International Biogeography Society

The Geography of Species Associations

Meeting Program

15-17 November 2013, Montréal, Québec, Canada

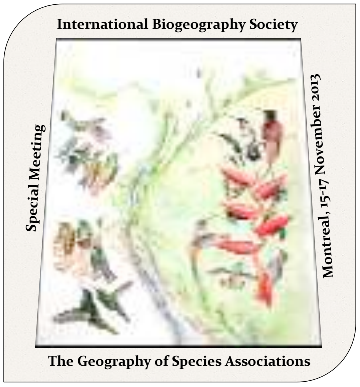
Special Meeting of the International Biogeography Society:

The Geography of Species Associations

The IBS is an international and interdisciplinary society contributing to the advancement of all studies of the geography of nature

Montréal, Québec, Canada

15 – 17 November 2013



Organizing Committee

Pedro Peres-Neto, Université du Québec à Montréal
Jonathan Davies, McGill University
Jean-Philippe Lessard, McGill University and the Quebec Centre for Biodiversity Science
Karen Faller, International Biogeography Society

Volunteers

Eraclis Araclides, Chelsea Chisholm, Sofia Endara, Renato Henriques-Silva,
Bailey Jacobson, Hedvig Nénzen and Andrew Smith

The organizers gratefully acknowledges the generous support of the Université du Québec à Montréal (UQAM) and the Canada Research Chair in Spatial Modelling and Biodiversity (UQAM)

International Biogeography Society 2013 – 2014 Officers

President	Rosemary Gillespie
President Elect	Carsten Rahbek
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Director-at-large	David Nogués-Bravo
Student-at-large	Leticia Ochoa Ochoa
Upcoming meeting host (ex officio)	Carl Beierkuhnlein
Past Graduate student representative (ex officio)	Ana Margarida Santos

IBS Mission Statement

Biogeography, the study of the geography of life, has a long and distinguished history, and one interwoven with that of ecology and evolutionary biology. Traditionally viewed as the study of geographic distributions, modern biogeography now explores a great diversity of patterns in the geographic variation of nature — from physiological, morphological and genetic variation among individuals and populations to differences in the diversity and composition of biotas along geographic gradients. Given its interdisciplinary and integrative nature, biogeography is now broadly recognized as a unifying field that pro- vides a holistic understanding of the relationships between the earth and its biota. Our abilities to develop more general theories of the diversity of life, and to conserve biological diversity may well rest on insights from the field of biogeography. Therefore, the International Biogeography Society (IBS) was founded in 2001, and incorporated as a non-profit organization in 2002, with the following mission:

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

More information at the IBS website: http://www.biogeography.org

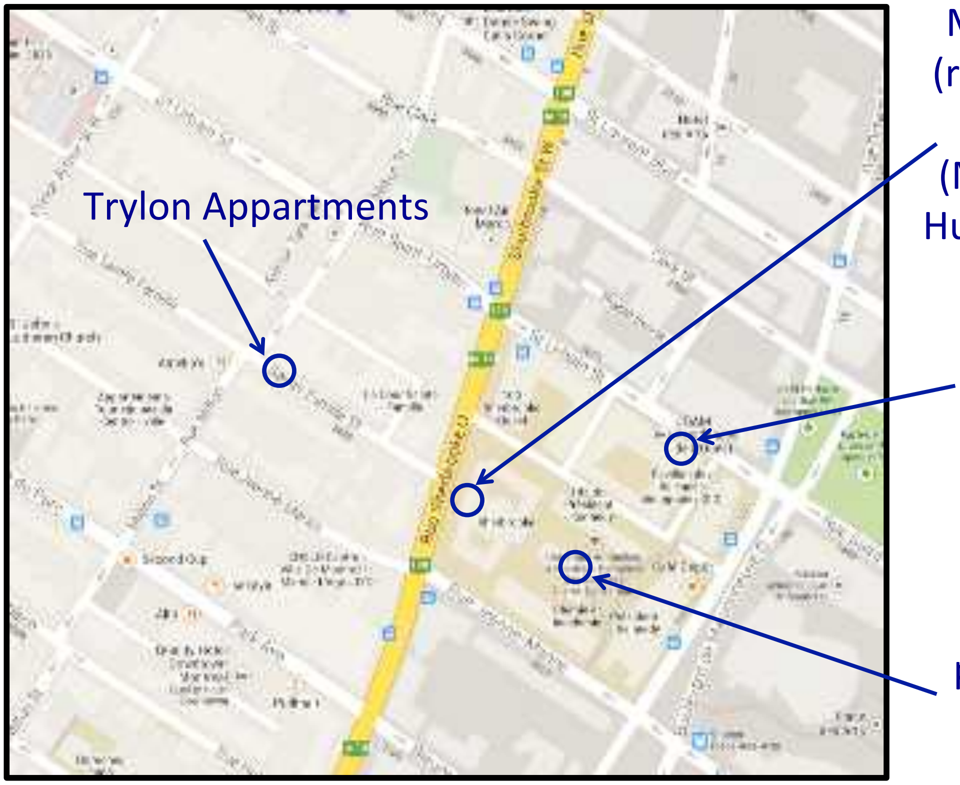
The Geography of the meeting

(small scale)

Physical address:

200 rue (street) Sherbrooke Ouest, H2X 3P2

Sherbrooke Pavillon (SH) – Main entrance on Sherbrooke street.



Trylon Appartments

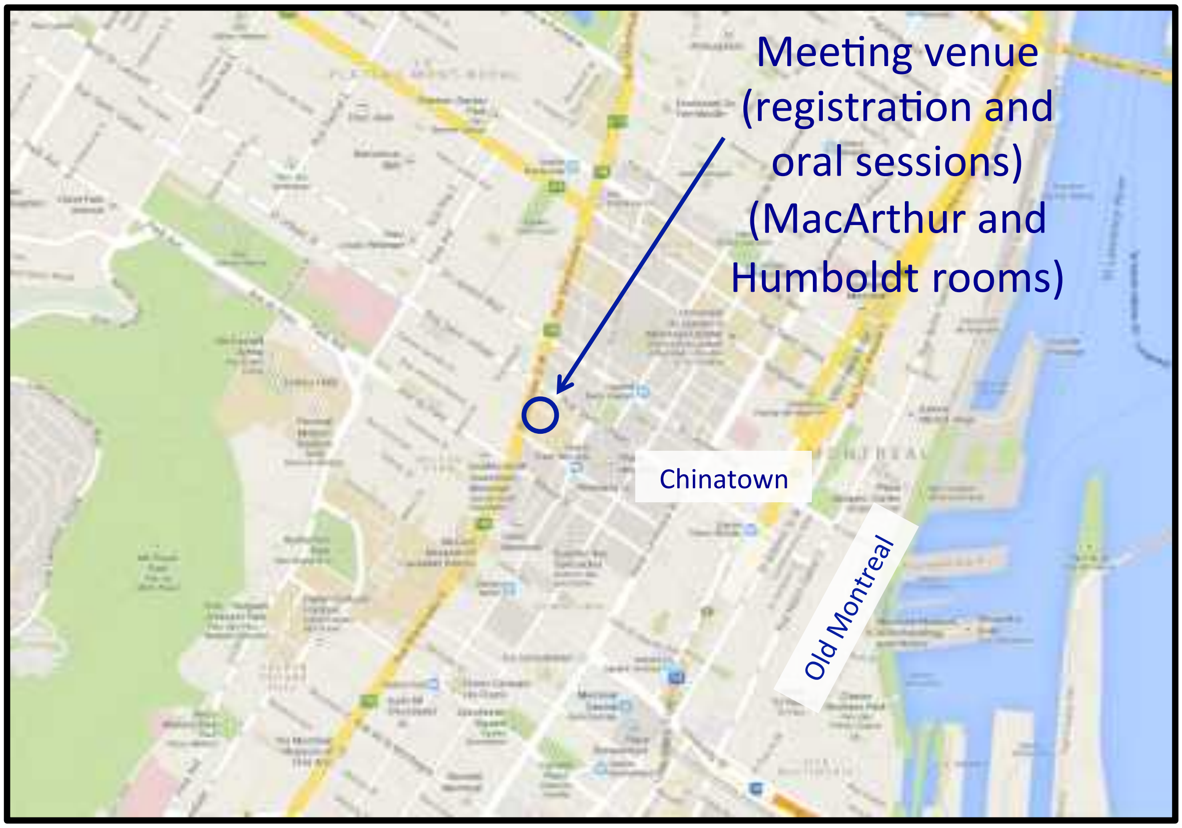
Meeting venue (registration and oral sessions) (MacArthur and Humboldt rooms)

UQAM Underground parking right side on St. Urbain St. ($12 per day)

Lunch, poster session and evening reception (Agora complex)

The Geography of the meeting

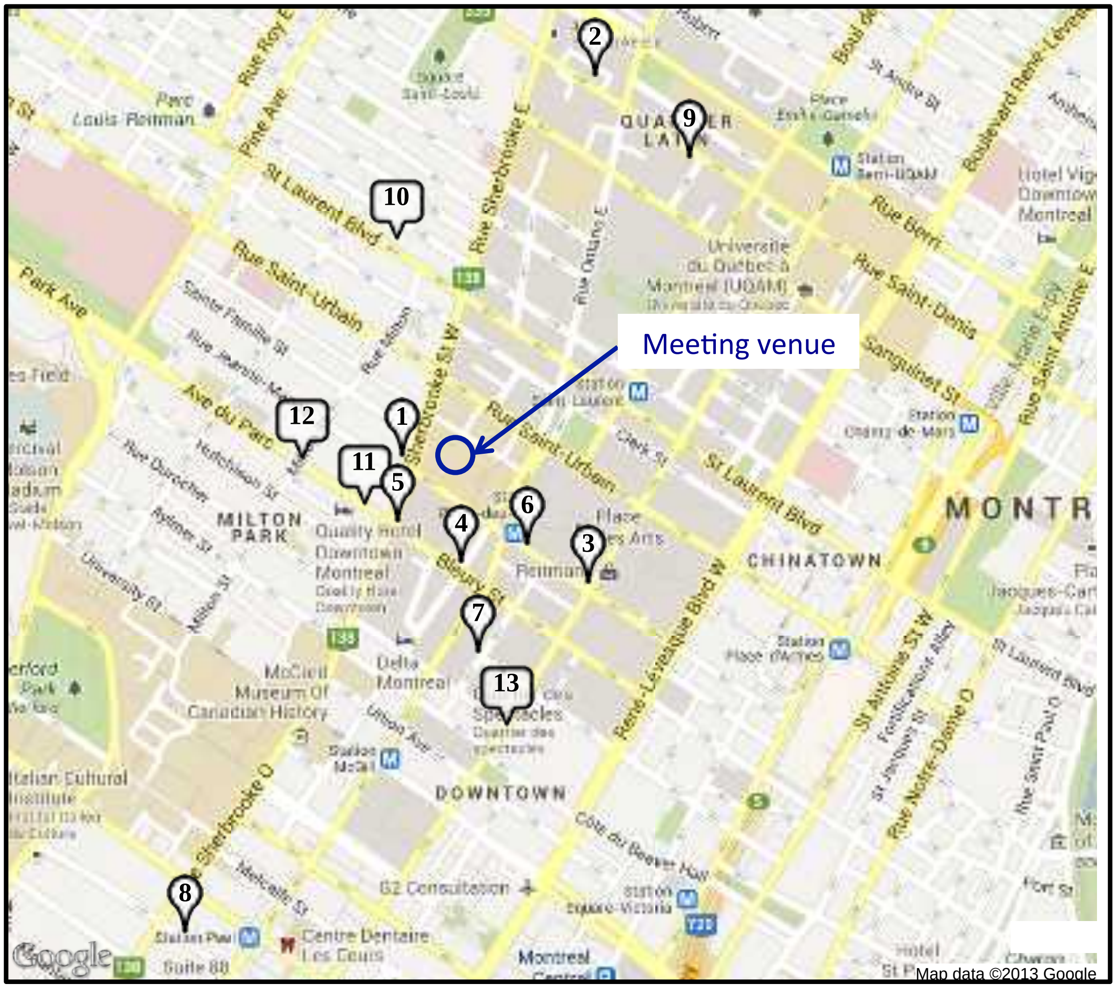
(large scale)



The ***Old Montreal*** district (Historic city center dating from 1605) is considered one of the main tourist attractions in Montreal. Among many attractions such as the architecture of the district and the old port, it has several restaurants and art galleries. It is a must in Montreal and it is only about a 20-minute walk from the meeting venue.

The Geography of the meeting

(restaurants, bars, breakfast, coffee houses)



	Walking distance
1: Benelux (Microbrewery, snacks but no meals– 245 Sherbrooke St. west)	1: 30 seconds
2: L'amère à boire (Microbrewery, no food – 2049 St. Denis St.)	2: 15 minutes
3: Brasserit T! (Bistro restaurant – 1425 Jeanne-Mance St.)	3: 1 minute
4: Café Dépôt (coffee/muffins/baggels – corner Bleury and President Kennedy)	4: 1 minute
5: Café Imagination (breakfast – 330 Sherbrooke St. west)	5: 1 minute
6: F-Bar (Portuguese style restaurant – 1485 Jeanne-Mance St.)	6: 1 minute
7: Furco (Restaurant/music - 425 Rue Mayor St.)	7: 7 minutes
8: Let Taj (Indian Restaurant - 2077 Stanley)	8: 17 minutes
9: Les 3 Brasseurs(Microbrewery with food – 1658 St Denis St.)	9: 15 minutes
10: McKibbins (Irish pub - 3515 St. Laurent Blvd.)	10: 7 minutes
11: Pullman (Wine bar and tapas – 3424 Parc Av.)	11: 45 seconds
12: Second Cup (coffee/muffins/baggels – 3498 Parc Av.)	12: 5 minutes
13: Zenya (sushi place - 486 Sainte-Catherine St., 2nd floor)	13: 10 minutes

Meeting Overview:

- 2 parallel sessions of contributed oral papers (***rooms Humboldt and MacArthur***)
- 4 keynotes
- 2 special talks
- 2 round tables
- 48 oral presentations
- Poster session

Conference Program - oral presentations

Friday, 15 November 2013

Sherbrooke Pavillion

Special Workshop		***room:* MacArthur**
12:00-13:45	*Mark Lomolino*	Teaching Biogeography
Opening ceremony		**MacArthur**
14:00		Introductory remarks and the geography of the meeting
Keynote 1		**MacArthur**
14:10	*Rosemary Gillespie*	Community assembly on isolated islands: macroecology meets evolution
Contributed papers 1: Community Assembly		**MacArthur**
15:20	*Steven Kembel*	Host plant traits and taxonomy drive microbial community structure on tropical forest tree leaves.
15:40	*Lacy Chick*	Similar enough to persist, but different enough to coexist: explaining the distribution of ant species along environmental gradients.
15:00	*Chelsea Chisholm*	Disentangling the multiple drivers of cryptogam taxonomic, phylogenetic and functional betadiversity
Contributed papers 2: Diversification		**Humboldt**
15:20	*Dan Warren*	Examining the geography and ecology of diversification in Banksia using new extensions to age-range correlation analysis
15:40	*Benoit Guénard*	Modern and historical ant biotas reveal dynamic processes in the formation of communities

16:00	*Rebecca Rundell*	Build up of ecologically similar rock- and leaf litter-dwelling land snails on the western Pacific islands of Belau (Republic of Palau, Oceania)
16:20-16:40	**Break**	**room besides Humboldt**
Contributed papers 1: Community Assembly		**MacArthur**
16:40	*Paul Martin*	Sympatry and the evolution of traits across latitudes: range dynamics, climate, and species interactions in birds
17:00	*Rafe Brown*	Evolution and assembly of amphibian community in island archipelagos of the Pacific
17:20	*Matthew Troia*	Community assembly mechanisms of stream fishes vary across environmental gradients and spatial scales
17:40	*Shai Meiri*	The number of competitor species is unlinked to sexual dimorphism
Contributed papers 1: Niche		**Humboldt**
16:40	*David Currie*	How are gradients of richness generated?
17:00	*Robert Anderson*	Which classes of biotic interactions represent scenopoetic variables and should be included in models of species Grinnellian niches?
17:20	*Véronique Boucher-Lalonde*	Does climate limit species richness by limiting individual species' ranges?
17:40	*Christopher Eckert*	Experimental transplants reveal stronger niche limitation of altitudinal than geographic range limits.

Saturday, 16 November 2013

Sherbrooke Pavillion

Keynote 2		**MacArthur**
8:30	*Pierre Legendre*	Partitioning beta diversity in landscape ecology and genetics
Contributed papers 1: Community Assembly		**MacArthur**
9:30	*James Stegen*	Quantifying community assembly processes and identifying features that impose them
9:50	*Mark Lomolino*	The silence of Biogeography

10:10	*Fabian Laroche*	Effects of connectivity and size of local sites on species diversity-gene diversity correlations within (meta)communities: insights from neutral theories
Contributed papers 2: Methods		**Humboldt**
9:30	*Brian McGill*	A new law of biogeography? - the Gause-Liebig law
9:50	*Raimundo Real*	Fuzzy logic is a helpful conceptual and operational tool for modelling the geography of ecological interactions
10:10	*Kalle Ruokolainen*	Relative explanatory power of environmental variables given by RDA and CCA are not always reliable
10:30-10:50	**Break**	**room besides Humboldt**

Contributed papers 1: Community Assembly		**MacArthur**
10:50	*David Nogués-Bravo*	Past climate-biodiversity dynamics forecast profound turnover in biotic systems
11:10	*Jessica Blois*	The influence of climate and dispersal limitation on the stability of biotic associations across the late Quaternary
11:30	*Robert Muscarella*	Functional and phylogenetic variation of tree communities across broad environmental gradients in Puerto Rico
11:50	*Kevin Burns*	Plant defence against megaherbivores: biogeography, heteroblasty and trait matching
12:10	*Carl Beierkuhnlein*	Spatial and temporal trends in plant community composition of Central European forest springs
Contributed papers 2: Methods		**Humboldt**
10:50	*Robert Beiko*	Visualizing species distributions and phylogeography using GenGIS
11:10	*Catherine Graham*	Node-based analysis of clade distribution
11:30	*Péter Sólymos*	Statistical assumptions in the distance decay relationship and their implications for biodiversity conservation
Contributed papers 2: Methods-application		**Humboldt**
11:50	*Adam Clark*	Defining communities by their interactions: Using process to identify pattern
12:10	*Hanna Tuomisto*	Using co-occurrence patterns of indicator species to infer broad-scale environmental and biotic structuring of Amazonia

Agora Complex

12:30-13:50	**Lunch and Poster session**	**Agora**

Sherbrooke Pavillion

Keynote 3		**MacArthur**
14:00	*Mark McPeek*	Reflecting on our current ecological and evolutionary theory in the context of past climate change
Round Table 1: Null Models in Ecology		**MacArthur**
15:00	*panel:* Nicholas Gotelli, Steven Kembel and Brian McGill; *mediator:* Jean-Philippe Lessard	
Round Table 2: Publication Opportunities in Biogeography		**Humboldt**
15:00	*panel:* David Currie, Editor of Global Ecology and Biogeography; Michael Dawnson, Associate Editor of Journal of Biogeography; Carsten Rahbek, Editor of Ecography; Richard Field, Deputy Editor-in-Chief of Frontiers in Biogeography; *mediator:* Pedro Peres-Neto	
16:30-16:50	**Break**	**room besides Humboldt**

Contributed papers 1: Community Assembly		**MacArthur**
16:50	*Allen Hurlbert*	When should species richness be energy-limited, and how would we know?
Contributed papers 1: Methods-application		**Humboldt**
16:50	*Israel Del Toro*	Community assembly of ants along environmental gradients: combining species distribution and macroecological models
Special Talk 1		**MacArthur**
17:10	*Mathew Leibold*	Colonization-extinction processes in metacommunities as 'mesoscale biogeography'
Special Talk 2		**Humboldt**
17:10	*Louis Bernatchez*	DNA barcoding: from sushi ID to determinants of continental wide pattern of genetic divergence and biodiversity in fishes

Agora Complex

17:40-20:30	**Poster session and reception***	**Agora**

*** The reception includes finger food, two paid drinks (beer, white wine or red wine) per person – a cash bar will be available as well.**

Sunday, 17 November 2013

Sherbrooke Pavillion

Keynote 4		**MacArthur**
8:30	*Nicholas Gotelli*	The past, present, and future of null model analysis in biogeograhy
Contributed papers 1: Large Scale A		**MacArthur**
9:30	*Len Gillman*	Latitude, Productivity and Species Richness
9:50	*Ignacio Morales-Castilla*	Biotic exchange, climatic niche conservatism and reversed latitudinal diversity gradients
10:10	*Hanieh Saeedi*	Global biodiversity and biogeography of razor clams (Bivalvia: Solenidae)
Contributed papers 2: Large Scale B		**Humboldt**
9:30	*Timothée Poisot*	Towards a biogeography of species interactions
9:50	*Dominique Gravel*	A quantitative framework to understand and predict spatial distribution of ecological networks
10:10	*Miguel Matias*	Estimates of species extinctions from Species–Area relationships strongly depend on ecological context
10:30-10:50	**Break**	**room besides Humboldt**

Contributed papers 1: Global Change		**MacArthur**
10:50	*Charlotte Germain-Aubrey*	Using museums to predict climate change response: modeling Florida plant diversity
11:10	*Katherina Searing*	Response of rodents to climatic variation in North America over the past century
11:30	*Sara Gagné*	How does city size affect the relationship between bird species richness and urbanization?
11:50	*Frank La Sorte*	The role of urban and agricultural areas for migrating birds: an assessment of within-year temporal turnover
12:10	*Qianlai Zhuang*	Incorporating the effects of permafrost dynamics into a dynamic vegetation model to improve the estimation of vegetation distribution and carbon cycling in northern high latitudes during the 21st century

Contributed papers 2: Phylogeography		**Humboldt**
10:50	*Michael Dawson*	Natural experiments and meta-analyses in comparative phylogeography
11:10	*Ana Carnaval*	Predicting phylogeographic endemism in a topographically complex Neotropical hotspot
11:30	*Nathan Lovejoy*	The biogeography of electro-crypsis in Gymnotus
11:50	*Cesc Múrria*	Whole-community dna barcoding of aquatic insects reveals extremely high endemicity and limited movement among highlands neotropics streams
12:10	*Barnabas Daru*	A phylogenetic reclassification of the phytogeographic zones of southern Africa
12:30-12:40	**Close of meeting**	**MacArthur**

Conference Program - poster presentations

Saturday, 16 November 2013

Agora Complex

All posters will be presented across the two poster sessions: 12:30-14:00 (lunch) and 17:40:20:30 (reception).

P1 – Community Assembly

P11	*Takayuki Shiono*	Drivers of the functional trait structure of woody plants in Japan: contrasting role of climate harshness and seasonality
P12	*Luka Negoita*	Patterns and potential effects of dispersal limitation on island plant community assembly
P13	*Victor Frankel*	Infection preference of an invasive parasite to a novel invasive host in a human dominated landscape, the Panama Canal
P14	*David Jenkins*	Metacommunity assembly affects the local-regional species richness relationship
P15	*Tammy Elliott*	The role of competition in structuring plant communities consisting of closely-related species

P16	*Sarah Loboda*	Multi-scale patterns of ground-dwelling spider (Araneae) diversity in northern Canada
P17	*Marie-Hélène Greffard*	If the Jack-of-all-trades were the master of dispersal and coexistence in heterogeneous metacommunities
P18	*Georgina Braoudakis*	Effects of lake size, isolation and piscivorous fish richness on nested fish community structure
P19	*Christian Messier*	Advancing biodiversity – ecosystem functioning science using high-density tree-based experiments over functional diversity gradients

P2 – Temporal Dynamics

P21	*Andrew Letten*	Tracking community stability through time: a phylogenetic and functional perspective
P22	*Evanilde Benedito*	Temporal dynamics in the size range of a fish population in neotropical reservoirs

P3 – Gradients

P31	*Felipe Saiter*	Climate and space promoting floristic variations among ecoregions in Doce River basin, Southeastern Brazil
P32	*Andrew Siefert*	Up the mountain, North to the pole: do species' elevational and latitudinal limits match?
P33	*Geneviève Lajoie*	Partitioning the sources of trait variation among plant communities along an elevational gradient
P34	*Kellina Higgins*	Plant species distribution in a patchy boreal forest-peatland landscape, Northwest Territories, Canada
P35	*Kaven Dionne*	Link between environmental parameters and cryptic species occurence in lakes: The case of amphipods of the Hyalella azteca complex
P36	*Daniel Gavin*	Development of forest communities over steep environmental gradients from the late Glacial to present in the Pacific Northwest

P4 – Large-scale studies

P41	*Renato Henriques-Silva*	Exploring species distributional patterns within metacommunities across large geographical areas
P42	*Michelle Chaput*	Holocene human- vegetation-climate interactions in North America

P43	*Sarah Steele*	Diversity and distribution of body size in Neotropical cichlid fishes
P44	*Richard Field*	Environmental convergence or historical contingency? Global body-size patterns of turtle assemblages

P5 – Conservation and Global Change

P51	*Tania Urquiza-Haas*	Can ecoregions be used as conservation planning units in a medadiverse country?
P52	*Sthephanie Shooner*	Local and regional species pool influences on subarctic mine restoration sites
P53	*Sapna Sharma*	The impacts of climate change on the invasion of warmwater fishes and extirpation of coldwater fishes
P54	*Jérôme Comte*	Bacterial biogeographic patterns in permafrost thaw ponds and implications for greenhouse gas emissions
P55	*Buntarou Kusumoto*	Logging practices and functional structure of forest tree and herbaceous plant communities across Japanese Archipelago
P56	*Wolke Tobón*	Assessing the capacity of Mexico's protected-area system to represent threatened and restricted-range vertebrate species
P57	*Michael Becker*	Vegetation and permafrost interactions in a polar desert oasis
P58	*Mohamed Anas*	Zooplankton communities as indicators to track environmental changes across broad geographical regions: the case of boreal lakes downwind of Athabasca oil-sands operations
P59	*Megan McCusker*	Modeling extinction risk of an endangered minnow in the upper St. Lawrence River
P60	*Karen Neil*	High-resolution paleoecological study of human-ecosystem interactions in relation to Holocene environmental change in Port Joli Harbour, Southwestern Nova Scotia, Canada
P61	*Corey Lesk*	Tree species diversity in Homegardens of Kerala

P6 – Methods

P61	*Ermias Azeria*	Identification and modelling of species-groups of bryophytes in the boreal region using co-occurrence based biodiversity deconstruction
P62	*Anne Fontaine*	Testing the influence of taxonomic group and taxonomic resolution on the delineation of ecological units in the Estuary and Gulf of St Lawrence (Canada)
P63	*Caterina Penone*	Imputation of trait datasets: which method performs the best?

P7 – Methods-application

P71	*Thomas Lamy*	Using beta diversity decomposition to understand ecosystem resilience
P72	*Alex Van Nynatten*	Improving the molecular detection of positive selection using biogeographic data
P73	*Karin Van Ewijk*	Predicting tree species abundance in a mixed mature forest using LiDAR.

P8 – Phylogeography

P81	*Julissa Roncal*	A phylogeographic model for lowland plant species diversification in western Amazonia.
P82	*Yuuta Miyagi*	Identifying the relative importance of historical and ecological factors on global diversity pattern on Scleractinian corals
P83	*Yasuhiro Kubota*	Historical interactions of isolation, palaeoclimate and volcanism determine plant diversity hotspots in the East Asian continental island
P84	*Gabrielle Malcolm*	Phylogeography of the Central American Neotropical electric fish Gymnotus (Teleostei: Gymnotidae)

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Keynotes

Community Assembly on Isolated Islands: Macroecology Meets Evolution

Rosemary G. Gillespie, Andy Rominger, Daniel S. Gruner, John Harte, Neo D. Martinez, Patrick M. O'Grady, Diana Percy, Donald K. Price, Kerry L. Shaw, Curtis Ewing, Fernanda Valdovinos, Kari Goodman & Karl Magnacca

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Islands have provided an arena for building and testing some of the fundamentals of ecology and evolution. The Hawaiian Islands in particular have expanded our understanding of island biogeography, with phylogeographic studies of rapid diversification and the dynamics of adaptive radiation overlaid upon a detailed understanding of ecosystem development and senescence. These studies demonstrate the overriding importance of *in situ* speciation in biodiversity patterns of highly isolated archipelagoes, beyond the reach of equilibrium colonization dynamics. We have initiated a study to synthesize ecological and evolutionary perspectives to analyze processes driving emergent patterns of island biodiversity. We use the natural experiment provided by the island chronology to develop a novel analytical pipeline that combines both macroecological (interaction networks and maximum entropy inference) and evolutionary (population genetics and phylogenetics) approaches. We aim to use this system to build a predictive understanding of the interplay between ecology and evolution in dynamically shaping the macroecology of complex ecosystems.

Partitioning beta diversity in landscape ecology and genetics

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Beta diversity is the variation in species composition among sites within a geographic area of interest. It can be measured in different ways. Among these, the total variance of the community data table Y is an estimate of beta diversity. We show how the total variance of Y can be calculated either directly or through an ecological dissimilarity matrix. This measure can be generalized to any community dissimilarity index. We address the question of which index to use by coding 16 indices using 14 properties that are necessary for beta assessment, comparability among data sets, sampling issues, and ordination. Our comparison analysis classifies the coefficients under study into five types, three of which are appropriate for beta diversity assessment. The total variance of Y links the concept of beta diversity with the analysis of community data by commonly used methods like ordination and analysis of variance. Total beta can be partitioned into Local Contributions of individual sites to Beta Diversity (LCBD: comparative indicators of the ecological uniqueness of the sites) and Species Contributions to Beta Diversity (SCBD: degree of variation of individual species across the study area). These new indices can be tested for significance. High LCBD values single out sites that have unusual species combinations and high conservation values, as well as degraded and species-poor sites in need of ecological restoration. Moreover, total beta can be broken up into within- and among-group components by multivariate analysis of variance (manova), into orthogonal axes by ordination, into spatial scales by eigenfunction analysis, or among explanatory data sets by variation partitioning. LCBD indices can also be computed for genetic data, using genetic distances, in the framework of landscape genetics.

Legendre, P. and M. De Cáceres. 2013. Beta diversity as the variance of community data: dissimilarity coefficients and partitioning. Ecology Letters 16: 951-963.

Reflecting on our current ecological and evolutionary theory in the context of past climate change

Mark McPeek

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The modern biota we study today was created and has lived through millions of years of climatic upheaval (i.e., the Pliocene and Pleistocene). However, the theoretical edifice we have constructed, particularly in community ecology and evolutionary biology, typically consider changes in a relatively static world. For example, species coexistence is evaluated by the criterion of “invasibility” in which new species must establish themselves in intact communities. Likewise, our most basic ideas of speciation are typically that relatively intact species ranges are subdivided by geographic or ecological barriers. However, the world that our modern biota experienced in the recent past was one of major upheaval, with species shifting huge distances across the landscape and consequently communities being disassembled in one place and reassembled in another. I will explore a number of empirical results from my own work on Enallagma damselflies (Odonata) that initially seemed anomalous, but that now are perfectly understandable when viewed through the lens of climatic upheaval and how that alters the form and consequences of ecological and evolutionary processes.

The past, present, and future of null model analysis in biogeograhy

Nicholas J. Gotelli

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Null model analysis is a widely used tool in biogeography for inferring mechanism from pattern in the absence of experimental manipulations. Null models occupy a philosophical middle ground between mechanistic theoretical models and statistical sampling models. They are tailored to the kinds of data that biogeographers collect, and they can be adapted to investigate many questions in contemporary and historical biogeography. Although null models were popularized by the controversy over ecological assembly rules during the 1970s, they originated in biogeographic analyses of species/genus ratios in the 1920s and again in the 1940s. Current challenges in null model analysis include the quantification of biogeographic patterns with an appropriate metric, benchmark testing and the evaluation of Type I and Type II statistical errors, and the detection of patterns hidden in sub-matrices of the usual species x site incidence matrix. With the exception of the mid-domain effect, surprisingly few null models have incorporated spatial effects. We present a framework for incorporating spatial data and measures of site quality into null model analysis. This framework provides a method for inferring mechanisms of species interactions, habitat associations, and dispersal limitation as potential causes of patterns of species aggregation and segregation.

Special Talks

Colonization-extinction processes in metacommunities as 'mesoscale biogeography'

Mathew A. Leibold

Integrative Biology, University of Texas at Austin, TX, USA.

Metacommunity ecology is a way of thinking about relatively large scale processes in ecology. As such it provides insights that also affect biogeographic ones that dominate at larger spatial scales. However metacommunity ecology has largely focused on spatial effects that dominate at relatively small spatial scales. Here I argue that critical insights about metacommunity processes that might affect biogeography involve colonization-extinction dynamics in environmentally heterogeneous landscapes. I describe recent results and experimental tests of this emerging theory and discuss future directions. In purely ecological settings, the main result is that environmental filtering is reduced while purely spatial and apparently stochastic ones increase as background extinction and dispersal limitation increase. In settings that also allow for significant local adaptation, the effects are more complex and likely produce patterns that further decrease apparent environmental filtering. How these effects relate to historic processes in biogeography such as vicariance and founder effects and in speciation is a major challenge for future work.

DNA barcoding: from sushi ID to determinants of continental wide pattern of genetic divergence and biodiversity in fishes

Louis Bernatchez

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Debated since Paul Hebert coined the term in 2003, DNA barcoding has nevertheless proven highly efficient to diagnostically identify species in many taxonomic animal groups. An additional benefit of broad scale barcoding DNA projects is that they allow collecting large, standardized genetic data base that can potentially be used for purposes extending well beyond the mere identification of diagnostic variation. In this talk, we will present the outcomes of such applications in a study of North American freshwater fishes. To provide an independent calibration of taxonomic uncertainty, we first generated a standard reference library of mtDNA sequences (DNA barcodes) for 752 North American freshwater fishes. This demonstrated that 90% of known species can be delineated using barcodes but also flagged numerous putative unnamed candidate species, which suggested a 28% increase in species diversity. Secondly, we showed that geographic patterns of intraspecific and interspecific genetic divergence support a dual role involving both the late Pliocene-Pleistocene climatic fluctuations and metabolic rate in determining latitudinal gradients of genetic divergence and very likely influencing speciation rates. Finally, in order to test the hypothesis that factors favouring allopatric speciation are the main drivers underlying the diversification of North American freshwater fishes, we combined mtDNA barcode data with that of nuclear DNA loci to show that the eastern Great Lakes drainage represents a multispecies suture zone for glacial lineages of freshwater fishes with variable levels of genetic divergence. Lineages with relatively deep levels of sequence divergence (>2%) developed strong reproductive barriers, while lineages with lower levels of divergence show weaker reproductive isolation when found in sympatry. These results offer strong evidence that allopatric speciation has contributed significantly to the diversification of north-eastern American freshwater fishes and confirm that Pleistocene glacial cycles can be viewed as a ‘speciation pump’ that played a predominant role in generating biodiversity.

Special Workshop

Teaching Biogeography

Mark Lomolino

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This workshop and open forum will launch what we hope will become a continuing series of initiatives by the International Biogeography Society to promote the teaching of what Charles Darwin described as “… that grand subject, that almost keystone of the laws of creation – Geographical Distribution.” Given its holistic nature, biogeography appears unrivaled in its potential to teach the most fundamental and compelling stories of science – the origins, diversity and spatial and temporal dynamics of the natural world. We will share some experiences and strategies for teaching Biogeography at undergraduate and graduate levels, and how IBS can promote and enhance the teaching of the geography of nature across disciplines and across the globe.

Oral presentations

The abstracts appear in the same order as in the programme

Friday 15 November, Contributed papers 1: Community Assembly

Host plant traits and taxonomy drive microbial community structure on tropical forest tree leaves

Steven Kembel

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In tropical forests, the phyllosphere - the aerial surfaces of plants including leaves - is home to a diverse community of microbes. Little is known about the processes responsible for microbial community assembly on leaves, or the biogeography of plant-microbe associations. In this study we addressed this lack of knowledge, using high-throughput environmental sequencing to quantify bacterial and fungal biodiversity on the leaves of 57 tree species growing in a neotropical rainforest in Panama. Tree leaves in this forest were host to more than 1,350 fungal and 7,250 bacterial taxa. Microbial community structure on leaves was correlated with host taxonomy and with a suite of host plant functional traits linked to host life history strategy, including leaf mass per area, leaf nitrogen and phosphorous concentrations, and wood density. We found evidence that filtering by host leaf traits drives the assembly of microbial communities on leaves. Host plant growth and mortality rates were correlated with the presence and abundance of different bacterial and fungal taxa on leaves. We discuss the implications of these results for our understanding of the biogeography of plant-microbe interactions in tropical forests.

Similar enough to persist, but different enough to coexist: explaining the distribution of ant species along environmental gradients

Lacy Chick[1], Jean-Philippe Lessard[2,3], Rob R. Dunn[4] & Nathan J. Sanders[1]

[1]Ecology & Evolutionary Biology, University of Tennessee, USA; Department of Biology, McGill University, Canada; [3]Québec Centre for Biodiversity Sciences, Canada; [4]Keck Center for Behavioral Biology, North Carolina State University, USA.

One of the most striking patterns in nature is that the number of species varies along environmental gradients. Explaining this pattern has attracted the attention of ecologists and biogeographers for decades and numerous mechanisms have been proposed to account for the (often) systematic variation. Species differ in how they respond to biotic and abiotic factors, and these differences among species in turn influence abundance, community structure, and broad-scale patterns of diversity. To illustrate the interplay between environmental constraints and biotic interactions on community membership, we collected data on occurrence, abundance, and thermal physiology on ant species along an elevational gradient in Great Smoky Mountains National Park, TN, USA. We examined competition, species segregation, and the degree of dependency on environmental temperature. We found that stressfully low temperatures limit abundance and species density at high-elevation sites and that these limitations are governed by an underlying physiological mechanism exerting a filter on community membership by allowing only certain taxa to establish and persist at high elevations. When examining co-existence, species were highly segregated at low-elevation sites but not high-elevation sites, suggesting that biotic interactions drive patterns of diversity in environmentally benign low-elevation sites. Our studies indicate that the mechanisms structuring communities vary along gradients and understanding these mechanisms may be important for predicting future biodiversity patterns.

Disentangling the multiple drivers of cryptogam taxonomic, phylogenetic and functional betadiversity

Chelsea Chisholm & Jonathan T. Davies

Department of Biology, McGill University, Montréal, QC, Canada.

Beta diversity has long been used in the examination of processes dictating community composition and structure across space. Recently, the inclusion of novel diversity metrics in community ecology has allowed for the assessment of changes in both phylogenetic and functional composition across space. However, little is known on how these diversity metrics vary with respect to each other and across environmental gradients. Our study examines different components of cryptogam betadiversity along an elevational gradient in subarctic Canada. Overall, taxonomic, phylogenetic and functional beta diversity metrics were auto-correlated, however, there was a difference in their strength of association with environmental drivers both within and between habitat types. Additionally, we demonstrate that phylogeny better approximates functional diversity when multiple traits are considered. This study was the first to assess phylogenetic and functional information of lichens in a community ecology framework. Our results suggest that multiple measures of diversity must be considered if we are to fully understand the processes determining community structure and function.

Friday 15 November, Contributed papers 2: Diversification

Examining the geography and ecology of diversification in Banksia using new extensions to age-range correlation analysis

Dan Warren & Marcel Cardillo

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The Southwest Botanical Province in Australia is home to more than 680 plants of the family Proteaceae, 96% of which are endemic to the region. The genus Banksia, with over 170 endemic species, is one of the largest components of this diversity. We examine the geographic and ecological components of this diversification using new statistical methods that extend age-range correlation analysis, one of the classic approaches in biogeography. These new methods allow us to examine patterns of sympatry and allopatry at both coarse and fine geographic scales, and to detect phylogenetic signal in correlations between ecological and geographic similarity between species. We document higher levels of sympatry than expected within recent clades of Banksia, and examine environmental, phenological, and morphological attributes of the species that may allow these unusually high levels of coexistence between closely related species.

Modern and historical ant biotas reveal dynamic processes in the formation of communities

Benoit Guénard[1], Vincent Perrichot[2], Michael Weiser [3] & Evan Economo[1]

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Despite tremendous advances in global biodiversity science, our understanding of biogeographic patterns has been restricted to a few groups of plants and vertebrates. Yet, invertebrates and among them insects represent the vast majority of species, and until now have been mostly excluded from this burst of new research. The inclusion of even one insect group would provide important insight to the construction of a global biodiversity framework. Here, we focused on ants, an insect family rich of over 15,000 described species and ecologically dominant in most terrestrial ecosystems, to present a first global analysis of the diversity and evolution of a major group of insects. First, we will introduce two databases on generic and species global distribution of ants and present the main diversity patterns observed. Then, combined with two other databases on past distribution of ant genera from the Eocene to the Miocene and a database on community structure of ants, we explored the dynamic aspect of ant assemblages over geological times. Congruent results both in terms of generic composition and of community structure support the hypothesis of a strong connection between past Western Palearctic and modern Indomalayan and Australasian assemblages and of a widespread Holarctic ant community. Massive extinction waves observed in both a continental and insular areas underline the dynamic nature and the importance of history in the formation of modern communities of ants.

Build up of ecologically similar rock- and leaf litter-dwelling land snails on the western Pacific islands of Belau (Republic of Palau, Oceania)

Rebecca J. Rundell

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Pacific island land snails are mostly tiny (< 10 mm) detritivores and fungivores that are simultaneously diverse, threatened and poorly known. The remote Micronesian archipelago of Belau (Republic of Palau, Oceania) harbors an enormous number of snails despite its small size, and multiple snails co-occur on each of the more than 500 islands. This is especially true within the Diplommatinidae, a morphologically fascinating and minute-sized group of snails with about 90 mostly undescribed species. These species are arrayed among neighboring limestone karst and leaf litter habitats yet have evolved in rather surprising ways on this relatively old archipelago. Molecular phylogenetic evidence suggests that species have diversified within each habitat type rather than switching between habitat types, as would be predicted in adaptive radiation. The pattern of co-occurrence of ecologically similar species within each island presents interesting opportunities for future work on island community assembly.

Friday 15 November, Contributed papers 1: Community Assembly

Sympatry and the evolution of traits across latitudes: range dynamics, climate, and species interactions in birds

Paul R. Martin

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The co-occurrence of closely related species can generate strong selective pressures on traits. Patterns of co-occurrence vary geographically, particularly with latitude, thus creating important variation in patterns of selection and evolution. Using a sister species framework proposed by Noor (1997, Am Nat), we show greater divergence of both colour pattern and body size among closely related species in sympatry compared with allopatry in a diverse array of birds occurring worldwide. We further show that sympatry among closely related species of birds occurs significantly faster at higher latitudes compared with the tropics, increasing the influence of species interactions among evolutionarily young species at high latitudes. We contrast latitudinal variation in the divergence of colour pattern and body size among young species of birds, considering the greater importance of both sympatry and climate as selective pressures at higher latitudes. Overall, the co-occurrence of closely related species presents a significant selective pressure that can explain geographic variation in trait divergence, but its relative importance depends on the trait and other selective pressures that also vary geographically.

Evolution and assembly of amphibian community in island archipelagos of the Pacific

Rafe M. Brown

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How do complex communities of amphibians form in distant islands archipelagos? For a given island, have today's diverse communities formed via evolutionary or ecological processes? At the low end of the spectrum of relative dispersal abilities, amphibians are arguably an exemplary vertebrate group minimally capable of dispersal to the islands of the Philippines, Indonesia, New Guinea, the Solomons, Bismarcks, and Fiji. And yet diverse communities of amphibians inhabit these distant landmasses. Because amphibians are not considered strong dispersers, we might predict that frog communities of Pacific archipelagos should be derived disproportionately from in situ diversification following infrequent colonization. In this study I used a phylogenetic approach to the study of community assembly to test this prediction with Melanesian forest frogs. I will present new empirical evidence for a combination of processes, with some complex communities apparently having arisen exclusively from ecological assembly (phylogenetic overdispersion) and others derived largely from speciation within archipelagos (phylogenetic clustering). An apparent shift from assembly to evolutionary formation of communities is associated with increasing isolation in the southwest Pacific. Many island assemblages are the result of a combination of processes that interact in novel ways, dictated by history of the taxa involved, the idiosyncrasies of individual lineages, the geographical template of the individual landmasses, and the scale of the local species pool. The end result, my data suggest, are diverse and seemingly structurally replicated assemblages of species, derived from disparate evolutionary and ecological processes in the island archipelagos of Australasia.

Community assembly mechanisms of stream fishes vary across environmental gradients and spatial scales

Matthew Troia & Keith Gido

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Functional traits shape abiotic tolerance and species interactions that drive the assembly of local communities from regional species pools. However, the position of local communities along environmental gradients, spatial scale at which the local community and regional pool is defined, and the types of functional traits investigated may influence the perceived importance of abiotic filtering versus limiting similarity. Stream fish communities are highly structured along hierarchically-organized habitat gradients, but the distribution of functional traits across gradients and spatial scales remains poorly studied. We used null models to quantify the dispersion of reproductive life history, feeding ecology, and fluvial morphology traits in local communities at three spatial scales (mesohabitats within a reach, mesohabitats within a basin, and reaches within a basin). Linear models were then used to test for environmental correlates of trait dispersion in local communities distributed along environmental gradients in a prairie stream network in Kansas, USA. Null models indicated that all three trait categories are underdispersed at the three spatial scales investigated. Linear models indicated that the dispersion of reproductive life history traits was associated with longitudinal network position at the reach resolution but not the mesohabitat resolution, suggesting that environmental filtering of reproductive life history traits is stronger in shallow, headwater streams and only apparent among reaches within the basin. Our results affirm that the assembly of stream fish communities is driven by abiotic filtering, but the mechanisms of assembly depend on the nature of functional traits, position along environmental gradients, and the spatial scale of investigation.

The number of competitor species is unlinked to sexual dimorphism

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Sexual size dimorphism can allow males and females of the same species to specialize in different sized foods and therefore minimize intraspecific competition. The existence of interspecific competition, however, is thought to limit such divergence, as larger competitors in the community will prevent the larger sex from growing larger, and smaller species may prevent the smaller sex from growing smaller. Because insular communities are depauperate, and guilds are species-poor, it is often assumed that enhanced sexual size dimorphism is common on islands. The intensity of interspecific competition, hindering enhanced dimorphism, is thought to increase with competitor richness. We examined these assumptions using data on the sexual size dimorphism of lizards, and mammalian carnivores, on islands worldwide. We tested whether intraspecific sexual size dimorphism decreased on species-rich islands. We further computed the average sexual dimorphism of species on islands and tested whether species-rich islands are inhabited by relatively monomorphic species. Within families and guilds across carnivores and lizards, and with both intraspecific and interspecific approaches, we consistently failed to find support for the notion that species-poor islands harbour more sexually dimorphic species. We conclude that either interspecific competition does not affect the sizes of insular lizards and carnivores (i.e., character displacement and species sorting are rare in these taxa), or that the number of species in an assemblage or guild is a poor proxy to the intensity of interspecific competition.

Friday 15 November, Contributed papers 2: Niche

How are gradients of richness generated?

David J. Currie, Kevin R. Walker, H. Vázquez-Rivera & Véronique Boucher-Lalonde

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"The factors that generate richness-climate correlations are poorly understood." This contention is distressingly common, despite abundant literature on the subject. If the contention is true, it is partly because there are, in fact, two canonical patterns of richness: a secular pattern of species diversification and colonization of biomes during the Phanerozoic, and finer-grained (both temporal and spatial) variation in species distributions that are manifested as patterns of species richness, range size, spatial turnover, species-abundance distributions, etc. The secular patterns of the evolution of life, for example those described by the tropical niche conservatism hypothesis, are in little doubt. Yet, there is little reason to postulate that fine-grained patterns of richness could equally be "understood" in terms of biome-level processes at geological time scales. Rather, processes that vary at fine grains seem much more likely to explain fine-grained variation in richness. Preston (1962) suggests a possibility. Individuals are distributed among species approximately log-normally. The total abundance of individuals does not vary strongly geographically. In contrast, minimum population size does so, in a manner strongly correlated with both climate and species richness. If continental populations of organisms colonize, and are extirpated from, environments in a manner similar to MacArthur & Wilson's (1967) island biogeography theory (or more recent meta-population theory) many of the fine-grained patterns of the distribution of life on Earth are likely to result.

Which classes of biotic interactions represent scenopoetic variables and should be included in models of species Grinnellian niches?

Robert P. Anderson

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A thorny problem for ecological niche modeling of species distributions is how to integrate biotic interactions. Here, I focus on correlative models of Grinnellian niches defined only by density-independent factors via scenopoetic variables: those not affected by the presence of the focal species. In contrast, models of Eltonian niches include density-dependent factors represented by variables that *are* affected by the focal species. As a starting point, I consider only species that interact directly with the focal species, asking whether some classes of biotic interactions could be considered scenopoetic. First, some classes are always scenopoetic (and important to the focal species): completely superior competitors, facilitators, and suffering-inducing ammensals. Second, some classes are never scenopoetic (but irrelevant anyway): completely inferior competitors, commensals, and suffering ammensals. Third, strictly speaking, all other classes are nonscenopoetic (yet potentially important): competitors of intermediate effects, mutualists, and all positive/negative interactions (predators/prey, consumers/resources, parasites/hosts). Interactions in the first category can be included as predictors in Grinnellian models, those in the second cannot, and those in the third require further information. Fortunately, in the third category, some interactions may be important to the focal species but only trivially affect the other species. Such interactors could be considered scenopoetic and used in Grinnellian models of the focal species. These determinations require natural

history information, e.g., regarding the symmetry of the importance and specificity of the interaction. Biotic interactions that cannot be considered scenopoetic must be taken into account in other ways (e.g., included in post-processing; or via Eltonian models).

Does climate limit species richness by limiting individual species' ranges?

Véronique Boucher-Lalonde, Jeremy T. Kerr & David J. Currie

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Broad-scale geographic variation in species richness is strongly correlated with climate, yet the mechanisms underlying this correlation are still unclear. We test two broad classes of hypotheses to explain this pattern. Bottom-up hypotheses propose that the environment determine species' ranges. Ranges then sum up to yield species richness patterns. Top-down hypotheses propose that the environment limits the number of species that occur in a region, but not which ones. We test these two classes of hypotheses using a natural experiment: seasonal changes in environment and seasonal range shifts of 625 migratory birds in the Americas. We show that richness seasonally tracks the environment. However, individual species' distributions do not. Rather, species occupy different environments in two seasons. Our results are inconsistent with bottom-up hypotheses. Instead, a top-down mechanism must constrain the number of species that can occur in a given region.

Experimental transplants reveal stronger niche limitation of altitudinal than geographic range limits

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The geographic and elevational distribution of a species is expected to be a spatial manifestation of its niche. Dispersal can also influence distributions: extending it beyond niche limits in vagile species, or constraining it in more sessile species. The effect of dispersal may also depend on the steepness of the ecological gradient causing the range limit. As steepness increases dispersal limitation should be rarer and range limits should either coincide with or exceed niche limits. We tested these predictions by synthesizing results from studies transplanting species across geographic vs. elevational range limits. As predicted, the frequency and magnitude of declines in fitness-related performance were greater for elevational than geographic limits. Range limits seemed to coincide with niche limits in 55% of tests across elevational limits but only 17% of tests involving geographic limits. These results could potentially arise from a methodological bias if experimental planting sites were placed climatically further beyond the range limit in studies of elevational than geographic ranges owing to the ease of covering larger climatic differences along steeper elevational gradients. However analyses accounting for climatic distance between within- and beyond-range planting sites produced similar results, further suggesting that elevational gradients are ecologically steeper than geographical gradients. Niche constraints and dispersal might play different roles in generating elevational vs. geographic limits. Our results indicate that dispersal seems to commonly constrain the location of geographic limits, whereas elevational limits more often coincided with niche limits, or exceed them as dispersal maintained sink populations beyond niche limits.

Saturday 16 November, Contributed papers 1: Community Assembly

Quantifying community assembly processes and identifying features that impose them

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Spatial turnover in the composition of biological communities is governed by (ecological) Drift, Selection, and Dispersal. Commonly applied statistical tools cannot quantitatively estimate these processes, nor identify abiotic features that impose these processes. For interrogation of subsurface microbial communities distributed across two geologically distinct formations of the unconfined aquifer underlying the Hanford Site in southeastern Washington State, we developed an analytical framework that advances ecological understanding in two primary ways. First, we quantitatively estimate influences of Drift, Selection, and Dispersal. Second, ecological patterns are used to characterize measured and unmeasured abiotic variables that impose Selection or that result in low-levels of Dispersal. We find that (i) Drift alone consistently governs ~25% of spatial turnover in community composition; (ii) in deeper, finer-grained sediments Selection is strong (governing ~60% of turnover), being imposed by an unmeasured, but spatially structured environmental variable; (iii) in shallower, coarser-grained sediments Selection is weaker (governing ~30% of turnover), being imposed by vertically and horizontally structured hydrologic factors; (iv) low-levels of Dispersal can govern nearly 30% of turnover and be caused primarily by spatial isolation resulting from limited exchange between finer and coarser-grain sediments; and (v) highly permeable sediments are associated with high-levels of Dispersal that homogenize community composition and govern over 20% of turnover. We further show that our framework provides inferences that cannot be achieved using pre-existing approaches, and suggest that their broad application will facilitate a unified understanding of microbial communities.

The Silence of Biogeography

Mark V. Lomolino[1] & Bryan C. Pijanowski[2]

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Biogeography is the study of geographic variation in all biological traits and, from the early classics of Darwin and Wallace and those of von Humboldt before them, biogeographers have explored a marvelous diversity of the patterns in nature across a broad range of spatial and temporal scales. Alexander von Humboldt's contributions, in particular the narrative account of his explorations to the Canary Islands and the New World tropics and his classic, comprehensive *Essay on the Biogeography of Plants*, not only inspired Darwin and Wallace and generations of others to become naturalists, but these works served as exemplars of holistic approaches for exploring the geography of nature. Although we can think of no other single work that is as holistic and eclectic as von Humboldt's Essay and its *Tableau* (illustrating in great detail the elevational gradients in biological communities and environmental conditions along the slopes of Mount Chimborazo, Ecuador) the collective interests of modern biogeographers has of course expanded to include an even greater diversity of biotic variables – ranging from genetic, physiological and morphological traits of individuals, to the characteristics of entire communities and regional to continental (whole ocean) scale biotas. Our purpose here, however, is not to praise our modern discipline for all its insights and breadth of visions, but to point out our glaring oversight of a potentially transformative frontier in the geography of nature.

Effects of connectivity and size of local sites on species diversity-gene diversity correlations within (meta)communities: insights from neutral theories

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In the last decade, there has been a growing interest in the simultaneous study of genetic diversity within populations and species diversity within associated communities. It has been argued that "neutral processes" such as drift and migration should similarly affect both organizational levels, thus contributing to positive covariation of diversities among sites, the so-called species-genetic diversity correlations (SGDCs). However, environmentally dependent competition and ecological characteristics of species may weaken, or even reverse, such SGDCs. Empirical studies have revealed both negative and positive SGDCs over a wide array of ecological situations, leading to discussions over the relative strength of "neutral" against "niche" processes in population / community construction. However, a proper quantitative neutral model including both levels has yet to be produced as a null model for SGDCs. We propose a unifying mainland-islands model with a sampling

theory to explore the effects of sites' connectivity and size, as well as the importance of intra-specific neutral mutation rate, on SGDCs. We show that variation in size and connectivity among sampled sites contributes to positive SGDCs through the relative strength of drift compared to migration. Moreover neutral gene mutation can significantly affect SGDCs, leading to negative correlations under realistic situations. We therefore argue that neutrality should not necessarily generate positive SGDC and provide some general guidelines for interpreting such joint patterns of diversity.

Saturday 16 November, Contributed papers 2: Methods

A new law of biogeography? the Gause-Liebig law

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Predicting how species will move in response to climate change is an important question. Current tools are either extremely mechanistic but very data hungry or completely based on correlation. Here I present evidence for a law which I call the Gause-Liebig law that describes how abundance varies along environmental gradients. I show how this law can be used to produce predictive models of abundance over space (as a function of environmental gradients). This result provides a tool with low data requirements but more mechanistically grounded than correlation. I assess the performance of this approach in predicting species abundances in interpolative and extrapolative contexts vs traditional niche models.

Fuzzy logic is a helpful conceptual and operational tool for modelling the geography of ecological interactions

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Fuzzy logic is a form of many-valued logic whose variables have a truth value that varies in degree. Spatial favourability for species occurrence may be considered a fuzzy concept, as historical, geographical, human, and environmental conditions make locations more or less favourable for the occurrence of particular species. The favourability function was conceptually conceived to define spatial favourability in a fuzzy gradient from 0 to 1, so facilitating the application of fuzzy logic to spatial modelling. Favourability values derived from the favourability function have the same meaning and the same mathematical value regardless the prevalence of the species, so enabling direct comparison of models built for different species and their combination using fuzzy logic operators. These characteristics make the favourability function particularly useful in the spatial modelling of ecologically interacting species. In particular, the fuzzy intersection of favourability for different species is useful to model the biogeographical consequences of different degrees of competition between species. Fuzzy logic operations allow also to combine autoecological and sinecological responses in a way that may account for the existence of parapatric distributions in current and future environments, as exemplified by hare species in Europe. Fuzzy logic may provide biogeographical modellers with the necessary flexibility in concepts and operational tools to deal with a highly unstable and intertwined biogeographical world.

Relative explanatory power of environmental variables given by RDA and CCA are not always reliable

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Redundancy analysis (RDA) and canonical correspondence analysis (CCA) are widely applied multivariate methods in community ecology when the researcher wants to know which explanatory variables are the best in explaining species data. The absolute values of explained variance that RDA and CCA produce are known to be rather uninformative because of inadequacies in the models that these methods fit for species abundances. However, it has been assumed that the relative explanatory power obtained for the explanatory variables can be considered reasonable reliable. We built a simulated environmental landscape in which species abundances were determined by two mutually uncorrelated independent variables, X_1 and X_2. Half of the species were defined as specialists and half as generalists. Specialists had their abundances more strongly controlled by X_1 whereas generalist species abundances were more strongly controlled by X_2. The species filled the landscape uniformly so that the species were spaced at constant environmental distance from each other. Then we sampled the landscape with a gradually widening systematic grid of community samples and subjected each grid of community samples at a time for an analysis by RDA and CCA. The results showed that both RDA and CCA switched the rank order of the explanatory power of the independent variables as the sample grid grew larger. This shows that RDA and CCA cannot give reliable results of the relative explanatory power of the independent variables when ecologically more specialist species respond to environmental factors differently from the response found among ecologically more generalist species.

Saturday 16 November, Contributed papers 1: Community Assembly

Past climate-biodiversity dynamics forecast profound turnover in biotic systems

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Quantitative assessments of 21st-century climate impacts on biodiversity typically predict heightened extinction risk. However, they have been questioned on various grounds, including a lack of long-term perspective, not using responsive indicators such as species abundances and for seeming inconsistency with sparse evidence for extinctions during recent glacial-interglacial cycles. Here we project changes in abundance and conservation status under a doubled-CO2 scenario for 147 European and North American tree taxa using models calibrated against taxa-climate relationships for the past 21,000 years. Our results provide a future scenario of profound changes in ecological communities but with low extinction levels.

The influence of climate and dispersal limitation on the stability of biotic associations across the late Quaternary

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Climatic and habitat conditions, dispersal lags, and biotic interactions are major factors structuring communities in the late Quaternary. Both environmental differences and dispersal limitation have been invoked to explain community structure across time and space (e.g., appearance of no-analog communities) or abundance change and geographic distribution shifts within single species, but biotic interactions are less commonly studied in the late Quaternary. However, quantifying the relative influence of environment, dispersal, and biotic interactions on patterns of species co-occurrence is not straightforward. We test a framework for assessing potential causes of species associations across space, thus identifying species pairs for which biotic interactions may be important. We focused on fossil pollen assemblages from lake sediment cores in eastern North America. We first determined significant pairwise associations among fossil pollen genera for every 1,000 years since 21,000 years before present. We then used geographic coordinates and simulated paleoclimates at each locality to determine whether significant pairs were influenced by environment, dispersal limitation, both processes, or neither. Few (0-1.9%) species pairs were significantly aggregated or segregated across space and overall, the potential role of biotic interactions was minimal for significant species pairs. Rather, the dominant processes were environmental differences or dispersal differences; often, both processes were detected. Even for those species pairs that potentially represented an actual biotic interaction in one time period, the association was usually nonsignificant at other times. The pairwise approach taken here emphasizes that assemblages of species are transitory and primarily tied to environmental changes or differences in dispersal ability.

Functional and phylogenetic variation of tree communities across broad environmental gradients in Puerto Rico

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Enhancing plant community surveys with functional and phylogenetic data can help resolve the influence of the various processes that govern species distributions and community assembly. Applying this approach to broad environmental gradients may reveal how communities respond to environmental change. We examined variation of Puerto Rican tree diversity across precipitation and soil gradients to understand how the relative influence of processes governing these patterns changes with respect to environmental conditions. We censused all freestanding, woody stems ≥1 cm diameter in 24, 0.25-ha plots located along Puerto Rico's broad precipitation gradient. For the species included in these plots (N=221), we measured five functional traits based on *a priori* hypotheses about their ecological relevance and response to environmental conditions (specific leaf area, leaf area, leaf thickness, maximum height, and wood density). In addition, we quantified the evolutionary relationships among nearly the entire native and naturalized tree flora of Puerto Rico (N=529) using a highly resolved molecular phylogeny. Using null models, we evaluated how functional and phylogenetic dimensions of tree community composition varied with respect to precipitation and soil gradients. For all five traits, community-weighted mean trait values responded to the precipitation gradient as we expected, although these relationships were only significant for the drier half of the gradient. Dry forest plots comprised species that were phylogenetically and functionally clustered compared to the island species pool. Specifically, dry forest plots comprised short statured trees with small leaves and dense wood compared to the overall pool. This pattern remained even when species pools were restricted to species occurring on particular soil types. Our study extends recent developments in community phylogenetics and functional ecology to address

community variation at an intermediate spatial scale and along broad environmental gradients. Integrating multiple dimensions of biodiversity may help illuminate the processes underlying community variation along environmental gradients. Broadening the spatial and taxonomic scale of analysis to address these issues at a regional scale integrates ecological and evolutionary processes structuring community diversity.

Plant defence against megaherbivores: biogeography, heteroblasty and trait matching

Kevin Burns

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Species interactions often promote trait matching, which occurs when species evolve traits that coincide with local interaction partners in ways that enhance their fitness. I quantified plant structural defences in two spatial dimensions (vertically and geographically) to test whether plants deploy prickles, thorns and spines in ways that match the distribution of mammalian herbivores. In mallee scrublands of Western Australia, where adult plants are within the reach of megaherbivores, plant structural defences increased vertically and were deployed preferentially by adult plants. Conversely, in woodlands of Eastern Australia and California, where adult plants commonly grow above the reach of megaherbivores, structural defences decreased vertically. Populations of closely related woodland taxa on Lord Howe Island and Santa Cruz Island exhibited significant reductions in structural defence in the absence of megaherbivores. However, Coprosma quadrifida, a member of a diverse clade of woody plants that radiated in New Zealand, evolved vertical changes in structural defence after colonising Australia, where it is exposed to megaherbivores. Overall results illustrate a diverse array of spatial patterns in plant structural defence that covary with the distribution and foraging behaviour of large mammals, providing a multi-scale perspective on how megaherbivores have shaped the evolution of plant form and function.

Spatial and Temporal Trends in Plant Community Composition of Central European Forest Springs

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Due to their inherently constant water supply and temperature regime, spring sites are “natural laboratories for ecologists” (Odum 1971) inhabiting numerous stenoecic species well-adapted to these conditions. Long-term constancy of the abiotic regime and the significant ecological differences to neighboring ecosystems are supporting the establishment of characteristic species assemblages of these ecological islands. However, their spatial isolation acts as a filter for dispersal, which is likely to limit rapid community adaptation to anthropogenic changes of environmental conditions. Central European forest ecosystems have been affected by acidic depositions until the end of the 20th century and are likely to respond to sudden and gradual climatic shifts in the near future. Spring sites and the related plant communities can be used to monitor these large-scale ecosystem changes in an integrative and standardized way. Here, we investigate the community composition of spring vegetation and physicochemical water characteristics of 102 Central European forest springs on siliceous parent material with forest catchments. Besides rare and small-scaled natural disturbances by wild game, these spring sites are not affected by any human disturbance. In consequence, the species composition is reflecting spatial gradients in the environmental regime of catchments. We show temporal trends and spatial patterns in species assembly and we analyze their ecological drivers. Spring communities react rapidly and sensitive to gradual but also sudden shifts in environmental conditions of the catchments reflected in the spring site conditions.. Ongoing work will confirm the potential of this biomonitoring-tool and support political decision-making regarding regional-scale climate change effects.

Odum, E.P. 1971. Fundamentals of Ecology. 3^{edn}. Saunders, Philadelphia, 574 pp.

Saturday 16 November, Contributed papers 2: Methods

Visualizing species distributions and phylogeography using GenGIS

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GenGIS (http://kiwi.cs.dal.ca/GenGIS) is a 3D geographic information system designed to support analysis of biodiversity data. Previous versions of GenGIS allowed interactive visualizations of georeferenced phylogenetic trees in two and three dimensions, and the exploration of species diversity in concert with environmental features. The latest major release of GenGIS includes support for the development of analysis plugins that can use functions from Python and R; currently available plugins include linear regression and the Mantel test, calculation of beta diversity, canonical correlation analysis and reference condition analysis. New data retrieval plugins allow users to retrieve data directly from online resources including the Global Biodiversity Information Facility (GBIF) and the MG-RAST metagenomics resource. In this presentation I will use a South American vertebrate dataset to illustrate how GenGIS can be used to retrieve and analyze data from online and local sources, in order to visualize species distributions and environmental properties. Using mitochondrial sequence data from several species, I will also show how trees can be used in GenGIS to test the geographic structuring of populations.

Node-based analysis of clade distribution

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The integration of ecological data with evolutionary relationships is one of the most rapidly moving research fields today, and has led to considerable advances in our understanding of the processes underlying biogeographical patterns. Here, we develop the node allopatry score that combines ecological and evolutionary approaches into a single framework, and avoids many of the problems that characterize community phylogenetic methods in current use. This approach goes through each node in the phylogeny, and compares the distributions of descendant clades to a null model. The node-based analysis identifies specific nodes associated with shifts in distribution or environmental tolerances, and in doing so provides insights into what nodes are responsible for patterns of phylogenetic structure and species co-occurrence. This provides the basis for more detailed studies, for example focusing on the ecological changes or adaptations that took place at the highlighted nodes. We demonstrate how this novel implementation can be used to generate hypotheses for biogeographical patterns with case studies with well-described biogeographical histories. The node-based analysis generates a set of intuitively interpretable patterns that are consistent with current biogeographical knowledge. Importantly, the results are statistically tractable, opening many possibilities for their use in analyses of the evolutionary, historical and spatial patterns of species diversity.

Statistical assumptions in the distance decay relationship and their implications for biodiversity conservation

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Distance decay relationship describes the decrease of compositional similarity between pairs observations and geographic distance. Statistically speaking, the distance decay relationship describes the covariance structure in the biological community. The simplest covariance structure which is often assumed for distance decay relationship in the ecological literature is stationary and isotropic. I show how the violation of these assumptions about the covariance structure affect the interpretation of the distance decay relationship in simulated and real-world data sets. Finally, I put these findings into the context of biodiversity conservation.

Saturday 16 November, Contributed papers 2: Methods-application

Defining communities by their interactions: Using process to identify pattern

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Much of contemporary community ecology focuses on intense study of pattern: Observed distributions of species and environmental variables are used to predict how communities and environments interact. This has resulted in a rich field of multivariate analysis techniques. Much less development has focused on using observations of changes to gain insight about ecosystem interactions. This alternative process-based view uses observational time series to estimate rates of change among populations of species (e.g. mortality and birth), and environmental properties (e.g. resource supply and consumption). These "demographic traits" could then be used to describe ecosystems using mechanistically informative and quantifiable variables, and may be useful for predicting future ecosystem behavior in response to management or perturbation. Using data describing almost a century of grassland succession following agricultural abandonment at Cedar Creek Ecosystem Science Reserve, I present an example of this process-based approach for estimating demographic traits in ecosystems, and show how these parameters can be analyzed. The demographic traits parameterized by this technique suggest a tradeoff between colonization and mortality rates, as predicted by many metapopulation models, and shows evidence for increased community stability with field age.

Using co-occurrence patterns of indicator species to infer broad-scale environmental and biotic structuring of Amazonia

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The use of indicator species has a long history in vegetation ecology and studies focusing on fossil assemblages. In particular, species whose habitat preferences are known have been successfully used to infer environmental conditions in sites or time periods for which no direct measurements of environmental variables are available. The inferred habitat conditions, in turn, can be used to make predictions about the potential distribution of other species and biotic communities. Amazonian rain forests are a prime example of an extensive and poorly known ecosystem, where broad-scale compositional patterns have been difficult to map. The challenges range from poorly resolved taxonomy of many organism groups to scanty information on species distributions and the spatial variation in environmental conditions. In the past year or so, several studies have documented that easily observable plant groups can be used to infer edaphic properties of rain forest sites. Since all plant groups to some degree respond to the same soil properties, this makes it possible to infer general compositional patterns in the forests even when direct data on most plant groups are absent. I will review some recent findings based on these inference methods, and assess how they could enhance understanding on Amazonian biogeography.

Saturday 16 November, Contributed papers 1: Community Assembly

When should species richness be energy-limited, and how would we know?

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Energetic constraints are fundamental to ecology and evolution, and empirical relationships between species richness and estimates of available energy (i.e. resources) have led some to suggest that richness is energetically constrained. However, the mechanism linking energy with richness is rarely specified and predictions of secondary patterns consistent with energy-constrained richness are lacking. Here we lay out the necessary and sufficient assumptions of a causal relationship linking

energy gradients to richness gradients. We then describe an eco-evolutionary simulation model that combines spatially-explicit diversification with trait evolution, resource availability, and assemblage-level carrying capacities. Our model identified patterns in richness and phylogenetic structure expected when a spatial gradient in energy availability determines the number of individuals supported in a given area. A comparison to patterns under alternative scenarios, in which fundamental assumptions behind energetic explanations were violated, revealed patterns that are useful for evaluating the importance of energetic constraints in empirical systems. We use a dataset on rockfish (*Sebastes*) from the northeastern Pacific to show how empirical data can be coupled with model predictions to evaluate the role of energetic constraints in generating observed richness gradients.

Saturday 16 November, Contributed papers 2: Methods-application

Community assembly of ants along environmental gradients: Combining Species Distribution and Macroecological models

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Global climate change threatens ecological communities by shifting species distributions and altering species assembly. To better understand and predict the consequences of global environmental change on biodiversity, we must first understand the current state of natural communities. Specifically, it is important to predict how community composition can change across broad environmental gradients that are likely to be impacted by climate change. Our main objectives were to: 1) document patterns of savanna ant species richness in northern Australia using macroecological and statistical models; 2) develop stacked species distribution models to predict community assembly; and 3) predict how community assembly might change under future climate scenarios. We hypothesize that ant richness patterns are driven primarily by the large rainfall gradient of the region (1600-600 mm north to south). We sampled ant communities at 15 sites along the rainfall gradient on two occasions, using pitfall traps. We also developed ensemble species distribution models using four algorithms for 35 species that are distributed throughout northern Australia. We stacked the distribution models to evaluate how accurately the models predicted community assembly. Finally we projected the species distributions on to future climate change scenarios and evaluated how species ranges might shift and how community assembly may change. Species richness remained fairly constant but there was marked compositional change along the rainfall gradient. Stacked species distribution models overestimated the occurrence of species at particular sites but shifts in species distributions and community assembly under future climate scenarios are expected.

Sunday 17 November, Contributed papers 1: Large Scale A

Latitude, Productivity and Species Richness

Len N. Gillman[1], Shane D. Wright[2], Jarrod Cusens[1] & Paul McBride[1] & Robert J. Whittaker[3,4]

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Net Primary Productivity on land has long been thought to be greatest in tropical forests and to decrease towards the poles. This view has recently been challenged with a report that annual net primary productivity of forests instead peaks at mid-latitudes. Understanding global patterns in primary productivity in natural ecosystems is important if we are to resolve questions relating to the influence of productivity on global carbon budgets and determine evolutionary processes such as those involved in regulating patterns of biodiversity. However, the claim that NPP peaks at mid-latitudes was made without

support from statistical analysis of the data. We find that applying ordinary least squares regression to these data, as well as to data obtained from the Oak Ridge National Laboratory database, yields strong support for a negative relationship between latitude and net primary productivity of forests. Given that species richness increases towards the equator, the parallel gradient in productivity we report is consistent with the findings that relationships between productivity and species richness of plants and animals in natural ecosystems are predominantly positive at both large and small spatial scales. These results are congruent with much diversity theory that invokes productivity as a causal factor.

Biotic exchange, climatic niche conservatism and reversed latitudinal diversity gradients

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That diversity patterns are imprinted by historical events is widely accepted but, what is the magnitude of the impact of history on current patterns? And how exactly have historical and evolutionary events functioned to influence the contemporary distribution of diversity? An approach to answer these questions is to focus in well-known examples of dispersal, a process recurrently used in Biogeography to explain species distributions. Here, we study the biotic exchange of mammals across Beringia, comparing the species richness patterns of the genera that dispersed to the Nearctic versus those that dispersed to the Palearctic. This case study allowed testing the following predictions: (1) if dispersers had conserved the adaptations that enabled them withstanding the cold temperatures of the Bering Strait, we would expect them to be species-rich in cold climates. (2) If climatic niches have been effectively conserved across evolutionary time, then macro-ecological models (MEM's) should be able to cross-predict diversity of dispersers between origin and destination biogeographic domains. (3) MEM's for species belonging to genera that dispersed would predict better the diversity of congenerics in other continent than diversity of species not belonging to dispersed genera. Results generally confirmed our expectations. Despite the long periods of time spanned since these dispersal events took place, exchanged faunas can still partially predict the distributions of congenerics inhabiting a different continent. In sum, dispersal coupled to thermal or climatic adaptations conserved along evolutionary history, provide a likely explanation for examples of a reversed latitudinal diversity gradient in mammals.

Global biodiversity and biogeography of razor clams (Bivalvia: Solenidae)

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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 0.083º 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.

Sunday 17 November, Contributed papers 2: Large Scale B

Towards a biogeography of species interactions

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Networks of species interactions are a powerful way to address the complexity of ecological communities. Yet, our understanding of networks is primarily static, species based, and overall poorly adapted to biogeographic questions. Nonetheless, understanding how and why networks vary through space is a key step in furthering the integration of community ecology and biogeography. Building on recent developments expanding the alpha -beta-gamma diversity levels to species interaction networks (Poisot et al. 2012), we propose a new paradigm for network research. We explore how embracing the fact that networks vary over space and time allow to develop statistical approaches to predict interactions, how it allows a more mechanistic approach to variation, and how it relates to the relationship between species interaction and species co-occurence. We show that working toward a biogeographic theory of interaction networks will have benefits for species distribution modelling, and allow to predict the re-assembly of ecological communities following environmental change.

T. Poisot, E. Canard, D. Mouillot, N. Mouquet & D. Gravel (2012). The dissimilarity of species interaction networks. Ecology Letters, 15 (12) 1353-1361.

A quantitative framework to understand and predict spatial distribution of ecological networks

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Integrating network theory to biogeography is among the most important and exciting challenges that macroecologists are currently facing, yet the idea that species interactions have a biogeographical structure of their own is often overlooked. Achieving this integration is necessary to progress towards understanding species interactions through time and space, and doing so to predict species geographical distributions and community dynamics. We propose a quantitative framework to infer spatial distribution of ecological networks. We start from the observation that local interaction networks are never simple random samples of a regional and stationary meta-network. We decompose the origin of this variation in several components with several probabilistic models of network structure. We find, not surprisingly, that spatial variation in community composition is the first factor responsible for the spatial variation in network structure. This variation is not random however, it is strongly driven by species-specific responses to variation in the environment. Secondly, we find that species non-random association (attraction and repulsion) is also a major component of the variation of network structure. Lastly, we underline the need to account for the reciprocal feedback between the meta-network structure and species co-occurrence. The framework we propose has potential practical implications such as the proposition of sampling guidelines for the inference of network structure, development of species distribution models accounting for biotic interactions and scenarios of future community structure following global changes.

Estimates of species extinctions from Species–Area relationships strongly depend on ecological context

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Species–area (SAR) and endemics–area (EAR) relationships are amongst the most common methods used to forecast species loss resulting from habitat loss. One critical, albeit often ignored, limitation of these area-based estimates is their disregard of the ecological context that shapes species distributions. In this study, we estimate species loss using a spatially explicit mechanistic simulation model to evaluate three important aspects of ecological context: coexistence mechanisms (e.g. species sorting, competition–colonization tradeoffs and neutral dynamics), spatial distribution of environmental conditions, and spatial pattern of habitat loss. We found that (1) area-based estimates of extinctions are sensitive to coexistence mechanisms as well as to the pattern of environmental heterogeneity; (2) there is a strong interaction between coexistence mechanisms and the pattern of habitat loss; (3) SARs always yield higher estimates of species loss than do EARs; and (4) SARs and EARs consistently underestimate the realized species loss. Our results highlight the need to integrate ecological mechanisms in area-estimates of species loss.

Sunday 17 November, Contributed papers 1: Global Change

Using museums to predict climate change response: modeling Florida plant diversity

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Integrated Digitized Biodiversity collections (iDigBio; www.idigbio.org), the National Resource for Advancing Digitization of Biodiversity Collections (ADBC), is an NSF-sponsored effort to digitize biological collections from all natural history institutions across the USA. This 10-year effort will make data from an estimated 1 billion specimens hosted in 1,600 collections available on a single portal. The scope of the research questions that this resource will enable the scientific community to address is unprecedented, and we are currently reaching out to the community to develop pipelines to make this resource user-friendly and broadly accessible to a diverse array of users. Here, we present a study of the vascular plants of Florida, using the historical information on museum specimens to predict the future of the flora of this biological hotspot. Using herbarium collections, we reconstructed niche models for more than 1,700 terrestrial plant species from throughout Florida and projected these models into the future. Mapping the index of plant diversity and endemism hotspots, we examined predicted future distributions of this diversity. Future distributions considered models of dispersal ability, sea-level change, and urbanization projections. Unexpectedly, two distinct regions respond differently to the future change in climate, with altered precipitation seeming to be a stronger determinant of these responses than increasing temperature. Furthermore, the regions with the greatest projected increases in species richness correspond to those most vulnerable to sea-level rise, with important implications for conservation and land management of the peninsula.

Response of Rodents to Climatic Variation in North America Over the Past Century

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Bergmann's rule, which describes the tendency for body size of animals to increase with increasing latitude and elevation, has recently been explored across temporal gradients to assess the relationship between body size and environmental conditions. Changing climates provide a unique challenge or opportunity that may result in a shift in body size of populations, consistent with the causal explanations for Bergmann's rule (i. e., increasing during periods of cooling and decreasing during periods of warming). The purpose of this research is to assess the capacity of members of small mammals to respond in an adaptive manner to recent climate change through shifts in body size of their populations. We predict that body size shifts over time will be inversely related to changes in mean annual temperatures. Specifically, we compared the body size (condylobasal length) of specimens representing five families and 23 species, where each species was collected at the same location over the past century. Given the fundamental importance of body size, our research will enhance our ability to predict potential evolutionary responses to future climatic change and provide transformative insights for conserving the natural character of species, including their body size and capacity to adapt to future environmental change.

How does city size affect the relationship between bird species richness and urbanization?

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Bird species richness changes along the urban gradient. The magnitude and direction of this change may be influenced by city size. For example, if the general pattern of bird species richness in response to increasing human density is humped-shaped with an overall decline, then the slope of the relationship between bird species richness and human density in individual cities should be positive in small cities (with small populations and low human density) and negative in large cities (with large populations and high human density). We tested hypotheses of the effect of city size on the bird species richness-human density relationship using Breeding Bird Survey (BBS) and U.S. Census Bureau data. We randomly selected 48 cities stratified by population size, latitude, and longitude. For each city, we summarized bird species richness for the BBS routes located within an exurban-density buffer and estimated the slope of the relationship between human density in landscapes surrounding routes and route bird species richness. We used these estimates as the response variable in models that included city population size, city age, temperature, precipitation, and elevation as predictors. We also directly tested for an effect of city population size on route bird species richness over and above the effects of other predictor variables, including human density. City population size was included in the most supported models and had a negative effect on bird species richness. These results have implications for the comparison of the effects of urbanization on biodiversity among cities and for urban planning and design.

The role of urban and agricultural areas for migrating birds: an assessment of within-year temporal turnover

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The impact of anthropogenic land-use change on avian diversity has been assessed from a variety of ecological perspectives, but primarily between-years with little attention given to within-year dynamics. Using citizen-science data on avian occurrences, we estimate how species richness and temporal decay in compositional similarity was structured within-years across an anthropogenic land-use gradient (intact vegetation, agriculture, and urban). Species richness peaked on average during spring and autumn migration, and intact vegetation had the highest and urban the lowest species richness on average. Temporal decay trajectories were similarly structured across the land-use gradient and were similarly affected by the geographic diffusion of migrating species. The level of temporal turnover was lowest for agricultural and especially urban areas, suggesting more homogeneous within-year species compositions. With increasing latitude, migratory species made up

a larger proportion of the breeding community, resulting in higher temporal turnover across the land-use gradient and a weaker effect of migration for intact vegetation. These results suggest land-use change degraded within-year temporal turnover and reduced species richness during migration and the breeding season. However, the effect of migration remained evident across latitudes within urban and especially agricultural areas. This suggests efforts directed towards maintaining or restoring landscape heterogeneity in these areas may enhance the quality of stopover habitat and the viability of migratory populations throughout North America. These efforts may also mitigate the temporal and spatial simplification of avian diversity that has occurred through human activities.

Incorporating the effects of permafrost dynamics into a dynamic vegetation model to improve the estimation of vegetation distribution and carbon cycling in northern high latitudes during the 21st century

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In northern high latitudes, permafrost plays an important role in affecting vegetation distribution and carbon (C) dynamics. This study incorporates a soil thermal model (STM) that couples water and heat transport into a dynamic global vegetation model (LPJ-DGVM) to simulate the permafrost and soil thermal dynamics, and to evaluate their effects on vegetation and C dynamics through the 21st century. With improved simulation of soil temperatures, LPJ-STM performs better in modeling carbon budget than LPJ does when results are compared to field observations for historical periods. Further model simulations are driven with a suite of climate projections with varying atmospheric CO_2 concentrations and climate sensitivity. The results indicate that both atmospheric CO_2 concentration and climate variability exert significant effects on vegetation distribution and ecosystem C dynamics, while CO_2 fertilization plays a greater role than climate variability. The warming climate will reduce the capacity of C sequestration in the region. Relative to the stand-alone LPJ-DGVM, incorporation of STM into LPJ-DGVM leads to: (i) slower replacement of boreal evergreen coniferous forest by deciduous forest and herbaceous vegetation; (ii) shorter growing season in present time primarily due to later thawing in spring; (iii) higher present-day ecosystem C sequestration but with a faster declining rate under warming climate; (iv) slight increase in vegetation C but a pronounced large gain in soil C by 2100.

Sunday 17 November, Contributed papers 2: Phylogeography

Natural experiments and meta-analyses in comparative phylogeography

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The challenge for phylogeography, like other observational sciences, is to extract general relationships representing causes and effects from complex natural data. I describe comparisons of synchronously diverging co-distributed (SDC) taxa, including sympatric sister species, to help meet this challenge. As an example, using narrative and best evidence synthesis, I re-evaluate ad hoc aggregate analyses relating population genetic structure (F_{ST}) to dispersal potential. I deconstruct an aggregate global analysis to generate a regional subset of data which I compare with datasets describing co-distributed taxa, SDC species and sympatric sister species. A weak negative relationship between F_{ST} and dispersal potential is implied by aggregate global analysis ($0.1 \leq R^2 \leq 0.29$). In contrast, regional datasets of co-distributed species show strong correlation between F_{ST} and dispersal potential ($0.78 \leq R^2 \leq 0.85$). Comparisons between SDC and sympatric sister species consistently evince higher gene flow in species with higher dispersal potential. This suggests that ad hoc aggregate analyses can be compromised by multiple sources of error. Comparisons of SDC taxa, including sympatric sister species, adapt the experimental scientific method to natural situations, providing robust and repeatable tests of phylogeographic hypotheses and accurate estimates of effect sizes. To make strong inferences about phylogeography we should seek out the hidden wealth of natural experiments that provide particularly clear opportunities to study the factors that influence patterns of

biodiversity.

Predicting phylogeographic endemism in a topographically complex Neotropilcal hotspot

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We ask how geography and environmental shifts over the last 120,000 years influence present-day patterns of phylogeographic endemism: a variant of phylogenetic endemism, based on the very tips of the Tree of Life, which we introduce to study the impacts of recent history on the spatial distribution of genetic diversity. Using the mega-diverse and threatened Brazilian Atlantic forest as a study system, we map phylogeographic endemism through a biome-wide synthesis that combines new and published sequence-level data from 25 vertebrate species or species groups. To ask how accurately one can predict the distribution of phylogeographic endemism in space, we investigate the roles of historical climate stability and current climatic heterogeneity on phylogeographic endemism. We identify two divergent bioclimatic domains within the forest (one in the north, one in the south). Independent modeling of these domains demonstrates that endemism patterns are subject to different drivers: while historical climatic stability predicts phylogeographic endemism in the north, contemporary climatic heterogeneity better explains endemism in the south. These results are consistent with recent speleothem and pollen fossil studies, which indicate that the northern and southern Atlantic forests have been acting as a dipole, providing a bridge between Neotropical genetic data and information from geomorphology and paleoecology. The correspondence also reinforces the conclusion that sub-regional differences in climate are central to explaining endemism patterns and historical demography across taxa and regions with divergent histories and environmental domains – a result expected to improve prediction of endemism patterns in other endangered or understudied ecosystems worldwide.

The biogeography of electro-crypsis in *Gymnotus*

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Neotropical weakly-electric fishes produce electric signals for navigation and communication. However, these signals are susceptible to eavesdropping by electro-receptive predators. It has been hypothesized that electric signals in some species of the genus *Gymnotus* have evolved to reduce detection by electro-receptive predators (electro-crypsis). We conducted a biogeographic and phylogenetic analysis of this hypothesis, by sampling electric signals from *Gymnotus* species within and outside the ranges of most electro-receptive predators. Our results support a correlation between geographic variation in predation pressure and *Gymnotus* electric signals. Thus, biogeographic patterns of species associations can affect the evolution of electricity-based communication and navigation systems.

Whole-community DNA barcoding of aquatic insects reveals extremely high endemicity and limited movement among highlands neotropics streams

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On-going massive extirpations of amphibians by chitrid infections in highland Neotropical streams lead to associated dramatic changes in ecosystem function. This study aims to elucidate diversity changes in unknown aquatic insect

communities (Ephemeroptera, Trichoptera, Coleoptera) comparing sites in stages of pre- and post-amphibian decline. We used a whole-community DNA barcoding approach to assess diversity simultaneously at species (divergence of lineages) and genetic (population dynamics) levels. Comparisons among eight sites revealed high β-diversity at species and genetic levels across a 400 km transect in Panama. This suggests high endemicity and limited movement among streams, with separation both at short- and large-temporal scales evident at the genetic and species levels, respectively. Testing patterns of total phylogenetic diversity within communities, opposing results were obtained for Ephemeroptera, whose diversity decreased from West to East along the gradient of chytrid introduction, and for Trichoptera and Coleoptera that increased over this transect. Our results did not reveal a homogenization of communities in the wake of amphibian extirpation that might have been expected because of the spread of insect species taking up vacant niche space. Therefore, differences in community composition may be driven by evolutionary and biogeographic factors unrelated to amphibian decline. In contrast to small-scale experiments where species composition is manipulated, our natural experiment at large scale evidenced effects of evolutionary history for predicting consequences of species loss and changes in ecosystem function. Each site is an independent evolutionarily unit, therefore, the evolutionary history of highland Neotropical streams is the highly erodible, unique and irreplaceable.

A phylogenetic reclassification of the phytogeographic zones of southern Africa

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The classification and delineation of biogeographical units provides a fundamental step in understanding the distribution of biodiversity across the globe. However, many bioregional classification schemes are laid down with little cognizance of phylogenetic relatedness, resulting in only a weak correspondence between bioregions and the evolutionary assemblages of species found within them. Because phylogeny captures information on the evolutionary history of diversification and dispersal, it provides a valuable tool for delineating biogeographical boundaries. In this study, we use a dated phylogeny of trees and a metric of phylogenetic β-diversity to delimit the phytogeographical zones of southern Africa. Based on cluster analysis, we uncover 12 phytogeographic regions which differ in evolutionary uniqueness. Our phytoregions match surprisingly closely to traditional classification, but we also find mismatches for some regions. Notably, we identify new phyloregions which differ in evolutionary distinctiveness. We suggest conservation premium should be placed on ecozones with highest evolutionary distinctiveness, such as the savanna and the coastal forests.

Posters

P1 - Community Assembly

Drivers of the functional trait structure of woody plants in Japan: contrasting role of climate harshness and seasonality

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We examined the hypotheses that geographic patterns of convergence and divergence in the functional trait structure of woody plants would be driven by environmental filtering and niche partitioning in relation to climate harshness and/or climate seasonality. Using a combined dataset of species distribution and leaf and stem traits in the Japanese archipelago, we analysed the influence of climate harshness (mean annual temperature and annual precipitation) and climate seasonality

(temperature and precipitation seasonality) on community mean trait values, functional richness and functional divergence. Climate harshness had a limited influence on the trait structure. Temperature seasonality played a significant role in determining the trait structure. For certain traits (wood density and leaf nitrogen concentration), functional diversity decreased with increasing temperature seasonality, indicating trait convergence associated with environmental filtering. For the majority of the traits (leaf thickness, specific leaf area and maximum height), however, functional diversity increased with increasing climate seasonality. Our results demonstrated the importance of climate seasonality in shaping the geographic variation of functional trait structures in the tree assemblages. In the Japanese archipelago under a warm and wet monsoon climate, climate seasonality resulted in the convergence and divergence of co-occurring traits across vegetation zones. This suggests that seasonal environmental variability acts not only as a filter of species traits, but also as a driver for creating a greater difference in ecological niches among tree species.

Patterns and potential effects of dispersal limitation on island plant community assembly

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Basic physiological limits and selection pressures can lead to resource use and investment trade-offs in plants. Arguably, one of the most interesting of these is the competition-colonization trade-off, also described in terms of r- versus K-selected species. Species leaning towards r-selection rely more on their colonization ability via large seed set and small seed mass, compared with K-selected species that allocate more energy into fewer seeds, relying on a more competitive strategy. Studies have shown that this trade-off can promote species coexistence in a local metacommunity context, but the large-scale island biogeographic implications of the competition-colonization trade-off are less well understood. By considering the effect of dispersal limitation, this trade-off may be a critical mechanism influencing community and ecosystem-level patterns on islands. We explored this conceptual framework by using species composition data from 27 Maine islands. We compared the functional composition of these islands to hypotheses predicted by the competition-colonization trade-off. Our results support the importance of dispersal limitation and the resulting competitive dynamics in this archipelago. This is an important step towards understanding the mechanistic role of dispersal limitation in island plant communities—providing an important link between island biogeography, functional ecology, and community assembly. We suggest methods to empirical test the importance of dispersal limitation on the plant communities of this and other archipelagos.

Infection preference of an invasive parasite to a novel invasive host in a human dominated landscape, the Panama Canal

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Infection preference of an invasive parasite to a novel invasive host in a human dominated landscape, the Panama Canal. The global spread of introduced species across broad biogeographical ranges provide excellent natural experiments with which to study the ecology and evolution of biological dependencies, such as predator-prey interactions and host-parasite associations. This is because introduced species are reshuffled with previously allopatric species in novel habitats, exposed them to novel selection pressures associated with biotic interactions. These interactions can limit or facilitate their demographic success, thereby affecting evolutionary trajectories, in new environments. Thus, understanding the extent to which introduced predators, herbivores and parasites, which can be generalists or specialists, interact with species in novel habitats provides the conditions to test alternative predictions on the processes that drive biotic dependencies in invaded systems, either niche conservatism or adaptive evolution. Parasites can have broad host specificity, yet their host range is highly adaptive and often mutable across spatial and temporal scales as natural selection can drive infection preferences to hosts that increase the parasite's transmission rate and fitness. Here, we investigate the extent to which an widespread invasive parasite, Centrocestus formosanus, interacts with a novel community of potential native and invasive second intermediate fish hosts in the Panama Canal. We report that parasitism of the peacock bass was significantly higher than

other co-occurring fish species in natural populations and laboratory experiments testing for infection preference and host compatibility. We speculate that the observed preference of C. formosanus on the peacock bass, a popular sportfish, demonstrates local adaptation to a novel invasive host driven by anthropogenic activities. This study underscores the importance of evaluating patterns of biological interactions in invaded communities to understand the ecological and evolutionary processes that influence the success of invasive species.

Metacommunity assembly affects the local-regional species richness relationship

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The relationship between local and regional species richness (LSR-RSR) has been debated, and multiple mechanisms likely cause the two possible LSR-RSR patterns (linear or saturated). Metacommunity theory is built on four paradigms (patch dynamics (PD), species sorting (SS), mass effect (ME), neutral (N)) that should represent those mechanisms. We present simulation results where metacommunities assembled per the four paradigms across a gradient of RSR and disturbance regimes. We hypothesized PD and SS would generate saturated LSR-RSR curves, whereas ME and N paradigms would generate linear curves. Also, we expected disturbances would depress curves and potentially convert linear curves to saturated at high disturbance levels. In simulations, species (N 12-200) colonized and competed in 100 sites for 500 time steps, where conditions (i.e., site and species similarity, colonization/competition tradeoffs) matched paradigms. Disturbances removed portions of species in portions of sites (range for both; 0-0.95). PD, SS, and N paradigms caused saturated LSR-RSR curves, with shapes maintained but depressed with disturbance. ME caused linear LSR-RSR curves, but curves shifted to a depressed saturated shape with high disturbance. The two LSR-RSR shapes can be explained by the four metacommunity paradigms. Neutral assembly caused results similar to those of PD or SS, supporting arguments for its use. Because only ME caused the often observed linear LSR-RSR, we infer that ME is fairly common in nature. Also, LSR-RSR curve shape was generally insensitive to disturbance. This work helps to connect two major diversity concepts and advance debate on LSR-RSR beyond methods and toward mechanisms.

The role of competition in structuring plant communities consisting of closely-related species

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Situations occur in nature where several congeners exist even though early competition theory predicted that species of the same genus would rarely co-exist because they occupied similar ecological niches, begging the question of how seemingly similar species do not competitively exclude each other. The importance of limiting similarity in community composition has been examined in a non-evolutionary context for decades, whereas phylogenies have only been included in these analyses in recent years. In this study I combine ecological and phylogenetic methods to provide more insight into the role of competition in structuring communities of closely-related plants. In particular, I examine whether competition prevents the coexistence of closely related species. To address these questions, I use data on the species composition of sedge communities (i.e., plants of the Cyperaceae family) collected from 35 focal species in 700 plots distributed in the boreal-subarctic transitional zone of Quebec to quantify the phylogenetic structure of these communities. I created a phylogeny of the sedges of this region by using DNA barcode markers and nuclear ribosomal DNA sequences. A mean pairwise distance metric and nearest taxon metric were created to test if focal plant individuals are less likely to occur with closely-related species expected by chance. Finally, I test whether focal plant abundance is lower when co-occurring species are more closely related. This work increases our understanding of the processes that determine the identity and abundance of closely-related species in biological communities.

Multi-scale patterns of ground-dwelling spider (Araneae) diversity in northern Canada

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Elucidating general patterns of diversity at multiple spatial scales requires fine resolution data collected over a large geographic extent. We examined how patterns of ground-dwelling spiders (Araneae) diversity (i.e. richness, evenness, composition and structure) vary at local, regional and continental spatial scales in northern Canada, using a hierarchical sampling design that covered 30 degrees of latitude and 80 degrees of longitude. Over 23, 000 spiders, representing 306 species in 14 families, were collected in 12 sites located in Arctic, Subarctic and North-Boreal regions. Spider diversity was structured at continental scale across ecoclimatic regions but not with latitude. At regional scale, western sites differed from eastern sites indicating the importance of longitudinal diversity gradients in northern North-America, perhaps due to post-glacial dispersal patterns. Vegetation and climate also influence Arctic diversity patterns, and thus predicted climate change may alter the distribution of spiders, an important ecological group in the Arctic food webs. Due to the large extent and fine resolution, this research contributes to a better understanding of hierarchical patterns of diversity and will help to define conservation strategies for the Arctic biodiversity.

If the Jack-of-all-trades were the master of dispersal and coexistence in heterogeneous metacommunities

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Long central in ecology is niche theory in which species are understood to ‘win’ niche space as a result of interactions between competitive-rank ability and dispersal, determined by the composition of species functional traits, for instance, taken together, quantifying local adaptation, or environmental tolerances in changing environments. Yet neutral theory challenges niche theory by implying that species traits, except for dispersal, have no role in structuring community assembly. To advance the discussion on niche and neutral theory taken together, I have developed an eco-evolutionary (individual-based) metacommunity model to demonstrate how species coexist regionally and locally in heterogeneous landscapes, when all that the species have that differentiates them from one another is a specialization-dispersal trait trade-off, as an alternative to the competition-colonization trade-off paramount in metacommunity theory. My findings reiterate that intermediately heterogeneous environments and intermediate dispersal potential allow greater coexistence of species. Most interestingly, my results show that intermediately heterogeneous environments buffer effects of increasing generalization on coexistence in metacommunities and promote coexistence via a spatial aggregation effect of species. Of greatest concern today is disentangling whether, how and why specialist species are dying off more rapidly than generalist species. My model reveals important counterintuitive results, mainly, that specialists may prevail though disadvantaged by a narrow niche breath (relative to generalists) and a regional dominance of generalists, and, though rare regionally, they may dominate locally. Thus, the model provides interesting information for mapping out processes that may underly community assembly in the 'real world' and at macroeco-evolutionary and biogeographical scales.

Effects of lake size, isolation and piscivorous fish richness on nested fish community structure.

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Numerous studies support the idea that fish communities exhibit non-random structure. This is attributed to biotic and abiotic conditions at both the local and regional scales. Using a presence-absence matrix of species distribution across several

sites, regional patterns of community assembly may be detected. Community nestedness is a commonly studied pattern of species occurrence. Recently, several studies have sought to elucidate the underlying mechanisms that result in this distribution pattern. Of these, few have focused specifically on freshwater ecosystems or on predator-prey interactions. The goal of our study was to determine whether fish communities in two Ontario watersheds were significantly nested and whether lake size, isolation and piscivorous predator richness contributed to this pattern. Using two nestedness metrics, we found that species occurrence patterns in these watersheds were significantly nested. Lake size was a significant driver of the nested pattern, but lake isolation and piscivore richness impacted community composition in only one of the two watersheds. However, examination of idiosyncratic species (species that have unexpected absences in the packed portion of the matrix or unexpected presences outside the packed area) demonstrated that piscivorous fish did, in fact, significantly affect community structure in both watersheds.

Advancing biodiversity–ecosystem functioning science using high-density tree-based experiments over functional diversity gradients

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Increasing concern about loss of biodiversity and its effects on ecosystem functioning has triggered a series of manipulative experiments worldwide, which have demonstrated a general trend for ecosystem functioning to increase with diversity. General mechanisms proposed to explain diversity effects include complementary resource use and invoke a key role for species' functional traits. The actual mechanisms by which complementary resource use occurs remain however poorly understood, as well as whether they apply to tree dominated ecosystems. Here we present an experimental approach offering multiple innovative angles to the field of biodiversity – ecosystem functioning research. IDENT (International Diversity Experiment Network with Trees) allows research to be conducted at several hierarchical levels within individuals, neighborhoods, and communities. The network investigates questions related to intraspecific trait variation, complementarity, and environmental stress. The goal of IDENT is to identify some of the mechanisms through which individuals, communities and species interact to promote co-existence and the complementary use of resources. IDENT includes several implemented and planned sites in North America and Europe, and uses a replicated design of high-density tree plots of fixed species richness levels varying in functional diversity. The design reduces the space and time needed for trees to interact allowing a thorough set of mixtures varying over different diversity gradients (specific, functional, phylogenetic) and environmental conditions (e.g. water stress) to be tested in the field. The intention of this paper is to share the experience in designing FD-focused BEF experiments with trees, to favour collaborations and expand the network to different conditions.

P2 – Temporal Dynamics

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.

Temporal dynamics in the size range of a fish population in neotropical reservoirs

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Studies on the size range allow inferring indirectly about the energy flow between organisms, by associating the abundance of individuals with their body size. This study aimed to evaluate the effect of cascade of reservoirs in the Iguaçu River basin on the stock and distribution in length of the population of Oligosarcus longirostris. To this end, fish were sampled every three months at five reservoirs located in the Iguaçu River, from March 2004 to December 2008. The stock size was estimated by the CPUE and to calculate the slopes of size ranges, we used a Pareto I model. There was a variation in the CPUE, being distinct among reservoirs. In relation to the population size distribution and to the constant c, we observed a lower proportion of smaller individuals in the first reservoir of the cascade, Foz do Areia (41.5% ≤ 32 g), and Segredo (21.3% ≤ 32 g) showed the greatest amount of larger individuals, with a progressive decrease as reservoirs succeed each other along the cascade: Salto Santiago (29.8% ≤ 32 g), Salto Osório (38.7% ≤ 32 g) and Salto Caxias (47.2% ≤ 32 g). The parameters indicated that reservoirs further down in the cascade tend to present higher abundance of smaller individuals, because the stock size has been reduced according to the initial hypothesis that the bottom-up mechanism is more intense than the top-down in the cascade, since a retention of nutrients occurs along the cascade, which limits the growth and development of individuals.

P3 - Gradients

Climate and space promoting floristic variations among ecoregions in Doce River basin, Southeastern Brazil

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We aimed to investigate the identity of ecoregions in Doce River basin, located in Southeastern Brazil, which has high levels of plants diversity and endemism. For this, we analyzed the role of environmental and spatial predictors on variation in the composition of tree species along the basin. We submit occurrence data of tree species and geoclimatic data for 61 sites to a set of analyzes (ordination, variance and cluster analyzes) and built multiple regression models based on key predictors of floristic changes. We also partitioned the variance between climate and space. The results showed the consistency of ecoregions because climatic characteristics supported the peculiarity of the composition of their floras. Temperature in the warmest quarter and precipitation in the coldest quarter were the main predictors of floristic variation. Climate and space provided significantly ($p \leq 0.05$) the explanation of phytogeographic patterns, although the fraction of the climate has been greater. The relevance of spatially structured climate was also confirmed. The space's fraction indicated possible influence of neutral processes in the distribution of species. Already the environment's influence allowed differentiation between three ecoregions types: (a) ecoregions containing a large set floristic; (b) ecoregions which are related to endemic flora conditioned by unique environmental conditions; (c) ecoregions which are constituted by groups of species tolerant to extreme environmental conditions. We suggest that with the results obtained, ecoregions (which are recognized for their species compositions and different climatic conditions) has to be included as a definite tool for planning conservation strategies at the regional level.

Up the mountain, North to the pole: do species' elevational and latitudinal limits match?

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It is a long-held assumption that species' upper elevational and latitudinal range limits are correlated—i.e., species that grow at higher latitudes also reach higher elevations—but the degree to which these limits match and the climatic factors controlling them have rarely been quantitatively assessed. We determined the upper range limits of 40 tree species along an elevation gradient in the Great Smoky Mountains (Tennessee and North Carolina, USA) and a latitudinal gradient in Eastern North America and compared values of climatic variables hypothesized to limit species' ranges: annual minimum temperature, mean January temperature, mean July temperature, growing season length, mean growing season temperature, and growing degree days. Species' elevational and latitudinal climatic limits were strongly correlated, but for most species the high-elevation range limit was not as cold as the high-latitude limit. This mismatch was greatest with respect to winter temperatures, providing evidence that cold tolerance is not the primary factor determining species' upper range limits. Our finding that species do not grow as high along an elevation gradient as would be expected from their latitudinal climatic range limits may indicate a lack of local adaptation in high-elevation populations due to gene flow from lower elevations.

Partitioning the sources of trait variation among plant communities along an elevational gradient

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Understanding the relative importance of processes responsible for maintaining the correspondence between trait variation and environmental gradients is important for predicting species' responses to environmental change. We quantified the relative contributions of intraspecific trait variation and species turnover to community-level trait variation in vegetation across a 400 m elevational gradient spanning a deciduous-coniferous forest transition in southern Québec, Canada. We assessed variation in three functional traits – specific leaf area (SLA), plant height, and peak flowering date (PFD) – for all herbaceous species present across the gradient. With increasing elevation, community weighted mean SLA decreased while PFD increased and height followed a unimodal pattern of variation, peaking at mid-elevation. We found that species turnover contributed most importantly to height and PFD trait variation among communities, while intraspecific variation was the main driver for SLA. The relative importance of the two processes however showed sensitivity to abundance-weighting (or not) of community-level trait means, either increasing or decreasing the detected influence of intraspecific variation on community trait variation. In contrast to previous studies, we tested for – and found – variation in the relative importance of intraspecific trait variation along the gradient itself, suggesting possibly different responses of the communities to environmental change in different portions of the elevational gradient.

Plant species distribution in a patchy boreal forest-peatland landscape, Northwest Territories, Canada

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While most studies on species distribution focus on dispersal between isolated patches or islands, comparatively little research has been conducted on species distribution in the connected landscape surrounding isolated patches that act as partial barriers. The heterogeneous boreal forest-peatland landscape in the southern Taiga Plains ecoregion, Northwest Territories, Canada (N 61°18, W 121°18) with a connected permafrost plateau covering only 50% of the landscape dotted by collapse bogs and linear channel fens is an ideal study area to explore such patterns of species distribution. The present study explores spatial distribution of vegetation including ten species of shrubs, three forbs, ten lichens, two sphagnums, two feather mosses and two liverwort species. We surveyed 80 permafrost peat plateau sites and 20 reference sites in permafrost-free bogs and fens with 6 quadrats (25cm x 25cm) per site spaced at 1-2m intervals (600 sampling locations) in July and August 2013. We also used remote sensing classification data to determine the distance across patches between sample sites. While there was some overlap in vegetation communities across landcover types, most species were restricted to a single landcover type. Thus, to a certain extent, the collapse bogs (a patch) represent a physical barrier to spread between areas in the continuous peat plateau. We intend to determine to what extent species spread is controlled by the shape of the peat plateau and to what extent species can spread across the collapse bogs. We expect to find different distribution patterns depending on reproductive strategies.

Link between environmental parameters and cryptic species occurence in lakes: The case of amphipods of the *Hyalella azteca* complex

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Cryptic species are species sharing similar morphologies but having important genetic differences among them suggesting their distinct species status. Many cryptic species occur together, and it is not evident at first that their similar morphologies enable them to occupy ecological niches different enough to coexist stably. As one of the steps necessary to understand the role of the ecological niche in the maintenance of cryptic diversity, our study aimed to verify if cryptic species of a complex can be associated with different levels of environmental parameters. To do so, we sampled freshwater benthic amphipods of the *Hyalella azteca* species complex in 60 lakes of Bas-Saint-Laurent and Gaspésie (Québec, Canada) and compared their association with the levels of various environmental parameters (pH, dissolved organic carbon and chlorophyll a concentrations, percentage of organic matter in the sediments, etc.). Species were identified to the *H. azteca* complex using morphological analyses and to the species of the complex using COI gene divergences (at least 20% among the species). Preliminary results suggest that the occurence of some species in lakes is linked in a complex way to environmental paramaters, suggesting that these species of the complex might occupy different ecological niches in lakes.

Development of forest communities over steep environmental gradients from the late Glacial to present in the Pacific Northwest

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A striking feature of forest community gradients in the Pacific Northwest (western Washington and southwest British Columbia) is the sharp transition in dominant tree species across elevation. The stability of this gradient during significant climate changes of the last 14,000 years may reveal the relative importance of climatic and competition at sorting species along steep environmental gradients. I hypothesized that past vegetation gradients were similar to modern vegetation gradients under the assumption that modern climatic gradients are similar to historical gradients despite changes in climatic means. I also hypothesized that the locations at which compositional turnover on modern gradients were greatest has shifted over time. I synthesized 19 lake-sediment pollen records from the Pacific Northwest and focused on a subset of five sites on the Olympic Peninsula that span temperature and precipitation gradients. Comparison of environmental (four climate variables) and community (ten pollen types) dissimilarity in 1000-year time slices revealed moderate linear correlations only in the past 8000 years. Generalized dissimilarity models (GDMs) that fit nonlinear responses to environmental gradients showed progressively increasing fit (to 50% deviance explained) over the Holocene. The Olympic Peninsula subset showed strong fit (85%) after modern communities established at 6000 years ago. GDMs that predict modern vegetation gradients used winter precipitation and summer temperature, but during the early Holocene summer precipitation was of greater importance and during the late Glacial only the locations today that are cool and wet revealed strong vegetation gradients. The drivers of modern forest zone transitions can explain these patterns.

P4 – Large-scale Studies

Exploring species distributional patterns within metacommunities across large geographical areas

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Ecological communities show complex patterns of variation, and quantifying the relative importance of spatial and environmental factors underpinning patterns of species distributions is one of the main goals of community ecology. Although we have accumulated good knowledge about the processes driving species distributions within metacommunities, we have few insights about whether (and how) environmental and spatial features can actually generate consistent species distributional patterns across multiple metacommunities. The elements of metacommunity structure (EMS) framework was developed to identify and classify metacommunities according to different patterns of species distributions. Given that each pattern has unique underlying structuring mechanisms, exploring and comparing such patterns across multiple metacommunities spanning large geographical areas provides a way to test the existence of general principles underlying species distributions within metacommunities. In this study, we applied the EMS framework into a dataset containing about 9000 lakes distributed across 85 fish metacommunities across Ontario, Canada, and estimated the relative importance of local and spatial factors in explaining their distributional patterns. Nestedness and Clementsian gradients were the patterns that fitted most metacommunities; nested metacommunities were distributed throughout the province, while Clementsian metacommunities were concentrated in the southeastern region. Sixty-five percent of nested metacommunities were located in low-energy watersheds (i.e., colder climate and shorter growing season), whereas metacommunities representing Clementsian gradients were present in high-energy watersheds (i.e., relatively warmer climate and longer growing season). Taken together, our results reveal that the environmental and spatial properties in which metacommunities are embedded are at least partially responsible for their species distributional patterns.

Holocene human-vegetation-climate interactions in North America.

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Long-term environmental change resulting from human activity, such as rising atmospheric concentrations of carbon dioxide, biological extinction and widespread land use change, has been so extensive since the beginning of the industrial era that the term "Anthropocene" has been used to describe the most recent geological epoch (Rull, 2013). However, there is evidence that the results of human-induced, global-scale environmental change can be measured several thousands of years into the past (Ruddiman, 2003; 2013). This study investigates the influence of human- induced changes in land cover on North American carbon dynamics and therefore climate, in an attempt to resolve some of the differences within these two perspectives. Preliminary methods will involve the analysis of pollen data (North American Pollen Database), historical fire data (Global Charcoal Database) and archaeological radiocarbon data (Canadian Archaeological Radiocarbon Database) to develop estimates of population density. Following this, data-assimilation techniques using paleoenvironmental data (e.g., pollen, charcoal) and models for reconstructing regional vegetation composition developed by members of the European Pollen Landscape Calibration Network (POLLANDCAL) will be used (Sugita 2007a; b). Although the goal of this research project is to eventually obtain a continental-scale estimate of the influence of European and Aboriginal peoples on the carbon cycle, this study will begin by using case studies in areas where sufficient data exist (e.g., eastern North America). Together, these methods will permit the study of human-vegetation-climate interactions in North America at different spatial and temporal scales.

Diversity and distribution of body size in Neotropical cichlid fishes

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The importance of body size on life history, ecology and species distributions has been frequently highlighted, yet few studies in fishes have explored the evolution of body size and the consequences of exhibiting a particular body size. We use Neotropical cichlids as a model to explore the role of body size in the immense diversity of Neotropical freshwater fishes. The body size distribution of cichlids is comparable to many Neotropical lineages, and much is known about the ecological diversity, morphological disparity and phylogenetic history of this group. Body size data and phylogenetic history were used to examine body size distributions in cichlids to test for phylogenetic autocorrelation, divergence and inter-clade partitioning of body size space. Neotropical cichlids show unexpectedly low phylogenetic autocorrelation and divergence, with considerable overlap among three primary regions of body size space. This pattern is consistent at several taxonomic levels, suggesting that lineages may be adapting towards particular size optima likely associated with ecological roles. In addition, body size evolution in South America appears to be constrained by the diversification of the most species-rich tribe, Geophagini. Within South America, other cichlid lineages occupying similar body size space are relatively species poor while expansion into Central America has allowed for tremendous species diversification within these same body size regions. With a strong knowledge of the ecology and phylogenetic history of these fishes, we can begin to link body size with ecology, life history and other aspects to determine the extrinsic and intrinsic factors of body size evolution.

Environmental convergence or historical contingency? Global body-size patterns of turtle assemblages

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Global-scale analysis of the respective contributions of environment and historical contingencies to assemblage-scale trait patterns has, to our knowledge, never been attempted for a large number of animal species. We aim first to evaluate the extent to which body-size distrib3utions of non-marine turtle assemblages (order Chelonia—turtles and tortoises) demonstrate convergence or divergence. Then we test whether the pattern results from (i) the environment, (ii) shared geography (and therefore shared history), (iii) a combination of these factors, or (iv) whether it is random. We develop the 'Assemblage Convergence Index (AsCI)' and use it to compare assemblage-scale body-size distributions in biomes and biogeographic realms, to test the environmental and geographic hypotheses, respectively. The greatest convergence was between assemblages in tropical moist forests, for both terrestrial and aquatic species. There was clear divergence between terrestrial desert assemblages. Some notable patterns within biogeographic realms were also observed, suggesting geographic convergence between aquatic assemblages of the Neotropical realm. Assessing significance using two separate null models, we found only weak support for both environment and geographical convergence. Although statistical power is a concern, it seems that observed body size patterns are largely random at this scale for non-marine turtles. The research can be extended by applying the method to other taxa and traits, and would benefit from the addition of phylogenetic analyses. In the context of the ongoing convergence–contingency debate, we suggest that our approach has the potential to provide a sound underlying framework for global convergence analyses.

P5 – Conservation and Global Change

Can ecoregions be used as conservation planning units in a medadiverse country?

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Ecoregions have been widely used as units of analysis in conservation planning, environmental and resource management assessments. Despite their widespread use there is no commonly accepted theoretical basis for ecological regionalization and their delineation is based on expert knowledge. We evaluate within versus between species compositional dissimilarity of Mexican ecoregions and the classification strength (CS) at different hierarchical levels. We used presence-absence data of non-flying mammals (326) obtained from predictive modeling of species geographic distributions to analyze the dissimilarity of equal-area grid cells (10 x 10 km). At Level I mean dissimilarity within ecoregions ranged from 0.49 to 0.69. The Mexican portion of the North American Deserts, the Temperate Sierras and the Tropical Dry Forests had the greatest compositional mean dissimilarity values whereas the Tropical Humid Forests had the smallest. Mean dissimilarity value decreased (from 0.6 to 0.35) as the classification detail increased (from Level I to IV). CS was significantly greater than expected from randomly grouped sites at all levels, but low CS value indicated a weak classification at Level I. Several ecorregions had large dissimilarity values (even at Level IV), while two Level III ecorregions had greater within than between dissimilarity values, meaning that their boundaries should be revised. We conclude that although ecoregions are useful units for conservation planning, they have limited use for maximizing the representation of species, especially in a country with high environmental heterogeneity such as Mexico, and thus should be used in combination with systematic planning tools to guide conservation efforts.

Local and regional species pool influences on subarctic mine restoration sites

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Phylogenetic tools have been used to detect evolutionarily conserved relationships between species in a community. Recently, they have been implemented in restoration ecology in an attempt to identify the species most suited for restoration. However, they have not yet been used to detect differences between mine piles and their surrounding vegetation, within the context of restoration. Our study focused on using phylogenetics to identify patterns of succession based on the natural regrowth of species on a chronosequence of three subarctic mine sites. We compared each pile with the other piles as well as its surrounding vegetation and investigated succession with phylogenetic tools, such as the net relatedness index (NRI). A phylogeny of the regional species was developed to address our hypotheses. Richness and phylogenetic diversity were significantly lower on the piles than in the surrounding vegetation, and diversity and richness did not increase as the time since abandonment increased. The NRI showed that the youngest and oldest piles were more phylogenetically clustered than the surrounding vegetation. Studying succession is important to understand and devise efficient plans for restoration. Based on the species and clades succeeding on each pile, it may be beneficial to plant related species with specific adaptations, rather than focusing on immediately increasing diversity by sowing random or diverse seeds. The application of phylogenetics to restoration and succession is a relatively new idea but it will provide insight into the dynamics of changing community structures.

The impacts of climate change on the invasion of warmwater fishes and extirpation of coldwater fishes

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Global air temperatures have increased by approximately 1°C over the past century and are projected to rise between 1.4 and 5.8°C over the next century. The objective of this presentation is to examine two potential impacts of climate change on aquatic ecosystems: the spread of invasive warmwater fishes at the northern extent of their range in Canada and the extirpation of native coldwater fishes at the southern extent of their range in the United States. First, I will present a case-study focusing on lakes across Canada illustrating that smallmouth bass, a non-native warmwater fish species, could reach the Arctic by 2100 under climate change. The spread of smallmouth bass could lead to the loss of 20,000 lake trout populations across the country, in addition to the loss of minnow and salmon populations. Second, I will examine the response of a coldwater fish species, cisco, at the southern extent of its range, to climate change. Depending upon the degree of climate warming, 25-70% of cisco populations could be lost by 2100 in Wisconsin lakes. I will provide evidence that climate change has been impacting lakes in the recent past and forecast the consequential impacts of continued climate change on the spread of invasive species and the loss of biodiversity in the future.

Bacterial biogeographic patterns in permafrost thaw ponds and implications for greenhouse gas emissions

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There is now clear evidence that microorganisms display biogeographic patterns, yet the processes that create and maintain such patterns are still unclear. Most importantly, our understanding of the implications of biogeographic patterns for ecosystem functioning is limited, which in the context of climate change becomes of vital importance. Permafrost thaw ponds are expanding in size and numbers in the northern Canadian landscape. These ecosystems are characterized by a great variability in their ambient limnological variables both within and across geographic regions and can be net emitters of greenhouse gases. Here we describe bacterial community composition and diversity (pyrosequencing of the 16S rRNA genes) in a set of ponds in Nunavik, Northern Quebec, Canada, that vary in their environmental and biogeochemical regimes. Results show a clear regional clustering among the ponds suggesting that some regions are compositionally distinct from the others whereas some regions tend to cluster together suggesting that they may share common taxa. Interestingly, some regions show high variability between ponds whereas in others, ponds cluster closely to each other. Raup-Crick analyses suggest differences in the main community assembly mechanisms, with dispersal being dominant in some regions whereas environmental filtering seems to be the major force in others. Ongoing analyses will evaluate the proportion of common taxa among the ponds, their degree of association and how taxon co-occurrence may vary between and within regions, using network analyses. Ultimately these compositional patterns will be linked to functional ecosystem processes measured in situ such as methane production and oxidation rates.

Logging practices and functional structure of forest tree and herbaceous plant communities across Japanese Archipelago

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Understanding of impacts of logging practices on biodiversity driving ecosystem processes is essential for ecologically sustainable forest management. To identify vulnerable forest vegetation types in terms of ecosystem functions, we examined the impacts of clear-logging on functional structures of tree and herbaceous plant communities across hemiboreal, cool-

temperate, warm-temperate and subtropical forests in Japan. We combined species functional traits (leaf, stem, flower and fruit) and vegetation plot data including intact and logged secondary-growth forests. In tree species, functional structure indices for leaf, stem and flower traits showed differences between intact and logged forests, while in herb species, that for a stem trait showed difference. Among forest vegetation types, there were various patterns of functional structure indices. In hemiboreal, cool-temperate and warm-temperate forests, community means of SLA and leaf nitrogen concentration were greater in logged forests than in intact forests, and functional richness and/or functional divergence of maximum height were lower in logged forests even though species richness was greater. In hemiboreal and cool-temperate forests, functional richness and functional divergence of SLA were also lower in logged forest. In contrast, subtropical forests showed no differences in species richness and functional structure between intact and logged forests. Our results suggest that functional redundancy differs between traits and between forest vegetation types. This emphasizes that adaptive management guidance promoting the maintenance of multiple ecosystem functions should be developed according to degree of functional redundancy in forest communities evolved along climate conditions.

Assessing the capacity of Mexico´s protected-area system to represent threatened and restricted-range vertebrate species

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Protected areas (PA) have become cornerstones of global conservation strategies. In Mexico, very few studies at the countrywide level have examined how well extant PAs are able to capture a comprehensive sample of known biodiversity components. In this work we assess the extent to which the protected area system of the country encompasses the spatial ranges of the Mexico’s terrestrial threatened and restricted-range vertebrate species and also assess the complementarity value of the network. Representation levels (gap, partial gap or covered) of vertebrate taxa were defined based on the overlap of the modeled species geographic distributions with the layer of protected areas. A species was covered if it met the conservation target set to identify priority sites for conservation at the country-wide level; targets were assigned based on criteria such as rarity, endemism, extinction risk status and pressure from international commerce, giving a higher target to species that met these criteria. Out of 2408 terrestrial species in Mexico of which we had information on their potential distribution ranges, 438 had a restricted-range and 347 were threatened species. More than half of the restricted-range species and 38% of the threatened species occurred entirely outside protected areas and target levels of protection were met for circa 36% of the total number of restricted-range and threatened species. The results show a clear need to ensure that new PA designations contribute towards the consolidation.

Vegetation and permafrost interactions in a polar desert oasis

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My doctorate examines the interactions between High Arctic ecosystems and permafrost ice-wedges in light of a changing climate. Ice-wedges of the polar desert may be particularly sensitive to a warming climate. Their decay may contribute moisture to a dry environment, and there may be significant ground subsidence over the ice-wedge due to a volumetric loss of ice, resulting in a depressed microtopography that may amplify the accumulation of moisture during precipitation. These depressions may form novel niches that act as a relative refuge for colonizing vegetation - creating an “oasis” ecosystem distinct in abundance, composition, and function from the surrounding polar desert. In turn, these colonizing communities have likely produced an alternative ice-wedge stable state from the surrounding polar desert. We hypothesize that stabilized thermokarst (melt) areas will have shallower active layers and degraded ice-wedges, with decreased vegetation diversity but higher abundance due to a changed hydrological balance. A comprehensive set of near-surface active layer and ecosystem measurements were gathered from an “oasis” on Ellesmere Island, Nunavut (79.85°N, 85.37°W). Probing and high-frequency Ground Penetrating Radar (500 MHz) were used to map the near-surface details of ice-wedges and active layer. Vegetation was measured using quadrat sampling for species richness and abundance. Soil measures of temperature at depth, moisture content, and bioavailable nutrients, were augmented with hourly microclimate data. Preliminary results suggest that an

initial climate-warming disturbance to the thermal regime of High Arctic ice-wedge polygon systems may result in long-lasting and significant effects on the polar desert landscape.

Zooplankton communities as indicators to track environmental changes across broad geographical regions: the case of boreal lakes downwind of Athabasca oil-sands operations

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The impact of regional environmental change on a biotic community is determined by responses of resident species to altered local environmental conditions as well as changes in composition due to dispersal processes. In this context, we evaluated effects of environmental factors and dispersal-related spatial factors on zooplankton communities of 244 headwater lakes in north-west Saskatchewan that are potentially influenced by acidifying/eutrophying emissions from Athabasca oil-sand region (AOSR). To test and quantify the relative importance of these individual processes, we conducted ordination analyses, spatial modeling and variation partitioning. Local environmental factors trumped the effects of dispersal in structuring the zooplankton communities. Our study provided intriguing environment-spatial-species patterns which suggest the potential influences of regional environmental change on zooplankton communities. This included the significant correlation of the community composition to two major environmental gradients susceptible to atmospheric emissions from AOSR i.e., acid-base status and productivity. Meanwhile, spatial structuring of these factors induced similar spatial structures in zooplankton distribution across the study region. However, disentangling any impacts of the AOSR on these environment-spatial-species relationships from the underlying natural variability was precluded by unavailability of baseline (pre oil sands development) data. Nevertheless, as our findings indicate that dispersal of zooplankton was not strongly limiting across this broad geographic region, zooplankton communities are highly appropriate indicators to track the effects of future regional environmental changes on lake ecosystems across north-west Saskatchewan.

Modeling extinction risk of an endangered minnow in the upper St. Lawrence River

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The Pugnose Shiner is an endangered species in Canada that has a fragmented distribution across the Great Lakes region. The St. Lawrence River may provide some of the best habitat for the Pugnose Shiner across its range and, therefore, may be of vital importance to the long-term sustainability of the species. We conducted species distribution modeling in the upper St. Lawrence River, which indicates that suitable habitat is likely well above the minimum requirements for the species. We have also analyzed the population structure of the species with microsatellite DNA, which suggests that population connectivity is high in the upper St. Lawrence River relative to the rest of the range. The relatively abundant habitat and limited genetic differentiation suggest that dispersal among populations may be greater here than elsewhere in the species' range. As we suspect that dispersal is very important to the long-term potential of the species, we explore the consequences of various levels of dispersal on extinction risk in the upper St. Lawrence River using the modeling program RAMAS-GIS. In particular, we ask how much habitat must be protected and how close suitable habitat patches must be from one another to maintain population connectivity and reduce extinction risk in the upper St. Lawrence River. Our results will have important implications for habitat protection in this species at risk.

High-resolution paleoecological study of human-ecosystem interactions in relation to Holocene environmental change in Port Joli Harbour, Southwestern Nova Scotia, Canada

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A high-resolution pollen record from Path Lake in Port Joli Harbour, Nova Scotia, Canada, provides a paleo-ecological perspective on Holocene climate and vegetation variability, as well as variations in sea level, within the context of local archaeological research. Native Mi'kmaw populations ca. 3000-350 cal. yr. BP were dependent on Atlantic marine and terrestrial ecosystems for survival, thus making them vulnerable to paleoenvironmental changes at century- and decadal-scale temporal resolutions. Human-ecosystem dynamics are studied by comparing pollen assemblages from the regional Acadian Forest to human settlement intensity of the Maritimes and Maine. Wetland (*(Alnus, Sphagnum*) and shallow water aquatic (*Isoetes*) taxa increased after 3400 cal. yr. BP in response to a transition towards wetter climatic conditions. At the beginning of this transitional period settlement intensity decreased in coastal Maritime sites, potentially as a result of unfavourable environments. Reconstructed coastlines from Port Joli show the progressive formation of a natural harbour beginning roughly ca. 3000 cal. yr. BP, and expanding to its present shape by ca. 1000 cal. yr. BP. The development of the harbour combined with periods of high effective moisture around ca. 1450 and ca. 700 cal. yr. BP would have increased abundance of soft shell clams (a main component of the Mi'kmaw diet). These periods correlate well with increased size and frequency of shell middens in Port Joli Harbour.

Tree Species Diversity in Homegardens of Kerala

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Homegardens have for millennia been prominent across the agricultural landscape of Kerala, southwestern India. These dense, multistory forest gardens featuring diverse species of intercropped trees can be found in nearly all rural smallholdings of Kerala. Homegardens are considered to be a promising example of sustainable agriculture, satisfying diverse needs of the household while preserving more ecological function than conventional cropping systems. Local scientists have speculated that over the past few decades, the diversity of trees cultivated in these homegardens has declined in favour of a few profitable species, but this hypothesis has not been rigorously tested. In this study, we estimate the biodiversity of the homegardens of Kerala as a test of the hypothesis that homegardens are becoming less diverse. During the summer and fall of 2013, we fully surveyed the tree community in 115 homegardens randomly selected from eight districts of Kerala and calculated the diversity of each. We find that the average diversity of the homegardens is comparable to that of natural forests in the region. Furthermore, no significant relationship is found between the tree diversity of a homegarden and its areal extent, age, elevation, or population density, all of which are proxies for the spatial location of the homegarden. These findings suggest that if homegarden diversity is diminishing, it is at present nascent and evenly distributed across the sample region. Our tree diversity estimates also provide baseline figures for future inquiries into land-use change in Kerala or the relationship between crop diversity and ecological function in agroecosystems.

P6 - Methods

Identification and modelling of species-groups of bryophytes in the boreal region using co-occurrence based biodiversity deconstruction

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Biodiversity patterns vary across space and time; this variation is partially driven by both shared and distinct species-level responses to underlying ecological and biogeographical processes. Aggregate assemblage-level metrics such as total richness are typically employed to characterize broad scale biodiversity patterns and infer underlying causes, which may, however, obscure the complexity of shared and distinct response patterns of species to underlying causes. In this presentation I will present a null model based biodiversity deconstruction approach, which aims to classify assemblages into sets of ecologically-related species based on non-random species co-occurrences. We used broad-scale bryophyte occurrence data in 558 long-term biodiversity monitoring sites in the boreal region of Alberta, Canada, to determine if there were discernible species groups with differential response patterns to forest composition, age structure and human footprint. Four bryophyte species groups with significant co-occurrence patterns related to stand composition and human foot print were detected. The first group was largely associated with upland forest types (coniferous, deciduous, and mixed wood), whereas groups 2 and 3 were mostly associated with lowland conifer forest. The richness of fourth group tended to increase with successional (mainly forestry) disturbances. An overall model examining richness patterns of all bryophyte species combined included most of the variables found important for group-level richness, but some of the relationships tended to be fuzzy and dominated by certain groups (e.g., positive relationship with lowland conifer). Overall, a biodiversity deconstruction based on null model analysis of species co-occurrence was a useful tool for effectively unravelling varied and complex macroecological bryophyte patterns in the boreal.

Testing the influence of taxonomic group and taxonomic resolution on the delineation of ecological units in the Estuary and Gulf of St Lawrence (Canada)

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Ecological maps, also called ecoregionalizations, are increasingly used to support marine management and conservation. However, the biological datasets used to produce those maps are always limited to specific taxonomic groups identified at specific taxonomic levels. In this context, one might question whether the resulting ecological units reflect the broader marine ecosystem independent of the nature of specific datasets used. This study tested the influence of taxonomic groups and taxonomic resolution on the process of ecological mapping. A dataset of more than 200 species of benthic megafauna collected in the Estuary and Gulf of St Lawrence (EGSL), Canada, was used to create a set of biological matrices corresponding to different taxonomic groups (e.g. vertebrates, invertebrates, arthropods) and different taxonomic levels (from species to classes). Multivariate Regression Trees were used to identify environmental drivers of taxa distribution and to establish ecological maps. Similarity between maps was assessed using pair-wise comparisons in two steps. First, the relationship between the two classification schemes was assessed using association plots on the partitions of the corresponding trees. Then, the spatial congruence of similar classes was quantified and mapped. The comparison across different taxonomic groups showed a substantial level of similarity between ecological maps, indicating that ecological units defined for a specific taxonomic group can be considered to some extent as representative for the whole benthic macrofauna. Little information was lost when working at the family level instead of the species level and common patterns could still be distinguished at the class level.

Imputation of trait datasets: which method performs the best?

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The functional dimension of biodiversity is more and more considered in large-scale analyses. However, in trait databases missing data are a common problem. As data do not usually miss at random, deleting missing values can introduce a taxonomical or phylogenetic bias that can lead to biased results in comparative studies or bad estimations of evolutionary parameters. Statistical alternatives to data deletion are available to deal with missing data, replacing it with estimated parameters. The aim of our work was thus to find which imputation method performed better for imputing trait data. We tested four imputation methods (Knn, MICE, MissForest and Phylopars) on a complete trait dataset where we artificially removed different amounts of missing values from 10 to 80%. We also tested if including phylogenetic information improved the imputation process. We considered that the imputation error became inacceptable when biological patterns were not anymore detectable in imputed data. We thus compared the relationship between two correlated traits in true and in imputed datasets. The imputation error increased with the amount of missing values for all the methods. When the methods were tested including phylogenetic information, they all performed better. Among the tested methods, the ones that performed better were Phylopars, a likelihood-based approach, and MissForest, a method based on random forest. The relationship between two correlated traits was maintained when missing data were lower than 70%, suggesting that imputing databases with higher amounts of missing values could mask biological patterns.

P7 – Methods-application

Using beta diversity decomposition to understand ecosystem resilience

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Understanding how species-rich communities respond to disturbances can provide critical insights into their resilience abilities. Three mechanisms can underlie species responses during disturbance: (1) stability – species presences and biomasses remain unaffected; (2) turnover – some species disappear or their biomasses decrease. In this case, the lost species will be replaced by new ones and the lost biomass will be transferred among species; (3) Loss (gain) – some species disappear (appear) or their biomasses decrease (increase) without being replaced or transferred. Based on beta-diversity measures along a disturbance gradient, we provide a practical framework to decompose an ecosystem response into the contributions of these three components. We apply this framework to understand the response of coral reef fish communities from Moorea Island (French Polynesia) to an extremely severe degradation in the coral habitat. 13 coral reefs were surveyed from 2004 to 2012, during which time an outbreak of the crown-of-thorns starfish, a major coral predator, occurred. Despite almost complete loss in coral cover, fish richness and biomass remained stable over time. Temporal dynamics in fish richness and biomass included (1) high stability in yearly variations in fish presences and biomasses and (2) high species turnover and biomass transfer among species. Overall, few additional species appeared. This example outlines the importance of stability and turnover as major drivers of ecosystem resilience during extremely severe disturbances.

Improving the molecular detection of positive selection using biogeographic data

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Bioinformatic techniques for detecting positive selection in molecular sequence data are useful for understanding the adaptive forces shaping biodiversity. Studies of opsins, the proteins responsible for initiating the visual cascade, have detected convergent adaptation to the spectral properties of the environment. Marine and freshwater environments are particularly spectrally divergent, making sister lineages inhabiting these water types excellent model systems for the study of visual adaptation. Our analyses of sequence data collected from closely related marine and freshwater anchovies (Engraulidae) and needlefishes (Belonidae) have identified evidence for positive selection in rhodopsin, the opsin responsible for dim light vision. We show that including habitat data in analyses can significantly improve their power and accuracy, demonstrating the importance of including biogeographic information in analyses of positive selection.

Predicting Tree Species Abundance in a Mixed Mature Forest using LiDAR.

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Knowledge of tree species abundance and how this abundance is distributed over the landscape provides forest managers with stand-level information for planning, modeling, and decision-making. Species may display different abundance patterns over the landscape due to many factors; each of which has implications for modeling species abundance. While climate is often the primary driver for global to regional species distributions, modeling of abundance patterns at finer scales, may require predictors that capture neutral, biotic, and disturbance processes, as well as local abiotic conditions rather than climate-niche based predictors. Remote sensing (RS) data are frequently used to derive topographic predictor variables (e.g., elevation, slope and aspect). However, light detection and ranging (LiDAR) data may also have the ability to capture fine-scale species abundance properties. Hence, the objective of this study was to investigate the importance of optical RS and LiDAR derived variables related to biotic and disturbance processes for predicting fine–scale abundance patterns of several tree species in a mixed mature forest in Ontario. Species' relative abundance was related to the RS predictors using boosted regression trees (BRT). Results revealed that optical RS and LiDAR derived fine-scale predictor variables improved the predictive accuracy for all species models by a minimum of 29% and maximum of 63%. Also, the relative contribution of such variables was high in all models underlining the importance of incorporating variables related to biotic and disturbance processes for fine-scale species abundance modeling.

P8 - Phylogeography

A phylogeographic model for lowland plant species diversification in western Amazonia

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Empirical evidence from dated phylogenies now suggests that most speciation of tropical American biota occurred in the last 10 million years, rejecting the commonly quoted Pleistocene refugia as forest remnants where biodiversity originated. The orogenesis underwent in western South America during the Neogene caused the formation arches or ridges some five to ten million years before present, and influencing the modern configuration of the upper Amazon drainage. These paleogeographical changes in topographic relief and river dynamics have been hypothesized to influence the diversification of biota through vicariance. We used a palm lineage of 15 species (Astrocaryum sect. Huicungo : Arecaceae) restricted to western Amazonia to test this hypothesis. We present a phylogeographic analysis based on the polymorphism at five chloroplast and two nuclear non-coding DNA fragments. We found evidence of past ancestral population expansion from central Amazonia into two western Amazonian regions with no clear genetic differentiation imposed by river barriers or arches. Our results support the role of dispersal in the historical assembly of lowland western Amazonian forests. Species within this complex did not form monophyletic groups suggesting an incomplete lineage sorting or current gene flow among species. The two genetically differentiated lineages within this complex diverged ~6 and ~3 million years ago in areas where the Fitzcarrald and Iquitos arches uplifted, respectively. These divergence times also corroborate a south to north Andean-associated speciation pattern.

Identifying the relative importance of historical and ecological factors on global diversity pattern on Scleractinian corals

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This study examined the relative importance of historical and ecological factors on global diversity pattern of Scleractinian corals. The analyses were based on three historical hypotheses (the centre of origin, the centre of accumulation, the vicariance hypothesis) and two ecological hypotheses (the environmental filter, the habitat area hypothesis). We analyzed the phylogenetic data 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 tropical Indo-Western Pacific (IWP), mean sea-surface temperature (SST) in the coldest month and coastline length on phylogenetic diversity, phylogenetic species variability, phylogenetic species clustering and phylogenetic beta diversity, by using spatial autoregressive models. Phylogenetic diversity and phylogenetic variability in the IWP were higher than in the Atlantic, Caribbean, and eastern Pacific, whereas phylogenetic beta diversity in the IWP was smaller than in the other regions. These phylogenetic diversity patterns were well explained by distance from the centre of the IWP and mean SST in the coldest month, and slightly explained by coastline length. Our results demonstrated the importance of dispersal limitations, environmental filters and habitat availabilities on shaping global diversity patterns. Global diversity pattern of Scleractinian corals should be formed by species accumulation from marginal regions to the IWP, diversification through the insularity in association with taxon-specific constraints on dispersal, and environmental filter and habitat availability during range expansions from the evolutionary centre to marginal regions.

Historical interactions of isolation, palaeoclimate and volcanism determine plant diversity hotspots in the East Asian continental islands

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We report on imprints of historical effects on vascular plant diversity patterns and endemism in the continental islands, based on species diversification associated with the isolation hypothesis and the habitat stability hypothesis. We delineated a fine-resolution map of vascular plant diversity (5614 species) in the Japanese archipelago by compiling over 2.5 million occurrence data, and examined the effects of the distance from the continent, elevation, historical temperature/precipitation anomalies, presence or absence of pyroclastic flow and of lowland alluvial plain and actual evapotranspiration on species richness and the number of endemic species. Temperature anomaly was significantly negatively associated with overall and endemic species richness. The presence of pyroclastic flow and of lowland alluvial plain was significantly negatively associated with overall species richness and endemic species richness of certain plant assemblages. The distance from the continent was significantly positively associated with endemic species richness. Elevation showed a significant positive association with overall species richness and especially endemic species richness across trees, herbs and ferns. Actual evapotranspiration was not positively associated with overall and endemic species richness. In conclusion, historical habitat instability (palaeoclimatic oscillation, volcanism and marine transgression during the Quaternary) played a prominent role in species accumulation through the balance of extinction and survival, and the combination of dispersal limitation from the continent and orogeny promoted speciation of endemic species in isolated mountainous areas. In situ diversification was an important evolutionary driver, demonstrating that the large-scale diversity pattern of plants in the East Asian continental islands is a historical product.

Phylogeography of the Central American Neotropical electric fish *Gymnotus* (Teleostei: Gymnotidae)

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The Neotropical electric knife-fish *Gymnotus* has the broadest geographic distribution of all the gymnotiform genera. Four species (*Gymnotus cylindricus*, *Gymnotus maculosus*, *Gymnotus panamensis*, and *Gymnotus henni)* are known to have distributions within Central America, with *Gymnotus cylindricus* and *Gymnotus maculosus* the most broadly distributed. These two species are distinct based on morphology; however, intermediate forms may exist in areas where the species have nearly overlapping distributions, particularly in Costa Rica. We conducted molecular phylogenetic analyses to determine phylogeographic patterns of relationships and to test the distinctiveness of *G. cylindricus* and *G. maculosus.* We sequenced approximately 1100 base pairs of the mitochondrial gene cyt b from 41 specimens, and conducted Bayesian and maximum likelihood phylogenetic analyses. Four distinct clades were identified using both phylogenetic approaches. Three of the clades were composed solely of *G. cylindricus* or *G. maculosus* individuals. The fourth clade included both *G. cylindricus* and *G. maculosus* individuals. The individuals in the fourth clade were sampled from the nearly overlapping region of the two species distributions in Costa Rica. We conclude that there is evidence supporting the distinctiveness of *G. cylindricus* and *G. maculosus*. However, hybridization may be taking place in regions where the two species have overlapping distributions.