may be widely applicable to questions of reserve design, habitat loss and climate change.

Keywords: phylogenetic diversity, β diversity, amphibia, conservation planning

The importance of dispersal for tropical forest biodiversity under climate change

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Many studies have predicted significant changes in the distribution of species and the composition of communities under climate change. These predicted changes in the spatial distribution of biodiversity will strongly depend on the dispersal capacity of species, yet dispersal is rarely considered in projections of future biodiversity outcomes. In the Australian Wet Tropics, the seeds of most plant species are dispersed by frugivorous vertebrates, hence changes in plant diversity of these tropical forests under climate change may depend on concomitant changes in the dispersal services provided by frugivores. Here we apply a recently developed dynamic macroecological modeling approach to assess the possible outcomes for all 4,313 plant species in the Australian Wet Tropics under climate change, incorporating complex changes in frugivore mediated dispersal over space and time. We also examine differences in projected outcomes for plant diversity when much simpler assumptions are made regarding the

dispersal capacity of tropical plant species. Our analyses demonstrate the crucial importance of incorporating realistic dispersal processes in improving our understanding of spatiotemporal change in biodiversity.

Keywords: community, frugivory, macroecology, modelling, plants

Measures of species and phylogenetic turnover weighted by range-restriction

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Measures of spatial turnover estimate the rate of change in species composition or phylogeny across two or more sites. These help us quantify variation in the spatial distribution of biodiversity across geographic and environmental gradients, and are of particular importance for the identification of biogeographic breaks and ecological transition zones for collections of taxa. A key limitation of existing turnover metrics is that they do not consider the geographic ranges of the taxa. When searching for geographic breaks, any wide-ranging taxa that span a break or transition zone may dominate the results, lessening the measured turnover in such locations and thus making the identification of breaks more difficult. We have developed a suite of range-weighted turnover indices for both species and phylogenetic turnover, implemented within the Biodiverse software (<http://purl.org/biodiverse>). These indices weight the relative contribution of each taxon, or branch in a phylogenetic tree, by the proportion of the geographic ranges that are found in the sites for which the turnover is calculated. In this way the indices result in higher turnover scores when those taxa that are different between sites have narrow geographic ranges, and lower turnover when those taxa that are different are wide-ranging. We demonstrate the turnover measures using a continental extent data set of Acacias in Australia, including a 520 species phylogeny. The measures described have potential to be used as drop-in replacements for standard metrics in analyses such as agglomerative clustering, moving window analyses, and Generalised Dissimilarity Modelling.

Keywords: biodiversity, biogeography, distributions, phylogeography

Incorporating beta diversity into estimates of tree species loss 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 present a clear methodological pathway that links beta diversity with species loss through habitat destruction and is thus valuable for conservation planning. 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 originally occurring tree species that was lost due to habitat loss in the same year. We compare our estimate of species loss using this spatio-temporal method to another estimate of biodiversity loss: the Species Richness Index (SRI). The SRI is also based on the MSA metric and the species-area relationship, and calculates the fraction of originally occurring species that survives land use change. Areas of high species turnover most affected by habitat loss include ecoregions in 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, conservation, land use change, biogeography, mean species abundance

Changes in phylogenetic structure of a bird community along an elevational gradient, in Eastern NSW

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There is an established negative relationship between elevation and species diversity (SD), but the relationship with phylogenetic diversity (PD) is poorly known. As such our study aimed to

assess the changes in bird PD across a range of altitudes (500-1450m) in Barrington Tops NP. As expected, a significant negative relationship between elevation and SD was found within our location. PD and functional diversity (FD) also decreased with elevation. PD however, increased significantly once covariance with SD had been corrected for, thus showing increasing phylogenetic dispersion with altitude. Corrected FD showed no significant relationship with elevation. There was significant species turnover with differences in elevation but this pattern was much weaker for phylogenetic and functional turnover. We propose that increasing phylogenetic overdispersion with increasing altitude is caused by a loss in ecological redundancy, with each major clade being represented by fewer species in higher altitude communities. If closely related species occupy similar ecological niches (phylogenetic niche conservatism), diminishing resources at higher altitudes will limit the number of members of each phylogenetic group. This hypothesis is further supported by the relatively weak phylogenetic turnover, indicating that the composition of major clades did not change with elevation. The differences in corrected PD and FD may be due to PD being a better functional surrogate than FD, with FD relying on a subjective choice of morphometric measurements, which do not always accurately reflect function.

Keywords: phylogenetic diversity, functional diversity, phylogenetic community analysis, avifauna, Australia

Influence of past sea-level changes on global-scale patterns of freshwater fish beta diversity

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Unrevealing the role of past climate changes on current biodiversity has been an active research area. During the Last Glacial Maximal, the sea was 120m below the current level and river mouths considerably progressed through kilometers of exposed marine shelves before reaching again the ocean, resulting in the connection of currently isolated rivers and an important reconfiguration of adjacent river basins (paleobasins). We test the hypothesis that paleobasins promoted freshwater fish species exchange producing high levels of species similarity and low beta diversity among connected river basins. By analyzing fish species composition of river basins within six biogeographic zones and controlling for key environmental factors, we found no differences in mean fish similarity but a slighter distance-decay of similarity in river basins that were connected during the LGM compared to disconnected ones. Using the shore depth at the point of river coalescence as a proxy of time since disconnection, we found support only in Indomalaya and Neotropical biogeographical zones to the hypothesis that a longer period of paleoconnection should result in greater fish species exchange (i.e. high fish similarity). Our results demonstrate the role of migration during low sea at the Last Glacial Maximal and

emphasize the role Quaternary climate change in determining current fish species beta diversity at broad spatial scales.

Keywords: Last Glacial Maximum, paleobasins, distance-decay of similarity, species turnover, historical climate effects, freshwater biogeography.

Turnover of deep-sea brittle stars (Ophiuroidea) across Australia, New Zealand and Antarctica.

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The deep sea is increasingly being exploited for fisheries and mineral resources. Describing and visualizing turnover of deep-sea (200-2500 m) biodiversity is urgently required by government and international agencies for area-based conservation and resource management. Despite thousands of research expeditions, our knowledge of large scale biogeography in the deep sea is largely based on qualitative analyses or environmental surrogates. A method of mapping turnover based on statistical analysis of distribution data has remained elusive. This study examined beta diversity of brittle star species (Ophiuroidea) across Australia and New Zealand, based on modelled distributions. The nature of data available from the deep-sea severely restricts the types of analyses available for use. Here we use a 'predict and then assemble' approach to determine regional and inter-regional changes in species composition. Our results suggest the presence of transitional zones rather than abrupt biogeographical breaks. Regions of high dissimilarity change drastically depending on the scale at which turnover is modelled, reflecting the contrast between local turnover and regional uniqueness. Models of turnover will help describe biogeography in the deep-sea and contribute to developing a strategy for broad-scale spatial prioritization for bathyal marine ecosystems.

Keywords: biodiversity, biogeography, beta-diversity, marine conservation, spatial scale.

Endemism, vicariance and distribution patterns of Cerrado herpetofauna (Brazil)

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The search for congruent geographic distribution patterns among groups with different evolutionary origins is fundamental to understand the events involved in the construction of

biotas. One prediction that can be derived from the vicariance model is the existence of Biotic Elements (BEs), groups of taxa whose ranges are significantly more similar to each other than to those of taxa of other such groups, as a result of historical barriers to dispersal. Another prediction is that closely related species belong to different biotic elements. Here we use biotic element analysis to find shared geographic distribution patterns among endemic squamates and anurans in the Cerrado, the largest block of Neotropical savannas, extending across central Brazil. We found four BEs for Anura and seven BEs for squamates. The closely related species of those two groups are homogeneously distributed across biotic elements. When we join all species of anurans and squamates in the same analysis, we found seven BEs with different species proportions in each group. However, in this case, closely related species belong significantly more often to the same biotic element than expected by chance. Despite the results with anurans and squamates alone, the vicariant signal disappears when we put together both groups with different evolutionary origins.

Keywords: Anura, Squamata, biotic elements, savanna, *hotspot*

Towards a global biogeography of the deep seafloor using distributional data of squat lobsters

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Maps of the world's seafloor fauna are long overdue. The most recent biogeographic classification including bathyal and abyssal depths (Global Open Oceans and Deep Seabed, 2009) relies on environmental surrogates. The lack of maps defined on the distribution of species hinders spatial marine management across nation's EEZs and the high seas. Our project aggregates distribution records for deep-sea brittle stars (Ophiuroidea) and squat lobsters (Galatheaidea and Chirostyidea) from museum collections, the literature and other databases. With the collaboration of expert taxonomists, we have collated more than 20,000 occurrences of squat lobsters from across the globe. Species distribution models were used to create maps of distribution. By combining multiple species distribution maps, we then use multivariate techniques of clustering and ordination to examine global biodiversity turnover and present biogeographic maps of the deep-seafloor.

Keywords: marine, modeling, presence only, species turnover, classification

Marine genetic diversity and connectivity around Australia: a synthesis

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While some marine species show limited genetic structure, due to long pelagic larval stages and large effective populations sizes, 'in others' genetic breaks' have been identified, and these can be geographically congruent across species. Combining information across many species can provide insight into broad patterns and processes, allowing greater understanding of a system. Knowledge of patterns that are common across many species can also provide a stronger basis for conservation and management. We have constructed a database containing published records of population genetic diversity and 'connectivity' from marine species around Australia. We identify regions of high and low genetic diversity using both randomization and Bayesian conditional autoregressive (CAR) analyses. We then identify locations of high and low 'connectivity' using a sliding window analysis of linearised pairwise F_{ST} estimates around the Australian coastline, as well as using a Bayesian approach. Using a suite of environmental variables we consider what factors may be driving these general patterns.

Keywords: phylogeography, marine, Australia

The value of ecology in conservation biogeography – elucidating bat community assembly patterns across a restored landscape in south-western Australia

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Biogeography and ecology share the similar view of seeking to identify patterns in the natural world, albeit at different spatial and temporal scales. Community assembly is one aspect of both disciplines where it is particularly important to integrate both, as ecological niche concepts incorporate biogeography. We examined community assembly using both traits-based and species-specific approaches to investigate the importance of scale on trait dispersion/convergence in an area affected by both local (habitat loss) and global (drying climate) processes. We studied bat echolocation call activity across a restored landscape, 64 sites in a mosaic of restored and unmined forest, in the biodiversity hotspot of south-western Australia. Our study occurred during one exceptionally dry year and one year with average rainfall. Bat community assemblage within restored forest was distinct from unmined forest, but only during the dry year. Larger, heavier bat species with long, narrow wings and low echolocation frequencies were associated with the younger restored forest while the more maneuverable species with higher echolocation call frequencies were associated with unmined forest and increasing canopy height and cover. Our findings resonate with general hypotheses of community assembly predicting: i) neutral assembly when environmental adversity is weak

(average rainfall) but not when strong (dry year); and ii) trait divergence at small spatial scales where species interact but neutral assembly as scale increases (bat use of restored sites differ but all bats occur within the restored landscape).

Keywords: ecological filtering, drying climate, bauxite mining

Climatic legacies in European plant functional diversity geographical patterns

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It is increasingly clear that both current and historical climatic conditions are two of the main determinants of species diversity patterns over large geographical scales. It is, however, less clear if historical effects also extend to functional diversity, which directly links species diversity to community and ecosystem functioning, but may itself be under stronger control by current environment. To address this, we here first quantified functional diversity (FD: richness, evenness, dispersion) for ~50×50-km grid cell plant assemblages across Europe, and estimated how current climate constrains maximum plant functional diversity (maximum FD). We then quantified the proportion of the maximum FD realized per grid cell (realized/potential [R/P] FD ratio). We predicted that the R/P FD ratio would increase with increasing climatic stability (slow Late Quaternary climate-change velocities) and decreasing distance from glacial refugia (reduced postglacial dispersal limitation). Across the evaluated region, R/P ratios were consistently high with lower bounds ranging between 40% and 86%. In accordance to our expectations, there was a significant effect of historical stability in the geographic variation of R/P FD ratios, with proximity to ice-age forest refugia (a index of postglacial re-colonization potential) showing the highest explanatory power. Our contrast of realized and maximum potential FD for the European flora provides evidence that local functional composition of a site often does not realize the full FD possible given the current local environment due to constraints posed by past climate instability and subsequent dispersal limitation.

Keywords: functional diversity; Europe; climatic stress; environmental heterogeneity; productivity; climatic stability; climate change; climate velocity; Quaternary; Holocene; Pleistocene; spatial autoregressive modeling

The race for new space: density-blocking masks dispersal and shapes biodiversity patterns

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Although dispersal is one of the fundamental processes underpinning the evolution and distribution of biodiversity, emerging evidence suggests that scientists routinely underestimate the frequency of dispersal events, and that most studies are inadequate for detecting such processes. This systematic bias occurs because competitive exclusion from residents can prevent the successful establishment of immigrants, even in cases where dispersal is frequent. Founding lineages can rapidly dominate the available niche space of newly-colonised territory, quickly reaching population densities that can effectively block colonisation by later arrivals. When founding populations monopolise resources, and local recruits substantially outnumber immigrants, this 'density-blocking' renders latecomers, including conspecifics, ineffective. Local extirpation of invasive species or lineages can, however, facilitate rapid new invasions by releasing population-density constraints. Evidence is mounting that a substantial component of global biogeography can be explained by these processes, and that they will continue to shape ecosystem structure in the wake of anthropogenic environmental change. This talk will discuss emerging molecular evidence for widespread density-blocking processes operating across a range of fields and spatio-temporal scales, and provide specific examples and insights from phylogeographic research on various taxa from penguins and invasive rats to seaweed.

Keywords: biodiversity, distributions, phylogeography, founder, density, invasive species, dispersal

Exploring moving range edges in parapatric distributed passerines: From climate, genes and biotic interactions

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Dynamic systems like moving contact zones are particularly interesting objects. First, climate and biotic interactions are major factors that shape species distributions, and disentangling their relative effects may be expected. Second, rapid range shift may strongly alter the genetic structure of a species which in turn may affect its dispersal, and the dynamics of the zone itself.

Many empirical and theoretical studies have dealt with only one part of the problem but they rarely tried to link the two questions which moving contact zone offer the opportunity to do. The two parapatric passerines *Hippolais icterina* and *H. polyglotta* form a moving secondary contact zone in Europe. The contact zone has been moving northeastward for at least 70 years. We used species distribution modelling to assess the relative effects of climate and interspecific interactions on the zone movement. We further analysed the genetic structure of the two species along a transect that crossed both allopatric ranges and the contact zone. Although the zone shift is consistent with a climate warming scenario, interspecific interactions limit the range edge of each species. Moreover, both species maintained their genetic diversity and structure despite the rapid zone movement, indicating their low susceptibility to climate change so far. Although an increasing number of moving zones is being reported, the proximate causes of movement remain unclear in most cases. In the general context of global change, we call for more research on interactions between these processes and the possible genetic consequences.

Thesis prize winner abstract

Population genetic and phylogenetic insights into the phyllosomal odyssey

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Most marine species maintain genetic connectivity through pelagic propagules, with pelagic duration hypothesized to limit dispersal potential. This dissertation investigates the geographic scale of genetic connectivity when pelagic duration is not limiting. I analyzed mtDNA sequences and microsatellites to determine patterns of genetic structure across the geographic distributions of three lobster species: *Panulirus penicillatus* (Red Sea to the East Pacific Ocean), *P. interruptus* (sub-tropical East Pacific), and *P. marginatus* (Hawaiian endemic). At the broadest spatial scale, significant genetic discontinuities for *P. penicillatus* correspond to provincial biogeographic boundaries, including putative species-level disjunction across the East Pacific Barrier. On a smaller scale, novel kinship analyses combined with traditional *F*-statistics indicate that larval behavior and oceanographic processes result in localized recruitment for *P. interruptus*. Geographic scales of connectivity vary by location and species, even in Hawai'i, where *P. marginatus* and *P. penicillatus* co-occur. These findings indicate the combined effects of geography, ocean currents, and biology overcome extremely long pelagic periods and result in variable degrees of dispersal.

Keywords: marine connectivity, larval behavior, pelagic larval dispersal, spiny lobster, phylogeography, population genetics

Poster Abstracts

For abstracts of Posters 1-14, please see Lightning Talks

Poster 15

24 years since the arrival of the invasive dung beetle *Digitonthophagus gazella* (Coleoptera: Scarabaeidae) to South America: dispersion process and population effects on native species

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The process of invasion of a foreign species consists of the overcoming of different barriers, managing to generate in some cases negative effects on biodiversity and ecosystem functionality. This is the case of the dung beetle *Digitonthophagus gazella*, which was intentionally introduced around the world with the main purpose of increasing the rate of waste removal, soil fertilization and fly control. The first introduction in America continent was in 1970's in USA, since then, it has increased its range through deliberate introductions and by natural spread, establishing a high mobility from Central to South America. Now, it is the most widespread dung beetle in tropical and subtropical pastures. In Colombia it was registered in 1995 and subsequently studies have been realized with the purpose of establishing their process of dispersion and to determine the magnitude of their effect on native populations. In one locality in Colombia its arrival and establishment was monitoring in three years: 2007 (before the arrival of *D. gazella*), 2009 (during the arrival) and 2011 (two years after the arrival) quantifying the abundance, richness and biomass of the assembly. In 2007 the dominant species was *Onthophagus marginicollis* (66%). In 2009 with the arrival of *D. gazella* the proportions of the dominant species changed and for 2011 *D. gazella* became the dominant species (96% of the assemblage) causing a noticeable reduction in the abundance of other species. This results evidence a negative effect on local populations, doing essential to generate monitoring plans to find control and conservation mechanisms.

Keywords: assemblage, biomass, ecosystem functionality, invasive species, *Onthophagus marginicollis*.

Poster 16

Biogeography and Biodiversity of Sri Lanka

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Sri Lanka is considered as a biodiversity hotspot in the world. Some of the contributory factors for high biodiversity and endemism are its location in the world & its geological affinity with mainland, topographic variation, climatic variation and biogeographic history. Sri Lanka is an

island in the Indian Ocean close to the equator and one of the oldest and most stable parts of the earth's crust. It has a total area of 65,610 km², with 64,740 km² of land and 870 km² of water. Climate of Sri Lanka is determined mainly from the north east monsoon and the south west monsoon. There are mainly 6 bioclimatic zones namely; low & mid country wet zone, dry zone, low & mid country intermediate zone, montane wet zone, montane intermediate zone and arid zone. When considering the biodiversity of Sri Lanka it has the highest diversity per 10,000 sq km in South Asia for amphibians, reptiles & flowering plants and second highest in birds. Sri Lanka has a remarkable percentage of endemism. 100 % (51) of freshwater crabs, 86 % (88) of amphibians, 83 % (204) of land snails, 54 % (44) of fresh water fishes, 51 % (94) of reptiles, 26 % (870) of flowering plants, 18% (57) of ferns are endemic. Sri Lankan biodiversity is under threat. 223 vertebrate species, 157 invertebrate species and 675 plants are threatened. 62 % of threatened vertebrates and 61 % threatened plants are endemic. 21 amphibians and 72 flowering plants used to be Sri Lankan endemics are already extinct.

Keywords: Endemism, hotspot, threatened species

Poster 17

Prediction of the distribution of arid shrublands in Australia as a function of climate

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Considering climate is the major control of shrubland distribution, we develop a model to predict the distribution of six types of shrubland in Australia (Mallee, Tall closed, Acacia, Heathlands, Chenopods, and Other shrublands). We used Canonical Correspondence Analysis to investigate relationships between 25 climatic variables, using ANUCLIM 6.1 and the Australian Water Availability Project (AWAP 3.1) datasets, and the abundances of shrubland types using NVIS dataset. We used generalized linear modelling to construct a model of the probability of shrubland occurrence as a function of the three climate variables as determined by the Akaike Information Criterion (AIC). We tested the agreement between observed and predicted shrubland probabilities using the kappa statistic. The distribution of shrublands in Australia can be predicted using climatic factors: photosynthetically active radiation during the period above 0 °C (PAR₀), the Prentice-Cramer plant moisture availability (α), and the difference in the moisture content of soil layers in summer (Dif_lyrs_sum). The overall distribution of shrubland vegetation was predicted with fair agreement (kappa: 0.4). The distribution of the shrubland types was geographically correct and the measured agreement with observations was excellent (kappa: 0.84). The extent of shrublands was overestimated, possibly reflecting the variability of vegetation within the major vegetation group classification used for the analysis. The distribution of arid shrublands of Australia can be predicted using the niche model approach specifically in response to the availability of energy during the growing season measured by PAR₀, annual moisture availability (α), and availability of summer moisture in deeper soil layers (Dif_lyrs_sum).

Keywords: Arid shrublands, climate, modelling, niche model, prediction

Poster 18**Coral reef fishes: the origins of biodiversity hotspots and biogeographic patterns**

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The world's largest marine biodiversity hotspot is centred in the Indo-Australian Archipelago (IAA). Much study in this region has concentrated on processes maintaining species richness within the hotspot, with less emphasis on the origin of the hotspot itself and the taxa that form it. Here, we explore the origins of four diverse reef fish families (Labridae, Pomacentridae, Apogonidae, Chaetodontidae) with phylogenetic and biogeographic methods. LTT plots reveal a possible late Eocene/early Oligocene cryptic extinction event coinciding with the collapse of an ancestral Tethyan/Arabian hotspot. Diversification models reveal elevated cladogenesis in all families in the Oligocene/Miocene. Lineages with a high percentage of coral reef associated taxa display significantly higher diversity than expected, with coral reef affinity providing a possible refuge from high extinction. Biogeographic reconstructions reveal marked temporal congruence in origination and dispersal across the marine tropics. The East Pacific and Atlantic have a history of isolation, developing from broader connectivity with the Indo-Pacific from the early Eocene. The IAA has a history of connectivity with adjacent regions, having sequentially, and then simultaneously acted as a centre of accumulation (Palaeocene/Eocene), survival (Eocene/Oligocene), origin (Miocene), and export (Pliocene/Recent) for reef fishes. Coral reef association may provide a mechanism for cladogenesis in several reef fish lineages in the Miocene, however, it appears that the expansion of reef habitat in the mosaic of island archipelagos in the IAA hotspot has allowed the survival, proliferation and expansion of coral reef fish lineages to form the hotspot that we see today.

Keywords: coral reef fishes, phylogeny, Lagrange, DEC model, ancestral biogeography

Poster 19**Plant diversity hotspot as a historical product under imminent threats**

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Understanding the conflicting pattern between biodiversity hotspots and anthropogenic activity is critically important for developing systematic conservation/prioritization, and further maintaining ecosystem services related to our sustainability. We report an exceptional historical process that generating plant diversity patterns and its endemism in the Japanese archipelago, in conjunction with our footprints. We built a database on geographic distributions of 5518 vascular plants by compiling primary sources including the data of species occurrence. Combining species occurrence and nine environmental variables, potential species distributions at 10 × 10 km grid scale were predicted by Maxent. Species distribution maps were overlaid,

and then geographical areas harboring high species richness and endemisms were identified. Historical constraints in the formation of hotspots were analyzed using linear model including historical and current factors, and spatial autocorrelation. We also evaluated anthropogenic impact using a human footprint index, and examined its geological overlapping with the diversity hotspots. Historical habitat stability (abiotic perturbation due to paleoclimate oscillation, Quaternary volcanism and marine transgression/regression) predominantly determined the diversity hotspot and centre of endemism through species persistence/accumulation during ice-age and allopatric speciation in isolated areas, which blurred the influence of energy on the current diversity patterns. Plant diversity hotspots as a historical product were congruent with geography of our ecological footprints, demonstrating that evolutionary potential of plant diversity hotspots is under imminent threats. Our results emphasize the importance of conservation biogeography from historical point of view in designing conservation area for plant biodiversity hotspots.

Keywords: Conservation biogeography, endemism, human footprint, Quaternary volcanism, vicariance

Poster 20

Identifying the relative importance of historical and ecological factors on global biodiversity pattern of Scleractinia corals

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One of the central goals in ecology is to reveal the mechanisms that generated geographical patterns of biodiversity. In the marine biomes, multiple mechanisms have been proposed to explain global biodiversity patterns, specifically focusing on ecological processes (the role of environmental filter and habitat area) and historical processes (the centre of origin and dispersal). Because the global biodiversity patterns are not the result of a single process, quantifying the relative importance of historical and ecological factors is a fundamental challenge for macroecological studies. In the previous studies, the role of historical processes in shaping biodiversity patterns has often been examined based on taxonomic information such as species richness. However, this approach is insufficient when evaluating the influence of historical processes on biodiversity patterns. Phylogenetic community approach is a promising framework to identify the relative importance of historical and ecological factors on marine biodiversity patterns. In this paper, we analyzed the phylogenetic data that comprising 128 scleractinian coral species from 68 genera of 16 families, and calculated the metrics of phylogenetic community structure at the global scale. We examined the effects of distance from the centre of the tropical Indo-Western Pacific, mean sea-surface temperature (SST) in the coldest month, seasonal variation of SST and coastline length on phylogenetic diversity, phylogenetic species variability, phylogenetic species clustering and phylogenetic beta diversity. These analyses were conducted using multiple linear regression models. Based on the results, we discussed evolutionary mechanisms that generated global biodiversity patterns of scleractinian corals.

Keywords: biodiversity hotspot, historical biogeography, marine macroecology, phylogenetic community structure, phylogenetic diversity

Poster 21**A methodology to estimate Extinction Debt for Mammals in a Fragmented landscape of Mexico**Mora Franz¹, Trejo Isabel¹, Munguía, Mariana¹¹CONABIO Mexico, Mexico City, fmora@conabio.gob.mx

Habitat loss is the most prominent impact on species survival. Extinction debts occur because of time delays between direct impacts on species', due to habitat destruction. Therefore many animals can persist in local habitats after they may be committed to extinction. In this study we detect the number of species likely to go extinct. The methods used included an allometric framework that evaluates the spatial requirements of species' survival, along with the loss of habitat. Habitat destruction change the landscape into a set of remnant patches with natural characteristics that allow their prevalence. Habitat loss may result in different mammalian composition within those remnant patches, particularly because some species are more sensitive than others in their spatial requirements. Results for 240 mammals in Mexico showed that individual life traits are highly associated to the proneness to extinction, and therefore to the extinction debt. The proneness (measured as the loss of habitat for viable populations) increases with body size, and for specialist at the higher trophic levels. Nearly 32% of all species analyzed have habitat loss greater than 40%. Species in this situation includes almost all meso-carnivorous (i.e, *C. latrans*) meso-omnivorous (*U. americanus*) and almost all meso- herbivores (i.e, *T. bairdii*) with the exception of big-size herbivores generalist (i.e, *O. virginianus*). The highest habitat loss rate was observed for top carnivores (i.e, *P. onca*). Transformed habitats in Mexico (roughly 35% of national territory) has resulted in a extinction debt > 50%, which is higher than estimates for climate change impacts.

Keywords: mammals, composition, distributions, patches, viable populations.

Poster 22**Plans for Phylogeographic Analysis of a Widespread Australian Lizard**Gabrielle Openshaw¹, Alison Fitch², Stephen Donnellan^{3,4}, J. Scott Keogh¹

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Ridge-tailed monitors (*Varanus acanthurus*) are a successful group of Australian lizards, widespread across Western Australia, the Northern Territory, northwestern Queensland, and associated offshore islands. Individuals differ greatly in morphology, as well as inhabiting a variety of habitats across their range, making them ideal for phylogeographic analysis. Mitochondrial DNA (ND4) in over 180 *V. acanthurus* specimens has recovered three major

lineages: (1) a lineage from Cape Crawford (NT) which is the sister group to the other lineages; (2) a lineage corresponding to *Varanus acanthurus insulanicus*, found on islands off the coast of Arnhemland, and most closely related to the 'sister' species *Varanus baritji*; and (3) a lineage containing all remaining samples, that is further subdivided based on geographic location. Broadly, these results suggest there is high diversity and genetic structuring in areas of environmental complexity through the Kimberley and NT, and low diversity through the expansive arid interior. We aim to extend this work to genomic-scale analyses and integrate topographic analyses to identify whether major splits in the tree, or changes in diversification rate, correspond with changes in Australia's landscape. Finally, we aim to test whether present-day genetic lineages relate to differences in morphology and habitat across the species' range.

Keywords: *Varanus acanthurus*, phylogeography, morphology, taxonomy

Poster 23

Ecological niche modelling and phylogeography of two sister species with different thermal ranges

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In Australia, arid regions have been dominating the ancestral mesic habitats, but phylogenetic conservatism of climatic tolerances constrained the ability of the majority of species lineages to shift from mesic to arid environments. Within *Carlia* skinks, an unusually mesic tropical genus, just few species have colonized the arid centre of Australia. One of the main interesting cases is the comparison of the widespread *C. triacantha* and its sister species *C. johnstonei*, which is restricted to mesic northwest Kimberley. The use of combined phylogeography and ecological niche modelling (ENM) is a powerful approach to understanding the relationship of environmental history, niche evolution and speciation. Hence using a combination of these methodologies we are exploring how the former species achieved its current distribution and how it relates to the niche divergence history within the genus. This work provide some preliminary results that combined with other methodologies (demographic and selection analysis of genomic data, and physiological information), will allow us to understand how species with different thermal constraints will respond to predicted future climate scenarios.

Keywords: skinks, *Carlia*, mtDNA, Australia, niche divergence

Poster 24

Divergent lineages overlap in geographic ranges and climatic preferences in a biodiversity hotspot

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The geographic and ecological processes that have led to species evolution and patterns of distribution around the globe have been central questions of evolutionary biology. One of these questions is how ecological preferences and geographic ranges change in relation to one another during species divergence. It has been suggested that divergent species can overlap along geographic or environmental axes, but not both. However, studies investigating both ecological and geographic patterns of species divergence simultaneously are scarce. The Cape Floristic Region (CFR) in southern Africa is an ideal region to study these patterns: it is one of the world's biodiversity hotspots, harbouring ca. 9,000 plant species, 70% of which are endemic to the region, within an area of approximately 90,000 km² with outstanding ecological diversity. Here, using extensive occurrence data and time-calibrated molecular phylogenetic trees, we investigate climatic and geographic patterns in the evolution of three largely endemic plant lineages of the CFR: the Proteaceae family, the legume tribe Podalyrieae and the genus *Babiana*. We find substantial overlap in geographic ranges and climatic preferences in the shallow nodes of the phylogenies. Further, when we explicitly test simultaneously for partitioning along the axes of geography and climate we demonstrate that species occupying similar niches tend to overlap substantially in their geographic ranges and vice versa, and this pattern was stronger for close relatives. Our results show that divergent species do not tend to partition geographic ranges or climatic preferences, suggesting that other mechanisms have driven plant species divergence in the CFR.

Keywords: Cape Floristic Region, geographic range, niche, species divergence

Poster 25**Estimating trophic complexity of predator-prey interactions in a fragmented landscape using complex network and species distribution models**Constantino González-Salazar¹, Franz Mora¹, Mariana Munguia¹, Isabel Trejo¹¹CONABIO, México, cgsalazar7@yahoo.com.mx

Habitat loss and fragmentation are major threats to biodiversity. Nowadays, in order to identify the effects of habitat loss, most studies have been focused on specific animal or plant species. However, few studies recognize that species are not isolated and they belong to a network within a biotic community. Therefore, studies in this direction are needed because when a specific species is lost, a complex network of interactions will be affected. Then, we studied the effect of species loss on complex networks within a fragmented landscape. We used Complex Networks (CN) and Species Distribution Models (SDM) to estimate and map the effect of species loss on predator-prey interactions of non-volant mammals in Mexico. We used data mining techniques to construct CN from geographic data and to infer potential predator-prey interactions. When analyzed, we identified seven top predators and their potential preys. Then, we used SDM's with and without habitat loss effects for predators and preys to estimate trophic complexity using geographic information systems. Complexity was calculated as $SC_{max} = S(L/S [S-1]/2)$; where L is the number of trophic links observed and S is the number of trophic elements in the network. Maps showing trophic complexity (i.e., the number of trophic links (L)) described a gradient from low to high complexity as a function of the presence and/or absence of a predator or prey. When patterns of habitat loss effects were compared, drastic changes in trophic complexity were identified after anthropogenic effects impacted natural habitats.

Keywords: biotic interactions, data mining, habitat loss, biodiversity, mammals**Poster 26****Genetic legacy of Quaternary climate changes in temperate East Asia: insights from the phylogeography of Chinese scorpion, *Mesobuthus martensii***Cheng-Min Shi¹, De-Xing Zhang¹¹ Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China. shicm@ioz.ac.cn

There is wide spread agreement that climatic changes have dramatically affected biota on the earth, as climate sets the baseline conditions under which species can persist and form viable populations across space and time. The Quaternary was characterized by extensive change of the global climate, but with varying modes and extents across the geographic locations. Temperate East Asia (TEA) is such a place where the Quaternary environment was profoundly influenced both by the global glacial oscillations and by localized geological/geographical features. Although no continental ice sheets developed in TEA during Quaternary, the far-field effects of ice sheets have led to drastic environmental changes in step with the global glacial cycles, expressed as sea level fluctuations near coast and aridification of inland. The biological consequences of these environmental changes have been suggested by palaeo-environmental evidences, but not explicitly tested using modern molecular phylogeographic approaches,

largely due to our unevenly limited knowledge in the Asia. We tested the relative role of these environmental changes on genetic architecture of TEA through range-wide phylogeographic analysis and ecological niche modeling of Chinese scorpion, *Mesobuthus martensii*. Our results indicated that the climate change impacted the phylogeography and demography of Chinese scorpion in different mode and extent at different geographic locations. The final outcomes were molded by both short-term climate oscillations (related to glacial cycles) and long-term climatic shifts (aridification trend), which were spatially tuned by geographic settings.

Keywords: demography, ecological niche modeling, aridification, sea level change, China

Poster 27

Monitoring of helocrenic forest springs as a solution to the riddle of regional-scale climate change effects

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Recent models about climate change impact on biodiversity and, thus, ecosystem functioning are based on knowledge about species response to environmental changes. This knowledge mainly derives from local-scale and short-run experimental studies. Based on a long-term (24 years) and regional-scale monitoring of helocrenic forest springs, which occur in a high spatial density in the lower mountain range of north-eastern Bavaria, we are able to assess and predict climate change effects on regional-scale ecosystem processes. Solutes from the whole spring catchment, which seep out of the ground punctually at the spring sites and are affected by long- but also short-term shifts in environmental settings were already shown to affect spring vegetation, which is evolutionary adapted to the naturally constant spring habitats. Furthermore, different degree of compositional vegetation turnover as a response to the climatic extreme summer drought 2003 could be shown for the surveyed springs in recent analyses. Both facts emphasize the potential of helocrenic forest springs to monitor climate change effects on regional-scale ecosystem processes in a comprehensive way. Information about spring water and vegetation response to short-term climatic events like extreme drought or precipitation as well as long-term climatic shifts like increasing average temperature will be used in our research project to understand system resilience and resistance of forest springs. The understanding about the drivers of compositional vegetation turnover in helocrenic springs will be used subsequently to model future effects of climate change on forest ecosystems. The results from this study will primarily assist forestry and nature conservation authorities to develop regional scale management strategies to cope with the effects of ongoing global climate change.

Keywords: forest ecosystems, crenic habitats, monitoring tool, physico-chemical water characteristics, vegetation turnover

Poster 28**Harnessing the Power of High-Throughput: Using Targeted Enrichment of DNA Ultraconserved Elements for the Phylogenomic Analysis of Coral Reef Fishes**

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Traditional phylogenetic methods have yet to uncover exactly how and when the modern coral reef fish fauna evolved. Increasing resolution in comparative phylogenetics would require the generation of datasets that sample large numbers of both taxa and genetic loci. The generation of such datasets poses a challenge to traditional PCR-based methods that are limited to performing a single reaction at a time, per gene per species. Alternatively, we present the use of a novel set of genetic markers, DNA ultraconserved elements (UCEs), in the first genomic-scale analysis of percomorph fishes. Percomorph fishes include over 16,000 species and the majority of the known reef-associated fish families. We used sequence capture, targeted enrichment, and high-throughput sequencing to efficiently and economically sequence over 1,000 UCEs and their variable flanking DNA—six times more loci than the largest published datasets to date. Species trees were constructed using maximum likelihood, resulting in a phylogeny that recovers previously disputed relationships with greater than 95-percent bootstrap support. These include the monophyly of Ovalenteria, sea-floor dwelling fish families, and the placement of wrasses separate from the other traditionally classified Labroid groups. Our results explicate the enormous potential of UCEs to finally generate a resolved phylogenetic hypothesis for coral reef fishes that can further be used as a framework for more complex questions regarding the timing and causes of diversifications in this fauna.

Keywords: next-generation sequencing, UCEs, evolution, phylogenomic markers

Poster 30**Diversification, extinction and global conservation status of lagomorphs**

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Unlike most mammalian lineages, lagomorphs exhibit higher species diversity in the fossil record than in the present. Eight out of thirteen extant genera of lagomorphs are monotypic and six of these are threatened. We combine data on lagomorph evolution and bioclimatic envelopes to explain present-day patterns of higher extinction risk for monotypic and species-poor genera. Taxa with more species may have phenotypes or ecologies that cause higher diversification rates. The ability to consume C4 plants efficiently may have led to a significant range expansion and diversification of leporids (rabbits and hares) during the late Miocene, when global climate change altered the composition of vegetation. Early-diverged leporid species depend on C3 plants, and include most of the currently threatened monotypic species. Specialization to narrow adaptive zones is considered one of the best predictors of species-poor clades.

Threatened lagomorphs in small genera include alpine, riverine and sagebrush specialists. Narrow habitat and diet breadths make species more prone to extinction from habitat loss, and projected climate change is expected to accelerate declines in bioclimatically suitable areas for C3 plant consumers. This combination of stressors threatens unique evolutionary history in leporids, as well as the entire and more diverse ochotonid (pika) lineage

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