



4th

International Conference
of the International
Biogeography Society



Merida, Mexico

2009
8-12 January

Fourth biennial conference of the
INTERNATIONAL BIOGEOGRAPHY SOCIETY
an international and interdisciplinary society
contributing to the advancement of all studies of the geography of nature

Mérida, Yucatán, México
8 – 12 January 2009



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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 provides a holistic understanding of the relationships between the earth and its biota. Our abilities to develop more general theories of the diversity of life, and to conserve biological diversity may well rest on insights from the field of biogeography. Therefore, the International Biogeography Society (IBS) was founded as a non-profit organization in 2000 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.

IBS website—www.biogeography.org

CONFERENCE PROGRAM

Thursday 8 January 2009 – Conference registration, workshops, and pre-conference field excursions

8:00 am – 3:00 pm	Dzibilchaltún ruins and Progreso town
8:00 am – 4:30 pm	Ría Celestún (flamingos)
8:00 am – 5:00 pm	Visualizing Evolution in Space and Time (Salón Maya)
8:00 am – 12:00 pm	Spatial Analysis in Macroecology: Basic (Salón San Jacinto)
10:00 am – 10:30 am	Coffee break (workshop participants)
12:00 pm – 1:30 pm	Lunch (<i>on your own</i>)
1:30 pm – 5:00 pm	Spatial Analysis in Macroecology: Advanced (Salón San Jacinto)
1:30 pm – 5:00 pm	Science Writing (Salón Santiago)
3:00 pm – 3:30 pm	Coffee break
8:00 pm – 9:00 pm	IBS Board Meeting (Salón San Jacinto)

**NOTE: Participation in the above excursions and workshops requires pre-booking.
Please see IBS Registration table for program additions or changes.
Registration will be open beginning on the afternoon of Wednesday, 7 January.**

Friday morning 9 January – Symposia & poster sessions

7:00 am – 8:00 am Poster session I & II (1-100) up (central garden)

8:00 am – 8:40 am OPENING CEREMONY

8:15 am Ella Vázquez-Domínguez & Héctor T. Arrita Yucatán : 65 million years of Biogeographic History

8:40 am – 12:00 pm SYMPOSIUM I : Pattern and Process at Biogeographic Boundaries

Organizers: Brett Riddle & Dave Hafner

8:40 am	Brett R. Riddle	Introduction and Overview: Pattern and Process at Biogeographic Boundaries
9:00 am	R. Toby Pennington	The history of neotropical forests; dispersal limitation, phylogenetic niche conservatism and the Panama Isthmus
9:20 am	Laurel S. Collins	Paleobiogeographic changes in benthic foraminifera associated with the closure of the Central American Seaway
9:40 am	John Klicka	Birds and the Great American Interchange: A Molecular Point of View

10:00 am – 10:30 am Coffee break

10:30 am	Juan J. Morrone	Fundamental biogeographic patterns across the Mexican Transition Zone: An evolutionary approach
10:50 am	Todd Castoe	Distilling Consensus Patterns of Middle American Biogeography from Multiple Lineages of Venomous Snakes
11:10 am	David J. Hafner	Nesting Behavior of Boundaries: North American Deserts
11:30 am	<i>closing discussion</i>	

Friday afternoon 9 January – Symposia & poster sessions

12:00 pm – 2:00 pm **Poster session I and II and buffet lunch**

2:00 pm – 5:30 pm **SYMPOSIUM II: The Biogeography of Disease: Examining the Forces that Drive Disease Distribution and Emergence**

Organizers: Sam Scheiner & Kate Smith

- 2:00 pm Peter Daszak Overview of human and natural forces that contribute to the geography of infectious disease
- 2:20 pm Christopher Mundt Models for continental-scale spread of epidemics, using plants as a model system
- 2:40 pm Kate Jones Predicting emerging infectious diseases in humans
- 3:00 pm Amy B. Pedersen The geography of cross species pathogen transmission in primates
- 3:20 pm *discussion*

3:40 pm – 4:10 pm **Coffee break**

- 4:10 pm Krystal L. Rypien The origin and impacts of *Aspergillus sydowi*, an opportunistic pathogen of Caribbean gorgonian corals
- 4:25 pm Amy S. Turmelle Impacts of historic and contemporary population structure on host-pathogen co-evolution and disease emergence
- 4:40 pm Sara States Geographic variation in avian community structure: implications for disease dynamics
- 4:55 pm Leon Blaustein Integrating infectious disease ecology and biogeography: Comments on the symposium talks and suggested future directions from an outsider
- 5:10 pm *closing discussion*

5:30 pm – 6:15 pm **Poster session I and II (with cash bar); presenters for even-numbered posters in attendance**

6:15 pm – 7:00 pm **Poster session I and II (with cash bar); presenters for odd-numbered posters in attendance**

7:00 pm – 8:00 pm **Graduate student discussion**

7:00 pm – 8:00 pm **Posters I and II taken down**

8:00 pm – 9:30 pm **Welcoming Reception**

Saturday morning 10 January – Symposia & poster sessions

7:00 am – 8:00 am Poster session III & IV (1-100) up (central garden)

8:00 am – 8:10 am **Announcements**

8:10 am – 12:00 pm **SYMPOSIUM III : Biogeographic Disjunctions between Asia and the Americas**

Organizers: Bob Ricklefs & Jun Wen

- 8:10 am Jun Wen Biogeographic disjunctions between Asia and the Americas: an overview

8:30 am Rick Ree Models and methods for inferring the history of biogeographic disjunctions

8:50 am Beth Shapiro Reconstructing demographic change through space and time

9:10 am Xiao-Quan Wang Evolution of biogeographic disjunction in conifers

9:30 am *discussion*

9:50 am – 10:20 am Coffee break

10:20 am Iván Jiménez Spatial structure of the environment of Eastern Asia – North America disjunct flora

10:40 am Jenny Xiang Use of fossils in biogeographic analysis - challenges and possible solutions

11:00 am Robert E. Ricklefs Ecology and timing of Asian-North American disjunctions

11:30 am *closing discussion*

Saturday afternoon 10 January – Symposia & poster sessions

12:00 pm – 2:00 pm Poster session III and IV and buffet lunch

2:00 pm – 5:30 pm SYMPOSIUM IV: Extinction Biogeography

Organizers: Jack Williams, Steve Jackson & Felisa Smith

2:00 pm Doug Erwin The fabric of mass extinctions: Biogeographic patterns and evolutionary history

2:20 pm Kirk Johnson Plant extinction and the K-T Boundary: The impact of one particularly harsh day in Earth History

2:40 pm Kate Lyons Where did all the mastodons go? Global patterns of late Pleistocene megafaunal extinction

3:00 pm Alison Boyer Biogeography of Pacific Island Avian Extinctions: Past, Present, and Future

3:20 pm *discussion*

3:40 pm – 4:10 pm Coffee break

4:10 pm Sandy Andelman A geographic framework for monitoring, understanding and conserving biodiversity in a changing world

4:30 John Anderson Plant diversity responses to climate and atmospheric change: Neo- and paleo-ecological perspectives from Africa

4:50 pm Josh Donlan Ecological history, latent conservation potential, and why are we aiming so low? Giant tortoises as a model for taxon substitutions

5:10 pm *closing discussion*

5:30 pm – 6:15 pm Poster session III and IV (with cash bar); presenters for even-numbered posters in attendance

6:15 pm – 7:00 pm Poster session III and IV (with cash bar); presenters for odd-numbered posters in attendance

7:00 pm – 8:00 pm Graduate student discussion

7:00 pm – 8:00 pm Posters III and IV taken down

Sunday morning 11 January – Keynote address and concurrent contributed paper sessions

8:00 am – 9:00 am KEYNOTE: 2007 Alfred Russel Wallace Award recipient, John C. Avise

9:15 am – 12:35 pm CONCURRENT CONTRIBUTED PAPER SESSION I

Moderator: Jens-Christian Svenning

- | | | |
|----------|-----------------------|---|
| 9:15 am | Jean-Philippe Lessard | Regional and local drivers of ant community structure |
| 9:30 am | Jonathan Davies | Phylogenies reveal the ubiquitous influence of competition on the structure of regional carnivore communities |
| 9:45 am | Walter Jetz | Toward a global biogeography of traits - avian clutch sizes across species and space |
| 10:00 am | Catherine Badgley | Ecological and evolutionary processes in the assembly of mammalian faunas |
| 10:15 am | Christy M. McCain | Janzen revisited: Are mountain passes physiologically higher in the tropics? |

10:40 am – 11:10 am Coffee break

- | | | |
|----------|----------------------|---|
| 11:10 am | David Nogués-Bravo | Predicting the past distribution of species' climatic niches |
| 11:25 am | Nathan J. Sanders | Niche theory and neutral theory as explanations for broad-scale diversity gradients: a test with ants |
| 11:40 am | Larisa E. Harding | Globetrotting: Patterns of similarity in mammalian distributions across continents |
| 11:55 am | Jonathan Lenoir | Recent upward shift in forest plant species' mean elevation from global to local scale |
| 12:10 pm | A. Townsend Peterson | Ecological niche conservatism: the domains and limits of conservatism, change, and convergence in ecological dimensions |

9:15 am – 12:35 pm CONCURRENT CONTRIBUTED PAPER SESSION II

Moderator: David J. Hafner

- | | | |
|----------|----------------------|---|
| 9:15 am | Michael J. Hickerson | Testing biogeographic models of community assembly, colonization and vicariance with comparative phylogeographic data and hierarchical Bayesian models |
| 9:30 am | Michelle R. Gaither | A marine biogeographic barrier at the Marquesas: limited dispersal across the Southern Equatorial Current |
| 9:45 am | Andrea Weeks | Historical biogeography of the pantropical cashew (Anacardiaceae) and frankincense (Bursaceae) families |
| 10:00 am | Gabriele Salvo | Molecular dating and biogeography of <i>Ruta</i> L. (Rutaceae): a case study from the Mediterranean basin |
| 10:15 am | Katriina L. Ilves | Comparative phylogeography of North Atlantic intertidal and coastal marine communities: tests of vicariance and colonization using a hierarchical Bayesian approach |

10:40 am – 11:10 am Coffee break

- 11:10 am Mark J. Statham Phylogeography of the North American red fox
- 11:25 am Rodrigo Vega Phylogeography of the Eurasian pygmy shrew, *Sorex minutus*
- 11:40 am Knud A. Jønsson Phylogeny and biogeography of Oriolidae (Aves: Passeriformes)
- 11:55 am Jason Malaney Phylogeography and niche partitioning of the western jumping mouse (*Zapus princeps*) detects deep, cryptic lineages in the southwestern United States
- 12:10 pm Ivan Horacek Bat fauna of the Eastern Mediterranean: historical biogeography vs. macroecological explanations

9:15 am – 12:35 pm CONCURRENT CONTRIBUTED PAPER SESSION III

Moderators: Ella Vázquez-Domínguez & José María Fernández-Palacios

- 9:15 am Michael K. Borregaard Range size heritability may form current range size distributions
- 9:30 am Kayce Anderson Evolutionary factors important to the formation of range limits and species distributions
- 9:45 am François Guilhaumon Taxonomic and regional uncertainty in species-area relationships and implications for conservation biogeography
- 10:00 am Alejandro Ordonez Comparison of trait strategies of co-occurring native and exotic plants: implications for predicting successful introductions
- 10:15 am Youhua Chen Latitudinal coincidence between biogeographic regionalization and diversity patterns: the precise boundary between Palaearctic and Oriental Realms in East Asia as a case study

10:40 am – 11:10 am Coffee break

- 11:10 am Kostas A. Triantis Catastrophic extinction debt on oceanic islands
- 11:25 am Ana D. Davidson Ecological pathways to extinction in mammals
- 11:40 am Héctor Vazquez-Rivera Richness-climate relationships in woody plants are consistent through the Holocene
- 11:55 am Irina Levinsky Where were refugia for African birds and mammals during the last glacial maximum?
- 12:10 pm Shawn B. Whiteman A tale of two continents: body size, ecology, and the Great American Biotic Interchange

Sunday afternoon 11 January – Poster session, business meeting & closing ceremonies

- 12:35 pm – 2:00 pm Poster session V and buffet lunch (presenters in attendance 12:30-1:15)**
- 3:00 pm – 4:00 pm BUSINESS MEETING**
- 4:00 pm – 4:30 pm Coffee break**
- 4:30 pm – 5:40 pm Awards Ceremony & Closing Ceremony**
- 5:40 pm – 6:00 pm Posters V taken down**
- 6:00 pm – 6:30 pm Board Meeting**
- 8:00 pm – Conference Banquet**

Monday 12 January – End of conference field excursions

- 7:30 am – 4:30 pm Chichén Itzá ruins**
- 7:30 am – 4:30 pm Loltún caves and Uxmail ruins**

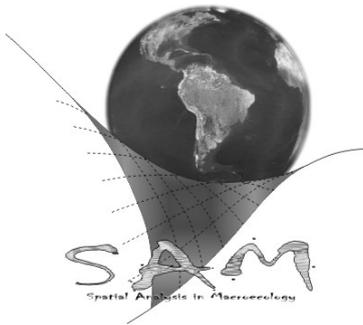
SPATIAL ANALYSIS IN MACROECOLOGY WORKSHOP

Salón San Jacinto

José Alexandre Felizola Diniz-Filho

Richard Field

Thiago Fernando L.V. B. Rangel

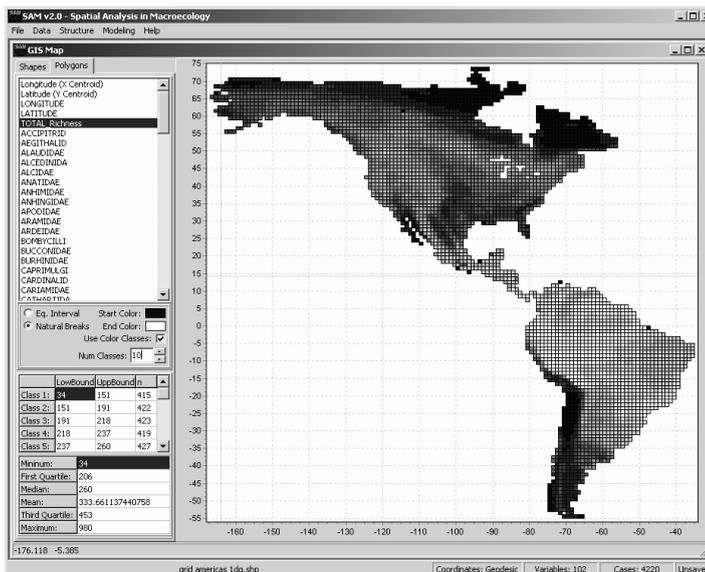


Spatial Analysis in Macroecology (SAM) was developed as user-friendly software to perform different types of exploratory spatial analysis and spatial modeling, which have been applied in different fields of macroecology and biogeography. It is now in its third version, and two levels of workshops will be available in Mérida.

Basic SAM (morning) - For those without experience with SAM, we will briefly discuss how available techniques can be applied and interpreted, and we will provide simple examples of how to run them in SAM. Practical classes in SAM will show how to input data and how to perform basic techniques, such as exploratory spatial autocorrelation using correlograms, basics on statistical inference, spatial correlation, and different techniques of spatial regression, including autoregressive models.

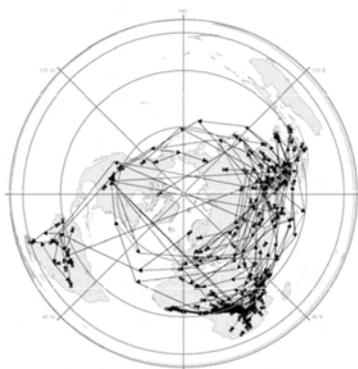
Advanced SAM (afternoon) - For those with some experience with SAM or spatial analysis, we will discuss new developments in spatial analysis as applied to macroecology and biogeography, including comparison of multiple forms of spatial regression, eigenvector-based spatial filtering, geographically weighted regression, multi-model inference, and autologistic methods. We also will show how the new routines of SAM 3.0 allow one to use these techniques.

Each session will be a half-day, pre-conference workshop (8 January 2009), each limited to 40 participants. If there is sufficient interest, we may be able to offer an additional half-day session (basic or advanced) for up to 20 people. Cost is \$50 US for each session, or \$75 US for both sessions.



Alexandre Diniz-Filho, Thiago Rangel, and Mauricio Bini have presented over 20 courses on spatial statistics in graduate courses and at conferences worldwide, using the SAM software that they developed. Along with Richard Field, they presented the initial tests of SAM version 2.0 at two very popular workshops organized by Richard and Lindsay Banin at the 2007 IBS meeting in Tenerife, and will be using the newly released SAM 3.0 in Mérida.

Please bring your own laptop computer if you have one.



VISUALIZING EVOLUTION IN SPACE AND TIME

Salón Maya

David M. Kidd

Geophylogenies are geographically referenced phylogenetic trees. This workshop will introduce the geophylogenetic data model and software to create and visualize them. Particular attention will be paid to using 'Geophylobuilder for ArcGIS' (https://www.nescent.org/wg_EvoViz/GeoPhyloBuilder) and 3D visualization with ArcScene, including the output of 'fly-by' movies. The use of KML and earth browsers will also be considered. Experience of GIS is desirable but not essential.

This will be a full-day, pre-conference workshop (8 January 2009), limited to the first 40 people who sign up. Cost is \$75 US.

Dave Kidd and **Xianhua Liu** designed and implemented 'Geophylobuilder for ArcGIS.'



COMMUNICATING BIOGEOGRAPHY

Salón Santiago

Rob Whittaker

Richard Ladle

The workshop will provide an overview of how to put together a paper for journal submission (adopting an appropriate writing style, organization of material, structuring a convincing narrative, pace of referencing, importance of identifying core questions/hypotheses, use of tables, figures, etc), what happens in the peer review process, what reviewers and editors are looking for, the role of co-authors, etc. Participants will be given some draft manuscript material and specific tasks to work on (e.g. how to write Aims statements, writing abstracts, editing texts, preparing legends). The template for the exercises will be the *Journal of Biogeography* format and guidelines, but the workshop is intended to be of general value in how to prepare manuscripts for submission to any scientific journal.

This will be a half-day, pre-conference workshop (8 January 2009), limited to 20 participants. It is intended primarily for postgraduates and those who have completed their doctorates in the last 2-3 years. If there is sufficient interest, we may be able to offer an additional, half-day session to 20 people. Cost is \$50 US.

Rob Whittaker was sole editor and then editor-in-chief of *Global Ecology and Biogeography* from 1995 to 2004, and has been editor-in-chief of the *Journal of Biogeography* since 2004. He takes a keen interest in assisting writers, particularly graduate students, to improve their ability to communicate their research through publication. **Richard Ladle** is course director for the Biodiversity, Conservation and Management MSc at the Oxford University Centre for the Environment. He has a special interest in science communication.

DZIBILCHALTÚN RUINS AND PROGRESO TOWN: 8 January 2009

Along the pilgrimage that the ancient Mayans performed towards the north of the Yucatán peninsula, they settled on those sites which they believed favored their development. Dzibilchaltún was one of those sites where grand buildings and cities were built, reflecting the great state of the art they had accomplished. For example, the Temple of the Dolls (Templo de las Siete Muñecas) is an imposing building on a pyramidal base with a short tower atop its roof. A monolithic stela stands at its front like a sentinel guarding its entrance. The doorways of the temple were built in exact solar alignment with the rising sun, such that the early rays pass through them on the Spring and Fall equinoxes, marking the beginning of planting season and the beginning of harvest season. Carvings that can still be seen on Dzibilchaltún tell the story of the king Kukulcan. There is also a beautiful cenote called Xlaca, where visitors can swim.



Progreso is a laid-back port town where you can enjoy the true flavor of Mexico. Progreso has safe, tranquil beaches with no currents or tides, which makes them great for swimming, floating, windsurfing and jet skiing. Palm trees, fresh seafood, the seaside boulevard called the malecón (mah-lay-CONE) and the friendly local Mayan residents make Progreso a great place to visit.



RÍA CELESTÚN: 8 January 2009

One of the most beautiful ports of the Yucatán coasts, Celestún, lies just 92 km northwest of Mérida, with many attractions worth visiting, including long beaches, many of them virgin, with excellent sea food. However, the main attraction is the huge number of flamingos that come each year to Celestún and turn the ría pink. Flamingos can be observed at very short distances in small boat tours, guided by local people.

CHICHÉN ITZÁ RUINS: 12 January 2009

The famous Mayan pyramids of Chichén-Itzá are over 1500 years old and are located only 120 km (75 miles) from Mérida. The name Chichén Itzá is Mayan: CHI (mouth) CHEN (well) and ITZA (of the Itza tribe). The magnificence of Chichén Itzá is well-known throughout the world. Chichén Itzá was a major regional focal point in the northern Maya lowlands from the Late Classic through the Terminal Classic and into the early portion of the Early Postclassic period. The site exhibits a multitude of architectural styles, from what is called "Mexicanized" and reminiscent of styles seen in central Mexico to the Puuc style found among the Puuc Maya of the northern lowlands. The site is divided into three sections. The northern grouping of structures is distinctly Toltec in style. The central group appears to be from the early period. The southern group is known as "The Old Chichén." All three can be seen comfortably in one day.



LOLTÚN CAVES AND UXMAL RUINS: 12 January 2009

Loltún, which means "stone flower," is a subterranean paradise 110 km south of Mérida, where one can admire beautiful cave formations and 7,000 year-old fresco paintings.



Uxmal means "built three times" in the Mayan language, and though its name is a mystery, its beauty is not. As a World Heritage site, it is one of the best restored and maintained ruins in the Yucatán, and certainly one of the most magnificent. Uxmal was the greatest metropolitan and religious center in the Puuc hills in the late classical period; it is located about 80 km (50 miles) southwest of Mérida.

Symposium I

**Pattern and Process
at
Biogeographic Boundaries**

INTRODUCTION AND OVERVIEW: PATTERN AND PROCESS AT BIOGEOGRAPHIC BOUNDARIES

Brett R. Riddle

University of Nevada, Las Vegas, 4505 Maryland Pkwy., Las Vegas NV 89154-4004 USA. Email: brett.riddle@unlv.edu

Biogeographers long have been attracted to the boundaries between the great biogeographic regions of the world. We recognize in these suture zones the potential insights regarding the dynamic interplay between Earth and biotic histories, and they have the further potential to serve as templates to gauge the impact of current and future human-mediated biotic invasions on biodiversity. Yet, while much insight has accumulated from intensive studies of focal taxa and exemplar zones of interchange (e.g., terrestrial mammals and the Great American Biotic Interchange), a new generation of biogeographers is revealing novel insights into patterns of dispersal, diversification, and extinction of species within and across biogeographic boundaries. Here, I provide an overview of the geographic and thematic threads that weave together the presentations in this symposium, which focus on a broad range of biogeographic patterns and processes associated with the transition zones that suture the Neotropical and the Nearctic biogeographic regions. These contributions collectively embrace a geographic scope ranging from northern South America to the southwestern deserts of North America, and marine biotas across the Isthmus of Panama. Thematically, they demonstrate the reciprocal dynamic emerging between a biogeography that increasingly incorporates analyses of multiple taxa into a comparative framework within an explicit temporal perspective, and a geology that identifies the causal events in a tectonically active Earth history.

THE HISTORY OF NEOTROPICAL FORESTS; DISPERSAL LIMITATION, PHYLOGENETIC NICHE CONSERVATISM AND THE PANAMA ISTHMUS

R. Toby Pennington, Matt Lavin, Sarah Cody & Valentí Rull

Royal Botanic Garden Edinburgh, , 20a Inverleith Row, Edinburgh EH3 5LR, UK. Email: t.pennington@rbge.org.uk

A meta-analysis of dated phylogenies of plant and animal clades with distributions in both Central and South America suggests that the closure of the Panama Isthmus was a less significant event in shaping plant biogeographies, reflecting their greater dispersal and colonisation capabilities compared to animals. However, a more detailed investigation of phylogenies of Neotropical plant genera endemic to distinct biomes suggests differing levels of historical dispersal limitation. In some rain forest genera, phylogenetic geographic structure is low, meaning sympatric species in a single region are not closely related. In contrast, in a single area of seasonally dry tropical forest, congeneric species tend to be closely related and often form monophyletic groups. In general, phylogenies suggest that niche conservatism has been a powerful force in plant evolution in the Neotropics and that dispersal limitation is probably most strong in seasonally dry tropical forests. Future research might focus on the relative permeability of biomes to lineages in order to address the question of the ease of evolving the necessary adaptations to survive in different environments.

PALEOBIOGEOGRAPHIC CHANGES IN BENTHIC FORAMINIFERA ASSOCIATED WITH THE CLOSURE OF THE CENTRAL AMERICAN SEAWAY

Laurel S. Collins & Carly J. Smith

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About 25 million years ago, foraminiferal and molluscan faunas from the Caribbean Sea and tropical Eastern Pacific Ocean were reported to be quite similar. As a result of the long-term rise of the Central American Isthmus, about four million years ago the tropical seaway that connected the two oceans closed completely, and today the two faunas are distinctly different. This project traces the paleobiogeographic divergence of the two benthic foraminiferal faunas from Miocene to Pleistocene time, and relates it to the geologic events that caused the rise of the isthmus and paleoceanographic changes that affected shallow-water conditions. The studied assemblages from Panama, Costa Rica, Ecuador and Venezuela have an excellent fossil record placed within the global biochronology of planktic foraminiferal and calcareous nannofossil zonations. Because of the virtual impossibility of collecting and identifying a sufficient number of fossil taxa from shallow to deep waters for each point in time, we are comparing coeval, isobathymetric assemblages from either side of the Central American isthmus to assess their similarities. The prediction is that with increasing constriction of the seaway, there was increased divergence of faunas between the two sides of the isthmus and increased similarity among regions of the Caribbean. Preliminary results of differences in similarity indices through the interval of seaway closure support these predictions.

BIRDS AND THE GREAT AMERICAN INTERCHANGE: A MOLECULAR POINT OF VIEW

John Klicka & Brian T. Smith

*Marjorie Barrick Museum of Natural History, University of Nevada Las Vegas,
4505 Maryland Parkway, Las Vegas, NV 89154 USA. Email: klicka@unlv.nevada.edu*

Separated throughout much of the Cenozoic era, North and South America were joined some 3.5 mya when a Central American uplift formed a landbridge between these two continents. This connection allowed an unprecedented degree of inter-continental exchange to occur between unique, previously isolated biotic assemblages. Due to a rich mammalian fossil record, we now have a fairly thorough understanding of how this "Great American Interchange" (GAI) impacted mammalian faunas on both continents, but; due to an extremely poor fossil record, the effect of the Panamanian landbridge formation on the exchange of avian lineages is much less well understood. In this study, we examine molecular data to investigate the timing of 116 trans-isthmus divergence events for a diverse array of avian taxa (9 orders, 29 families, and more than 90 genera). Although most divergences occurred within the last 3.5 my, our results indicate that inter-continental diversification began well before isthmus completion. We are able to reject a model of constant diversification and note that an apparent decrease in diversification rates over time is consistent with density-dependent cladogenesis. For the lineages examined, exchange within the tropics (N to S or S to N) was symmetrical. However, exchange between temperate and tropical regions is highly asymmetrical. We compare and contrast the evolutionary history of birds in the context of the GAI and with the known history of mammals.

FUNDAMENTAL BIOGEOGRAPHIC PATTERNS ACROSS THE MEXICAN TRANSITION ZONE: AN EVOLUTIONARY APPROACH

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Transition zones, located at the boundaries between biogeographic regions, deserve special attention because they represent events of biotic hybridization and intense biotic interaction, promoted by historical and ecological changes. In its more general sense, the Mexican Transition Zone is a complex area where the Neotropical and Nearctic biotas overlap. Parsimony analyses of endemism and track analyses have led us to restrict the Mexican Transition Zone to the mountainous areas of Mexico and to recognize five smaller biotic components, or biogeographic provinces, within it: Sierra Madre Occidental, Sierra Madre Oriental, Transmexican Volcanic Belt, Sierra Madre del Sur, and Chiapas. A cladistic biogeographic analysis, based on 40 plant and animal taxa, challenged the prevailing hypothesis that the Mexican Transition Zone is biogeographically divided along a north-south axis at the Trans-Mexican Volcanic Belt, as the two major clades identified divided Mexico in an east-west axis. This implies that Tertiary geological events leading to the convergence of Neotropical and Nearctic elements may be younger (Miocene) than those that led to the east-west pattern (Paleocene). Within the Mexican Transition Zone, three cenocrons have been identified: Paleoamerican, Nearctic, and Mountain Mesoamerican.

DISTILLING CONSENSUS PATTERNS OF MIDDLE AMERICAN BIOGEOGRAPHY FROM MULTIPLE LINEAGES OF VENOMOUS SNAKES

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Despite decades of intense study of Neotropical Middle American fauna and flora, the historical biogeographic processes that have shaped patterns of speciation in the region remain much debated, largely anecdotal, and poorly understood. We used inferences of phylogenetic relationships and divergence times for three lineages of highland pitvipers to identify broad-scale historical events that have shaped the evolutionary history of Middle American highland taxa, and to test previous hypotheses of Neotropical speciation. Our results suggest strong correspondence across three highland lineages for temporally and geographically coincident divergences in the Miocene and Pliocene, and further identify widespread within-species divergences across multiple lineages that occurred in the early-middle Pleistocene. These data implicate the existence of at least three major pre-Pleistocene historical events in Middle America that had broad impacts on species divergence and lineage diversification among highland taxa. In addition, we find widespread within-species genetic structure that may be attributable to the climatic changes that affected gene flow among highland taxa during the middle-late Pleistocene. With this as a foundation, we further explore the potential for constructing a comprehensive model of tectonic/biotic evolution for highland and lowland, as well as arid-adapted and wet-forest-adapted lineages in the region based on comparative analyses of lineage diversification.

NESTING BEHAVIOR OF BOUNDARIES: NORTH AMERICAN REGIONAL DESERTS

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Temporally nested geological and ecological barriers and filter-barriers provide important opportunities for deciphering complex biogeographic histories within broadly defined ecological regions. Recent advances in approaches that more confidently estimate dates of lineage divergence, test for temporal and spatial congruence of divergence events in multiple lineages, and incorporate dispersal and vicariance in testable hypotheses have finally allowed us to place molecular-based phylogenies in their correct geological context. For example, theories of assembly of the North American regional deserts previously were dominated by a Pleistocene speciation paradigm in which all recoverable divergence events were thought to be due to glacial climatic oscillations over a static geological landscape during the last 700 ky; the dynamic Neogene geologic history of the region revealed by plate tectonics was largely ignored. Increasingly sophisticated phylogeographic approaches have revealed a far deeper and more complex biogeographic history in the current biota of these regions, and have led to the identification of barriers and filter-barriers of disparate ages from 6 ky to 10 my, often at the same geographic site. I'll review the current understanding of the assembly of the North American regional deserts, focus on two particularly dynamic regions of the Baja California Peninsula as examples of the growing interplay of phylogeographic and geological inquiry, and suggest optimal approaches for sorting out temporally nested barriers and filter-barriers. Delineation of both core and transitional subregions has important implications for conservation applications.

1.—DISPERSAL, CLIMATE, AND THE GREAT AMERICAN BIOTIC INTERCHANGE

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There is a good fossil record for the mammalian families and genera that dispersed between North and South America during the Great American Biotic Interchange 9 million years ago, when the subcontinents were connected at least four times by low sea level and plate movements. Despite the opportunities, not all taxa dispersed between the subcontinents. Here, we examine whether successful dispersal of genera was contingent on the existence of potentially suitable climate space in the target subcontinent. Our results invite the interpretation that changes in climate availability, distance to suitable climates, and the size of the potential climate area available determined whether genera were able to successfully colonize the other subcontinent. The analyses include projections of the potential distributions of extant mammal genera during the periods (Miocene to the recent interglacial period) when dispersal took place. Our results can help explain the well-known, but little understood dispersal asymmetry between the two subcontinents during the Great American Interchange: We propose that past dispersal of genera between the two continents was a function of patterns in the climate availability for species.

2.—SPECIATION AND BIOGEOGRAPHY IN THE ARIDLANDS OF CENTRAL MEXICO

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The Trans-Mexican Volcanic Belt (TMVB) shows high species richness and endemism in several vertebrate groups. Only a handful of investigators have used molecular tools to study speciation and biogeography in this region, and most of these researchers have focused on species of the TMVB highlands. Previous workers have implicated vicariant events, including the rise of the TMVB and climatic fluctuations in the Pleistocene, as the major cause of speciation in this region. Herein, we present preliminary results from our study of rodents inhabiting the arid and semi-arid lowlands of the TMVB. Specimens representing seven rodent species (five of them endemic to the TMVB) were collected from nine localities in the Oriental Basin of the TMVB, and the mitochondrial gene, cytochrome- β , was sequenced for at least one specimen per species per locality. Using these preliminary data, we analyzed relationships within each species using Maximum Likelihood and Bayesian Inference methods. Reconciliation analysis using Treemap was performed to compare the topology (branching structure) of the resultant phylogenetic trees. Preliminary results suggest that the TMVB has been a significant geographic barrier to gene flow in some species of rodents, but has failed to stop dispersal through the volcanic mountains in others.

3.—COMPARATIVE PHYLOGEOGRAPHY IN THE BAJA CALIFORNIA PENINSULA

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The terrestrial biota of the Baja California Peninsula (BCP) has been the focus of recent phylogeographic research, including 36 vertebrate species, 8 invertebrates and 4 plants. These data indicate an overall high degree of phylogeographic structure: three-quarters of the species surveyed have at least one Deep Phylogeographic Break (DPB, i.e. at least two reciprocally monophyletic phylogroups) and these average 2.6 phylogroups per species. Plants and volant animals show relatively less structure. However, from all the species showing DPBs, 91.6% are from analysis of mitochondrial DNA, and there is not a single explicit case of geographically concordant DPBs between the mitochondria and nuclear loci. Interestingly, few of these species (20%) and DPBs (12.5%) show latitudinal geographic overlap between distinct phylogroups. The distribution of DPBs along the BCP is not random and two areas have similar frequencies that are unusually high: the mid-peninsular region (between 26° and 29°N latitude); and the base of the BCP (between 30° and 32°N). Coalescence simulations confirmed that DPBs can arise relatively quickly in the mitochondria whenever the effective size and the time (in generations) are on the same order of magnitude, even in areas where migration has never been completely hampered in the past, but only reduced to less than one effective migrant per generation. This suggests that besides hypothesized marine transgressions (seaways), reduced but uninterrupted migration, for instance across regions showing drastic changes in phylogeography, can also explain the presence of DPBs.

4.—BIOGEOGRAPHY PATTERNS IN THE GULF OF CALIFORNIA: THE HOLOPLANKTON CASE

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The distribution and abundance of different taxonomic groups of the Gulf of California have been studied by several authors who have proposed a variety of models to explain the general distribution patterns of the benthonic, planktonic and nectonic organisms of the Gulf. In this work we analyzed the holoplanktonic mollusks from zooplankton samples collected in seven oceanographic surveys (2005 – 2007), in order to obtain their general distribution and abundance patterns and to look for a general bio-regionalization of the Gulf based on the distribution of species assemblages. Our results demonstrate the presence of two main species assemblages: a cold assemblage of temperate affinity distributed in the north of the Gulf, mainly during the cold season; and a warm assemblage in the south found during summer. Both assemblages merge in the central region of the Gulf. We suggest a general model of the Gulf of California consisting of three main bio-regions, with borders that are dynamic in time and space in response to the warm water mass entering to the Gulf during summer. We contrasted our results with the previous regionalization of the Gulf based on different taxonomic groups and attempted to obtain a general regionalization model as well as determining the main mechanisms and environmental variables that provoke this regionalization.

5.—ASSESSING THE STRENGTHS AND LIMITATIONS OF AN INTEGRATIVE APPROACH TO INFER RESPONSE OF A GREAT BASIN ENDEMIC TO THE LAST GLACIAL MAXIMUM

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Geographic and demographic responses of populations, species, and species assemblages to Quaternary climatic changes have been studied using genetic, fossil, and ecological niche modeling (ENM) approaches, increasingly in an integrative biogeographic framework. Genetic signatures reveal historical range shifts and population expansions or declines. The fossil record documents the presence of a taxon during certain time periods, changes in biotic assemblages through time, and shifts of entire biomes, indirectly used to evaluate habitat suitability for a particular taxon. Finally, ENM facilitates evaluation of species range shifts by projecting species environmental niches on simulated paleoclimatic reconstructions (transferal modeling). Here, I use these approaches to evaluate how climatic conditions of the Last Glacial Maximum (LGM) affected distribution and population structure of the chisel-toothed kangaroo rat (*Dipodomys microps*), an endemic of the Great Basin of North America. The fossil record and climatic niche reconstruction suggest that populations of this species were extirpated or severely reduced in geographic extent throughout the Great Basin during the LGM, persisting primarily within the southern Mojave Desert. Conversely, phylogeographic analysis revealed high genetic diversity and pronounced geographic structure indicating persistence within the Great Basin without significant geographic or demographic changes. These contradictory results triggered the recognition of obstacles accompanying the integration of transferal modeling, fossil records, and genetic data. Additional challenges include niche evolution, phenotypic plasticity, or biotic interactions. Results such as these provide important opportunities to address the current limitations of this increasingly popular approach to reconstructing species responses to climate change.

6.—DWARF CARDÓNS AND ICE AGE RELICTS: SOME BIOGEOGRAPHICAL PLANT STORIES FROM ISLANDS IN THE GULF OF CALIFORNIA, MEXICO

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Like rocks, from large boulders to small pebbles, lying in the middle of a flowing stream, the Midriff Islands of the Gulf of California stand as a bridge between the Baja California Peninsula and the Sonoran Mainland. These desert islands display a continuum of adaptation to arid environments in isolated settings. Our recent work on the botanical diversity of these islands has illuminated multiple intriguing biogeographical stories. For example, the cardón (*Pachycereus pringlei*), a massive columnar cactus, is common through most of the Gulf of California region, but on several islands it occurs in densities and has regeneration indices at orders of magnitude greater than anywhere else throughout its range. On Isla San Pedro Mártir, the most isolated island in the Gulf, the cardóns are uniquely dwarfed and form a dense forest that dominates the island. A markedly distinct growth pattern is seen in this species on many Gulf of California islands. Among other biological intrigues are the insular disjuncts. At the highest elevations of Isla Tiburón (ca. 600-800 m), the largest island in Mexico, we have discovered multiple species with outstandingly disjunct distributions. For many, they occur on no other gulf island and their next nearest localities are over 200 km away and above the intervening Sonoran Desert. Their occurrence on Tiburón is best explained as Pleistocene relicts indicative of an historical vegetation much different than the current suite of desert species.

7.—A PHYLOGENETIC ANALYSIS OF THREE TROPICAL FORESTS

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The tropical dry forests (TDF) of Mesoamerica extend from southern Sonora, Mexico to Central America, where they terminate in Costa Rica. The nature of the relationship between TDF floras across this latitudinal expanse as well as the relationship between these dry forests and surrounding wet forests remain enigmatic. To gain insight into the differences between these geographically linked forests, two tropical dry forest sites (Alamos, Sonora, Mexico and Palo Verde, Guanacaste, Costa Rica) and one tropical wet forest (La Selva, Costa Rica) were compared using phylogenetic community structure analyses. We tested for patterns of phylogenetic clustering and dispersion among the three floras and also compared our phylogenetically-controlled results to those obtained using traditional comparisons of overlap based on Linnaean ranks. Phylogenetic analyses showed all floras differed significantly from the null expectation of random associations. Linnaean analysis for taxa shared between two or more floras showed the greatest amount of shared diversity among all three floras is at the generic level, with more shared genera between Palo Verde and La Selva than Palo Verde and Alamos. However, differences between the two methods were seen at the species level with Linnaean comparison indicating a roughly equal number of shared species between the two dry forest sites and the phylogenetic results showing these shared species to not be significantly different from the null expectation of a random distribution. Our analyses demonstrate the additional information gained when a phylogenetic perspective is incorporated in studies of community ecology.

8.—A DESERT RUNS THROUGH IT: COMPARATIVE PHYLOGEOGRAPHY OF THREE RODENT TAXA ACROSS THE HIGHLANDS OF MEXICO AND THE SOUTHERN UNITED STATES

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The Mexican vole, *Microtus mexicanus* occupies a distribution from southern Mexico north to the southwestern United States. Levels of morphological and karyological variation support the elevation to species status of a Mexican vole subspecies, *M. m. mogollonensis*. An analysis using ecological niche modeling suggests that each taxon requires significantly different abiotic conditions, indicating a possible role for vicariance in divergence. An analysis of variation in the cytochrome-b gene was conducted to test the hypothesis that the Mexican vole is composed of more than 1 species. Results suggest 2 well-supported reciprocally monophyletic clades: a Mexico clade found south of 32° latitude in Mexico, and a Southwestern clade located north of approximately 32° latitude in the United States. The recovered phylogenies of several taxa associated with the Mexican vole suggest a north/south division similar to the Mexican vole. Vicariance is supported if the species are co-distributed, demonstrate similar topologies, and are temporally congruent. I sought to elucidate whether the associated taxa are co-distributed using spatial overlay techniques. I simulated phylogenies defined by 4 colonization hypotheses, and estimated divergence times for northern and southern clades. Results of analyses suggest that the biodiversity that characterizes the region's fauna is the result of several abiotic events.

9.—BIOGEOGRAPHY OF THE MAMMALS OF THE NORTH PACIFIC COAST

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The North Pacific Coast of North America includes several large archipelagos including >2000 islands of the Alexander Archipelago. Molecular genetic analyses of selected mammals have demonstrated substantial spatial structure across this region. Repeated Pleistocene glacial advances along the coast fragmented these species with contemporary elements of this biota being the result of recolonization events from outer coastal refugia or from northern (Beringia) or southern refugia (West Coast and Continental). Several species show multiple, independent colonization histories from more than one source. During the Holocene, the highly fragmented landscape of the Alexander Archipelago further diversified this fauna and produced distinctive populations that are endemic to one or more islands.

10.—EVOLUTIONARY BIOGEOGRAPHY OF SHALLOW WATER JELLYFISHES (SCYPHOZOA: DISCOMEDUSAE) FROM THE GULF OF CALIFORNIA, MEXICO

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Scyphozoans are important pelagic predators throughout the world's oceans, but their diversity, distribution, ecology, and systematics are poorly known. The Gulf of California (the Gulf) presents a microcosm of this problem; the area is renowned for high endemic diversity in other taxa, but only three scyphomedusae of unknown biogeographic affinity have been documented previously. To test biogeographic hypotheses about the origin of the Gulf fauna, we surveyed bays along the Gulf and Pacific coasts of Baja California in 2008, collecting eight species of scyphomedusae, five previously unrecorded. One species, new to science, belongs in the Family Lobonematidae, previously known only from the western Pacific. Global phylogenetic analysis of another genus, *Aurelia*, demonstrates a new species that is sister taxon to a western Atlantic clade. These data suggest a tropical origin for the Gulf scyphofauna and hint at the first calibration for rates of molecular evolution in Scyphozoa based on closure of the Isthmus of Panama (~ 12-3 Mya) of ~2-6% per MY (an upper bound as more closely related trans-isthmian congeners may exist in Central America). Rates of molecular evolution will be examined in additional western Atlantic / eastern Pacific geminate species pairs, including a new species of *Stomolophus* from the Gulf. The affinities of the remaining five taxa collected – *Cassiopea* (global), *Chrysaora achlyos* (eastern North Pacific), *Cyanea* (2 spp.; global), and *Phyllorhiza* (Indo-Pacific) – affirm the importance of studying Gulf of California and Central America medusae for understanding global patterns of diversity in Scyphozoa.

11.—PHYLOGENETIC SPECIES SPLITS IN ASIAN OLD WORLD WARBLERS (AVES: PASSERIFORMES, PHYLLOSCOPUS)

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Systematics and taxonomy of Old World warblers (*Phylloscopus*, *Seicercus*) is under a lively debate, particularly with respect to recently suggested phylogenetic species splits between vicariant Southeast Asian taxa. We present molecular and bioacoustic data suggesting considerable differentiation within four traditional species: Blyth's Leaf Warbler (*P. reguloides*), White-tailed Leaf Warbler (*P. davisoni*), Dusky Warbler (*P. fuscatus*) and Tickell's Leaf Warbler (*P. affinis*). In phylogenetic reconstructions based on mitochondrial genes each of the four taxa were found to be a paraphyletic assemblage with at least one further highly distinctive warbler species nested in the respective molecular clade. Genetic distances ranged from 2.3% to higher than 7% p-distance (cytochrome b) among subspecies. Most recent lineage splits referred to terminal sister taxa from the Sino-Himalaya dating back to the Pleistocene. Southeast Asian lineages from S China and adjacent countries (Thailand, Vietnam) were dated back to earlier Pliocene splits from their Sino-Himalayan relatives. In all warbler groups investigated genetic divergence was paralleled by marked differentiation of territorial songs. Acoustic differentiation between taxa – quantified by pairwise differences between discriminant functions for the *P. reguloides* and the *P. davisoni* group – significantly increased with pairwise genetic p-distances. Deep phylogenetic splits between *Phylloscopus* clades corresponded to evolutionary changes of song syntax pattern. Ancient DNA from museum type specimens was used for clarification of taxonomic ambiguities in one case.

12.—HISTORICAL BIOGEOGRAPHY AND POSTGLACIAL RECOLONIZATION OF SOUTH AMERICAN TEMPERATE RAIN FOREST BY THE RELICTUAL MARSUPIAL *DROMICIOPS GLIROIDES*

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Long-term natural climatic variation has acted upon ecosystems to produce historic expansions and contractions of species' ranges, with accompanying fragmentation and population bottlenecks. These historic processes thereby influence the contemporary distribution and genetic structure of populations. We examined the geographic structure and demographic history of the phylogenetically and biogeographically relictual marsupial *Dromiciops gliroides* ("monito del monte") across its geographic range (36–43°S) in the temperate rainforest of southern Chile and adjacent Argentina. Using mitochondrial DNA (877 base pairs of cytochrome-b and control region) we evaluated the potential influence of major montane and island-mainland barriers. Both Bayesian and maximum-likelihood inferences revealed a phylogeny with three clades. Nearly all of the haplotypes belong to two geographically expansive clades: a northern clade (36–39°S) and a southern clade (40–43°S), both of which contain haplotypes found on both sides of the Andes. This pattern suggests recent maintenance of gene flow across the Andes within both clades. Within the large southern clade we also found little differentiation between insular and mainland forms within Chile. Tests of recent population expansion revealed a modestly declining population in the north and recent population expansion in the southern portion of species range, suggesting postglacial colonization. Our results indicate that population structure of *D. gliroides* has been strongly shaped by recent geoclimatic cycles.

13.—PHYLOGEOGRAPHY OF THE SOUTH AMERICAN RODENT *TYMPANOCTOMYS BARRERAE* (RODENTIA, OCTODONTIDAE) ALONG ITS GEOGRAPHIC RANGE.

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The red vizcacha rat, *Tympanoctomys barrerae*, is a highly specialized octodontid rodent endemic to the central and southern aridlands of Argentina. It lives in complex burrows and occurs at low population densities in isolated patches associated to salt basins and sand dune habitats along the Monte and Patagonian deserts. To investigate the genetic structure and biogeography of this species I analyzed mitochondrial DNA control region sequences of 60 individuals occurring in 8 sites along its distribution. I found 26 haplotypes in the analysis of 800–base pair sequences. Most were restricted to single populations, although a few haplotypes were shared between populations. I found low levels of nucleotide diversity compared with other subterranean rodents. Central populations had the lowest nucleotide diversity compared to southern and northern populations. Molecular variance analyses indicated a slow geographic structure of the populations. Phylogenetic analyses and a haplotype network generated using statistical parsimony recovered 2 groups: A (Northern and Southern populations) and B (Central and Southern populations). Most of the populations were polyphyletic. Neutrality tests indicate no signal of population expansion. I discuss the likely southern origin of this species and suggest that topographic and climatic attributes could result in differentiation and isolation of central populations. Furthermore, these results have implications in the conservation of isolated populations of the endangered red vizcacha rat.

14.—THE GLOBAL BIOGEOGRAPHY OF AVIAN DIETARY GUILDS

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Broad–scale geographic patterns of species distributions are central to ecology and evolution, but little is known about how whole-clade dietary niches and geographic distributions interact at broad spatial scales. Here, we analyze the geographic variation in the occurrence of avian dietary guilds worldwide and investigate potential contemporary and historical determinants. Biogeographic patterns in species richness and proportional diet specialization show marked differences across the globe, suggesting that the structure of regional bird assemblages is the result of guild-specific requirements and processes. We conclude that spatial and evolutionary constraints on animal’s dietary niches need to be taken into account for a general understanding of the broad-scale distribution of organisms.

15.—DIVERSITY OF ANDEAN RODENTS: LATITUDINAL AND ALTITUDINAL PATTERNS

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Altitudinal and latitudinal gradients have become excellent examples to test macroecological patterns in biodiversity. Although the Andean cordillera played an important role in the evolution of South American biota, there are few studies addressing its diversity patterns. The aim of our study was to characterize and quantify the composition and diversity of rodent assemblages along latitudinal and altitudinal gradients in the Southern Andes (10°N to 39°S). We compiled and developed a presence/absence matrix from the scientific literature. We compared assemblage composition and similarity among elevational/latitudinal bands to explore species turnover. We identified a northern and a southern group along a latitudinal gradient. Latitudinal and elevational species richness showed a hump-shaped pattern between 20° and 35° and between 2000 and 3500m, respectively. As latitude covaries with altitude, we analyzed the altitudinal pattern according to the latitudinal groups. The southern group showed highest richness between 500 to 2500 m. In contrast, the northern group has a richness peak at 3000 m. The patterns in the analyzed Andean assemblages reflect the influences of two major biomes: the high Andean Puna and Patagonia. Furthermore, our research of altitudinal gradients on Andean small mammals represents ecological baseline data for long term studies on climate change.

16.—DISPERSAL OF INDO-PACIFIC DEEP-SEA SNAPPERS (*ETELIS* SPP.) INTO THE TROPICAL WESTERN ATLANTIC

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Many marine organisms exhibit biogeographic connections between the Indo-Pacific and Atlantic oceans, but the pathway and timing of these connections remain largely unknown. Deep-sea snappers (Lutjanidae) in the genus *Etelis* are represented by three species in the Indo-Pacific Ocean (*E. carbunculus*, *E. coruscans*, *E. radiosus*), but only a single species (*E. oculatus*) in the Atlantic. Phylogenetic analyses of 507 bp of the mtDNA cytochrome-b gene indicate a close affinity (approximately 1.5% divergence) between Indo-Pacific populations of *E. coruscans* and western Atlantic populations of *E. oculatus*, two morphologically similar snappers. These data indicate a colonization pathway from the Indo-Pacific around South Africa and directly into the tropical western Atlantic, a pattern also observed in recent studies of gobies (genus *Gnatholepis*) and angelfishes (genus *Centropyge*). During recent interglacial periods, relaxation of the cold Benguela Current along the coast of Africa may have allowed fish larvae in the tropical Agulhas Current to enter the southern Atlantic and be transported by the South Equatorial Current directly into the western Atlantic. The goby and angelfish data indicate invasions of Indo-Pacific reef fishes into the western Atlantic approximately 145,000 and 250,000-500,000 years ago, respectively. Using conventional mtDNA molecular clock estimates for marine fishes (approximately 2% per million years between lineages), our data for *E. coruscans* and *E. oculatus* suggest an Atlantic founder event occurred approximately 750,000 years ago. Collectively these findings demonstrate a novel biogeographic pathway for colonization between ocean basins that clearly enhances Atlantic reef biodiversity.

17.—ENVIRONMENTAL AND GEOGRAPHIC LANDSCAPES: THEIR ROLE ON SPECIES' DISTRIBUTIONS

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It has been suggested that barriers that constrain the distribution and dispersal of species can be created by environmental conditions, and that such barriers are more pronounced in the Tropics than in temperate areas given the relative stability of environmental parameters and species' long-term adaptations to such conditions. Here, I analyze quantitatively the effect of environmental diversity on species' potential distributions across South America. A set of 1000 virtual species was created to represent environments available across the continent; their distributions were obtained by: 1) placing a random point on the map (seed point); 2) calculating Euclidean distances in a 7-dimensional ecological space from all points in South America to the seed point; and 3) applying different thresholds of ecological similarity within which the species is allowed to disperse into adjacent (contiguous) pixels. The area making up the species' distribution (i.e., suitable area that is contiguous to the seed point) was measured and compared to the total areas indicated as suitable for the species as indicators of geographic fragmentation of the species' distribution. The results indicate that the temperate versus tropical contrast is supported in general, but not in detail—for example, Andean ranges are extremely dissected, even in Equatorial regions. Implications of these dissected ecological landscapes for creation of dispersal barriers and how they fragment landscapes for species, translating into broader-scale processes such as speciation, remain to be explored.

18.—ICE AGE DISTRIBUTIONS OF EUROPEAN SMALL MAMMALS: INSIGHTS FROM SPECIES DISTRIBUTION MODELLING

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In addition to the traditionally recognized Last Glacial Maximum (LGM, 21 ka BP) refuge areas in the Mediterranean region, more northerly refuge areas for temperate and boreal taxa in Europe are increasingly discussed based on palaeoecological and phylogeographic evidence. Our aim was to further this discussion using species distribution modelling to estimate the geographic distribution of suitable climatic conditions for selected rodent species during the LGM. Presence/absence data of seven rodent species with a well-developed northern range in the temperate (3 spp.), boreal (2 spp.), or arctic zone (2 spp.) were used in the analysis. We developed predictive distribution models based on the species' present-day European distributions and validated these against their present-day Siberian ranges. The LGM projections of the models showed that areas with a suitable LGM climate for the three temperate species were largely restricted to the traditionally recognized southern refuge areas, i.e., mainly in the Mediterranean region. In contrast, suitable climatic conditions for the two boreal species were predicted in southern England and across southern parts of Central Europe into the northern Balkans and southern Russia. For the two arctic species, suitable climate was predicted from the Atlantic coast eastward across Central Europe and into Russia. Our results lend partial support to the idea of more northerly refuge areas in Europe, indicating that boreal species would have found suitable living conditions over much of southern Central and Eastern Europe. In contrast, strictly temperate species would have primarily found suitable conditions in the traditional southern refuge areas.

19.—BIOGEOGRAPHY OF CAPYBARA (*HYDROCHAERIS HYDROCHAERIS*) IN THE CHACO REGION OF PARAGUAY

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Anthropogenic habitat alteration has the capacity to alter the distribution of species. The capybara is widely distributed throughout most of South and Central America, but restricted to areas of standing water. As the Gran Chaco ecosystem of Paraguay is converted from dry tropical forest to pastureland, we hypothesize that this alteration has created potential for invasion by capybara. We used a three-pronged approach, combining occupancy modeling with phylogeographic analyses to investigate the hypothesis of a recent expansion into the Chaco Region of Paraguay. First, we conducted surveys for capybara throughout the Chaco to estimate the distribution of capybara and collect noninvasive genetic samples. Second, we used a niche modeling program (GARP) to model habitat suitability for the species both presently and prior to habitat modifications. Third, we verified the signal of range expansion found with our GARP model using phylogeographic analyses. Based on 6 environmental variables associated with the current distribution of capybara, GARP suggested that populations had indeed expanded into the Gran Chaco after habitat alterations occurred. Analyses of the mitochondrial D-loop suggest that three distinct clades of capybara persist in the Chaco and signals of range expansion were detected. Anthropogenic land transformation appears to be a major factor influencing the distribution, as predicted by the niche model and confirmed by genetic data. Habitat modification changes connectivity of populations across the landscape allowing capybara to invade new areas in which the species was not previously present.

20.—PATTERNS OF GENETIC AND DEMOGRAPHIC CONNECTIVITY IN THREE STOMATOPOD SPECIES: ORIGINS OF DIVERSIFICATION IN THE CORAL TRIANGLE

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The Coral Triangle is the center of the world's marine biodiversity. Although it has been suggested that this region is a center of origin, there is limited evidence for the diversification processes driving this pattern. To help understand the origins of biodiversity in this region, we examined phylogeographic patterns and genetic connectivity of three stomatopods, *Siamosquilla laevicaudata*, *Haptosquilla hamifera*, and *Hoplosquilla said*. All three species show strong evidence of limited gene flow and connectivity across the Coral Triangle. *Siamosquilla laevicaudata* exhibits a strong genetic break across Maluku Sea with pronounced genetic structure between populations east and west of this region. *Haptosquilla hamifera* shows more regional structure with strong differences between Papua New Guinea, Central, and Western Indonesia. Finally, *H. said* exhibits fine scale regional partitioning across its entire range, suggesting particularly pronounced limits to genetic connectivity. Results suggest multiple processes shaping lineage diversification in the Coral Triangle, including limited water transport across the Maluku Sea, historical divergence during lowered sea levels during Pleistocene glacial maxima, and species specific dispersal potential. Identification of the processes that create marine biodiversity, particularly the identification of regional barriers to larval dispersal, can help delineate boundaries for marine reserves and protected areas to help conserve and maintain the biodiversity of the Indo-West Pacific.

21.—BUCKING THE TREND: DRY FOREST TREES AND THE ABUNDANCE-RANGE RELATIONSHIP

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Data from two sites in the tropical dry forest (TDF) of Pacific Coast Mexico suggest that the majority of tree species do not conform to the macroecological theory that posits a positive correlation between local abundance and geographic range size. We compared field data from primary forest in Oaxaca and Jalisco to occurrence data from national and online databases to examine how local patterns relate to putative geographic range areas and latitudinal breadth. Results showed no significant correlation between abundance and range size. Overall, many more locally abundant species had small ranges than large ones. We found that most species occupy the majority of the TDF range north of the Panama Canal, and those species present in South America occupy the majority of that continent's TDF range as well. This pattern was independent of local abundance. We also found no relationship between range size and local niche breadth as measured by elevation, or between local abundance and distance to range center. We hypothesize that the absence of abundant species with large ranges is due to opposing environmental constraints that prevent a species from thriving everywhere.

22.—GEOGRAPHIC PATTERNS OF *DERMANURA* (CHIROPTERA: PHYLLOSTOMIDAE) IN COLOMBIA

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Recent phylogenetic studies on small fruit-eating bats, *Dermanura*, have revealed an increased diversity and better defined species boundaries. A general biogeographic pattern was also found, including Middle American and Chocóan species in a basal position, and a derived group restricted to the Amazonian versant of the Andes. Due to its geographic connection to Middle America, and the presence of three Andean Cordilleras, Colombia is expected to harbor particular distributional patterns for small mammals. To explore and clarify these patterns, we revised series of museum vouchers and updated the taxonomy and distribution information for the seven species recognized in Colombia. Whereas *D. rosenbergi* is associated to the humid forests of the Chocó region, *D. rava* extends along the Pacific coast and through the dry Andean forests of the Cordillera Occidental, and *D. phaeotis* (with an extensive range in Middle America) occupies the northern dry Andean forests. Although *D. anderseni* is mostly Amazonian in range, isolated populations occur in the dry Andean forests. On the other hand, *D. bogotensis* is restricted to the montane forests above 1200 m in the Cordilleras Central and Oriental as well as in Serranía del Perijá. Along the Amazonian versant of the Andes, there is an altitudinal replacement with *D. glauca* being pre-montane and montane, and *D. gnoma* being the lowland Amazonian form. Our data suggest the northern Andes as a colonization route for Middle American species and as a refuge for South America ones. This study shows the importance of appropriate geographic sampling for interpreting biogeographic patterns within a complex group.

23.—GEOGRAPHIC DIFFUSION OF NEW WORLD BIRD SPECIES: ENERGETICS, INTER-CONTINENTAL DISPERSAL, VICARIANCE, AND DIVERSIFICATION

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Studies of body size have sought to understand how energetics both cause large-scale spatial patterns and are also influenced by environmental and developmental constraints. We used a spatially explicit comparison of sister taxa (1) to test whether the evolution of body size at the species and genus levels is controlled more by phylogenetics or environment and (2) to determine whether the probability of a taxon being distributed across two large, recently connected continents is at all determined by its body size, and thus energetics. Using data on bird species of North and South America we (1) simulated subsamples of body size, (2) compared frequencies of size change and diversity for sister taxa on each continent and (3) evaluated the relative importance of taxon diversity, body size and evolutionary history. Within the New World bird fauna, we find evidence for the environmental constraint of body size evolution. However, the importance of body size in determining diffusion of taxa across North and South America is less clear. Our simulation results support the importance of body size. However, phylogenetic analyses indicate that taxon diversity drives the probability of diffusing across both continents.

24.—TREE-BASED PHYLOGEOGRAPHY OF CODISTRIBUTED FISH GROUPS IN CENTRAL MEXICO

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In Central Mexico the freshwater ecosystems are characterized by their genesis dynamism, destruction, and compartmentalization induced by intense geologic activity and climatic changes since the early Miocene. We addressed the phylogeography of five codistributed groups of fishes in Central Mexico and uncover and describe biogeographic patterns of the main river basins to understand the processes that determine them with respect to the molecular clock and the geological events that have taken place in the region since the Miocene. This study demonstrates that the dynamics of genesis and destruction of the Mesa Central drainages, induced by the high tectonic and volcanic activity since the Miocene, produced a complex pattern in the evolutionary and biogeographic history of the freshwater fish fauna of Central Mexico. This complexity, combined with the climatic history of the past 15 million years, gave the biogeographic history of these freshwater fish a high degree of complexity, characterized by a taxon-pulse dynamic in which dispersal, isolation and extinction events occurred in different spatial and temporal scales. Co-distributed species are not always affected in the same way when a common geological event determines, for instance, the connection between two water bodies, or the isolation or fragmentation of the original habitat.

25.—COMPARATIVE PHYLOGEOGRAPHY OF THREE SPECIES OF GOODEINES (CYPRINODONTIFORMES: GOODEIDAE) IN CENTRAL MEXICO

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Freshwater fishes of Central Mexico represent a model study to understand the evolution of complex areas and biotas. The ichthyofauna of Central Mexico is a key component in the evolutionary history of the area. The species *Xenotoca variata*, *Zoogoneticus quitzeoensis* and *Allophorus robustus* are widely distributed in Central Mexico, sharing most of their distributional range. We investigate the biogeographic and demographic history, and the role of geologic and climatic events on the evolutionary history of these species. The evolutionary history of the species did not share the same biogeographic scenario. *Xenotoca variata* and *Zoogoneticus quitzeoensis* are genetically well structured, showing high genetic divergences, relatively low migration rates, high effective population size and high genetic diversity within populations. *Allophorus robustus* exhibits low genetic structure, low divergences, high migration rates, low population sizes and low genetic diversity within populations. The geologic and climatic activity of the area is closely related to early diversification of different groups within each species, but the differences in phylogeographic patterns shed some light into the possible influence of the intrinsic characteristics of the species in the evolutionary history of the freshwater fish fauna of a complex geological and climatic area.

26.—COASTAL SIBLING SPECIES PAIRS SEPARATED BY LATITUDE ALONG THE SHORES OF WESTERN NORTH AMERICA

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On the temperate North American west coast, about a third of all genera have multiple species and about five percent of genera surveyed have pairs of morphologically similar species whose respective ranges partly overlap. Such species are potentially informative for understanding recent speciation events. Chitons and limpets are ecologically important grazers on rocky intertidal shores. In collaborative molecular and morphological phylogenetic studies of most of the about 100 chiton and 30 limpet species along these shores, we have identified seven chitons and four limpet inferred sibling species pairs whose ranges overlap. The region of overlap varies from pair to pair and this presents multiple opportunities for investigating hybridization, introgression, competition, resource partitioning, character displacement, and molecular divergence. We are investigating the extent to which the present dynamics of the transition zone between a pair of species might reflect their presumed history of allopatric speciation. Much remains unknown, including whether biogeographic barriers to dispersal or selection operating to promote divergence might be acting to maintain the present transition between species. We have also documented at least one case in which a transition zone has shifted substantially northward in less than two decades, providing an opportunity to use the species pair as a model system to track further climate change.

27.—A MOLECULAR PHYLOGENY OF THE MANAKINS (AVES: PIPRIDAE) GIVES FURTHER EVIDENCE FOR THE OLD AGE OF LINEAGES RESTRICTED TO FLOODPLAIN AND TERRA FIRME FORESTS IN THE AMAZON BASIN

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The phylogenetic relationships within the manakin family (Pipridae) were investigated with sequence data from three nuclear introns and one mitochondrial protein-coding gene. Main phylogenetic results include: 1) a sister group relationship between *Neopelma/Tyrannneutes* and the typical manakins; 2) a division of a majority of the typical manakins into one small clade largely distributed outside of the Amazon basin and a larger clade consisting of eight genus level subclades with overlapping distributions centered on the Amazon basin; and 3) polyphyly of the non-lekking genus *Chloropipo*. Divergence date estimates indicate that deep lineages of typical manakins originated during the mid Miocene, and that the eight Amazonia-based clades diversified during the late Miocene. This diversification involved specialization into different forest habitat types, such as terra firme forest, floodplain forest and forest edge. Most of the extant species diversity has its origin in the Pliocene. These results add to the evidence of an ancient history of habitat specialization into floodplain or terra firme forest types that has been reveal for several other groups of Amazonian birds.

28.—PATTERNS OF SPECIES RICHNESS IN MEXICAN FRESHWATER FISHES

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Mexico possesses a rich and diversified freshwater fish fauna, with Nearctic and Neotropical elements as well as taxa originating from marine ancestors and a large autochthonous subfamily: Goodeinae. General descriptions of current distribution of this fishes have been provided by some authors. It is therefore important to summarize patterns of species richness and endemism at local and regional scales. The aim of the present work is to analyse patterns in species richness for Mexican freshwater fish fauna at the hydrographic region level. We compiled data of fish species richness for the 37 hydrographic regions of Mexico from museum collections. Data used in this study included only native freshwater fish species, i. e., species are unable to disperse through sea waters and are therefore restricted to the drainage basins. The following variables were measured for each region: surface area, length of drainage basin, mean altitude, mean latitude, latitudinal extent, mean longitude, longitudinal extent, and climate types. The contribution of these factors for the variation among regions in terms of species richness was analyzed by correlation analysis and regression techniques. A total of 390 species were present in the data set. No data were obtained for the Mapimí region. The largest family is Poeciliidae, with more than 20% of the total number of species. The latitude was the most important factor explaining the variation of fish species richness across Mexico's freshwater habitats.

29.—DETERMINANTS OF BROAD SCALE PLANT RICHNESS ACROSS THE NEOTROPICS

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Explaining broad scale spatial variation in plant species richness has long been a major challenge. Recent work has focused on three major hypotheses that contend that plant species richness reflects 1) variation in energy and water availability among sampling units (the species-energy hypothesis), 2) habitat and topographic heterogeneity within sampling units (the spatial heterogeneity hypothesis) and 3) variation among spatial blocks of sampling units in rates of speciation, immigration and extinction (the regional effects hypothesis). We used a large botanical database and spatial and non-spatial regression models to simultaneously confront the predictions from these three hypotheses against an estimate of vascular plant richness across three major paleophysiographic divisions of the Neotropics: Northwest South America, Southern Central America (Southern Costa Rica and Panama) and Northern Central America (from Central Mexico through Northern Costa Rica). Variation in estimated plant richness was primarily explained by the spatial heterogeneity hypothesis, with secondary contributions from the species-energy and regional effects hypotheses. Regression models that incorporated the relative contributions of the three hypotheses predicted the highest plant richness in topographically complex areas. In contrast to recent mapping efforts, lowland Amazonia was predicted to be a plant richness trough. We suggest that diverging portrayals of plant richness across the Neotropics result from differences in estimates of the relative importance of the species-energy and the spatial heterogeneity hypotheses.

30.—RANGE FILLING AND RANGE LIMITS IN ANDEAN BIRDS

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A fundamental question in biogeography is what factors determine species range limits; a question particularly important in mountains known for their high levels of endemism and beta diversity. We use ecological niche modeling (ENM) and environmental clustering to study range filling (i.e., the extent to which the species exists in all the areas it is predicted to exist) in 71 endemic birds of the Colombian Andes. Further, we evaluate how climate and geographic barriers may shape range limits at two scales. At a broad extent (i.e., across several mountain ranges within the northern Andes) ENM predicts that suitable habitat exists in close proximity indicating that there are regions where the environmental conditions for a species are appropriate, but where the species does not exist likely as a result of dispersal limitation or biotic interactions. In contrast, at a smaller scale (within a given cordillera) species generally exist across the entire area predicted to be suitable by a given niche model. The relatively small geographic barriers within cordilleras do not generally correspond to range limits; instead range limits correspond to changes in environmental conditions. These results suggest that different mechanisms influence niche filling at these two different scales. More broadly, we show that ENM modeling can provide some insight into the importance of isolation and environmental gradients in generating and maintaining diversity in a complex montane region.

31.—BIOGEOGRAPHICAL ANALYSIS OF THE PLIOCENE SHARKS AND RAYS FAUNA IN AMERICA

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The elasmobranch fossil records from the Baja California Peninsula, Mexico comprise teeth, dental plates, dermal denticles, vertebrae, gill arches and caudal spines. The main localities in the Salada Formation (Fm) are Arroyo La Salada (Type locality), El Rifle, Santa Rita, Santa Teresa and El Médano, which are dated as Early Pliocene based on fossil shark teeth and as Miocene to Early Pliocene based on mollusk's fossils. The present study reports a faunal list, in this area, containing 20 shark and six ray species in which *Negaprion brevirostris* and *Carcharias taurus* are the most abundant. Currently three of the species found in this formation are absent in the Western Central Pacific (*Carcharias taurus*, *Rhizoprionodon* aff. *terranovae* and *Rhynchobatos* sp.) and three are extinct (*Parotodus benedeni*, *Carcharocles megalodon* and *Hemipristis serra*). This faunal list was compared with other contemporaneous published records from formations dated as Pliocene in America: San Diego Fm in California; Pisco Fm in the Ica Basin and the Miramar Fm in Piura, Perú; Uscari Fm in Alto Guayacán, Costa Rica; Río Pungo Fm and Yorktown Fm from Lee Creek Mine in North Carolina; Cubagua Fm in Venezuela and Caldera Fm from Bahía Inglesa in Chile. With these data, possible biogeographic patterns have been elucidated in the Pliocene elasmobranch fauna from America.

32.—BIOGEOGRAPHY OF TREE RICHNESS IN THE BALSAS BASIN OF THE STATE OF MEXICO

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Ecological and biogeographical relationships among sixteen areas of endemism in the Balsas Basin of Mexico state are analysed by PAE, based on richness of arboreal species. Endemism areas include Amatepec (AMA), Bejucos (BEJ), Holotepec (HOL), Ixtapan de la Sal (IS), Iztaccíhuatl (IZT), Malinalco (MAL), Nanchititla (NAN), Ocuilan (OCU), Sultepec (SUL), Tejupilco (TEJ), Temascaltepec (TEM), Tlatlaya (TLA), Valle de Bravo (VB), Villa de Allende (VA), Xinantecatl (XIN) and Zacualpan (ZAC). These localities divide in two groups; a northern group including TEM, SUL, ZAC, OCU, VB, HOL, IZT, VA and XIN; this set is characterized by recent, probably Pleistocene isolation of tree species in the Transmexican Volcanic Belt, with a high refill of species (beta diversity equal 0.292), but low gamma diversity (84 spp). The southern group, consisting of TEJ, BEJ, MAL, NAN, TLA and IS, is characterized principally by trees from tropical forests with higher endemism, low beta diversity (0.094) and higher gamma diversity (159 spp). Amatepec is an isolated locality, not grouped with those groups and localized to the southwest of the state of Mexico.

33.—MORPHOMETRIC ANALYSES OF GEOGRAPHICALLY ISOLATED SHREWS OF THE *CRYPTOTIS NIGRESCENS* SPECIES COMPLEX (MAMMALIA: SORICOMORPHA)

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Small-eared shrews of the genus *Cryptotis* (Soricidae) are mostly Nearctic in distribution, but some species extend as far south as northwestern South America, including Colombia, Ecuador, Venezuela, and Peru. No explicit phylogenetic study is known for this genus, but at least four groups are recognized within it, some of them only from Middle America (i.e., *mexicana* group) or from South America (i.e., *thomasi* group). The *nigrescens* group includes seven species; at least two of which occur in South America. The few available studies have been based on small series from South America, thus precluding further comparisons with more extensive studies in other parts of the range. We analyze over 90 specimens of *C. mayensis* (from southern Mexico) and *C. colombiana* (from central Colombia) to assess geographic variation among and within species in this species group. Statistical analyses of 14 cranial and dental measurements confirmed interspecific (*mayensis* vs. *colombiana*) variation that is equivalent to morphological differences between these species. On the other hand, there was broader variation among populations of *C. colombiana* compared to *C. mayensis*. However, morphometric variation in *C. colombiana* does not correspond with preliminary assessment of morphological discrete variation. These results improve morphological characterization of some populations within this highly diverse genus. This study is a first step towards an improved definition of populations and taxa, within a broader geographic sampling, for a usually neglected genus such as *Cryptotis*.

34.—PHYLOGENETIC RELATIONSHIPS OF TAIWAN ENDEMIC PASSERINES (AVES: PASSERIFORMES)

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The Island of Taiwan is considered one important hotspot of avian biodiversity in Southeast Asia with fourteen endemic species and about 70 endemic subspecies. We investigated the phylogenetic relationships of five passerine endemics from the Central Mountain Range within the Taiwan subtropical evergreen forests ecoregion. Phylogenetic reconstructions were inferred from mitochondrial gene sequences (cytochrome-b and 16S rRNA) and partly from flanking bioacoustic analysis, too. Closest relatives of all Taiwan endemics investigated were found in the Sino-Himalayan region. Even the Taiwan Firecrest, *Regulus goodfellowi*, formerly considered conspecific with the European Firecrest (*R. ignicapillus*), resulted as the sister species of the Eurasian Goldcrest assemblage (*R. regulus*). Discriminant and cluster analysis of song parameters confirms this molecular sister-group relationship due to strong similarities of Taiwan Firecrest songs and those of Goldcrests from the Sino-Himalaya. A rate-smoothed molecular clock approach dated the invasion of ancestral *R. goodfellowi* to Taiwan to the mid Pliocene. Similarly high genetic divergence of Taiwan populations from their continental relatives was found in two finch species: the Grey-headed Bullfinch (*Pyrrhula erythaca*) and the Vinaceous Rosefinch (*Carpodacus vinaceus*). Two other passerine species showed no particular phylogeographic structure with respect to the populations from Taiwan: the Brown Bullfinch (*Pyrrhula nipalensis*) and the Coal Tit (*Parus ater*) are probably among the youngest descendants from continental Chinese populations that invaded Taiwan during the Pleistocene or even post-Pleistocene era.

35.—*NASSARIUS NITIDUS*, A CRYPTIC GASTROPOD FROM EASTERN ATLANTIC: DNA BARCODING AND FIRST PHYLOGEOGRAPHIC DATA

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Taxonomic certainty is essential in biogeographic research. Still, delineating species is not always straightforward, especially among cryptic species complexes (i.e. groups of true species not readily/reliably distinguishable on a morphological basis). Here, we deal with a particular example of the latter: the species complex *Nassarius reticulatus*/*N. nitidus*, two sibling marine gastropods that have been the subject of considerable taxonomic confusion. Actually, the taxonomic consensus until the early 1990s considered only *N. reticulatus* as a valid species with obvious consequences for the accuracy of the records (and distribution range) reported in the literature. In contrast with alternative morphological and geometric morphometric approaches, we show that DNA barcoding allows a clear and infallible (9.6% sequence divergence) distinction between these two congeners. Moreover, when DNA barcoding was used with samples of the complex collected along Atlantic and Mediterranean European shores, we found that *N. nitidus* was the only species in the Adriatic (Venice lagoon) and North Sea (Lysekil, Sweden; Oostende, Belgium), while it was either absent or in sympatry with *N. reticulatus* between these extremes (i.e., along the eastern Atlantic shoreline from the entrance of the English Channel to the Alboran Sea). Albeit limited, our results also suggest differences in the haplotypes recorded in those two separate areas (North vs. Adriatic Sea) where *N. nitidus* might be the only representative of the complex; this pattern resembles what has been recently found for other marine gastropods.

36.—A GENERAL DYNAMIC MODEL OF OCEANIC ISLAND BIOGEOGRAPHY: PREDICTIONS AND EVALUATION

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In a recent paper in *Journal of Biogeography* (June 2008), we presented a theoretical model of rates of immigration, extinction, and speciation on oceanic islands as a function of island ontogeny (life cycle). The central premise of the model is that the ecological capacity of remote volcanic islands typically describes a hump-shaped trend as an island grows to maturity and then declines through erosion and subsidence, eventually disappearing again. The model generates several predictions for emergent biogeographical patterns within archipelagos comprised of such islands, focusing on numbers and proportions of endemics, relative importance of adaptive and non-adaptive processes, etc. Here we (i) outline the key properties of this general dynamic model, (ii) present some additional tests of the model using snapshot data based on numbers of endemic species, and (iii) highlight the potential for phylogenetic data to be used in evaluating the model.

37.—GLOBAL PATTERNS IN THE NICHE WIDTH OF ISLAND PARASITIC WASPS

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Islands have long been the focus of interest for researchers, being natural laboratories for the study of evolutionary and ecological patterns. Moreover, islands are one of the most threatened ecosystems in the planet. One of the consequences of islands' discrete and isolated character is the relaxation of natural selection and the evolution of generalist species. Parasitoids are probably no exception to this, as they may have to attack novel or unusual hosts on islands, compared to those on the mainland. It is therefore expected that parasitoids arriving on islands may make do with less preferred hosts, and that island parasitoid faunas will have higher proportions of generalists (biased towards idiobiont species). We use a published database on the species distribution and biology of Ichneumonoidea (Hymenoptera) to analyse the influence of historical, environmental and ecological factors on the niche width of well-surveyed parasitoid island faunas.

38.—THE ROLE OF FORGOTTEN SEAMOUNTS IN SHAPING THE MACARONESIAN RELICT LAUREL FOREST

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The important development achieved in the last years by the sea floor mapping and the seamounts-dating technology has enabled the reconstruction, albeit still with a high degree of uncertainty, of the geologic history of the Eastern Central Atlantic during the Cenozoic. Today we know that as early as 60 My BP there were already some volcanic islands (PalaeoMacaronesia) in this region, located much closer to the mainland than today's extant archipelagos, reflecting the long-lasting activity of the Madeiran and the Canarian volcanic hot spots. Many of these palaeoislands, now submerged as guyots (flat-topped seamounts) due to erosion and sea floor subsidence, still retain summits less than 120 m below the sea level, which enabled them to emerge during the Pleistocene sea level regressions and act as stepping stones. The present essay tries to vindicate the important role played by these palaeoislands both in the long-distance Europe-North America Trans-Atlantic dispersal of tropical taxa between 40 and 25 My BP, after the closure the North Atlantic (Scotland-Greenland) corridor, as well as in their role in the colonization of the present archipelagos by palaeoendemic species, especially those constituting the Macaronesian relict laurel forest, an impoverished remnant of the South Europe and North Africa Tethyan laurisilva.

39.—AEGEAN BIOGEOGRAPHY: A LANDBRIDGE ISLAND PERSPECTIVE

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The thousands of Aegean islands, with their complex palaeogeographical and palaeoecological history, diversity of ecosystem types, rugged topography, and the wide range of areas they span, offer an excellent natural experimental set-up for island biogeography studies. An increasing number of phylogenetic and phylogeographic analyses based largely on molecular markers are gradually revealing the importance of vicariance events, dispersal, and in situ speciation in shaping current distributional patterns of a variety of organisms in this region. This body of knowledge leads to new insights into the effects of crucial historical events especially for endemic forms. At the same time, important contributions to ecological biogeography have been made after analyses of insular communities on Aegean islands. These include the Choros model, new approaches to the Small Island Effect, the application of structural equation models in biogeographical analyses, concepts regarding non-adaptive radiation and several other innovations and elaborations of new ideas. The richness and variety of Aegean islands provide a valuable tool for testing hypotheses of island biogeography and macroecology, e.g., regarding species turnover, the role of habitat diversity, species co-occurrence. Here, we present a concise account of major contributions to Aegean biogeography. Furthermore, we combine these with new insights gained regarding patterns and processes that characterize landbridge islands in general and oceanic archipelagos such as Hawai'i and the Canaries with the aim of obtaining a more comprehensive understanding of spatial biodiversity patterns in the Aegean region.

40.—THE GEOGRAPHIC SPREAD OF EARLY DOGS IN ISLAND SOUTH EAST ASIA

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Human colonization of the Pacific occurred in multiple waves, potentially out of China/Taiwan between 45,000 and 5,000 BP, with subsequent movement and introgression. The commonly held “Out of Taiwan” hypothesis dates the second wave, the Austronesian expansion, starting around 5,500 BP, with subsequent waves and mixing of neighboring populations. It has been suggested and supported with archaeological evidence that the most recent colonizers (around 5,500 BP) brought dogs with them to these islands from Taiwan/China. Recent molecular analysis of the Dingo, New Guinea Singing Dog and village dogs on Bali suggest an ancient SE Asian origin with divergence times (based on rho-aging of endemic clades) of the Dingo and Bali dogs corroborating with estimates of human colonization from SE Asia. Our goal is to determine the extent to which ancient dog haplotypes still exist in village dogs throughout Island South East Asia (ISEA). Our group has begun investigating the colonization route by analyzing mtDNA, Y chromosome, and autosomal microsatellites in dogs from ISEA. Purported archeological dates give us potential divergence times that should be corroborated by molecular analysis in village dogs from these locations if they are direct descendants of the dogs of the Austronesian expansion. Our goals are to determine if: 1) the locations of the Austronesian expansion contain an ancient Southeast Asian origin; and 2) dogs show divergence times similar to what archaeological and human molecular evidence suggests.

41.—REGIONAL VARIATION IN THE DIVERSITY OF CORAL-DWELLING FISHES IS DRIVEN BY GRADIENTS IN CORAL ASSEMBLAGE STRUCTURE

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The size of the regional species pool may influence local patterns of diversity. However, it is unclear whether certain spatial scales are less sensitive to regional influences than others. I sampled fishes within branching-corals in three geographically distinct regions in the Indo-Pacific (Red Sea, Western Indian Ocean, Great Barrier Reef) that contain increasingly larger regional diversities of reef fish. First, additive partitioning was used to separate diversity at multiple spatial scales to its alpha and beta components. I then examined how the relative contribution of these components changes with increased regional diversity. Although alpha and beta diversities within each region were consistently different from random-placement null models, the increase in beta diversities among regions was similar to that predicted once heterogeneity in coral habitat was accounted for. Next, I compared the number of fish species that reside within specific coral species across regions. The number of fish species per coral species was similar among regions with different regional diversities. Moreover, I found that fish richness within coral species was lower than that expected from random-samples of the species pool, and that richness in rich regions was reduced comparably more than in poor regions. These results suggest that higher regional diversity of coral-dwelling fish is rooted in higher coral richness and therefore ecological interactions between functional groups (coral and fish) can be powerful drivers of regional biodiversity.

42.—INSECT AND SPIDER RARITY IN ISLAND TREE CANOPIES: TRUE RARE AND PSEUDO-RARE SPECIES

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Until now the mechanisms of how recent historical land-use changes in island ecosystems shape the distribution of individual insect species have been poorly understood. Here, we concentrate on the contribution of island habitat composition (i.e., habitat resource availability) to island spider and insect distribution patterns. In this context we study in detail the distribution patterns of four functional groups (herbivorous sucking insects, herbivorous chewing insects, spiders and other arthropod predators) of endemic, native and exotic arthropod species on a well-studied island of the Azores archipelago (Terceira). Within the larger context of a standardized sampling program for canopy arthropods we want to find out which species are truly rare and which are pseudo-rare species in each target habitat. Habitat tourists have proved to contribute substantially to arthropod density in the ecological community of the laurisilva canopy. Two types of local pseudo-rare species were identified: “habitat (or land-use)” and “host plant” pseudo-rarities. Insufficient spatial replication in sampling can lead to the conclusion that numerous species appear to be rare because they were sampled in marginal sites or in the edge of their distribution. Our results provide clear evidence that without adequate spatial data on abundance and habitat requirements, rarity status for insects and spiders on islands and elsewhere cannot be appropriately assessed.

43.—HAWAIIAN REEF FISHES: ARE ENDEMICS POOR DISPERSERS?

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It remains controversial whether a general correlation exists between range size and dispersal ability, where range-restricted endemism would be indicative of lower dispersal ability. To evaluate this hypothesis we surveyed mitochondrial cytochrome-b sequence variation in three surgeonfish species with vastly different ranges: *Ctenochaetus strigosus*, Hawaiian endemic, $n = 531$; *Zebrasaoma flavescens*, North Pacific, $n = 560$; *Acanthurus nigrofuscus*, Indo-Pacific, $n = 298$. Collections were made throughout the 2500 km expanse of the Hawaiian Archipelago and adjacent Johnston Atoll. Analyses of molecular variance demonstrate that each species is capable of maintaining population connectivity on a scale of thousands of kilometers. However, collections of the endemic *C. strigosus* revealed significant restrictions to gene flow within the Papahānaumokuākea Marine National Monument. These results are consistent with current phylogeographic surveys of Hawaiian reef fauna where widely distributed species exhibited genetic homogeneity across the archipelago, while endemics revealed significant population subdivision over the same range. These findings invoke the intriguing hypothesis that Hawai'i's endemic marine fauna evolved from species with reduced dispersal ability that, after initial colonization, could not maintain contact with parent populations.

44.—BIOGEOGRAPHICAL AFFINITIES OF THE SPONGE FAUNA OF BERLENGAS ARCHIPELAGO (PORTUGAL)

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Sponges have an unrealized potential importance in biogeographic analysis. Berlengas Archipelago is located 10 km off the coast of Peniche (Portugal), comprising 3 islet groups and showing an enormous diversity of subtidal habitats, some of which are included in the Habitats Directive. The poriferan fauna of Berlengas is composed of a total of 69 species, most of which were collected during three summer sampling campaigns: 2003, 2005, and 2007. The complete list of sponge species of Berlengas under analysis also included other data from the literature. The comparison of this fauna with other faunas from neighbouring geographical areas such as the Macaronesian Archipelagos, the Mediterranean Sea and the North East Atlantic Coasts is made. Cluster and multidimensional scaling (MDS) were used to look for similarities between poriferan fauna from these regions. Although presenting high similarities with the Iberian Coasts, Berlengas seems to constitute a meeting point for the faunas from the Lusitanian, Mauritanian and Mediterranean regions.

45.—BIOGEOGRAPHY OF ROCKY SUBTIDAL MACROINVERTEBRATES OF THE REVILLAGIGEDO ARCHIPELAGO, MEXICO.

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In order to analyze the relationship and biogeographic affinities of islands in the Revillagigedo Archipelago (Socorro, San Benedicto, Roca Partida and Clarion) based on rocky subtidal macroinvertebrates, quantitative visual scuba surveys were conducted in February 2006 at four depths (10, 20, 30 and 40 m) and at four habits (wall, flat reef, boulders and small boulders). 60 species were recorded of which 22 (37%) are new records. The sponge *Aplysina* cf. *fiistularis*, the corals *Pocillopora eydouxi*, *Porites lobata* and *Tubastraea coccinea*, the sea urchins *Euclidaris thouarsii*, *Diadema mexicanum* and *Tripneustes depressus*, and the sea cucumber *Isostichopus fuscus*, were the dominant species (86% of the total density and occurrence more than 20%). Within Socorro, the San Benedicto and Clarion islands are differentiated by habitat, while in Roca Partida a separation by depth exists, perhaps reflecting the structural complexity and physical factors associated with a thermocline. Each dominant species is associated to a specific habitat. The analysis of similarity and ordination analysis showed a divergence between the Socorro (San Benedicto and Clarion) islands, where Indo-Pacific, Eastern Tropical Pacific, Oriental Pacific and Endemic species were predominate; and Roca Partida, where Eastern Tropical Pacific and Oriental Pacific species predominate. In Roca Partida a change at 30 m was observed, where species from affinities of California-Gulf of California (*Muricea appressa*), and Gulf of California-Mexican Tropical Pacific (*M. austera*, *A. gerardogreeni*) appear, which may indicate that the depth of the thermocline can control the distributional limits of species.

46.—PHYLOGEOGRAPHY AND GENETIC VARIATION OF RELATED SPECIES PAIRS ON AEGEAN ISLANDS: SIGNALS OF ECOLOGY AND HISTORY

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Patterns of geographic variation of species among island populations are still a hot issue, lying on the common ground between historical and ecological biogeography. Organisms with low dispersal abilities may differentiate largely in strict allopatry, therefore more strongly exhibiting adaptive and non-adaptive radiation processes. We analysed mtDNA variation of several insular populations of four terrestrial isopod species distributed on Aegean islands (Greece) and estimated their genetic divergence and phylogenetic patterns. Each pair of species belongs to the same genus, with each species exhibiting either different ecological characteristics (generalist-specialist) or different distributional range (local endemic - more widespread). The results provide useful insights to the biogeography of Aegean islands and the evolution of the species studied.

47.—COMPARING PATTERNS OF DIVERSITY AND ABUNDANCE OF GROUND-BEETLES IN THE LAURISILVA OF AZORES AND MADEIRA ARCHIPELAGOS

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The Macaronesian islands of Azores and Madeira have a unique type of native forest, the “Laurisilva.” We used standard techniques to collect data on ground-beetles species richness covering the Laurisilva of seven islands in Azores and the Madeira Island. The aims of this work were to: 1) compare alpha, beta and gamma diversities between the native forests of both archipelagos; 2) evaluate patterns of rarity; and 3) evaluate the number of forest patches needed to preserve all the endemic species sampled, using the complementarity method. Interestingly in both archipelagos we sampled 39% of the endemic epigeal species (5 out of 13 in Azores and 29 out of 74 in Madeira). Maximum endemic alpha diversity is 9 in Madeira and 2 in the Azores. The unified abundance-variance-occupancy model fits extremely well to data. At least one fragment on each Azorean island where carabid beetles were found (Terceira, S. Miguel and Pico) was required to accomplish conservation efforts for the 5 endemic taxa sampled. In Madeira, almost one-third of the sampled transects (11 out of 36) are needed to protect the 29 endemic sampled species. Although in a single island, the Laurisilva of Madeira is a hotspot of ground-beetle diversity with a remarkable turnover of species within the forest.

48.—ISLAND BIOGEOGRAPHY AND EVOLUTION IN MARINE ENVIRONMENTS

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Island theory has been largely neglected in marine science for 30 years. Island theory does not appear in marine ecology texts (e.g. Nybakken 1997; Castro & Huber 2003), nor do marine examples appear in island biogeography texts (e.g. Whittaker & Fernandez-Palacios 2007). Yet, as evidence has accrued that dispersal in marine systems is not as high as assumed, so has increased the probability that ‘rules’ of island ecology and evolution are also pertinent to marine species. Here, I summarize our decade-long study of marine lakes – islands of seawater entirely surrounded by land – which examines whether patterns in species richness, genetic diversity, and size and shape evolution in sponges, ascidians, echinoderms, jellyfish, fish, and/or molluscs are consistent with the predictions of species-area relationships, colonization dynamics, ‘the island rule’, and changes in predation. In all cases we find patterns of evolution consistent with those previously reported for terrestrial species on oceanic islands. This finding demonstrates that marine and terrestrial systems are not ‘fundamentally different’ as has often been stated, and encourages application of the rich body of island theory in studies of marine faunas, for example those inhabiting oceanic islands, guyots, hydrothermal vents, and networks of island-like reserves.

49.—USING THE SEA CUCUMBERS *HOLOTHURIA ATRA* AND *HOLOTHURIA WHITMAEI* TO TEST HAWAII CONNECTIVITY HYPOTHESES

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The coral reefs of the Hawaiian Archipelago are the most isolated in the world. This isolation has been a significant factor contributing to the high endemism and lower biodiversity in Hawai'i compared to reefs in the South and West Pacific. In order to test hypotheses about biogeographic connections that can drive biodiversity within Hawai'i, we examined the genetic population structure of the wide-ranging tropical sea cucumbers *Holothuria atra* and *Holothuria whitmaei* across the Hawaiian Archipelago and among neighboring habitats in the southern and western Pacific: Japan, the Marshall Islands, Line Islands, and Johnston Atoll. We found significant genetic structure between the inhabited Main Hawaiian Islands and the Northwestern Hawaiian Islands, and between the widespread locations in the South and West Pacific, with the strongest barriers between Japan and Hawai'i and between the Line Islands and Hawai'i. In contrast, we observed no significant genetic structure between the Northwest Hawaiian Islands and Johnston Atoll, 800 km to the southeast and Hawai'i's closest neighbor. These results support previous hypotheses about connectivity based on faunal comparisons and computer modeling, indicating that Johnston Atoll may be a gateway into the Hawaiian Islands. The production and maintenance of Hawaiian biodiversity, which is the basis of a healthy island community, may depend on this critical link to other Pacific reef ecosystems.

50.—THE MADEIRAN LAURISSILVA: WHERE ARE THE HOTSPOTS OF BRYOPHYTE DIVERSITY?

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The Macaronesian flora display characteristics typical of oceanic islands, including a high degree of endemic plants. The predominance of endemic plant species makes the Macaronesian Islands an exceptional area for studies concerning extant diversity, evolution and speciation. The Madeiran Archipelago hosts a diverse bryoflora with 529 bryophyte taxa with the highest diversity on Madeira Island (the main island of the archipelago), where 511 bryophyte taxa have been recorded. In Madeira, the main forest formation, the Laurissilva, which is considered a relict of the forests of the Tertiary, is the most species-rich and most valuable habitat type of Madeira Island. In order to determine the bryophyte hotspots within the Madeira Laurissilva, the bryophyte flora and vegetation of distinct habitats were surveyed. In total 329 bryophyte taxa including 21 Macaronesian endemics and six Madeira endemics were identified. Distribution models for 97 species which had at least 5 occurrences were performed based on topographic and climate variables using Maxent. For 39 species we found good models in terms of cross-validated AUC values. The minimum number of occurrences for these species was 10. As a first result, preliminary bryophyte 'hotspots' within the Laurel Forest were identified. While most of these areas are situated within the still existing and protected Laurel forest, some hotspots are predicted to occur outside of the remaining forest. Moreover, we observed that the hotspots also contained very rare species and species of conservational concern according to recent IUCN criteria. Therefore, the preliminary richness hotspots may also be rarity hotspots. Further analyses testing the robustness of the hotspots are under way.

51.—VARIATION IN LOCAL OCEANOGRAPHY CONTROLS THE NATURAL HISTORY AND DEMOGRAPHY OF AN AZOOXANTHELLATE CORAL

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Despite many well-documented effects of oceanography on biological systems at large spatial scales, the effects of local oceanographic variability on the life history and demography of marine species have received little attention. Here, we report the effects of local oceanography (14 parameters considered) and substrate orientation on the survival, growth, and demography of an azooxanthellate coral, *Tubastraea coccinea*, at 6 sites (maximum inter-site distance 106 km) in the Galapagos Archipelago. Relevant oceanographic parameters were identified using AIC-based model selection and model averaging techniques. Repeated surveys indicate that sites with higher horizontal flow rates and warmer temperatures had larger, younger colonies of *T. coccinea* at greater densities. In a year-long experiment, coral survival varied >30% among sites, and was strongly controlled by substrate orientation and vertical flow speed. A concurrent experiment indicated that coral growth varied >50% among sites and increased with vertical and horizontal flow, and water temperature. Stable isotopic data indicate that *T. coccinea*'s food sources do not vary among sites, suggesting that changes to the coral's survival, growth, and demography are causally related to oceanographic processes. Together, these data suggest that local variability in oceanographic conditions is more important to the life history and demography of subtidal organisms than previously believed, and may confuse biogeographic patterns observed at larger spatial scales.

52.—BRYOPHYTE DIVERSITY OF SÃO TOMÉ E PRÍNCIPE ARCHIPELAGO: A BIOGEOGRAPHICAL APPROACH

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São Tomé e Príncipe is an archipelago in the Gulf of Guinea. The largest island São Tomé is 32 x 48 km and Príncipe is 19 x 12 Km. The highest mountain of the archipelago, Pico Gago Coutinho (2024 m) is located on São Tomé. The climate is tropical, hot and very humid, with small termic amplitude. The forest of São Tomé e Príncipe was classified in 1988 by the International Scientific Association as one of the two most important of this type in Africa, due to the high plant diversity, including a large number of endemic species. Data on the bryophyte flora was obtained from bibliographic references, herbarium material and recent field work during 2007 and 2008. The bryophyte of São Tomé e Príncipe archipelago is presented and some (main) biogeographic tendencies of its bryophyte flora are presented and compared with other island and archipelagos. The bryophyte flora of the islands shows western and central African affinities, with high rates of endemism at the species levels. The influence of some variables such as, altitude, soil use, forest type, island size, distance to African continent, and other factors on the development of some bryophyte assemblages is discussed.

53.—UNEXPECTED EVOLUTIONARY RELATIONSHIPS AFFECT BIOGEOGRAPHIC PATTERNS IN PHILIPPINE HORSESHOE BATS

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Diversity in the Philippine archipelago has been strongly influenced by both colonization of islands and in situ speciation, resulting in flora and fauna indelibly marked by geography. Possibly the least well studied vertebrates in the archipelago are the nocturnal, echolocating bats and in at least one group patterns are obscured by cryptic variation within islands. Variation in noseleaf morphology defines species groups within the Old World horseshoe bats (Rhinolophidae) and therefore may also be useful in determining species boundaries. DNA sequences from the mitochondrial genome show that genetically divergent lineages of these horseshoe bats (genus *Rhinolophus*) do correspond to subtle noseleaf differences and as they are broadly sympatric in the archipelago, may warrant taxonomic recognition. However, currently recognized taxa that exhibit less genetic differentiation to these lineages than to their own putative conspecifics also were discovered. Thus cryptic diversity may not simply reveal hidden sister taxa, but may uncover much deeper divergences. Additionally, in this study the character sets that define groups suggest that the evolution of some characters of primary importance in traditional taxonomy (such as body size) may be relatively labile while older evolutionary events may be characterized by subtle morphological change. Understanding phylogenetic relationships is necessary in biogeographic analyses and in this case reveals lineage specific levels of conformity to predictions from Pleistocene and modern island geography

54.—PHYLOGENETIC INSIGHTS INTO THE ORIGINS OF THE HAWAIIAN FLORA

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The Hawaiian Islands arose in isolation, and therefore harbor a biota that is derived entirely from long distance dispersal. In 1948, F. Raymond Fosberg identified groups of species in the Hawaiian angiosperm flora derived from each putative colonist and estimated the geographical origin of each long distance dispersal event. He identified colonists as having arrived from one of the following regions: Austral, Indo-Pacific, American, Boreal, Pantropical, and Obscure. Utilizing a wealth of phylogenetic analyses now available, we compared Fosberg's treatment to a new analysis of the origins of the Hawaiian flora. For a more detailed analysis, we subdivided Fosberg's broadly defined Indo-Pacific region into Malesian and Pacific Island regions, and the American Region into Neotropical and Nearctic regions. Despite upholding many of Fosberg's original assessments, we report several notable differences. It has been shown that several groups comprise diverse adaptive radiations derived from a single colonist (where Fosberg hypothesized multiple colonization events), and thus our analysis recognizes somewhat fewer original colonists. We estimate that colonist origins are: 6% Austral, 5% Malesian, 35% Pacific, 14% Neotropical, 10% Nearctic, 2% Boreal, 18% Pantropical, and 10% Obscure. Our analysis recognizes more colonists from the Americas (63) compared with Fosberg's estimate (50). Several groups that are newly recognized as American in origin appear to be from temperate North America and include several key adaptive radiations. Our analysis also suggests that Hawai'i may be an important source of colonists to South Pacific archipelagoes, with several clear cases of out-of-Hawai'i dispersal.

55.—BODY SIZE, NICHES, AND (DIS)ASSEMBLY RULES FOR INSULAR MAMMAL COMMUNITIES

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A central problem in biogeography and ecology is to understand how the differential extinction of species and populations influences the assembly and disassembly of biotas. Here, we integrate niche theory, insular biogeography, metabolic ecology, and rules of community assembly to develop a conceptual and mathematical model describing the central role of body size in moderating the disassembly of insular communities. The theory underscores the interrelatedness of several disparate phenomena and empirical patterns in macroecology and biogeography. In order to evaluate our theory, we constructed and analyzed a species list and database of body masses for the entire terrestrial, non-volant mammal fauna of the Sunda Shelf Islands, which are landbridge islands once connected to the southeastern mainland before the late Pleistocene's rising sea levels. As predicted, the insular communities of mammals are highly nested, significantly deviating from several relevant null models. As the communities disassemble into smaller subsets on smaller islands, these subsets converge on species of intermediate body sizes of around 100 to 300 grams. These species have the greatest number of island occurrences and the highest species richness. The large islands contain the largest and smallest mammals, whereas the small islands only have intermediate body sizes. Our theory and empirical findings have important implications towards community ecology, insular and extinction biogeography, conservation, and understanding the disassembly of communities resulting from habitat fragmentation.

56.—MIOCENE AND PLIOCENE RADIATIONS AND BIOGEOGRAPHY OF LEIOTHRICHINAE BABBLERS (AVES, TIMALIIDAE)

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The phylogenetic relationships of babblers (family Timaliidae) have recently been resolved, which enables us to outline their earliest biogeographic history. However, for one of the four recognised timaliid subfamilies, Leiothrichinae (laughingthrushes, song babblers and ground babblers), the basal relationships have proven hard to infer, although a mainland Southeast Asian origin can be estimated, as in the other subfamilies. During the mid Miocene a rapid radiation occurred, followed by extensive radiations of several clades at the Miocene-Pliocene boundary. We estimate that most of the Sundaic representatives of Leiothrichinae babblers spread to the Sunda region separately, most of them in the Pliocene. One major change of habitat choice has taken place, the adaptation to arid habitats of *Turdoides* ground babblers from a life in the forest has enabled this group to spread over India, the Middle East and Africa. The African genera *Kupeornis* and *Phyllanthus* are exceptional in having “returned to” a forest living. Most radiation events in the Leiothrichinae babblers can be associated with large-scale changes in geology, climate and habitat, such as the build-up of continuous forest coverage of Eurasia and northern Africa during Miocene followed by desertification in the end of Miocene, and the uplift of Greater Sundas in Pliocene.

Symposium II

**The Biogeography
of Disease:
Examining the Forces
that Drive
Disease Distribution and Emergence**

OVERVIEW OF HUMAN AND NATURAL FORCES THAT CONTRIBUTE TO THE GEOGRAPHY OF INFECTIOUS DISEASE

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Understanding the forces that drive infectious disease biogeography is critical to global public health, crop production, and the conservation of biodiversity. In this overview, I will highlight what is known, and not known, about the drivers of diseases in these systems. I will begin with an historical perspective on over five phases of disease emergence throughout human history and pose a key question for the 21st Century: How can we understand and predict the process of pathogen emergence and spread? This pattern is one of demography, human development and anthropogenic environmental change driving repeated pathogen emergence and spread from areas of high pathogen diversity. To understand this process requires an understanding of pathogen evolution, host-parasite ecology and the broad changes that drive pathogen invasion of novel systems. I will discuss how this process can be modeled in roughly the same manner as an invasive species "waiting time" model, and how this might provide a framework for prediction of the process of disease emergence. I will then review some recent attempts at addressing different aspects of this process, from SARS to plant pathogens to vector-borne diseases to the next new zoonosis. I conclude that we are at an important juncture in infectious disease biogeography, with such a detailed knowledge of pathogen biology, demography and ecological theory that simply fusing these disciplines will provide a dramatic leap in our understanding of disease risks globally. Furthermore, the rapid development of molecular techniques will lead to significantly finer resolution of the global diversity of infectious agents over the next decade. However, many gaps remain, including global datasets on the key drivers of infectious disease emergence and spread, and surveillance in remote regions, particularly in the Tropics, where it seems that potential pathogens are more biodiverse, and the drivers of their emergence and spread are concentrated.

MODELS FOR CONTINENTAL-SCALE SPREAD OF EPIDEMICS, USING PLANTS AS A MODEL SYSTEM

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Classic approaches to modeling biological invasions predict a "traveling wave" of constant velocity determined by the invading organism's reproductive capacity, generation time, and dispersal ability. Traveling wave models may not apply, however, for organisms that exhibit long distance dispersal (LDD). We used simple empirical relationships for accelerating waves, based on inverse square law dispersal, and applied them to diseases caused by pathogens that are wind-dispersed or vectored by birds: the within-season spread of a plant disease at spatial scales of <100 m in experimental plots, historical plant disease epidemics at the continental scale, the unexpectedly rapid spread of West Nile virus across North America, and the transcontinental spread of avian influenza strain H5N1 in Eurasia and Africa. The analyses suggest that location of the epidemic front will double per unit time used to measure initial velocity and that a plot of velocity versus distance will have a slope of 1/2. When treated as unknowns, estimates of the inverse power law exponent for dispersal that would be required to attain the rates of disease spread observed in the field varied from 1.74-2.36, despite more than a five-fold range of spatial scale among the data sets. Properties of the inverse power law also allowed us to scale epidemic spread in experimental plots to the size of the initial focus and to the density of susceptible hosts; the same relationships may hold at the continental scale as well. Our approach may provide a more realistic basis for studying the spread and control of organisms capable of significant LDD.

PREDICTING EMERGING INFECTIOUS DISEASES IN HUMANS

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Biodiversity and ecosystems are changing at an unprecedented rate in human history as the world population grows and impacts global systems. We urgently need to evaluate the effect of human development on global ecosystems and the services they provide, in particular on the risk of the emergence of infectious diseases. We take a multidisciplinary approach to address this question using a global database of human emerging infectious disease (EID) events. We use a number of socio-economic, environmental and macroecological spatial databases to produce the first global EID risk model, from which predictive models of regions where new EIDs are most likely to originate (emerging disease ‘hotspots’). From these spatial models, it seems that global resources are poorly allocated, with the majority of the scientific and surveillance effort currently focused on areas where the next important emerging pathogen is least likely to originate.

THE GEOGRAPHY OF CROSS-SPECIES PATHOGEN TRANSMISSION IN PRIMATES

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Many of the most virulent emerging infectious diseases, e.g. AIDS and Ebola, are zoonotic – shifting from wildlife to humans. A critical question is what determines when and where a disease first crosses from one species to another. Over 60% of human and wild primate pathogens and 80% of carnivore and ungulate pathogens can infect more than one host; and these multi-host parasites are the most likely to emerge on a new species. Using primates, we have shown that infectious diseases are more often shared between species which are closely related and inhabit the same geographic region. A higher frequency of pathogen host shifts between close relatives and neighbours may explain this result. We also find that host relatedness is the best overall predictor of whether two host species share the same pathogens, and this is consistent for both wild primates and humans. Here we translate these results into “hotspot” maps, where we highlight regions where the risk of cross species pathogen transmission between wild primates and humans is greatest. We also test how ecological factors, such as human population density and land-use patterns, affect the risk of pathogen transfer to wild primates. We identify SE Asia as a potential new hotspot for emerging diseases in humans due to pathogen transfer from wild primates, and highlight areas where disease threats from humans may pose the greatest risk to primate conservation.

THE ORIGIN AND IMPACTS OF *ASPERGILLUS SYDOWII*, AN OPPORTUNISTIC PATHOGEN OF CARIBBEAN GORGONIAN CORALS

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Coral reefs are increasingly suffering outbreaks of disease, causing dramatic declines in population abundance and diversity. One of the best-characterized coral diseases is aspergillosis, caused by the fungus *Aspergillus sydowii*. *Aspergillus sydowii* is a globally distributed saprophyte commonly found in soil, so its presence in marine systems raises questions about its origin. Using microsatellite markers, I analyzed the population structure of *A. sydowii* from diseased sea fan corals, diseased humans, and environmental sources worldwide. The results indicate that *A. sydowii* forms a single global population, a diversity of nonrelated isolates able to cause disease in corals. Concurrent studies of genetic diversity in the coral host indicate a signature of disease outbreaks; sites with a larger historical impact of disease show evidence of a bottleneck in sea fan populations. Overall, the combined use of population genetic studies in both the host and pathogen has revealed critical information about the origins and impacts of aspergillosis in the Caribbean.

IMPACTS OF HISTORIC AND CONTEMPORARY POPULATION STRUCTURE ON HOST-PATHOGEN CO-EVOLUTION AND DISEASE EMERGENCE

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Historic and contemporary host evolutionary dynamics have profound impacts on viral diversity, virulence, and associated disease emergence. Bats have been recognized as vectors and reservoirs for a diversity of emerging viral pathogens, and are unique among mammals in their vagility and potential for long distance dispersal. Evolutionary theory predicts that hosts with high levels of dispersal should drive the evolution of more virulent pathogens, although connections with the ecology and evolution of chiropteran hosts have been lacking. We demonstrate through meta-analysis that, despite the potential for long-distance dispersal, bats vary widely in population structure and migration strategies. We generate predictions on viral evolution and emergence from observed variation in the historic and contemporary population structure of bat hosts, and discuss the influences of viral characteristics and dynamic spatial landscapes. We investigate host biogeography, or phylogeography, for predictions on viral diversity in relevant reservoir species, and describe models which combine host population genetics and selection for evolutionary stable strategies in viral pathogens. Host biogeography and population structure are critical for spatial predictive disease modeling of viral pathogens, and provide a model for evaluating the relative contributions of environmental, immunological, and anthropogenic selection on viral evolution and emergence.

GEOGRAPHIC VARIATION IN AVIAN COMMUNITY STRUCTURE: IMPLICATIONS FOR DISEASE DYNAMICS

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Because many pathogens can infect multiple host species within a community, disease dynamics in a focal host species can be affected by the composition of the entire host community. We examine the extent to which spatial variation of an avian host community may contribute to geographically-varying prevalence of a recently emerged wildlife pathogen. *Mycoplasma gallisepticum* is a pathogen novel to songbirds that has caused substantial mortality in one songbird species in eastern North America. This host, the house finch (*Carpodacus mexicanus*), is apparently the primary songbird host species for *M. gallisepticum*, but American goldfinches (*Carduelis tristis*) and house sparrows (*Passer domesticus*) are secondary hosts that live in the same general habitat. Laboratory experiments have demonstrated *M. gallisepticum* transmission among these species; however, the impact of among-species transmission on real-world disease dynamics is unknown. We analyzed data from winter-long citizen science bird and disease surveys to determine whether alternate hosts influence disease prevalence in house finches in eastern North America. Our analyses indicate that the abundances of multiple potential hosts do affect disease prevalence in house finches. Thus, spatial variation in bird communities has the potential to cause geographic variation in disease prevalence in house finches.

INTEGRATING INFECTIOUS DISEASE ECOLOGY AND BIOGEOGRAPHY: COMMENTS ON THE SYMPOSIUM TALKS AND SUGGESTED FUTURE DIRECTIONS FROM AN OUTSIDER

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Increasing global mobility by humans, global trade and anthropogenic changes to the landscape have made taking a biogeographic approach to understanding disease dynamics and spread increasingly important. The Symposium on Biogeography of Disease is an attempt to bring together both experts and experts in training to advance the field. Being somewhat an outsider to this field, I will attempt to bring an outside view on the ideas presented at this symposium as well as suggest future directions in the field.

57.—DOES LANDSCAPE INFLUENCE VIRAL EMERGENCE IN THE CENTRAL GREAT PLAINS?

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The role of landscape features as barriers to dispersal has been extensively studied for many plant and animals species, but how landscape influences disease epidemiology is poorly understood. We compared viral molecular epidemiology in North and South Central skunk rabies strains, population genetic structure of striped skunks, and the influence of rivers on viral emergence to determine what factors affect disease epidemiology in the Midwest. North Central strain had a higher nonsynonymous to synonymous substitution ratio than South Central strain (northern $dN/dS = 0.26$; southern $dN/dS = 0.10$), suggesting that South Central strain is under more stabilizing selection pressure than North Central strain; demographic analysis of the number of infections indicates that South Central strain rapidly increased, while North Central strain did so gradually. In striped skunk populations, high migration rates ($Nm = 41$ individuals/generation) of skunks across rivers suggest that in the Midwest landscape features do not appear to be dispersal barriers to striped skunks. Rabies strains, however, appear to be slowed by rivers. Phylogenetic analysis indicated that North Central strain has crossed the Missouri River three times, but South Central strain has not crossed it despite being present in counties adjacent to the river. South Central strain breached the Platte River only once to occupy northeast Nebraska. It is possible that viral or ecological properties such as differences in virulence, latency, transmission efficiency, or host density are driving the observed epidemiological variation.

58.—BIOGEOGRAPHY OF GENETIC RESISTANCE TO CHRONIC WASTING DISEASE

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Genetic resistance to disease is driven by both endogenous and exogenous factors affecting the distribution of susceptibility across the landscape. Resistant genetic forms can be locally abundant due to natural selection, but this may be mitigated by gene flow among populations. Gene flow is dependent on biological properties of the species as well as historic and recent biogeographical features of the landscape. To assess the interplay between natural selection, gene flow and landscape features, we sampled DNA from 268 white-tailed deer across Kansas. We sequenced 771 bp of the PRNP gene to assess the prevalence of an allele associated with lower susceptibility to Chronic Wasting Disease (CWD), and genotyped animals at 8 microsatellite markers to assess levels of gene flow among populations. We found the highest frequency of the lower susceptibility allele in animals from populations adjacent to CWD positive locations. Populations at the leading edge of the distribution of the disease had significantly higher prevalence of resistance than areas which were not adjacent to CWD positive areas. Genetic differentiation of populations measured with multilocus microsatellite genotypes was not attributable to Euclidian distance which suggests that other factors, such as landscape characteristics, influenced population connectivity. Furthermore, the geographic pattern of genetic differentiation of the PRNP gene did not correlate with the pattern of differentiation in microsatellite loci suggesting that natural selection, but not gene flow, drives the frequency of the disease resistance factor.

59.—RABIES EPIDEMIOLOGY IN THE MIDWESTERN UNITED STATES: CONSTRUCTION OF CONTACT NETWORKS TO PREDICT THE INFLUENCE OF HOST ECOLOGY AND LANDSCAPE HETEROGENEITY ON DISEASE SPREAD.

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Anthropogenic habitat alteration can have a significant effect on a variety of important ecological processes including disease emergence. In the Midwest, the striped skunk (*Mephitis mephitis*) is the reservoir host of rabies and presents a risk of disease exposure to humans, particularly in urban and suburban areas. To understand the altered epizootic potential of rabies in the Midwestern United States due to human habitat alteration, we are constructing a model of human exposure risk based on ecological parameters of the host species, the striped skunk, and current and predicted anthropogenic changes. As initial steps towards this risk assessment objective, we present habitat use data for the striped skunk and modeling techniques developed to predict the emergence and initial spread of rabies across a heterogeneous landscape. Thirteen striped skunks were monitored on the Konza Prairie Biological Research Station using radio-telemetry methods from October 2007 to June 2008. During the spring months, the skunks were found to prefer forest habitat with 86% of den sites located within forested areas. Disease latency, infectivity, and location of initiation were varied in Susceptible-Exposed-Infected-Recovered (SEIR) contact network models of disease spread based on predicted host densities in the Upper Kansas River Watershed. The degree of disease latency and the habitat type of disease initiation had a significant effect on the speed and expansion of the disease. Understanding these models in terms of the underlying habitat heterogeneity will have significant implications for determining human exposure risk to rabies.

60.—SCOPE, SCALE AND IMPLICATIONS OF U.S. LIVE WILDLIFE TRADE

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The U.S. imported >1.48 billion and exported >198 million live wildlife animals from 2000 through 2006. 55% of imports were wild-caught individuals and 92% were intended for commercial sale. Only 36.5% of shipments were identified taxonomically lower than the family level, making it impossible to assess the diversity of animals imported or calculate the risk of non-native species or pathogen introduction. We propose that strategic scientific risk analyses, at the lowest possible taxonomic level, are necessary to effectively reduce these risks, coupled with targeted screening according to a set of national, agreed-on priorities at ports of entry. These measures are paramount to minimizing threats to public health, the environment and economy, such as the 2003 monkeypox outbreak and introduction of Burmese pythons to the Florida Everglades.

61.—MULTIPLE NICHE SHIFTS DURING GLOBAL INVASION OF THE ASIAN TIGER MOSQUITO, *Aedes albopictus* SKUSE

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Niche-based species distribution models are now being used to predict invasive species spread. These models assume niche conservation during invasion, but numerous examples of niche evolution during invasion exist for successful invaders. I used MAXENT to model native and introduced ranges for the Asian tiger mosquito (*Aedes albopictus* Skuse) to test if the species' niche was conserved during its 25-year invasion of 5 continents. This multi-continent invasion provides a naturally replicated test of niche conservation during invasion. I show that the native niche poorly predicts introduced ranges for this species. Likewise, reciprocal models based on introduced ranges poorly predict the native range. Specifically, models trained with North American and European niche characteristics predict a native range fully outside the actual native range. Models trained with South American characteristics shift the native range into Australia. Thus, niche characteristics on invaded continents are not merely a subset of the native niche, but reveal clear shifts. Multivariate analyses support modeled differences in niche characteristics among continents, and reveal important variables explaining these differences. My analyses indicate that *Ae. albopictus* has adapted to different conditions on different continents, and provides further evidence that successful invasive species rapidly evolve during invasion. These models generate hypotheses that will frame empirical evaluations of the mechanisms driving rapid adaptation by *Ae. albopictus* to novel conditions. Such mechanisms are discussed.

62.—PATTERNS OF NATIVE AND EXOTIC PLANT RICHNESS ALONG A SEA LEVEL TO SUMMIT MACRO-TRANSECT, APPALACHIAN MOUNTAINS, USA

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Species richness generally decreases from low to high elevations. Explanations for this trend fall into three categories: historical, climatic and spatial. Its shape varies from humped to monotonic, and may reflect the length of the sampled gradient, indicating a sampling effect. Previous studies have focused on total species richness, and relatively few have investigated how patterns of native and exotic species richness differ. We used local floristic studies (floras) to test the patterns of plant species richness from sea level (Atlantic coast) to the summit of the Appalachian Mountains, USA. The use of floras enabled us to investigate elevational patterns over a large gradient and to examine the effect of spatial scale on elevational patterns. In addition, we investigated whether elevational patterns of native and exotic species richness differed. We modeled the effects of size of study area, year of study, and elevation on native and exotic plant richness using a dataset of >70 floristic studies. After accounting for area and year, native and exotic species had contrasting richness patterns along the elevational gradient. These results suggest that different processes may govern native and exotic plant richness patterns. The protocols used here are being expanded to facilitate biodiversity informatics within the herbarium network SERNEC, as part of a project to use floras and specimens to explore regional diversity patterns.

63.—CAN CLIMATE-DRIVEN RANGE EXPANSIONS BE INFORMED BY NON-NATIVE SPECIES INVASIONS?

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Shifts in species' ranges are a predicted and realized effect of global climate change; however, few studies have addressed the consequence of such shifts, particularly in marine systems. Given ecological similarities between expanding and invading species, we examine how our understanding of range expansions may be informed by the more established study of species invasions. Our review and meta-analyses revealed that: 1) spread rates of expansions are lower than those of invasions; 2) marine expanders spread faster than terrestrial expanders; and 3) directions of community effects are largely negative and magnitudes are often similar for expanders and invaders, although this comparison is limited by few data for expanders. Because invasions are considered one of the primary threats to biodiversity, it follows that, like invasions, expansions have the potential to seriously affect biological systems.

64.—USING A HIERARCHICAL MODELLING APPROACH TO PREDICT POTENTIAL PLANT INVASIONS AT A FINE SCALE

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To improve the fine scale predictions of potential invasive species distribution we integrated into a species distribution model both coarse scale climatic data on the home range and fine scale land cover data on the new range. We chose four species that are considered invasive in several USA states, but are believed to not have reached their full distribution. We predicted potential invasive species distribution in the central USA through a series of hierarchical models that are based on climate, at the coarsest level, and land cover at the finest. First, we modelled the suitable climatic environment within the species native range. The potential distribution based on climate was then projected into the US where the species are considered invasive. We integrated the climate based model predictions into a finer scale model that included land cover. Combining the continental scale climate model and the fine scale land cover suitability model will help to limit invasion prediction to likely habitats. Results from this type of modelling approach can be used to help concentrate the effort for early invasion detection, especially in sensitive natural areas and better inform land managers of the potential for invasion in their area.

65.—RAPID MORPHOLOGICAL EVOLUTION OF EXOTIC PASSERINE BIRDS ON ISLANDS

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Islands have figured prominently in the study of biogeography and evolution because they are simplified systems in which processes can be more easily studied. The introduction of birds to islands provides us with a large-scale “natural experiment,” one in which we know the date of introduction, propagule size, and source population. These data were often recorded by the individuals and acclimatization societies responsible for the introductions. Well-documented introductions provide an opportunity that is rarely if ever encountered when examining natural colonizations. We examined morphological changes of passerine birds introduced to Bermuda, Puerto Rico, and Hawai'i by comparing field and museum specimen measurements of the exotic populations with museum specimen measurements of the native mainland source populations. These comparisons allow an examination of the magnitude and direction of morphological divergence that has occurred over contemporary time scales, and determine if there are any large-scale patterns related to island area and time of isolation. Our results indicate that native and exotic populations have diverged rapidly; in some cases morphological change is discernible after only a few decades. Furthermore, many of these morphological changes appear to be contrary to predictions made by classic evolutionary theory, such as the Island Rule. Our study highlights the utility of using exotic species to examine evolutionary and biogeographical questions in contemporary time.

66.—SPATIAL HETEROGENEITY OF PARASITE SPECIES RICHNESS: A CASE STUDY OF NORTH AMERICAN CARNIVORES

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Research on diversity patterns of species has demonstrated integral ecological and evolutionary relationships. However, few empirical studies have focused on parasites, despite their ecosystem functions and high species diversity. Here, we present a model of parasite diversity across North America using mammalian carnivores. We obtained species distribution maps of 29 terrestrial carnivores to estimate host diversity and conducted a systematic review of the literature to compile a list of parasites for each carnivore host. To inclusively explore patterns of parasite diversity, we included microparasites (viruses, bacteria, protozoa), macroparasites (nematodes, platyhelminthes), and ectoparasites (fleas, ticks) in our analysis. Our analysis included three hierarchical levels of parasite species diversity (alpha- average number of parasites per host; beta- number of specialist parasites per host; gamma- total number of parasites per grid cell) and we corrected for unequal sampling effort across carnivore species. Our literature search yielded over 500 parasite species and about 1200 host-parasite combinations with macroparasites being the most diverse parasite group. We found a strong positive, linear relationship between gamma parasite diversity and carnivore diversity. There were both latitudinal and longitudinal gradients to all levels of parasite diversity, but alpha and beta parasite diversity exhibited similar spatial patterns. Our findings identify potential parasitic hotspots for carnivore parasites, which has implication for disease management of parasites that threaten other species (including humans) and conservation of parasites that are at risk themselves. As such, our results provide a framework to consider spatial patterns of coendangerment and problematic diseases.

67.—FORECASTING DISTRIBUTION OF TWO ADVENTIVE ORCHID BEES IN THE UNITED STATES (HYMENOPTERA: APOIDEA)

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Orchid bees are remarkable due particularly to their metallic coloration and the chemical collecting behavior of the males, mainly from flowers of Orchidaceae. Restricted to the neotropical region, this group of bees reaches its northernmost distributional range in the mountains of northwestern Mexico. In recent years an isolated record of a male *Eulaema polychroma* (Mocsáry) from southern Arizona aroused the possibility of the presence of permanent populations of this species in the area, thereby pushing the extreme limits of the *Euglossini* northwards. In a separate case, *Euglossa viridissima* Friese has successfully established in southeastern Florida after a seemingly accidental introduction first noticed in the summer of 2003. By applying species distribution models we show the absence of suitable conditions in southern Arizona for *E. polychroma* to maintain populations there, as well as establishing the northernmost limit for the species at around 29°N in northwestern Mexico. *Euglossa viridissima* is predicted to spread to occupy roughly the southern half of the Florida peninsula. We discuss the naturalization of *E. viridissima* in Florida in the absence of perfume orchids and its implications for understanding the biology and biogeography of the *Euglossini*.

68.—THE BIOGEOGRAPHY OF INVASIONS: WHAT THE ENVIRONMENT OF THE NOVEL REGION AND THE PATTERN OF INVASION TELL US ABOUT RANGE LIMITATION

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Understanding how species range margins are determined is a fundamental biogeographical goal, but species range data often do not give reliable information on range limitations. For example, when species are introduced to novel regions, they often end up occupying a wider set of physical environmental conditions than in their native region. This suggests that in their native region, these species are restricted to a subset of the conditions in which they are truly able to persist. Therefore, we compare native and naturalised ranges for hundreds of plants, birds and mammals; to ask how often species are able to persist outside of their native environmental conditions. Furthermore, the circumstances under which species become established outside their native environmental conditions have important implications for native range determinants. If native ranges are determined by physical environmental tolerances, the degree of difficulty of invading new environmental conditions should be high, as a species must adapt to the novel conditions. Thus, the degree of assistance a species requires to become established should be greater under novel environmental conditions than under conditions that match the native range. If this is not the case, then species native ranges may be limited by a factor that is not present in their naturalised region, such as a biotic interaction or geographical feature. Therefore, we ask whether the establishment of invasive species outside their native environmental conditions is largely due to natural dispersal or to facilitation by human association (e.g., as an agricultural crop, seed contaminant or livestock).

69.—INTER-HEMISPHERIC PHYLOGEOGRAPHY OF “WEEDY” SKIPPER BUTTERFLIES

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Human activities have had many impacts on species distributions. We studied phylogeographic variation of two Pan-American butterfly species, *Hylephila phyleus* and *Lerodea eufala*, which are largely restricted to human-modified habitats. Both genera are basically Neotropical; *Hylephila* is entirely South American except for *H. phyleus*. Across their ranges, both species routinely feed on Bermuda Grass, a naturalized Palearctic plant, in mowed lawns. These “weedy” associations have led some to suggest that these species are actually recent introductions into temperate North America. To test this hypothesis, we sampled populations spanning the global distribution from the United States to Argentina and sequenced a homologous region of mitochondrial DNA. Intraspecific divergence was low, and the most abundant haplotypes are shared across continents in each species. AMOVAs indicate that within-population variation explains much more of the overall variation (60-66%) than the variation across continents (20-25%). Interpopulation variation within continents is very low (about 5%). Nonetheless, both North and South America have several unique haplotypes that are not shared across continents (mostly one mutational change removed from the shared haplotypes), which suggests that North American populations of *H. phyleus* and *L. eufala* are not the exclusive result of human introductions and have evolutionary histories independent from South America. These patterns are compared with other Pan-American butterflies that are not tightly associated with humans.

70.—DISTRIBUTIONAL RECORDS OF THE ADVENTIVE GIANT RESIN BEE, *MEGACHILE SCULPTURALIS*, IN THE UNITED STATES AND ITS PREDICTED POTENTIAL DISTRIBUTION (HYMENOPTERA: MEGACHILIDAE)

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The giant resin bee, *Megachile sculpturalis* Smith (Megachilidae: Megachilinae), a species originally native to eastern Asia, was first discovered as an adventive species in North America in 1994. An ecological niche model produced in 2005 predicted *M. sculpturalis*, then confined to the eastern United States, to potentially inhabit the entire eastern half of the United States, eventually spreading as far south as southern Florida, as far north as southern Ontario and Nova Scotia, and as far west as South Dakota, western Kansas, and northwestern Texas. Earlier observational predictions based on the bee’s native range projected a similar range although seemingly more restrictive than the ecological niche model prediction. This conspicuous bee species has steadily spread since its presumably accidental introduction, reaching as far north as Massachusetts and southern Ontario, and (as recent as June of 2008) as far west as eastern Kansas. The current distributional records of the bee support the predicted potential distribution produced via ecological niche modeling. Despite the absence of systematic monitoring of the expansion of this species, its spreading pace seems remarkable.

71.—SPATIAL NONSTATIONARITY AND SCALE-DEPENDENT EFFECTS OF DISTURBANCE AND TOPOGRAPHY ON INVASIVE BRACKEN FERN IN SOUTHERN YUCATÁN

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The presence of invasive bracken fern (*Pteridium aquilinum*) in the southern region of the Yucatán Peninsula has become an increasingly important problem over the last 20 years. Established populations of bracken fern are difficult and costly to remove, and the impacts of bracken invasion include decreased biodiversity and encumbrance of natural forest succession. The present research aims to further comprehend the relationship between the presence of bracken and environmental determinants such as topography (elevation and slope) and disturbance (distance to road and fire history). It is likely that one or all of these variables are scale dependent and an accurate understanding of this scale-dependence is crucial for conservation efforts. Spatial nonstationarity is another important factor related to the scale that alters the biological effect of an environmental determinant and is problematic for global regression models. Therefore, we have used a geographically weighted regression model to investigate the scale and spatial nonstationarity of the relationship between topography and disturbance and bracken presence. Also, this analysis allows us to vary the scale parameter of the model and observe the effect of variation of spatial scale on the bracken-determinant relationship. Through this sort of analysis we are able to accurately increase our descriptive and predictive power in modeling future Bracken spread.

72.—WHAT MAKES INVASIONS SUCCESSFUL? A COMPARATIVE DISTRIBUTION MODELING ANALYSIS BETWEEN TWO AFRICAN CARNIVORANS INTRODUCED TO SOUTH-WESTERN EUROPE

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Species distribution modeling has become a major tool in predicting ranges of invasive species. Here we examine the case of two African small carnivorans (Mammalia), *Genetta genetta* and *Herpestes ichneumon*, with long-time established populations in southwestern Europe. On the basis of taxonomic and phylogeographic investigations, we partitioned their native ranges into 5-6 sub-regions. We used GARP and Maxent algorithms to model distributions using 662 (*G. genetta*) and 522 records (*H. ichneumon*). Our main objectives were: 1) generate models at the regional level to compare niche characteristics (marginality and specialization) among species partitions; 2) generate invasive predictions, comparing models from region-based partitions and entire range datasets; and 3) project models onto future European climate scenarios. The highest marginality values were obtained for European and western African regions for *G. genetta* and *H. ichneumon*, respectively, whereas the situation was reversed for specialization. Invasive predictions trained on African and European presences had the lowest omission rates. Range expansions were predicted eastward in Europe for *G. genetta* into Germany and Italy, whereas projections of *H. ichneumon* models showed much lower expansion. Our results highlighted the importance of model variations among species geographic partitions and suggested that an ‘ecological shift’ drove the successful (more widespread) invasion of *Genetta genetta* in Europe.

73.—MODELING THE RANGE EXPANSION OF *CACTOBLASTIS CACTORUM* INTO NORTH AMERICA: KEY SITES FOR MONITORING THE SPREAD OF THE SPECIES

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Cactoblastis cactorum Berg (Lepidoptera) was introduced into Australia as a biological control for the cactus *Opuntia* spp. during the 1920's. After the success that *C. cactorum* had in Australia, it was introduced into South Africa and Hawai'i to control non-native *Opuntia* populations. However, in these locations it has reduced the populations of not only *Opuntia* but other species in the family Opuntioideae (*Nopalea*, *Cylindropuntia* and *Consolea*) as well, placing several species in danger. *Cactoblastis cactorum* has expanded its geographical range in the Antilles and was first documented in continental North America in 1989. This raised concerns about the possible biological and economical impacts of colonization in mainland USA and, more importantly, in Mexico, where at least half of the *Opuntia* species are endemic. An effort to predict the possible invasion of *C. cactorum* into Mexico was made in 2001, with the overall goal of implementing sound regulatory mechanisms to prevent the spread of *C. cactorum* in the country. Nonetheless, *C. cactorum* was recorded in 2006 on the offshore islands of southeastern Mexico and was fortunately eradicated in 2008. Here, we modeled the potential distribution of *C. cactorum* in continental North America (USA, Mexico), correlating the known historical geographic spread of the species and 19 climatic variables using MaxEnt. We present a framework aimed at identifying the risk areas for *Opuntia* spp. as well as key sites for establishing sound monitoring plans in order to control the spread of *C. cactorum* in the USA.

74.—PHYLOGEOGRAPHY, EVOLUTION AND CRYPTIC DIVERSITY OF PINE-FEEDING *CHIONASPIS* (HEMIPTERA: DIASPIDIDAE) ACROSS NORTH AMERICA

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Currently there are thought to be two species of pine feeding armored scale insects in the genus *Chionaspis*, *C. pinifoliae* and *C. heterophyllae*. Both are pests native to North America, but the extent of their geographic distribution and host associations are unknown. We have collected *Chionaspis* scale insects from nearly every species of pine, throughout the range of *Pinus* in the Western Hemisphere. We have sequenced 2,400bp of DNA for over 400 individuals including one mitochondrial and two nuclear gene regions (CO1-CO2, Efl-a, 28s). Phylogenetic analyses reveals high levels of haplotype diversity, especially in Mexico and the Western USA. Gene genealogies are to some extent congruent across loci, and in some cases correspond to diagnosable morphological variation, implying the presence of cryptic species. Both geography and host association (*Pinus* spp.) contribute to observed patterns of genetic variation. There is one apparent case of closely related sympatric cryptic species feeding on different hosts: *Chionaspis* feeding on *Pinus strobus* differs at all three loci from sympatric *Chionaspis* feeding on other species of pine.

75.—EXPLORATION OF THE VARIATION AND RELATIONSHIPS IN POPULATIONS OF TWO DIFFERENT GROUPS OF *ALEXANDRIUM* FROM DISTINCT LOCATIONS

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The biogeography and population genetics of dinoflagellates of the genus *Alexandrium* are important in the understanding of blooms of this harmful alga worldwide. The “harm” associated with these algal blooms is due to toxins that are produced by these dinoflagellates. These toxins affect multiple trophic levels in the ocean, as well as the fisheries and recreation industries in affected regions (Turner *et al.* 2000). The economic losses and potential human health concerns associated with these blooms have led to much research into possible reasons for the increases in blooms and biogeographic ranges of these algae. Previous work has used ribosomal RNA genes to create phylogeographic reconstructions, and has documented cases of human introduction (Lilly *et al.* 2002, Lilly *et al.* 2007). However, the rRNA gene data have not yielded sufficient variation to track the spread of closely related species. Therefore, we have collected data for two important groups of *Alexandrium* using additional mitochondrial, chloroplast, and nuclear markers, including genes for cytochrome oxidase (cox1), cytochrome-b (cob), the D1 protein of PSII (psbA), and the large subunit of RubisCO (rbcL). Detailed information can be drawn on the relationships of *Alexandrium* populations from different locations through the use of the combined data set. This may lead to insights in natural and human assisted dispersal of this harmful alga, aiding in the future avoidance of such introductions.

76.—BIOGEOGRAPHY IN THE HUMAN MOUTH

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Periodontal disease is one of the most common infectious diseases among humans, yet there is no one organism so far found responsible for this condition, indicating that this and other oral diseases may be the result of interactions at the community level, rather than infection by individual species of bacteria. We have begun to use the tools of biogeography to explore the spatial distribution of bacterial communities in the healthy human mouth, both to understand the contrasts between oral health and disease, and to inform the goals of clinical treatment. Previous studies have typically pooled samples from diverse sites within a mouth or between people to describe the oral microbiota. As the human mouth presents a diversity of habitats at the bacterial level, we hypothesized that the community structure of the bacteria may be distributed according to the physical structure of the mouth. We have sampled two healthy humans as 23 subgingival sites, comparing the bacterial communities as described by 16S DNA sequences. Based on this survey, subgingival samples are distinct from one another, though the distinctions do not appear to be explored by a simple physical pattern (left vs. right, top vs. bottom, molar vs. incisor). Use of checkerboard scores to analyze the distribution in each mouth indicates that the communities are consistently exhibiting co-occurrence patterns indicative of segregation. Analysis is continuing to determine the causes of these differences, and consequences for human health.

77.—POSITIVE CORRELATIONS BETWEEN NATIVE AND EXOTIC DIVERSITY DECREASE OVER TIME IN COASTAL PLANT COMMUNITIES

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Recent research in invasion biology suggests that species invasions can increase diversity at local and regional scales. Here, I show evidence that this increase may be temporary and that time-lags may play an important role in determining community composition. Using coastal plant communities of the Narragansett Bay Estuary in New England, I looked at changes in native and exotic richness over a ten-year time period. In 1998 exotic and native species richness was positively correlated. Over time however, this pattern has changed and exotic species have increased in diversity, while natives have declined. Interestingly, replacement of natives by exotics tends to be highest at sites with high levels of diversity, which could indicate that ecological saturation may play a role in these communities. These findings suggest that incorporation of a temporal component may be essential in evaluating the impact of species invasions.

78.—SPREAD OF SUDDEN OAK DEATH: APPLICATION OF STOCHASTIC EPIDEMIC MODELING TO REALISTIC LANDSCAPES

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As the number of emerging infectious diseases continues to rise, spatial prediction of disease outbreaks is critical for effective management and prevention of epidemics, especially in complex spatially heterogeneous landscapes. Epidemiological models of Susceptible-Infectious (SI) transitions increasingly incorporate effects of spatial heterogeneity, but are rarely applied to realistic landscapes, limiting our ability to examine the geography of disease dynamics. We present a stochastic epidemic model, applied to temporally and spatially heterogeneous landscape data, to predict the spread of the emerging forest disease sudden oak death across California. We describe how field and lab data were used to parameterize key system variables affecting disease, including weather variability, host density and infectiousness, and a Markov Chain Monte Carlo estimated dispersal kernel. Implemented on a 250m grid at a weekly time step (1990-2030), three spatially-explicit epidemiological processes are considered in the geographical model: production of inoculum, dispersal of inoculum, and infection. Model predictions have a high degree of correspondence with field observations, illustrate the integral role that landscape heterogeneity plays in disease spread, and identify numerous forest ecosystems at high risk of infection. The nature of prediction errors are examined by ecoregion, plant community, and climate, and we discuss how application of epidemiological models to realistic geographies fosters understanding of spatial processes and designing management strategies to control disease spread.

79.—MULTIPLE RESTORATION EFFORTS IN DRY AND MESIC UNDERSTORY COMMUNITIES

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Biological invasion is of serious concern to land managers worldwide. Restoration to control non-native species depends on the plant community. Management decisions become complicated when anthropogenic activities interrupt successional processes. For instance in oak savanna, fire is commonly used to restore understory composition and manage non-native species, otherwise light partitioning can impact species richness and promote invasion. In one Midwestern savanna, fire suppression resulted in increased shade, lower species richness, and many shade-tolerant invaders. In this situation, a combination of fire and mechanical removal is required. However, mechanical removal alone could be successful depending on the level of understory diversity in mesic communities, where fire is not important. In a highly diverse mesic deciduous forest, only one non-native invader has threatened species composition whereas nearby degraded remnants were dominated by non-native species. After three years of only mechanical removal in the highly diverse site, very few first-year non-native plants persisted and species composition was responding favorably. This study suggests that management decisions for restoration should be driven by the plant community, dominant disturbance type, and level of diversity in the understory. This research can be extended to other oak savannas and mesic forests at risk of invasion.

Symposium III

**Biogeographic Disjunctions
between Asia and the Americas**

BIOGEOGRAPHIC DISJUNCTIONS BETWEEN ASIA AND THE AMERICAS – AN OVERVIEW

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The biogeographic disjunctions between Asia and the New World have attracted many recent studies, especially concerning phylogenetic relationships of disjunct lineages and the timing of major biogeographic patterns. In this talk, I review the recent advances on the disjunctions between Asia and the Americas, focusing on four disjunctions: 1) between temperate Asia and North America; 2) between the neotropics and tropical Asia; 3) between temperate South America and Asia; and 4) between Eurasian and western North American deserts with the Mediterranean climate (the Madrean-Tethyan disjunctions). Studies so far have revealed important patterns on the timing of the disjunctions and the diversification processes in various lineages. The diversification across temperate and tropical zones appears highly complex. The rates of morphological diversification are not always correlated with molecular rates. Integration of evidence from phylogeny, ecology, physiology and fossils is needed to better understand the patterns and processes of diversification in various lineages through time and space. With the much better understanding on the complexity and dynamics of temperate disjunct groups, it is important to work with colleagues in Mexico, neotropical regions and Asian tropics on tropical disjunct lineages. We also need to analyze the Asian-American disjunctions in the global biogeographic context.

MODELS AND METHODS FOR INFERRING THE HISTORY OF BIOGEOGRAPHIC DISJUNCTIONS

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Disjunct lineages highlight the role of historical biogeographic connections in the assembly and evolution of continental biotas. Methods for inferring the phylogenetic history of disjunctions have traditionally emphasized vicariance, with limited support for alternative modes of range inheritance. They have also emphasized parsimony, to the exclusion of prior knowledge/assumptions about geological history, the spatial configuration of areas, paleoclimate, and other factors relevant to opportunities for lineage movement through time. Recently, new methods based on parametric models of range evolution have begun to address these issues, allowing for more flexible hypothesis testing and a more balanced view of phylogenetic vs other lines of evidence. An intriguing challenge for future work is the development of models that incorporate statistical parameters for range-dependent lineage diversification, similar to those recently developed for reconstructing character evolution.

RECONSTRUCTING DEMOGRAPHIC CHANGE THROUGH SPACE AND TIME

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Recent advances in ancient DNA extraction and Bayesian statistical analysis techniques have made it possible to reconstruct complex demographic dynamics of large mammal populations across long evolutionary time periods. We have shown, for example, that Beringian populations of bison, horses and mammoths experienced very different demographic histories over the most recent 100,000 years, with each taxon responding differently to the environmental stresses associated with human use of the region and the most recent glacial maximum. However, until recently, these methods have ignored spatial structure: a key confounding factor in any coalescent-based population genetic analysis. Here, I present new phylogenetic/demographic models that explicitly incorporate space as well as time in demographic reconstructions. Focusing on the use of the Beringian landscape, I discuss how dispersal patterns and habitat use in several Beringian taxa vary both across space and over time, and correlate these differences with environmental changes during the Late Pleistocene/early Holocene.

EVOLUTION OF BIOGEOGRAPHIC DISJUNCTION IN CONIFERS

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The center of diversity is not necessarily the place of origin, which is particularly true for conifers. The species diversity of many coniferous genera, such as *Picea* and *Pseudotsuga*, is higher in East Asia than in North America. Most of the genera, however, might have originated in North America rather than East Asia, according to the DNA-based phylogenies and fossil evidence. In addition, the circumscription of some conifer genera such as *Chamaecyparis* and *Cupressus* has recently been modified, providing new insights into the biogeographic history of these groups. Although it is well known that the conifers have a long evolutionary history, many species such as spruces from northeastern Asia are young and could have arisen from recent radiations given the very low interspecific genetic differentiation. Moreover, in plants, most previous studies on the eastern Asia-North America disjunction are based on uniparentally inherited cpDNA and (or) directly sequenced nrDNA ITS data, and thus the historical reticulate evolution in the studied groups might have been underestimated. This could be partially responsible for the difficulty in elucidating the relationship between eastern Asia, and eastern and western Northern America. Therefore, we suggest that multiple genes from different genomes, especially low-copy nuclear genes, be used in this research area in the future.

SPATIAL STRUCTURE OF THE ENVIRONMENT OF EASTERN ASIA – NORTH AMERICA DISJUNCT FLORA

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Disjunct Eastern Asia – North America plant genera in a distinct Eastern North America (ENA) assemblage have fewer species than those in Eastern Asia (EA) and Western North America (WNA) assemblages. Higher physiographic heterogeneity, temperature, or larger area may have resulted in higher net diversification rates in EA and WNA than in ENA. We examined assumptions about regional differences in current environment implicit in these three hypotheses. The latitudinal gradient of 19 temperature and precipitation variables was shallower in ENA than in EA, but similar between ENA and WNA, while the respective longitudinal gradient was similar across regions. After subtracting these gradients, spatial eigenvectors revealed much less climatic spatial structure across ENA than across EA and WNA, particularly at broad spatial scales. The mean of annual mean temperature was lower in ENA (9.3°C) than in EA (9.7°C) and WNA (9.9°C), while the rank of annual mean temperatures was lower across ENA than across WNA but similar between ENA and EA. The area occupied by the ENA assemblage (5,601,017 km²) was smaller than that occupied by the EA (10,835,652 km²) and WNA (8,010,358 km²) assemblages. The results were consistent with assumptions implicit in the three hypotheses, but regional differences in temperature seemed small relative to those in physiographic heterogeneity and area.

USE OF FOSSILS IN BIOGEOGRAPHIC ANALYSIS - CHALLENGES AND POSSIBLE SOLUTIONS

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Inferring the biogeographic history (e.g., origin, persistence, dispersal, and extinction) of lineages is fundamental to understanding the origin and evolution of the modern distribution of biodiversity. It is widely recognized that fossil taxa provide important information, but the practice of using them in biogeographic analysis has been rare due to many potential problems. The major challenges are assessing the phylogenetic affinity of fossil taxa and accounting for phylogenetic uncertainty of fossils. A few approaches have been proposed, and some have been implemented in case studies. Here, we explore the utility of these methods using three genera, *Cornus*, *Alangium*, and *Aesculus*, all of which have good fossil records. To assess fossil affinities, we used phylogenetic analyses of all morphological characters, only those present in fossils, and all characters constrained by a molecular tree. We also used morphological synapomorphies of clades to place fossils onto molecular trees. Biogeographic analyses including the fossil taxa were conducted for these genera using the tree topology-based method DIVA, the newly developed chronogram-based likelihood method LAGRANGE, or both. The results were compared to analyses without fossil taxa to show the impact of fossils. To account for phylogenetic uncertainty, ancestral distributions were optimized for a sample of Bayesian trees. Our results showed a strong influence of fossils in biogeographic analyses, and critical interpretation of fossils and careful assessment of their impact on the analysis must be emphasized.

ECOLOGY AND TIMING OF ASIAN-NORTH AMERICAN DISJUNCTIONS

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Disjunct lineages of plants in eastern Asia and North America have provided an opportunity to study independent evolution and diversification of sister lineages under similar environmental conditions—a replicated experiment, so to speak. The broad range in the estimated timing of disjunction in different groups also allows us to ask whether the ecological filter imposed by the land connection between Asia and North America has left a signal in the present-day ecological distributions of species. In particular, cooling through the last half of the Tertiary may have imposed an ecological filter that resulted in higher cold tolerance of more recent disjunct taxa. We examine this working hypothesis by comparing the climate characterizing the contemporary distributions of disjunct genera in North America to the estimated timing, based on molecular phylogenetic analyses, of their separation from their Asian sister lineages.

1.—MOLECULAR PHYLOGENY AND HISTORICAL BIOGEOGRAPHY OF THE TRIBE PHYLLODOCEAE (ERICACEAE: ERICOIDEAE)

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Based on recent phylogenetic analyses of multiple nuclear and chloroplast markers, the angiosperm tribe Phyllodoceae (Ericaceae: Ericoideae) is comprised of six genera in three major clades. Clade 1 (*Elliottia*—4 spp.) is found in northwestern and southeastern North America and Eastern Asia. Clade 2 (*Kalmia*—10 spp.) is widespread in North America and includes one circumboreal species (*Kalmia* [= *Loiseleuria*] *procumbens*). Clade 3 is comprised of two smaller clades: Clade 3A is comprised of the sisters *Phyllodoce* (7 spp.) and *Kalmiopsis* (1-2 spp.), which together are roughly circumboreal, while Clade 3B is comprised of *Epigaea* (3 spp.) which are disjunctly distributed in North America, Eastern Asia and the Caucasus, and *Rhodothamnus* (2 spp.), which are found in the same areas except being absent in North America. Parsimony, likelihood and Bayesian phylogenetic analyses of six molecular markers all suggest that Clade 1 (*Elliottia*) is sister to Clade 2 (*Kalmia*) + Clade 3 (*Phyllodoce et al.*). As a consequence, a detailed examination of the historical biogeography of the group is possible. Here, results of recent phylogenetic analyses are presented, along with a comparison of traditional (e.g. Fitch optimization) and cladistics-based (e.g. DIVA, likelihood) methods. Particular emphasis is placed on the North American/Asian disjunction and the impact of circumboreal distributions on biogeographical analyses.

2.—THE PHYLOGENETICS AND HISTORICAL BIOGEOGRAPHY OF *LEIBNITZIA* CASS. (ASTERACEAE: MUTISIEAE): AMERICAN SPECIES IN AN ASIAN GENUS

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Evolutionary relationships among the seven genera of the *Gerbera*-complex remain largely untested due to their well-acknowledged need for taxonomic revision. Here we present a phylogenetic analysis of the *Gerbera*-complex that tests the monophyly of one constituent genus, *Leibnitzia* Cass. (6 spp.). Historically *Leibnitzia* comprised four species distributed from the Himalayan Plateau to eastern Asia. Two montane southwestern North America species, *Leibnitzia lyrata* (Sch.Bip.) Nesom and *L. occimadrensis* Nesom, were subsequently placed in *Leibnitzia* based on similarity of achene trichomes. The distribution of these two species overlaps with that of *Chaptalia* Vent., a morphologically similar New World genus of the *Gerbera*-complex. Nuclear and chloroplast DNA sequence data from accessions of *Leibnitzia*, *Chaptalia*, and other *Gerbera*-complex genera were analyzed in order to test the hypothesis that American *Leibnitzia* are more closely related to *Chaptalia* than to Asian *Leibnitzia*. Our findings confirm the monophyly of *Leibnitzia* and its remarkable biogeographic disjunction. Asian-American disjunctions are typically observed in temperate forest taxa distributed between eastern Asia and eastern North America, *Leibnitzia*, by contrast, occupies open, semi-arid temperate to sub-tropical montane habitat. To our knowledge, this disjunction is unique in the flowering plant family Asteraceae.

3.—*ALNUS* FOSSILS FROM THE LOWER EOCENE: IMPLICATIONS FOR THE EVOLUTIONARY HISTORY AND BIOGEOGRAPHY OF THE GENUS

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The genus *Alnus* (Betulaceae) is comprised of about 35 species of early successional, actinorhizal trees distributed widely across the Northern Hemisphere, generally in wet, nitrogen poor soils. *Alnus*-like pollen occurs as early as the Late Cretaceous, however the oldest unequivocal macrofossils are Eocene. The abundance of *Alnus* fossils during and after the Eocene probably results from their durable, woody, reproductive organs and their preferred growth in environments that typically accumulate sediment. *Alnus* provides an excellent system for addressing evolutionary questions because of the relatively small number of species and the abundant fossil record. Compressed *Alnus* leaves and aments recovered from the Lower Eocene Willwood Fm. of the Bighorn Basin, Wyoming are the oldest macrofossil evidence of *Alnus* in North America. Arrangement of the pistillate catkins, the absence of subtending leaves, and general leaf shape suggests these fossils represent the most derived of the three subgenera (subgenus *Alnus*). The abrupt appearance of the most derived subgenus suggests the more basal clades evolved elsewhere, perhaps in Asia, and arrived in North America via high latitude land bridges open during the globally warm early Cenozoic. Previous work on the genus suggests that phylogenetic trees based on morphological characters (Furlow 1979) correspond closely with those based on nrDNA ITS sequences (Navarro et al. 2003; Chen and Li 2004). Consequently, a thorough study of morphological characters in living and fossil members of the genus should yield a much clearer picture of the evolution and biogeography of *Alnus*.

4.—BIOGEOGRAPHIC DISJUNCTION BETWEEN EASTERN ASIA AND NORTH AMERICA IN THE MAIDENHAIR FERN *ADIANTUM PEDATUM* COMPLEX

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The *Adiantum pedatum* complex (Pteridiaceae) consists of four species disjunctly distributed in western North America (*Adiantum aleuticum*), eastern North America (*Adiantum pedatum* and *A. aleuticum*), eastern Asia (*A. pedatum* and *A. myriosorum*) and a hybrid *A. viridimontanum* between *A. pedatum* and *A. aleuticum*. Phylogenetic analyses with the chloroplast *rbcL*, *trnL-F* and *rps4-trnS* sequences strongly support the monophyly of the complex. The eastern Asian *Adiantum pedatum* does not form a clade with the eastern North American *A. pedatum*, instead it is sister to *A. aleuticum*. The Asian *Adiantum myriosorum* is sister to the *A. pedatum*-*A. aleuticum* clade. The divergence of the *A. pedatum* complex from its close relatives in *Adiantum* was estimated to be at least 4.09 (1.24-7.69) million years ago (mya). The divergence between the Asian *Adiantum pedatum* and *A. aleuticum* was 0.77 (0.12-1.62) mya, and that between the eastern Asian *Adiantum pedatum* and the North American *A. pedatum*-*A. aleuticum* clade was 1.44 (0.35-2.80) mya, using the Bayesian dating method based on *rbcL* sequences with fossil calibration. The dispersal-vicariance (DIVA) analysis suggests an eastern Asian origin of the complex and its migration into eastern North America via the Bering land bridge, with subsequent migration into western North America.

5.—INCOMPLETE DATA SETS: ASSESSMENT OF GEOGRAPHICAL SAMPLING BIAS ON THE FOSSIL RECORD OF ORDOVICIAN EDRIOASTEROIDS

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Edrioasteroids (Echinodermata) have a fossil record spanning over 300 million years, from the Early Cambrian through the Late Permian. Plotting known Ordovician edrioasteroid localities reveals an anomalous geographic distribution. This may result from either the ease with which post-mortem disarticulation occurs, thereby necessitating rapid burial for the preservation of articulated specimens, or sampling bias. Edrioasterids appear to be endemic to the Laurentian continent with recorded distribution in modern day Utah, Michigan, Kentucky, New York, Oklahoma, and Ontario.

Isorophids, on the other hand, appear to have a more cosmopolitan geographic distribution including Utah, eastern North America, peri-Gondwanan Europe, and Morocco. Enigmatic cyathocystids are known from Laurentia and Baltica. Stalked rhenopyrgids first appear in Avalonia and Baltica and later become cosmopolitan.

Although Cambrian and Silurian/Devonian edrioasteroids are found in Australia and other undescribed Cambrian and Silurian edrioasteroids are found in China and South America, no Ordovician taxa have come forward from these areas. The paucity of Ordovician edrioasteroid specimens may truly reflect their rarity, with populations sparsely but broadly distributed. However, we propose that Ordovician edrioasteroids are likely located in these locations, but that a historical lack of paleontological field research resulting from inaccessibility coupled with sampling bias may be contributing to our limited understanding of their global dispersal patterns.

6.—BIOGEOGRAPHY OF THE COLD AND COLD-TEMPERATE ASCIDIAN FAUNA IN THE SOUTHERN HEMISPHERE

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Traditional biogeography is important in organisms for which phylogenetic studies are still scarce such as ascidians. The biogeography of the ascidian fauna of the cold and cold-temperate regions of the Southern Hemisphere is described and compared to the biogeography of other fauna in the same regions. Species and biogeographical areas were classified using cluster analysis combined with MDS ordination. The results indicate an association between Tasmanian and Southern African regions, while Southern New Zealand was more related to colder regions (South America, sub-Antarctic and Antarctic). Endemism was high in all the considered regions, but a high percentage of cosmopolitan and widespread Southern Hemisphere species were also identified. Species in the widespread fauna were re-classified using existing invasion criteria (Chapman and Carlton, modified to suit ascidian characteristics) to determine if these species are native, cryptogenic or introduced.

7.—PHYLOGENY AND BIOGEOGRAPHY OF *DENDROPANAX* (ARALIACEAE), A GENUS DISJUNCT BETWEEN TROPICAL ASIA AND THE NEOTROPICS

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Dendropanax (Araliaceae) is a genus of about 70 species disjunctly distributed in Asian tropics/subtropics and the Neotropics. To better understand the tropical disjunctions between Asia and the Americas, we constructed the *Dendropanax* phylogeny using sequences of the nuclear ribosomal ITS and six chloroplast regions (*ndhF*, *trnL-F*, *atpB-rbcL*, *rps16*, *rpl16*, and *psbA-trnH*). Both cpDNA and the combined cpDNA and ITS data support the monophyly of the core *Dendropanax* except that *D. lancifolius* and *D. hainanensis* from tropical Asia group with other genera. The New World and the Old World *Dendropanax* each forms a robustly supported clade, and they are sister to each other. Fossils of *Dendropanax* date back to the middle Eocene. The trans-Pacific intercontinental divergence of *Dendropanax* was estimated to be 30.05 million years ago (mya) (95% HPD: 21.71-38.73 mya) using fossil-calibrated Bayesian method with the combined data. Within the phylogenetic framework of Araliaceae, *Dendropanax* was inferred to have originated from continental tropical Asia and migrated into the New World via the North Atlantic land bridge. Our analysis suggests two evolutionary radiations of *Dendropanax*, once in the New World at 18.06 mya (95% HPD: 11.81-25.41 mya) and another in the Old World at 16.54 mya (95% HPD: 10.04-24.27 mya).

8.—PHYLOGENETIC AND BIOGEOGRAPHIC COMPLEXITY OF MAGNOLIACEAE IN THE NORTHERN HEMISPHERE INFERRED FROM THREE NUCLEAR DATA SETS

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Based on morphological, molecular, and fossil evidence, Magnoliaceae has been considered to be one of the earliest extant lineages of flowering plants and has played a crucial role toward our understanding of the origin and diversification of angiosperms. The limited divergence of chloroplast sequences has made it difficult to resolve the evolutionary relationships within the family. This study employs three nuclear genes (*PHYA*, *LFY*, and *GAI1*) to reconstruct the phylogenetic and biogeographic history of Magnoliaceae. A total of 104 samples representing 86 taxa from all sections and most subsections were sequenced. Twelve major groups are well supported to be monophyletic within Magnoliaceae and these groups are largely consistent with previous chloroplast results and the recent taxonomic revision at the sectional and subsectional levels. Evolution of intercontinental disjunctions of the family involving both temperate and tropical lineages appears to be complex. The two well-recognized temperate lineages disjunct between eastern Asia and eastern North America occurred after the middle Miocene. The other disjunctions in the family are tropical and warm temperate elements and their intercontinental splits were more ancient, dated no later than the Oligocene.

9.—PHYLOGENY AND BIOGEOGRAPHIC HISTORY OF THE WILD-RICE GENUS (*ZIZANIA*, POACEAE), AN AQUATIC DISJUNCT MODEL BETWEEN EASTERN ASIA AND NORTH AMERICA

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The wild-rice genus *Zizania* includes four species with an intercontinental disjunction between eastern Asia and North America. *Zizania* is one of the few aquatic genera disjunctly distributed between the two continents. We employed the chloroplast *matK*, *atpB-rbcL*, *trnL-F*, *trnH-psbA*, and *rps16* and the mitochondrial *nad1* regions to infer the phylogeny and its biogeographic history. Results indicate that: 1) *Zizania* is monophyletic with two distinct clades corresponding to eastern Asia and North America; 2) among the three North American species, populations of the widely distributed *Z. palustris* and *Z. aquatica* group into separate clades, while the population of the endangered species *Z. texana* comprises a single genotype and falls into the clade of *Z. palustris*; and 3) the divergence time between the intercontinental species was estimated to be 3.94 (1.54 ~ 6.98) million years ago using the Bayesian method with the combined *matK*, *trnL* and *nad1* data. The recent divergence of *Zizania* correlates with that in other aquatic disjunct taxa including *Acorus* and *Nelumbo*. Our results favor a North American origin of *Zizania* and its migration into eastern Asian via the Bering land bridge.

10.—INTER- AND INTRACONTINENTAL DISJUNCTIONS IN THE HOLARCTIC: AN EXAMPLE OF TRIBE OENANTHEAE (MAGNOLIOPHYTA, APIACEAE)

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Tribe Oenanthae is one of the most extensively studied major clades of angiosperm family of umbellifers (Magnoliophyta, Apiaceae). The morphological adaptations to water and marsh habitats, inter- and intracontinental disjunctions of its member genera, and comprehensive sampling with respect to molecular phylogenetic markers make the tribe an excellent model for testing biogeographic and evolutionary hypotheses on umbellifer diversification. Using cpDNA and nrDNA ITS based phylogeny of the tribe and outgroups with nodes dated based on fossil data, we infer its biogeographic history, estimate the number of dispersals between Eurasia and North America, and identify its disjunction patterns in the Holarctic.

11.—BIOGEOGRAPHY AND SYSTEMATICS OF ASIAN TREE-VIOLETS (*RINOREA*, VIOLACEAE): DISJUNCT AND NARROWLY ENDEMIC SPECIES DISTRIBUTION IN THE MALAY ARCHIPELAGO

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Recent taxonomic revision and ongoing phylogenetic investigation of Asian *Rinorea* reveal disjunct and narrowly endemic species ranges in the Malay Archipelago. Our study provides intriguing geographic distribution patterns reflective of greater species richness and spatial complexity than previously understood. Examination of herbarium specimens (BO, WAN, L, K, BM, and MO) delineates 9 geographically coherent species groups and reveals that several broadly circumscribed, polymorphic species characterized by Jacobs and Moore (1971), e.g., *R. bengalensis* and *R. javanica*, are complexes of multiple narrowly delineated species. Many divergent vegetative and reproductive traits distinguish the 29 distinct taxa, in comparison to 11 taxa broadly defined by earlier taxonomists. Geographically separated taxa with many shared features are retained at the subspecies level. Preliminary molecular phylogenetic studies of the trnL-F chloroplast spacer show Asian *Rinorea* to be a monophyletic (natural) group nested among Neotropical and African taxa. Approximately 65% of Asian taxa, derived from eight of nine groups, are present in Borneo. Initial spatial analysis of georeferenced specimens delimits narrowly endemic species most evident in *Macrantha* and *Iliaspaiei* complexes. The *Longeracemosa* and *Javanica* complexes best exemplify disjunct distributions of taxa. Collectively, group-level evolutionary trends suggest multiple, parallel, geospatially intricate modes of dispersal for Asian *Rinorea*.

12.—NON-STATIONARITY IN THE RELATIONSHIP WITH CLIMATIC STABILITY REVEALS STRONG ICE AGE LEGACY ON DUNG BEETLE DIVERSITY GRADIENTS

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Most analyses of biodiversity patterns assume that the relationship between species richness and environmental predictors is spatially stationary. We assessed the relationship between Scarabaeidae dung beetle species richness in Europe, contemporary environment and climate stability since the last glacial maximum. To do this, we use Geographically Weighted Regression (GWR) to assess stationarity, identifying the areas where each predictor has a consistent effect on richness. A regression function of current environment showed a high coefficient of determination. However, GWR revealed that the relationships between richness and all environmental predictors (except AET) were non-stationary, and therefore do not have a consistent relationship with richness throughout all Europe. Temperature stability was less explanatory, but showed a stationary relationship in all the area that was glaciated in the past. However, there the slope of richness/temperature stability relationship was indistinguishable from zero, showing that other factors are shaping richness patterns in that area. Thus, although the current richness gradient is a by-product of glacial ages, northern assemblages also are affected by post-glacial dispersal and species responses to current climate.

13.—A METHOD FOR DETECTING CHARACTER DISPLACEMENT WHEN SIZE CLINES ARE PRESENT

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When species diverge more in sympatry than they do in allopatry, character displacement is thought to be operating. However, the presence of geographic clines in the trait selected is thought to act upon may either (1) prevent us from detecting character displacement, or (2) make us infer character displacement is operating when, in fact, it is not. While the detection of displacement when clines are present is increasingly recognized as important, methods used so far are usually complicated, rely on unrealistic assumptions, or lack power. Here I present a simple method based on multiple regression to detect character displacement in the presence of geographic clines. I use this method to test for character displacement in the three smallest members of the Holarctic weasel (*Mustela*) guilds. Treating males and females as different morphospecies, and examining two morphological traits (skull length and canine diameter), I demonstrate the relative strengths and some possible weaknesses of this technique. The method seems powerful and readily detects character displacement when the number of species in a guild and clines incorporated are low. With larger guilds and multiple clines, sample sizes become small. Some rescaling of relevant variables is needed in order to compare sizes in allopatry and sympatry.

14.—ISOLATION BY DISTANCE IS DEAD, LONG LIVE IBD

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Isolation by Distance (IBD) is rapidly being dethroned by landscape genetics as a method to understand population genetic structure. To test its persistent value as a reference for landscape genetics, we evaluated the published IBD knowledge base by asking: 1) How have existing analyses varied in method and study scale? 2) After standardization, what patterns emerge? and 3) How have analytical differences among studies affected IBD results? We collected and analyzed >450 articles from peer-reviewed journals. IBD was often expressed as pairwise F_{st} or $F_{st}/(1-F_{st})$ per km, although diverse statistics exist. Most studies measured genetic variation using microsatellite loci, used model I regressions (assumes precise geographic distance), and reported R^2 and significance for regressions, but omitted slope (the measure of effect). Our standardized analyses using Mantel tests of $F_{st}/(1-F_{st}) : \ln(\text{distance})$ and model II regression (assumes uncertain geographic distance) found that: A) standardized results can differ from those published; B) study scale (geographic range and number of populations) differed among taxa; and C) IBD significance was related to number of populations studied. Thus, phylogenetic differences in frequency of significant IBD and IBD slopes may be due to phylogeny and/or study bias. We recommend standardizing analyses and accounting for study scale when calculating IBD, so it can better serve as a reference for landscape genetics and for macroecological tests of population genetic structure.

15.—BIOLOGICAL CORRELATES OF RANGE DISTRIBUTION AREA IN IBERIAN BUTTERFLIES (LEPIDOPTERA) - A PRELIMINARY APPROACH

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This study was aimed at identifying potential relationships between the size of the geographic ranges and broad life-history parameters in SW-European butterflies. The data used were from diurnal butterflies (Lepidoptera, superfamilies Papilionoidea and Hesperioidea) of the Iberian Peninsula (the continental territories of Spain and Portugal in South-West Europe). Range size was measured as the number of 10-km squares occupied. The available life-history data were coded for the most *a priori* relevant potential information, including variables that represent larval polyphagy, the adult and immature phenology, size, ability for dispersal, potential fecundity, and abundance. The available information for several of the required fields remains limited. Within these limits, however, the results strongly suggested that the area of occupation within this region is primarily related to traits linked to phenology, e.g., the number of broods per year. Re-analysis of the data within a phylogenetic framework may be necessary, for taxonomic effects are evident at the family level at least.

16.—DO PENINSULAR EFFECTS OCCUR IN PENINSULAS? IBERIAN BUTTERFLIES

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Previous authors have argued that the Iberian Peninsula (SW-Europe) provides a test case for the pattern termed the 'peninsular effect' (a decline in species richness with increasing distance to the continental mainland); this is due to the geometry of the Iberian land mass, and to the north-eastern location of the isthmus. Positive evidence for this pattern was formerly provided using distribution data from Iberian butterflies, although such studies relied on data gathered from 'expert-drawn' distribution maps, and spatial effects other than the distance to the isthmus were not thoroughly assessed. In this study we analyse the presence/absence data matrix of Iberian butterflies, covering ca. 230 species, at a grid size of 50 x 50 km. Further, we incorporate information on estimated sampling effort, relevant physiographic variables, and nonlinear spatial effects. The results suggest that some physiographic variables, particularly altitude, are primarily correlated to species richness, and that controlling for sampling effort may importantly modify the results. A 'diagonal' (peninsular) effect cannot be completely ruled out, however.

17.—BERGMANN’S RULE IN PLETHODON SALAMANDERS OF EASTERN NORTH AMERICA AT THE ASSEMBLAGE LEVEL: INSIGHTS FROM A PHYLOGENETICALLY INFORMED BIOGEOGRAPHIC APPROACH

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Bergmann’s Rule, a trend of increasing body size towards colder regions, has long attracted the attention of biogeographers. Specially, there is a lively debate on the applicability of this ecogeographical “rule” to ectotherms. Here, we use an assemblage-based approach complemented with Phylogenetic eigenVector Regression (PVR) to generate insights into potential evolutionary and ecological mechanisms determining variation in body size of *Plethodon* salamanders in eastern North America. We found a clear reversed Bergmann’s cline strongly associated with thermal availability in the environment for both the phylogenetic (P) and ecological (S) components of body size obtained from PVR. Our results are consistent with the ‘heat balance hypothesis’ as a plausible explanation for the observed pattern. Accordingly, species smaller than expected by their phylogenetic relatedness are more frequent in cold environments, whereas species larger than expected are mostly distributed in warmer areas. However, the individual responses of species to temperature appear not to be the only cause for the overall gradient in body size, as we also found a climatic signal in the phylogenetic component (P). This is likely to be related to the particularities of recent diversification in this woodland-adapted salamander group since the early Pliocene.

18.—USING SPATIAL STATISTICS FOR MAPPING DISTRIBUTIONAL SPECIES PATTERNS

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We propose to use the spatial mean and standard deviation ellipses, obtained by spatial statistics of point pattern analysis, to produce summarization maps of large groups of distributional species areas. The distribution of 55 columnar cacti species was used as a study case. Data of species’ presence-absence were assigned to 1° x 1° grid. A species richness map was produced for comparison with the alternative spatial statistical maps. The second map was produced using the spatial mean. The third map was produced grouping the standard deviation ellipses of each distributional species area. The spatial mean map could help decide if the richness of a region is the product of local species only or the product of wide distributed species. The standard deviation ellipses map accounts for overlapping distributional areas, and also for disjointed and nested ones. Although the species richness map is a valuable tool for biogeographers, it neglected the richness contribution of a set of species: a unique richness pattern could be formed by diverse arrays of specific distributional areas. Because the ellipses represent general distributional areas of one or more species, the standard deviation ellipses map accounts for general biogeographical patterns and could help define biogeographical regions. These kinds of maps could be valuable tools for describing distributional species patterns, detecting biogeographical patterns, and defining biogeographical regions.

19.—LOCAL STATISTICS IN GEOGRAPHICAL ECOLOGY

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Species richness patterns on broad geographical scales still remain to be fully understood by ecologists and biogeographers. The long list of potential mechanisms hypothesized to be drivers of those patterns may be classified in two different groups: historical/evolutionary and current/ecological processes. Analyses of species richness patterns are usually restricted to line-fitting methods, although computer simulations are now also being employed. Local spatial statistical methods have recently been developed in geography, proving to be useful tools to explore and understand processes that vary in geographical space. However, their application in geographical ecology has been limited so far, although no one doubts that the processes driving high species richness in mountainous regions are not the same as those driving low richness in cold and dry areas. Here I use Geographically Weighted Regression to show that the spatial pattern in species richness of birds, mammals and amphibians in the Western Hemisphere can be explained by few environmental variables. In order to estimate the magnitude of explanatory power of each environmental variable, in each locality of the domain, I used model selection and multi-model inference based on Akaike Information Criterion. Results reveal a strong latitudinal turnover in local drivers of species richness. At higher latitudes, temperature (a measure of energy availability) is the strongest environmental driver of species richness, whereas rainfall (water availability) is the major environmental explanatory factor in warm tropical areas.

20.—PREDICTING PALM SPECIES DISTRIBUTIONS IN AFRICA USING REMOTE SENSING DATA AND SPATIAL FILTERS

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This study investigates what determines the distribution of African palm species using species distribution modelling (SDM). Specifically, we assess the relative importance of four classes of potential distribution-controlling factors, namely climate, habitat, human influence, and spatial constraints. In the modelling we tackle several challenges that face species distribution modelling (SDM): the reliance on spatially interpolated environmental data and the equilibrium postulate. Large-scale species distribution modelling has generally been based on more or less spatially interpolated data in particular climate. However, remotely sensed environmental data of fine spatial resolution is now increasingly available and has been shown to improve SDM predictive accuracy. In the present study we use both interpolated climate and other ground-based environmental data and fully or partially remotely sensed data on both habitat and human influence. In SDM it is assumed that species' distributions are in equilibrium with the contemporary environment. However, this equilibrium postulate will not hold when a species is dispersal-limited and may lead to overpredictions and inaccurate models. Recently, it has been shown that using spatial filters as predictors in SDM may overcome this limitation. We therefore represent the potential broad-scale spatial constraints on palm distributions by spatial filters. The modelling was implemented using Maxent at 1-km resolution over the African continent for all African palm species with >20 georeferenced observations.

21.—"DIVERSITY FIELD," A CONCEPTUAL TOOL LINKING DIVERSITY AND DISTRIBUTION

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Underlying large-scale diversity patterns is the geographic distribution of species. Many studies consider range size for investigating the determinants of such patterns and the mechanisms constraining species ranges. Nonetheless, there are other equally important attributes of geographic ranges such as their internal structure. Also, most studies of large-scale patterns focus on either the distribution of species or the diversity of sites, ignoring the link between these two variables. In this study we introduce and describe a new concept, "diversity field", linking richness and geographic distribution by analyzing richness variation within each species' range (its internal structure). We built geographic databases and digital maps for the bat family Phyllostomidae to analyze each species' diversity field, and compare patterns among equal-sized species' ranges and trophic groups. Our results show most species share their ranges with many other species. More interesting, high richness values are present throughout most part of their ranges indicating a high number of potential interactions anywhere within the range. Patterns do not differ between different-sized species' ranges, implying that range size might not be as important as may be location. Furthermore, regardless of ecological differences, trophic groups show the same patterns suggesting common, non-ecological, mechanisms. Thus, for these bats, ecological factors seem to be weak determinants of geographic richness patterns, supporting an important role for regional/historical factors in the structure of geographic ranges and large-scale biodiversity patterns.

22.—THE BIOGEOGRAPHY OF BREEDING RANGES IN *SYLVIA* WARBLERS

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The range of a species is one of the most important parameters in biogeography, ecology and conservation. Understanding the complex interplay of factors influencing the size and configuration of species' ranges remains a challenge. Species ranges can be shaped by present species characteristics including body size, habitat choice or dispersal ability, a species' history including its phylogenetic age, biotic interactions including competition and present and past geographic and environmental conditions. As a first approach to better understand the factors behind the present configuration of breeding ranges in the bird genus *Sylvia*, we use species distribution models to create potential geographic distributions based on climate and vegetation and compare these to the actual breeding ranges. In the genus *Sylvia* we find both species with high range filling, whose distributions are likely limited by present environmental conditions, as well as species that do not occupy all potentially suitable regions. To further investigate what might cause these differences, we test whether *Sylvia* warblers who exhibit low range filling tend to have low dispersal ability, be phylogenetically young, and face more intrageneric competition in the unoccupied parts of their potential range.

23.—USING SIMULATED COMPLETE BIOGEOGRAPHIC HISTORIES TO TEST METHODS OF INFERENCE IN HISTORICAL BIOGEOGRAPHY

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Simulation methods have been used extensively in statistical phylogenetics to test models of sequence evolution and character evolution. However, the simulation approach only rarely has been used to test methods of inference in historical biogeography, despite a variety of such methods (parsimony analysis, DIVA, maximum likelihood, and Bayesian) and their widespread use in published analyses. A draft version of such a simulation program is presented, including major parameters, objects, processes (extinction, dispersal, cladogenesis, etc.), and methods of representing space, time, and range. Sample runs will be presented along with the results of a pipeline running these known “histories” through available analysis programs. Conceptual and modeling challenges will be discussed.

24.—BIOCLIMATIC AND CARTOGRAPHIC MODELLING OF CLIMATE IN BIOGEOGRAPHY

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The geographical distribution of biodiversity on the Earth surface is explained, apart from many complex and intertwined causes such as phylogeny, geological history, and paleoclimates, by climatic conditions. Therefore, we need particular climatic studies applied to biogeography that also allow us to map the bioclimatic units. Here, a worldwide bioclimatic classification, useful for making bioclimatic maps at different scales, is presented. Mapping can range from the large bioclimatic zones of the Earth to the very tiny areas with biologically uniform climatic conditions. Several examples of bioclimatic cartography are given: from very remote places in Asia and Europe; from big countries as Kazakhstan to small regions, such as Navarra province. The method allows mapping the largest bioclimatic units as Macrobioclimates, as well as the amounts of incoming thermal energy, degree of hydro-comfort, or the annual thermal amplitudes.

25.—ESTIMATING UNCERTAINTY AND THE EFFECTS OF SPATIAL AUTOCORRELATION IN ECOLOGICAL NICHE MODELS BUILT WITH FEW OCCURRENCE RECORDS

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Ecological niche models (ENMs) of species potential distributions have been used for a variety of purposes, from conservation assessments to studies of niche evolution. Despite their broad application, the predictive ability of these models has recently come under scrutiny, especially for small sample sizes of occurrence records. We implement the delete-1 jackknife as a statistical tool for assessing the performance and uncertainty of maximum entropy (Maxent) models built with small sample sizes. As composite measures of performance among jackknife iterations, we calculate averages for: 1) omission rates of test localities and 2) the Area Under the Curve (AUC) of the Receiver Operating Characteristic (ROC) plot. For both omission rate and AUC, we then calculate estimates of variance as a measure of uncertainty, correcting for non-independence of jackknife iterations. In addition, to minimize spatial autocorrelation in ENMs, we filter occurrence records based on pair-wise distances. We present implementations of these approaches for the spiny pocket mice *Heteromys australis* and *H. teleus* in Ecuador and southwest Colombia. Preliminary results indicate that using a larger distance for spatial filtering results in better-performing models. In addition, if accompanied by an estimate of uncertainty, measures of performance (omission and AUC) provide a more informative indication of model utility.

26.—EXAMINING THE ROLE OF CLIMATE IN *MICROTUS* TOOTH-SHAPE DISTRIBUTION USING GEOMETRIC MORPHOMETRICS

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Geometric morphometric techniques provide a way to examine detailed shape data independent of size and, when combined with geographical data, are powerful tools to trace different phenotypes across landscapes through time. Here, I apply these techniques to examine how climate influences dental morphology in *Microtus californicus*, a rodent that spans many biogeographic boundaries in an evolutionary hotspot, California. Specifically, I quantified the shape of the first lower molar (m1) in *M. californicus* and compared that shape with climate parameters and distance models. I found that *M. californicus* m1s are relatively straight in the northwestern, cooler, moister portion of California and more curved in the southeastern, hotter, drier portion of the state. The variance in shape is best captured by a model that depends on the specimen's distance along the geographic singular axis, which is consistent with the hypothesis that selection acting along geographic and climatic gradients is influencing tooth morphology. Models that assume diffusion of morphology, representing a phenotypic drift hypothesis, are rejected. Potential climate-related selective forces that influence tooth morphology include direct effects of parameters such as temperature, precipitation, and growing season, as well as indirect effects such as changing vegetation, which in turn affects the diet of *M. californicus*. Studies are underway to parse out which effects are most crucial.

27.—A DYNAMIC NEUTRAL MODEL FOR LARGE-SCALE PATTERNS OF DIVERSITY AND DISTRIBUTION

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In macroecology there has been a long tradition that works with null models for the study of biodiversity and geographic distribution, but this kind of work does not imply a mechanism of community assembly. In this study we use a neutral model to incorporate a dynamic mechanism that generates quantitative predictions to be compared with patterns of diversity and geographic distribution of species in a real data set as a null model. The model incorporates a demographic process with speciation and dispersal parameters where all the individuals have identical demographic probabilities. We compare the results of species distributions generated by simulations with the geographic distribution of the family Phyllostomidae, a neo-tropical family limited to the American Continent. The geographic analysis was made for the entire family at a continental scale considering two recently described concepts. The neutral dynamics produce spatial patterns in species richness and occupancy distribution showing a particular structure, right-skewed frequency distribution of range size and heterogeneous distribution of richness among sites. The results are evidence that neutral models are capable of providing appropriate null hypotheses for the evaluations of macroecological questions.

28.—ANTITROPICAL DISTRIBUTIONS: A GLOBAL PHYLOGENETIC APPROACH

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The New World phylogeny of patellogastropods reveals a sister relationship between limpets of the temperate waters of Chile in the Southern Hemisphere and the NEP in the Northern Hemisphere. This “antitropical,” “trans-equatorial” or “bipolar” distribution is not unique to limpets. Representatives from nearly every class of terrestrial and marine organisms have been described as having antitropical distributions (Hubbs, 1952; Ekman, 1953; Nelson, 1985; White, 1986; Lindberg, 1991). Here, I reveal a global phylogeographic hypothesis for the antitropical distribution of limpets and for antitropical distributions in general.

29.—SPATIAL TRANSFERABILITY OF NICHE-BASED DISTRIBUTIONAL MODELS IN THE CARIBBEAN SPINY POCKET MOUSE *HETEROMYS ANOMALUS*

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The use of niche-based distributional modeling has been hampered for several critical applications (e.g., invasive species, effects of climatic change) by questions of transferability. Transferability is the ability of a model to make correct predictions when projected across space or time (e.g., onto unsampled geographic regions or novel climatic scenarios). Because datasets from other time periods seldom exist, we assess transferability across space in the Caribbean spiny pocket mouse *Heteromys anomalus* using the maximum entropy algorithm, Maxent. Models were trained in north-central South America (the principal distributional area of the species) and transferred to the Río Magdalena valley (where an isolated set of occurrence records exists). We partitioned the 124 occurrence records from the training region twice: first randomly and then geographically, both times dividing records into four bins of equal sample size. The latter strategy provides test data that are spatially independent of the training data. We ran models in a delete-1 jackknife fashion, each time using a different bin as the test group for a model made using the other three (= k-fold cross-validation). To tune for optimal performance, we ran models across a range of regularization multipliers (protection against overfitting). Randomly partitioned models provided inflated estimates of performance when compared to geographically partitioned models. Parameter tuning did little to improve transferability.

30.—PHYLOGENETIC SIGNALS IN CLIMATIC NICHE SIMILARITY OF THE WORLD'S AMPHIBIANS

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Over the last decade, studies investigating the linkage between ecological similarity and phylogenetic relatedness have accumulated rapidly. Although one might expect that phylogenetic relatedness would also be reflected in shared ecological traits, the existence and generality of such a phylogenetic signal are still a matter of debate. To date, no study addressing the issue has been conducted for an entire class of organisms on a global scale. Here, we test the hypothesis of phylogenetic signal in climatic niche similarity for the world's amphibians (5527 species). We make use of a novel taxonomy that is based on the recent advances in amphibian phylogenetic research, thus representing the evolutionary history of lineages. To characterize climatic niches, we use niche positions in two-dimensional climatic space calculated by the Outlying Mean Index ordination technique. Firstly, we test if climatic niche similarity is larger for species within a taxonomic group than for species belonging to different groups. Secondly, we quantify the proportions of inter-species niche variance that can be explained at higher taxonomic levels, and then compare these values with null models simulating the absence of a phylogenetic signal. Niche similarity was consistently higher within than between taxonomic groups. Furthermore, a large proportion of inter-species variance in climatic niches was explained at higher taxonomic levels. The observed proportion was always larger than the null model proportion. These results indicate the existence of a strong phylogenetic signal in climatic niche similarity.

31.—USING NICHE-BASED GIS MODELING TO DETERMINE WHETHER SMALL MAMMALS INHABIT NOVEL CLIMATIC CONDITIONS ON THE PENÍNSULA DE PARAGUANÁ IN NORTHWESTERN VENEZUELA

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Isolated populations may evolve different climatic tolerances. We address this possibility on the Península de Paraguaná, which is connected to the mainland of South America only by a narrow isthmus of sand. *Marmosa robinsoni*, *Heteromys anomalus* and *Proechimys guairae* are three species of small non-volant mammals found in northern Venezuela and Colombia. We make maximum entropy (Maxent) models of the potential geographic distributions of these species, based on climatic data and occurrence localities from the mainland. We then use records of these species (or close relatives) from the peninsula to determine if populations there are predicted by the models. Most occurrence records for *Heteromys* and *Marmosa* on the peninsula fall within the prediction, indicating only low-to-moderate evolution of climatic tolerances in those groups. Results for *P. guairae* are inconclusive and likely suffer from high spatial autocorrelation associated with sampling bias in the dataset for that species. To remedy this in our ongoing research, we are adding additional occurrence localities of *Proechimys* and spatially filtering them (by randomly removing localities in close proximity). Detailed analyses are ongoing with these and other species.

32.—SPATIAL NON-STATIONARITY AND THE SCALE OF SPECIES-ENVIRONMENT RELATIONSHIPS IN THE MOJAVE DESERT, CALIFORNIA, USA

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This research explores spatial non-stationarity in the relationships between species' distribution and environmental gradients in the Mojave Desert by using geographically weighted regression (GWR). More traditional generalized regression methods assume spatial stationarity in the modelled relationship, however, in reality there may be other processes and patterns that make the species-environment relationship vary spatially. For example, precipitation may have a different effect (either magnitude or direction) on species' distribution given the temperature regime. GWR was used to explore the spatial non-stationarity and the scale of the influence of each of ten environmental factors on four different plant species in the Mojave Desert. The environmental variables describe important gradients such as temperature and precipitation extremes and simple and complex topographic variables. The four species represent distributions characteristic of plants in the Mojave Desert, ranging from habitat generalist to habitat specialist. The variation in the coefficient for each variable (among all observations) is used as an 'index of stationarity' (Fotheringham *et al.*, 2002). This index of stationarity can be plotted against each bandwidth tested to determine at what scale the species-environment relationship became stationary. Results indicate that there is non-stationarity in all three species-environment relationships. Higher levels of non-stationarity were usually associated with smaller bandwidths. Some species-environment relationships became stationary at a certain spatial scale (bandwidth), but others remained non-stationary for all bandwidths tested.

33.—THE TROPICS: CRADLE, MUSEUM OR CASINO? A DYNAMIC NULL MODEL FOR LATITUDINAL GRADIENTS OF SPECIES DIVERSITY

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Several ecological and evolutionary hypotheses have been proposed to explain the latitudinal diversity gradient, but a general model for this conspicuous pattern remains elusive. By necessity, studies on the gradient have relied on indirect methods, such as analyses of the fossil record, interpretation of present-day patterns, and mathematical models. We present a dynamic model that generates null expectations for the diversity gradient based on very simple random-walk processes of range shifts, extinction, and speciation. Despite its simplicity and neutrality, the model generates latitudinal patterns that resemble predictions of some of the leading ecological and evolutionary hypotheses. In particular, the model predicts higher species richness and higher extinction and speciation rates in the Tropics, and a strong influence of range movements in shaping latitudinal patterns of diversity. Thus, the model predicts a higher turnover of species in the tropics, making the Tropics good cradles but poor museums, using Stebbins' metaphor. These null expectations should be taken into consideration in studies aimed at understanding the many factors that generate latitudinal diversity gradients.

34.—BIOINFORMATICS AND THE GEOGRAPHY OF LIFE: SYNTHESIS PROGRAMS OF THE ENCYCLOPEDIA OF LIFE

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The fundamental question of where species live, and why, is crucial for conservation and understanding the impact of global climate change. The Encyclopedia of Life (EOL) is an emerging effort to provide a comprehensive online resource for information about species, including their past, present, and future geographic ranges. The Biodiversity Synthesis Center (BioSynC), located at the Field Museum in Chicago, USA, is an EOL component dedicated to innovative research on biogeography. Examples of ongoing biogeographic projects by researchers at BioSynC include: 1) Using phylogeography to understand the evolution of tropical marine biodiversity; 2) The integration of biogeographic data into studies of host-parasite coevolution; 3) Analyzing patterns of tetrapod diversity and paleobiogeography relative to fossil-bearing outcrops; and 4) Establishing species boundaries and geographic patterns of genetic variation and genetic pollution in freshwater turtles. BioSynC hosts "synthesis meetings" that bring together complementary groups of biodiversity scientists to work toward specific goals, e.g. developing new mapping tools, synthesizing databases, and integrating museum specimen data with global geologic history, ecological niche modeling, and regional ecosystem threats. For these groups, BioSynC provides travel funds, a meeting space, and logistical support. We invite proposals for synthesis meetings that would make significant contributions to the EOL, and involve international groups of biogeographical researchers. We are especially interested in proposals that emphasize climate change and species range shifts.

35.—A STATISTICAL APPROACH TO BIOGEOGRAPHIC INFERENCE USING DIVA UNDER PHYLOGENETIC UNCERTAINTY

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Widely used quantitative methods for reconstructing ancestral areas on a phylogeny require a fully bifurcating tree. We propose a statistical approach using DIVA without fully bifurcating trees. Ancestral distributions are optimized repeatedly for a sample of Bayesian trees. The probability (P) of an ancestral area (A) at a node is calculated as $P(AY) = [FT_1 + \dots + FT_N]/N$, where Y is the node of interest, F is the probability of an ancestral range at node Y for a given tree, and TN is one of N randomly sampled Bayesian trees. F is determined as the frequency of all the optimal solutions resulting from DIVA optimization. This probability accounts for two types of uncertainties: phylogenetic uncertainty and uncertainty of DIVA optimization on a given phylogenetic tree. Where placement of a well supported terminal clade was uncertain, the ancestral distribution of the node connecting the specific terminal clade and its unspecified sister (x) can be estimated. Using simulated data, we show that the probability of an ancestral area at a node with phylogenetic uncertainty is not truly factored by the posterior probability, as $pp[F(AY)]$. This is because different x can result in the same optimal area (A) in DIVA, leading to combined frequencies greater than the posterior probability supporting the node. We applied the method to *Aesculus* L., which lacks a fully bifurcating phylogenetic tree. The analysis provided estimates of ancestral distributions of major clades with statistical probabilities. We also applied this approach to determine the effects of wildcard fossils on biogeographic analysis of *Aesculus*.

36.—GEOGRAPHICAL CONTROLS ON THE DISTRIBUTION OF AVIAN RICHNESS IN COLOMBIA

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Colombia is a megadiverse country not fully inventoried. This represents a major challenge to conservation; a situation aggravated by deforestation, climate change, poverty and armed conflict. The Darwin–Hernandez database compiled by Project BioMap in 2005 represents an opportunity to assist inventory and conservation using data from museum collections. The dataset was revised and estimations of error conducted to filter it, retaining entries with complete taxonomy and localities with a georeferencing precision error below 1 km (169,221 accessions). Maxent 2.3.0 was used to model distributions of 71 families and 491 genera. Exercises were performed using five bioclimatic variables, models were evaluated using 30% of the data and presence was accepted above values of 30% of cumulative probability. Richness was estimated in equal altitude interval bands (EAIB) of 100 m and approximate equal surface area bands (AEQSB) of ~ 103 km². Models performed better than random, having AUC values usually above 0.7. Effort showed a sampling bias towards western Colombia. When this was eliminated, a correlation between richness and environmental resources and spatial heterogeneity was apparent for western Colombia; Spearman's coefficients absolute values ~ 0.4 – 0.9 for the total and the average richness ($p < 0.01$, $n = 56$ EAIB, 51 AEQSB). The relationship with resources was positive, whilst negative with heterogeneity. The interaction between the two variables is suggested here as the main control of the altitudinal richness pattern for birds in the country.

37.—THE BIOGEOGRAPHY OF GROUP SIZE IN SOCIAL SPECIES

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Social organisms, such as termites, parrots, and primates, form interactive groups through mutual attraction. A key difference among social species is the size of these groups. Like body size of individual organisms, different group sizes presumably reflect both different phylogenetic histories and different ecological conditions. Ecological conditions may underlie the tendency for mammal and bird species to be larger-bodied at higher latitudes, a pattern called “Bergmann’s rule.” Interestingly, membership in ant colonies and traditional human foraging societies also varies positively with latitude. Despite their obvious differences, larger ant and human societies can presumably extract resources from larger areas and store more food, capacities that become more important in seasonal environments. We expand this search, examining geographic and environmental correlates of group size in social species generally. We hypothesize that: 1) group size in social species will increase with latitude; 2) this pattern will be a positive function of social complexity (i.e., the more closely a taxa comes to a “superorganismal” social structure); and 3) variation will partly reflect resource variability and climate, for which latitude is an imperfect proxy. Using data from the literature, we used simple and multiple regressions to assess patterns of group size and the relative influence of key environmental and social variables on group size. Preliminary findings support the hypotheses, but phylogeny clearly affects the macroscopic patterns. The findings have important implications for both biogeography and allied fields.

38.—THE BIOGEOGRAPHY OF MEXICAN FERNS: USING BIBLIOMINING AND GIS TO MAKE MAXIMAL USE OF FLORA DISTRIBUTION INFORMATION

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We present a species richness map of the ferns of Mexico and explain the techniques used to generate it. This map is based on the distribution data of Mickel and Smith (2004), including species presences for each Mexican state and species elevational range. We use Perl to automate data extraction, and GIS to generate state X elevation OGUs (Operational Geographical Units). The resulting OGUs are highly reticulated GIS polygons that correspond to all regions within each state that are at each elevation, binned at 100m increments, allowing us to make maximal use of the flora’s locational information for each species. The resulting richness map differed substantially from a map based on state presences alone and represents richness patterns more realistically. We suggest that using elevation data in conjunction with state presence data alleviates the problem of lumping disparate ecological regions into single OGUs. Finally, we present basic biogeographical analyses of Mexican pteridophytes including climatic correlates of richness and compositional attributes. Biogeographic data of floras are not ideal because they are summarizations of high resolution specimen records. However, if all information is leveraged, it is possible to pull out ecologically relevant geographical units. In addition, floras are based on an accumulation of knowledge; they have been the standard for synthesis of biological knowledge for decades. The resulting maps are suitable for a broad range of evolutionary and ecological analyses, and similar techniques are being applied by the authors to map all ferns of the New World.

39.—WHY DO COMMON SPECIES CONTRIBUTE TO THE GEOGRAPHICAL DIVERSITY PATTERN MORE THAN RARE SPECIES?

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Common species have a greater effect on observed geographical patterns of species richness than do rare ones. Here we present a link between individual species occurrence patterns and patterns in species richness, which allows purely geometrical and statistical causes to be distinguished from biological ones. Central to the theory is frequency distribution of species richness among sites. The ability of common species to explain the overall diversity pattern is promoted by the fact that species occupancy distributions are mostly right-skewed. However, biological processes can lead to deviations from the predicted pattern by changing the nestedness of a species' spatial distribution with regard to the distributions of other species in an assemblage. Using data from several continents, we have identified the species with significantly stronger or weaker correspondence with the overall richness pattern than predicted by null model. In sum, whereas the general macroecological pattern of a stronger influence of common than rare species on species richness is predicted by mathematical considerations, we can reveal biologically important deviations at the level of individual species.

40.—THE SPATIAL ECOLOGY OF *SPARTOCYTISUS SUPRANUBIUS*, A DOMINANT ENDEMIC SHRUB IN THE HIGH-ALTITUDE DESERT OF TENERIFE

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Arid and semi-arid systems are typified by non-equilibrium dynamics and are believed to be among the most sensitive ecosystems to anthropogenic and climatic change. Understanding the distribution and dynamics of arid plant populations is essential for their conservation, especially for narrow-ranged endemics such as *Spartocytisus supranubius*, a dominant endemic shrub of the high-altitude Cañadas caldera, Tenerife. However, there is a temporal mismatch between traditional observational and experimental methods (years) and the time scales of vegetation change (centuries) which has made arid vegetation dynamics difficult to investigate. Here, I apply techniques from mathematics and remote sensing to try to overcome this difficulty via a more macroecological approach. I use spatial statistics and individual-based simulation modeling to investigate the population dynamics and processes underlying the spatial organisation of *S. supranubius*, and one-class spectral classification to map the size and location of 17,551 *S. supranubius* individuals over 162 hectares. Contiguous plots (ranging from 10 to 50 ha) sample five spatially adjacent substrates (lava flows) that differ in age and topography. I quantify the spatial organisation of the *S. supranubius* population on each of the five substrates via univariate and bivariate spatial analyses. Based on analyses to date, I hypothesize that the spatial structure of the *S. supranubius* population results from intra-specific competition and asexual reproduction via branch layering, with these processes superimposed on an environmental control driven by substrate characteristics. I have developed an individual-based simulation model, based on the field-of-neighbourhood approach of Berger and Hildenbrandt (2000), to test this hypothesis.

41.—PALEOECOLOGY OF AN ENDEMISM HOTSPOT: EVIDENCE FROM POZA AND MARSH SEDIMENTS OF CUATROCIÉNEGAS, MEXICO

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The unique desert wetlands of the Cuatrociénegas Valley of Mexico support more endemic species than any comparable area of North America. Endemic fish, snails, and stromatolites inhabiting pozas (ponds) constitute important study systems for phylogeography, microbial evolution, astrobiology, and the geographic mosaic theory of coevolution. Here we present evidence of dramatic shifts in poza community composition obtained through paleoecological analysis of sediment cores from the Reserva Privada Pozas Azules. In 2007, we collected surface sediments from seven pozas and short (<1 m) sediment cores from three pozas to investigate fossil preservation and provide reference sediments from modern pozas. We found snail shells, fish scales, diatoms, pollen, and biogenic carbonates from stromatolites in recent sediments, all with potential for elucidating poza community dynamics through paleoecological analyses. In 2008, we collected four sediment cores from three marsh sites identified as possible paleo-pozas. Our longest core (12.3 m) consists of marsh-derived peats overlying poza-type sediments containing biogenic carbonates, *Nymphaea*-dominated peats, and shells of the endemic hydrobiid snail *Nymphophilus minckleyi*. This sedimentary record provides the first evidence of the transition from a deep poza to a marsh and suggests a dynamic history for the aquatic habitats that support many endemic species of Cuatrociénegas.

42.—ANALYSIS OF BIOLOGICAL SOIL CRUST MAPPING IN THE MOJAVE DESERT, USA

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Biological soil crusts (BSCs) are critical ecological components in arid regions around the world. These crusts form a living, desert skin that reduces soil erosion, influences soil fertility, manages soil moisture/temperature, and prevents desertification. BSCs are fragile resources, easily destroyed by physical disturbances and potentially impacted by climate change. Despite their ecological importance, the environmental factors controlling BSC distribution in the Mojave Desert are poorly understood. Furthermore, no predictive modeling technique exists for BSCs in Mojave landscapes. Our investigation employs a novel, interdisciplinary approach to investigate BSC ecology and to develop a predictive model of BSC biotic potential. We discuss initial results from various BSC mapping techniques (remote sensing indices, field-based mapping, and geomorphic mapping) and surface characterization. Our data indicate the application of two remote sensing indices (Karnieli et al., 1997; Chen et al., 2005) with high resolution Quickbird® multispectral imagery (2.44m) effectively delineates BSC density into three mapping units. In contrast, our field-based map is divided into 10 mapping units reflecting BSC distribution, density, morphology, and species composition. Field-based mapping further addresses surface characteristics that control soil stability and resistance to disturbance. Initial field data and mapping reveal geomorphology is a primary controlling factor in BSC distribution within the Mojave. Because geomorphology largely determines soil characteristics that influence crust distribution, geomorphic maps could be incorporated into a BSC predictive model. The science of BSCs is still in its infancy, with few conclusive answers regarding their biology. Our interdisciplinary approach to BSCs bridges gaps between biology, ecology, soil science, hydrology, statistics, chemistry, geomorphology, GIS, and remote sensing. Our research aids in understanding interrelationships between biological soil crusts, soils, geomorphology, and land stability.

43.—FINE-SCALE HABITAT FRAGMENTATION AND SPECIES COEXISTENCE

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Spatial aggregation fosters the persistence of weak competitors in the neighborhood of stronger ones by reducing interspecific interaction intensity. Fine-scale habitat fragmentation that disrupts interactions between individual plants should have a similar effect. I test this proposition using a spatially explicit simulation model and using observational data from the Carrizozo Malpais, a basalt flow in southern New Mexico. In the simulation model, time to extinction of the weakest species in a two-species simulation is positively correlated to habitat fragmentation. In the field study, habitat fragmentation explains over 60% of the variance in species richness. These lines of evidence suggest that spatially-induced competitive uncoupling may be an important mechanism contributing to species coexistence and the persistence of weak competitors in rocky habitats. If so, such environments may serve as refugia for marginal species. They may also be more open to colonization and invasion than are continuous habitats where competitive interactions are not disrupted.

44.—ENVIRONMENTAL CONDITIONS USED BY CLOSELY RELATED HUMMINGBIRD LINEAGES

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Environment shapes the distribution and abundance of organisms and, consequently, biodiversity patterns. Because species are physiologically adapted to particular sets of conditions, and these adaptations have an evolutionary basis, it has been proposed that closely related species should exist in similar environments. If environmental niches are conserved we expect that the degree of environmental differences among lineages parallels their genetic divergence. As a result we expect that environmental variation among species should be greater than among subspecies. We explored these predictions in the Andean *Metallura* hummingbirds. We found that polytypic species use broader environmental conditions than monotypic species, and, as a consequence, variation among species is not significantly greater than variation within species. However, when the distributions of species overlap, *Metallura* hummingbirds tend to segregate in the environment by occupying different altitudinal bands. Additionally we found that geography plays an important role in the diversification of the genus because lineages generally inhabit different regions and slopes of the Andes. Our results provide a first step in understanding the relative influence of abiotic factors on the distribution of lineages, and will guide collection of more detailed ecological data so we can explore how both regional (i.e., climate) and local (i.e., food plants, species interactions) factors influence species distribution.

Symposium IV

Extinction Biogeography

THE FABRIC OF MASS EXTINCTIONS: BIOGEOGRAPHIC PATTERNS AND EVOLUTIONARY HISTORY

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Mass extinctions have been recognized in global compilations of the fossil record, but are generally studied in individual sections. Thus one of the greatest challenges, particularly for older events, is to understand their biogeographic fabric -- the patterns between global databases and individual sections. This is particularly so for the end-Permian event, 252 million years ago. Although this was the most severe mass extinction of the past 550 million years, the limited distribution of both marine and terrestrial sections have severely hampered our understanding of the biogeographic patterns of extinction, and of the subsequent biotic recovery. For the earliest extinction event, at the end of the Middle Permian, we know of only two marine sections, both in China, where there is a preserved record across the Guadalupian-Lopingian boundary; the record is elsewhere missing. For the end-Permian event more marine sections are available, but the biogeographic pattern of extinction remains difficult to discern, at least in part because it many have been less significant than depth for marine localities.

PLANT EXTINCTION AND THE K-T BOUNDARY: THE IMPACT OF ONE PARTICULARLY HARSH DAY IN EARTH HISTORY

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The Cretaceous-Tertiary Boundary occurred 65.51 million years ago when an extraterrestrial body struck the Yucatán Peninsula and formed the Chicxulub Impact crater. The fallout from this impact formed a thin layer that can still be found at many sites around the world and is a unique global timeline that allows the concept of global extinction to be tested. Terrestrial K-T boundary sites are well-known only from North America and New Zealand. The North American sites demonstrate continent scale devastation of vegetation and a subsequent extinction of more than 50% of plant species. The New Zealand sections show evidence of devastation but little extinction. Active research in Colombia, Patagonia, and Manchuria is adding additional texture to this pattern. Recovery to pre-K-T boundary levels of floral diversity appears to take 2-10 million years in North America.

WHERE DID ALL THE MASTODONS GO? GLOBAL PATTERNS OF LATE PLEISTOCENE MEGAFUNA EXTINCTION

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What happens to a biota after a size-biased extinction? Approximately 10 kya in North and South American and 46 kya in Australia, virtually all of the mammalian megafauna disappeared. This extinction was fundamentally different from previous ones in that it was highly size-biased and directly affected only a portion of the available biota. Moreover, unlike earlier events, the pattern and timing of the late Quaternary extinction across the globe suggests that migrating humans played a large role. Using body size and species composition as metrics, we evaluated the effects of the late Quaternary extinction at multiple spatial scales. At the continental scale, the removal of megafauna had profound and dramatic effects on the biota. There were significant trends in extinction risk related to the taxonomy of mammals, with only specific orders of large bodied mammals affected. The body distributions of continental biota were significantly and fundamentally altered. At the local scale, there was significant turnover in community composition likely related to the extinction and climate change. However, community body size distributions before and after the extinction do not show significant changes in shape. Comparison to current communities indicates that body size distributions show greater changes in shape across latitudes now than we see in the temperate zones before and after the extinction. The similarity in community body size distributions across time, despite changes in taxonomic richness and composition, suggests that body size plays an important role in structuring local communities.

BIOGEOGRAPHY OF PACIFIC ISLAND AVIAN EXTINCTIONS: PAST, PRESENT, AND FUTURE

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Endangered Pacific island birds are the most recent victims of a biodiversity crisis which began thousands of years ago with initial human colonization of the islands. On many islands, the arrival of Polynesian colonists is linked to the extinction of more than 40% of indigenous landbird species. Were these extinctions biogeographically structured, and if so can this information aid our understanding of contemporary extinctions? I used a comprehensive dataset of fossil and modern avian species from 43 Pacific islands to test the ecological and biogeographic selectivity of extinctions in the prehistoric (3500 – 200 ybp) and historic (200 ybp – present) time periods. Endemism was one of the best predictors of extinction risk through time, and fossil evidence shows that many extant single-island endemics were more widespread in the past. Prehistorically, small, low islands had higher extinction rates, but this pattern was reversed for historic extinctions. More isolated island groups showed higher rates of extinction, which is linked to the endemism of their avifaunas. Melanesian islands experienced lower extinction rates, possibly because they tend to be larger and less isolated, with a longer history of human occupation. Although human impacts on birds and their habitats have changed over time, modern endangered birds share many of the same ecological characteristics as victims of previous extinction waves.

A GEOGRAPHIC FRAMEWORK FOR MONITORING, UNDERSTANDING AND CONSERVING BIODIVERSITY IN A CHANGING WORLD

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Abstract unavailable at time of printing.

PLANT DIVERSITY RESPONSES TO CLIMATE AND ATMOSPHERIC CHANGE: NEO- AND PALEO-ECOLOGICAL PERSPECTIVES FROM AFRICA

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ECOLOGICAL HISTORY, LATENT CONSERVATION POTENTIAL, AND WHY ARE WE AIMING SO LOW? GIANT TORTOISES AS A MODEL FOR TAXON SUBSTITUTIONS

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Starting in the 1980s, ecologists began viewing present-day species interactions through the lens of history. For the first time, the ecology of large-seeded fruits in the Americas and divaricating plants in New Zealand were viewed as anachronistic, due to the missing large vertebrates that once influenced their evolutionary ecology. Two decades later, conservationists are now considering the role of ecological history in conservation practice, and some have called for restoring missing ecological functions and evolutionary potential with extant conspecifics and related taxa. This proactive approach to biodiversity conservation has proved controversial. Yet, taxon substitutions, or species analogs, are now being integrated into conservation programs around the world, from Russia and Latvia to the Netherlands, New Zealand, and the United States. On islands, conservation practitioners are starting to repatriate giant tortoises to ecosystems where they once played keystone roles; more than 30 species of giant tortoises went extinct since the late Pleistocene. Empirical evidence is emerging that supports the notion of using species analogs to restore missing ecological functions. We use giant tortoises as a model to examine the evidence, latent conservation potential, benefits, and risks of using species analogs as a strategy for biodiversity conservation.

45.—THE BIOGEOGRAPHY OF FOREST CHANGE: DROUGHT AND CROWN FIRE IN THE AMERICAN SOUTHWEST

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Our research questions whether the regional pine forest can persist in the unprecedented conditions of a novel fire regime combined with extreme climate conditions. Climate warming changes are expected to produce large and rapid forest biogeographic shifts, yet we currently lack predictive models largely due to the lack of empirical data. The research will focus on the role of climate in limiting pine recovery after severe fire, by examining tree recruitment after six high-severity crown fires that burned New Mexico, USA, forests in a severe drought that prevailed in the 1940-50s. The absence of abundant precipitation during the study period allows us to separate and quantify the influence of the post-fire environment from climate effects, using the tools of tree-ring reconstructed climate and water budget models. Our research results include (1) whether ponderosa pine trees in the US Southwest can successfully recover from anthropogenic high-severity fires during drought conditions; (2) a database of post-high-severity fire establishment processes influencing ponderosa pine recruitment during droughts in order to test biogeographical hypotheses; (3) predictions of post-disturbance forest dynamics under future climate scenarios, including the potential for recovery following high-severity fires during deeper or longer droughts in a warming climate scenario; and (4) guidelines for resource managers to improve strategies that can bring an important regional forest within historic natural ranges of variability.

46.—THE USE OF POPULATION GENETICS TO EVALUATE LANDSCAPE PERMEABILITY

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Fragmentation and loss of habitat as a result of human activities is a chief threat to global biodiversity, yet how species view and utilize fragmented landscapes is still relatively unexplored. The Flint Hills of Kansas represent a fragmented prairie landscape, which contains >90% of the remaining tallgrass prairie in the U.S. Prairie loss has been implicated in declines of numerous grassland species including Greater Prairie-Chickens (*Tympanuchus cupido*). We captured chickens on leks throughout the Flint Hills, collected blood samples and constructed a microsatellite DNA profile for each individual. Despite high genetic diversity, we detected interrupted gene flow. Gene flow among populations is indicative of population connectivity which depends on landscape permeability to species dispersal. To explore how anthropogenic land use affects regional connectivity of populations, we used regional landcover data of the Flint Hills parameterized with habitat-specific values of permeability based on biological inferences and telemetry data collected as part of ongoing research. Isolation by resistance was calculated using CIRCUITSCAPE, which estimates landscape permeability using models derived from electrical circuit theory. Spatial autocorrelation between genetic distance and habitat resistance were compared among landscape permeability models to identify which model best explained gene flow across the Flint Hills. This approach allows us to identify important landscape barriers and corridors among prairie chicken populations, as well as evaluate the role of matrix configuration on landscape permeability.

47.—CONSERVATION BIOGEOGRAPHY IN MONTANE EAST AFRICA: ENDEMISM, β -DIVERSITY, COMPLEMENTARITY, AND RESERVE DESIGN

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The montane avifauna of East Africa, including in the Albertine Rift, Eastern Arc, and Rift Valley highlands, exhibits a high degree of endemism. Habitat loss and conversion have threatened many of these endemics with extinction. Biogeographic affinities of birds in these mountains have received some attention, but determining biogeographic boundaries—points of high floral or faunal turnover (i.e., high β -diversity)—can be highly subjective. Of equal difficulty is presenting boundaries in an easily understandable manner that is repeatable. Monmonier's algorithm, a spatially explicit technique, offers a means of assessing boundaries in a way that provides insight into regional faunistic relationships and is readily interpreted. We used this algorithm on avifaunal lists we compiled for 46 sites throughout the east African mountains, and we created bootstrap matrices to determine the relative support for mapped boundaries. We used results to assess how patterns of β -diversity (and thus complementarity) could be used to shape reserve design, and we compared resultant reserves with those that would be identified by focusing on endemism and species richness. We argue that spatially explicit techniques such as Monmonier's algorithm should be a part of the conservation biology toolkit, as determining biogeographic patterns is more important than ever if we are to make efficient use of limited management resources.

48.—THE IMPACTS OF LAND-USE CHANGE ON VEGETATION PATTERNS IN KYRGYZSTAN'S WALNUT-FRUIT FORESTS

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The walnut-fruit forests of Kyrgyzstan are the most extensive walnut forests worldwide and of global significance for biodiversity conservation, in particular due to high diversity of trees and shrubs. At the same time the forests are of considerable importance for sustaining the livelihoods of over 100,000 people living in the forest area. A wide range of valuable resources (wood, nuts, fruits, hay) has caused intensive forest use since pre-Soviet times. Present institutional settings, external demands on specific products and the economic constraints of the local population lead to the exploitation of these forests. In order to assess the effects of human impacts on vegetation patterns we conducted detailed vegetation analyses along a complete utilization gradient. Classification resulted in four forest communities, differentiated primarily by form and intensity of forest use. Ordination analyses showed that anthropogenic site factors exert a greater influence on variation in vegetation patterns compared to natural site factors. Impoverished stand structures, regressive successions and insufficient regeneration point to considerable changes in the walnut-fruit forests and to their uncertain future.

49.—THE CAUSAL RELATIONSHIP BETWEEN CLIMATE, VEGETATION AND DISTURBANCE, AND ITS CONSEQUENCE FOR PREDICTING A BIRD'S RESPONSE TO CLIMATE CHANGE

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Effects of climate change on a species' distribution range are commonly predicted from models of the current distribution range in dependence of climate. However, climate is only one of several environmental factors that cause a species' distribution. Others are (for example) vegetation structure, disturbance, resource availability or species interactions. Most of these factors are themselves ultimately determined by climate. Considered together, the determinants of a species' distribution may form a complex chain of causal relationships of which climate is one origin. Climate change thus may cause a cascade of indirect effects within this chain including disruptions or decelerations if time scales of effects differ. We hypothesize that the ultimate effect of climate change on a species' distribution will depend on how precisely the environmental factors are ordered and weighted along this causal chain. We test this idea using the sociable weaver *Philetairus socius*, a colonially breeding, endemic passerine bird species of southern Africa, as an example. We apply and compare different hierarchical models that combine environmental determinants and their causal relationships to investigate how assuming different causal relationships influences the prediction of the species' response to climate change.

50.—THE CHANGING FACE OF AFRICA – THE EFFECT OF ABIOTIC AND ANTHROPOGENIC FACTORS ON LAND-COVER TYPES IN AFRICA

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In natural systems, vegetation types are thought to be primarily determined by climatic factors at coarse scales, while a number of other factors may also be important at fine scales, e.g., soil, hydrology, and, in Africa specifically, fire. However, humans are increasingly altering natural vegetation globally through, e.g., agriculture, urban development and other changes in landscape management. Therefore, classification of current land-cover types is usually based on both natural vegetation types and anthropogenic effects. Mayaux *et al.* used remote sensing data on vegetation cover to define 27 different land-cover types for the African continent in the GLC2000 land-cover map. Here, we examine how climate (specifically temperature and precipitation), fire, soil, topography and hydrology, and measures of human influence predict land-cover types on the African continent at a fine spatial scale. Based on this we develop predictive land-cover models and use these to look at how predicted climate change and human pressures may alter land-cover in Africa over the 21st century.

51.—SPECIES DISTRIBUTION MODELS PREDICT CURRENT RANGES WELL, BUT FAIL TO PREDICT RANGE CHANGES AS A RESULT OF CLIMATE CHANGE

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Species distribution models are often used to predict how species ranges will shift as a result of climate change. There are many uncertainties in predicting future distributions, including interactions among species, dispersal limitation and adaptation to new environments. Testing the accuracy of the projections is difficult because they are predicting changes that have not yet occurred. One solution is to predict changes that occurred in the past (hindcasting). Using time series data on the distributions of British birds and hoverflies, we show that species distribution models predict contemporary ranges very well. However, models that include known changes in the climate predicted range shifts significantly worse than models that assumed that climate change had no effect on the distributions of species at all.

52.—CLIMATE-INDUCED CHANGES IN THE SEA CURRENTS RANGES, ZOOPLANKTON COMMUNITIES AND LITTLE AUK FEEDING ECOLOGY AND DISTRIBUTION IN SPITSBERGEN

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The effects of global warming are accentuated particularly in the Arctic. Here, we present results on the Little Auk (LA) *Alle alle*, which is a keystone species in the Arctic ecosystems due to its huge numbers. LA deposit large amounts of organic matter of marine origin near breeding colonies, thus increasing production and diversity of ornithogenic tundra. LA inhabits the west coast of Spitsbergen, but with a highly spatially heterogeneous distribution - the largest colonies are situated in the SW and NW parts of the island. This pattern quite precisely reflects the range and influence of cold Arctic waters and the occurrence of its preferred prey, the large energy-rich Arctic calanoid *Calanus glacialis*. Enlarged inflow of warm Atlantic water results in dominance of small Atlantic *C. finmarchicus* in the Arctic zooplankton and in consequence less efficient feeding of LA chicks. Indicating the negative impact of this climate change on LA, there is a negative correlation between its median hatching dates with spring ground temperature in the colony and positive relationship with sea-ice concentration in the feeding grounds. Further climate warming may force a northward shift of the LA breeding range and have serious negative consequences for the ecosystem. The southernmost LA populations in Greenland and Iceland have already collapsed after warming following the Little Ice Age.

53.—IS GEOGRAPHICAL VARIATION IN SIZE OF THE LITTLE AUKS A RESPONSE TO CLIMATIC CONDITIONS IN THEIR BREEDING GROUNDS?

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The Little Auk is the most numerous seabird of the Palearctic, has a circumpolar breeding distribution, and is considered well-adapted to the severe Arctic conditions. In this study we tested relationships between body size variation of Little Auks from different breeding areas and latitude and harshness of the local climate (defined as sea surface temperature during the breeding period). We found significant biometrical differences between the Little Auk populations inhabiting different parts of the Arctic. The largest birds breed in the northernmost Franz Josef Land Archipelago, >80° N), characterized by the severest climate conditions. Little Auks breeding on Bear Island and West Spitsbergen (77-80°N), where the climate is milder due to impact of warm sea currents, appear to have intermediate size, while the smallest birds breed on NW and SE Greenland (Kap Hoegh and Hakluyt; 70-77°N) in areas which are considered rather cold due to strong influence of Arctic currents. Our results do not fit precisely to Bergmanns' rule and this discordance is a subject of discussion. Investigations, which are in progress, on the genetic structure of particular Little Auk populations and rates of gene flow between them, should help understanding these findings.

54.—THE GEOGRAPHICAL RANGE OF EUROPEAN TREE SPECIES EXPLAINED A BIT FURTHER: THE ROLE OF CLIMATE, SOILS, AND ECOPHYSIOLOGICAL TRAITS

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Given the jeopardy that biodiversity is currently facing, robust assessments on future shift of the geographical range of species are of utmost importance. Species Distribution Models (SDMs) are widely used to estimate current and future potential distributions of many organisms. However, a frequent lack of pertinent data on variables other than climate in SDMs, despite these being known to influence range dynamics, has often precluded an integrative approach to account for the effects of species-specific functional traits on the geographical ranges of species. Here, we use an ongoing database (GEOFEN) with information on geographical range of trees in Europe, climate, soils, and several phenotypic traits to make clear the effects of abiotic and biotic drivers on range size and range filling (i.e., the proportion of the potential range delimited by niche modelling that is actually occupied; [Svenning & Skov 2004, *Ecology Letters* 7: 565-573]). First, we use several modelling techniques to map the climatic niche of 55 tree species in Europe. Second, we apply a common classification of tree soil preferences to fine-tune the modelled distribution of species by accounting for soil water retention capacity and pH effects. Third, we test whether ecophysiological traits (growth rate and tolerances to drought and shade) bear upon range size and range filling of European tree species. Disentangling the role of ecophysiological traits in the geographical range of tree species through this approach will enhance the understanding and prediction of range shifts in response to climate change.

55.—MODELING POTENTIAL IMPACTS OF CLIMATE CHANGE ON THE DISTRIBUTION OF MOUNTAIN SPECIES IN PENINSULAR SPAIN

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Given that mountain species are particularly at risk due to climate warming, we selected one amphibian (Baetic midwife toad), one reptile (Lataste's viper), one bird (Bonelli's eagle), and one mammal (Iberian wild goat; all species present in Spanish mountains) to model their distributional response to climate change during this century. Climatic forecasts for the whole century were provided by the National Meteorological Institute of Spain, which adapted the global circulation models CGM2 and ECHAM4 to Spain and produced expected temperature and precipitation values according to the A2 and B2 emission scenarios for each circulation model. We modelled the response of the species to spatial, topographic, human, and climate variables separately. We also produced a combined model using stepwise selection of the variables previously selected according to each factor. In this way every factor was represented in the final explanatory model of the distributional response of the species to environmental conditions. We forecasted the distribution of the species by replacing current climatic values with those expected according to each climate change scenario, while preserving spatial, topographic and human variables. We computed the coincidence between predictions for different emission scenarios in the same global circulation model, and the consistency between predictions for the same emission scenario applying different global circulation models. In general, coincidences were higher than consistencies and, thus, discrepancies between predictions were more attributable to our insufficient knowledge of the effect of the oceans and the atmosphere on climate than to the putative effect of different emission scenarios on future climates.

56.—WALNUT-FRUIT FORESTS OF SOUTHERN KYRGYZSTAN: THE 2000-YEAR HISTORY OF VEGETATION DEVELOPMENT UNDER HUMAN IMPACT

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The walnut-fruit forests of southern Kyrgyzstan are the most extensive walnut forests worldwide and of global significance for biodiversity conservation. Until recently, they were considered to be an impoverished relic of mesophyllic forests of the Tertiary period, and even an evolutionary center of *Juglans regia* by some scientists. However, pollen analyses of the sediments of a sedge fen provide new data to infer the forest history. The results suggest that the walnut stands are only about 1000 years old and have obviously developed in the presence of grazing domestic animals. Only around 1500 AD *Juglans* forests reached their approximate present extension. The results point to an anthropogenic origin of the walnut stands. The intimate interaction with human activities continues today. Walnut forests are of considerable importance for sustaining the livelihoods of local people. Forests are adversely affected by the high amount of firewood and nuts collected, hay making, and by livestock grazing. Detailed vegetation analyses along utilization gradients revealed massive human impacts. Ordination analyses showed that anthropogenic site factors exert a greater influence on variation in vegetation patterns compared to natural site factors. Impoverished stand structures, regressive successions, and almost complete failure of seed-produced regeneration point to an uncertain future of walnut-fruit forests.

57.—THE EFFECTIVENESS OF A METHODOLOGY FOR SIMULATING CLIMATE CHANGE BY MANIPULATING SOIL MOISTURE AND TEMPERATURE IN A SUGAR MAPLE FOREST UNDERSTORY, ONTARIO, CANADA

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To fully capture the range of expected environmental changes associated with climate change, we implemented a two-factor (air/soil temperature and soil moisture) split-plot field design in a sugar maple dominated forest in our study site in Ontario, Canada. To manipulate rainfall input in our seedling plots, we erected open-sided polythene-topped rain-exclusion structures. Under each structure, plots were watered with one of three treatments: 1) “Average” – 1961-1990 average rainfall for local weather station, 2) “Wet” –20% greater than “average”, and 3) “Dry” – 20% less than “average.” Water application amounts were adjusted monthly to track seasonal precipitation patterns. Plots were also manipulated to simulate changes in ambient air temperature based on the Canadian Regional Climate Model predictions for the study area, we established three heat treatments (0°C, 2.5°C, and 5°C) using infrared heaters. Environmental conditions under each structure and within the controls were monitored every 30 minutes with a Decagon EM50 data logger tracking air temperature, soil temperature, soil moisture, and photosynthetically active radiation. Additionally, we measured rainfall and relative humidity at the site outside the rain exclusion structures. Statistical analysis of environmental conditions demonstrates that the temperature manipulation was most effective at maintaining target temperature during the early part of the growing season, but it was more difficult to keep the warmest treatment at 5° C above ambient in the late summer. Target moisture regimes were generally achieved despite microtopography and skeletal soils.

58.—ABIOTIC STRESS AS A RANGE-LIMIT DETERMINANT FOR EUROPEAN PLANTS: INSIGHTS FROM SPECIES’ RESPONSES TO CLIMATIC GRADIENTS

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We examined whether species’ occurrences are primarily limited by physiological tolerance in the abiotically more stressful end of climatic gradients (the asymmetric abiotic stress limitation hypothesis, AASL) and the geographical predictions of this hypothesis: abiotic stress mainly determines upper-latitude and -altitude species’ range-limits, and the importance of abiotic stress for these range-limits increases the further northwards and upwards a species occurs. The AASL hypothesis predicts that species have skewed responses to climatic gradients, with a steep decline towards the more stressful conditions. Based on presence-absence data we examined the shape of plant species’ responses along three climatic gradients across latitudes in Europe (1577 species) and altitudes in the Swiss Alps (284 species) using Huisman-Olff-Fresco and generalized linear and additive models. We found that up to 1/2 (Europe) and 1/3 (Swiss Alps) of the species show responses consistent with the predictions of the AASL hypothesis. Cold temperatures and a short growing season seem to determine the upper-latitude and upper-altitude range-limits of up to 1/3 of the species, while drought provides an important constraint at lower-latitude range-limits for up to 1/5 of the species. We found a biome-dependent influence of abiotic stress and no clear support for abiotic stress as a stronger upper range-limit determinant for species with higher latitudinal and altitudinal distributions.

59.—A REGIONAL VEGETATION-CLIMATE MODEL FOR CENTRAL AMERICA

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Dynamic Global Vegetation Models (DGVMs) simulate the distribution and structure of vegetation as a function of climate. These models are used to simulate biogeochemical cycles and vegetation shifts in response to past, current and future climate change. DGVMs have been criticized for using generic plant functional types (PFTs), various limitations due to the coarse resolution of grid cells, and their assumption of perfect dispersal (where plants can arrive at any location regardless of distance or physical barriers). New DGVMs have been developed to address some of these issues, including the regional dynamic vegetation model LPJ-GUESS. LPJ-GUESS combines an ecophysiological and biogeochemical vegetation model with a regional forest gap model. Competition for light, interactions between shade tolerant and intolerant PFTs, stand structure and succession are simulated in a more realistic manner. In addition, LPJ-GUESS can be run at a finer resolution and can capture the effects of microclimates, elevation and provide a more appropriate scale in which to simulate dispersal. Regional models have been developed for parts of northern hemisphere. However, there has been relatively little effort placed in developing regional models for the tropics. We used LPJ-GUESS to simulate the vegetation in Central America. New tropical PFTs were described and implemented, which allowed the model to represent tropical biomes not included in previous simulations, such as tropical pine-oak forests. Future applications of the model will involve applying paleo- and future climate scenarios, and include mechanistic dispersal limitations for different plant functional types.

60.—RECENT RANGE EXTENSIONS AND CONTRACTIONS OF BIRDS OF TAMAULIPAS

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Distributions of many species in the state of Tamaulipas are changing, as tropical species move north and temperate-zone species move south. During the past decade, Olivaceous Woodcreeper (*Sittasomus griseicapillus*), Streaked Flycatcher (*Myiodynastes maculatus*), Mangrove Swallow (*Tachycineta albilinea*), and Scrub Euphonia (*Euphonia affinis*; nesting) extended their range north to south-central Tamaulipas. Melodious Blackbird (*Dives dives*) and Masked Tityra (*Tityra semifasciata*) were noted in additional areas in south-central Tamaulipas, indicating consolidation of previous range expansions. Agami Heron (*Agamia agami*) has been observed for the 4th time in northeastern Mexico. Some species have spread southward, such as Western Kingbird (*Tyrannus verticalis*), which nested for the first time in Tamaulipas and occurred south to the Ciudad Victoria area, and European Starling (*Sturnus vulgaris*), which nested in south-central Tamaulipas for the first time. Lesser Goldfinch (*Carduelis psaltria*) a highland species, is establishing itself in the lowlands. The ranges of some species, such as Red-Billed Pigeon (*Patagioenas flavirostris*), Red-crowned Parrot (*Amazona viridigenalis*), Green Parakeet (*Aratinga holochlora*), Audubon's Oriole (*Icterus graduacauda*), and other species appear to be contracting due to habitat fragmentation and/or capture for the pet trade. The directions and causes of changes in distribution need to be carefully analyzed.

61.—CLIMATE CHANGE EFFECTS ON MOUNTAIN VEGETATION DISTRIBUTIONS IN THE USA PACIFIC NORTHWEST

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Vegetation types are the aggregate of, and a critical influence on, species compositions. Because of steep topographic, edaphic, and meteorological gradients, minor changes in climate can have significant effects on the distribution of mountain vegetation types. To assess the sensitivity of mountain vegetation types to predicted climate change, we downscaled data from nine general circulation model simulations (three GCMs each run at three CO₂ emission scenarios) to an 800-meter resolution grid spanning a region of the Oregon and Washington Cascade mountain range in the United States. We then used MC1, a dynamic vegetation model, to simulate changes in the Cascade vegetation types and carbon fluxes during the projected 21st century climates. MC1 simulates competition for water, nutrients, and light between plant functional types and uses a biogeographical rule base to classify vegetation type. It also contains a detailed and interactive fire module. Changes in ecotone elevation, ecosystem spatial extent, and carbon storage are shown to reflect non-linear responses to temperature and precipitation forecasts. Two hydrologic factors associated with higher temperatures interact to be the dominant mechanisms of change: 1) an increasing synchrony between precipitation and the beginning of the Pacific Northwest growing season, and 2) earlier snowmelt. Both act to increase the available water content at the start of the growing season, but also increase drought stress later in the summer.

62.—RECONSTRUCTING PALEOHURRICANE DISTURBANCE REGIMES IN THE DOMINICAN REPUBLIC

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Hurricanes are important disturbance agents in tropical ecosystems of the Caribbean region. Although an increasing body of literature has documented the short-term (subdecadal) impacts of hurricanes on tropical vegetation, little is known about their long-term effects on vegetative composition at decadal and centennial scales. It is also unknown whether Caribbean hurricane activity has varied over long-term and how such variations might have affected vegetation development in the region.

Paleotempestology, a young science that studies paleohurricane activity by means of geological proxy techniques, can shed light on this question. We seek to reconstruct the late-Holocene history of hurricane strikes in the Dominican Republic by studying coastal sedimentary records using the principles and methods of paleotempestology. Twenty-five cores were obtained from six coastal lakes in the Dominican Republic and analyzed by loss-on-ignition techniques to identify storm deposits attributed to past hurricane strikes. By correlating events temporally and spatially we are able to establish long-term changes in the disturbance regime in the context of regional climate changes. Evidence from other Caribbean locations has suggested millennial-scale fluctuations between active and inactive hurricane regimes. Palynological analysis is underway to investigate the vegetation response to these prehistoric storms. Furthermore, microscopic charcoal data, in conjunction with the pollen and sedimentary records, will be used to evaluate the interactions between hurricanes and fires in the tropical ecosystems of the Dominican Republic.

63.—RANGE LIMITS AND THE AFROTROPICAL AVIFAUNA

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Although understanding large-scale spatial variation in species' distributions is a major goal in macroecology, relatively little attention has been paid to the macroecological factors limiting species' ranges. An understanding of these factors may help to improve predictions of species' movements in response to global change. We present a measure of landscape impermeability, defined as the proportion of resident species whose ranges end in an area. We quantify and map impermeability for Afrotropical birds and test a suite of hypotheses of its potential environmental correlates. Non-spatial analyses emphasize the importance of broad-scale environmental patterns of energy availability and habitat heterogeneity in limiting species' distributions. Spatial analyses focus attention on smaller-scale factors of habitat and topographic complexity, and also indicate an association with human population density. All our analyses highlight that range edges are concentrated in heterogeneous habitats. Global change is expected to alter the nature and distribution of such habitats, necessitating range movement by resident species. Impermeability provides a simple measure for identifying regions where continuing global change and human encroachment are likely to cause profound changes in regional diversity patterns.

64.—IMPACTS OF TROPICAL FOREST DISTURBANCE UPON RANGE-RESTRICTED AVIFAUNA: EXTINCTION VULNERABILITIES ACROSS ZOOGEOGRAPHICAL ZONES

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Continued modification and degradation of tropical ecosystems is predicted to have severe implications for avifaunal communities, particularly among birds with restricted distributions. These species experience a much greater extinction risk than those with broader ranges, but scant research has been conducted comparing vulnerabilities of these species across zoogeographical zones. We examine and compare the ecological response of range restricted birds to habitat disturbance in two widely separated biological 'hotspots'; a small island ecosystem in the Wallacea region of South-East Asia and a tropical cloud forest in Mesoamerica. Point count surveys of range-restricted species were conducted along disturbance gradients in the Lambusango forest reserve, Sulawesi, and Cusuco National Park, Honduras. Results indicate target species in Mesoamerican cloud forest as being highly vulnerable to environmental disturbance, with populations of range-restricted birds being largely confined to high quality forest types. Wallacean range-restricted species, however, exhibit greater ecological tolerance, despite the theorised biogeographical fragility of small island ecosystems. Our results indicate no significant difference in abundance of range-restricted species between primary, established and heavily disturbed secondary forest. Abundance of these species is only low in cleared agricultural sites. In this paper we consider the biogeographical factors which may influence differential vulnerabilities between Neotropical and Wallacean range-restricted avifauna.

65.—INTRA- AND INTER-CONTINENTAL PATTERNS OF EXTINCTION AMONG SOUTH AMERICAN PLEISTOCENE MAMMALS

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The end-Pleistocene extinctions claimed at least 170 species and more than 90 genera of mammals around the globe, disproportionately affecting large-bodied (>44kg) taxa. South America lost more megamammal genera during these extinctions than did any other continent, yet the causes and dynamics of these die-offs are largely unresolved. To better understand how South America fits in with global late-Quaternary extinction patterns, we compiled and evaluated published radiocarbon dates for Pleistocene megafaunal occurrences, early (>8000 RCYBP) archaeological sites and late-Pleistocene environmental shifts on this continent. We then used the vetted dates to compare timings of human arrival, climate changes and megafaunal extinctions throughout South America and the Western hemisphere. Fourteen genera had robust dates. Last Appearance Dates for these taxa indicate: 1) megafaunal extinctions in South America likely were protracted, occurring between about 45,000 and 8,000 years ago; 2) some taxa persisted significantly longer in South America than in North America; 3) biogeographic patterns of extinction across the continent varied among taxa; 4) megafaunal taxa survived several hundred to several thousand years after the arrival of humans in various regions of South America; and 5) the extinctions of South American megafauna likely were accelerated due to an interaction between human activities and Younger Dryas climate change. These findings suggest that the unusually rapid climate change and heightened anthropogenic impacts occurring today may combine to exacerbate the current biodiversity crisis.

66.—FORECASTING CLIMATE-INDUCED DISTRIBUTION SHIFTS FOR ARBORESCENT CONIFERS OF NORTH AMERICA'S ARID INTERIOR WEST

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We evaluated climate-induced geographic distribution shifts for 29 species of arborescent conifers inhabiting North America's arid interior west. Magnitude of climate change for the current century was calculated from the Hadley Climate Center HadCM3 model run with the Intergovernmental Panel on Climate Change emission storylines A2 and B1, representing severe and moderate scenarios, respectively. The classification technique Random Forests was used to generate distribution models on a species-by-species basis using forest inventory data from across the entirety of each distribution. This technique allowed the identification of climatically distinct varieties within some species, and indicated important variables that were then used to construct minimum-volume ellipsoids representing their realized niche. The application of climate change scenarios to the distribution models resulted in the detection of areas becoming suitable to colonizing populations, as well as areas no longer suitable for regeneration of existing populations. The selection of a regional pool of functionally and taxonomically related species enabled us to gauge shifts in the co-occurrence of species.

67.—ECOLOGICAL NICHE MODELING OF EQUIDS IN THE GREAT PLAINS DURING THE MIOCENE

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Geographic distributions of Miocene horses (subfamily Equinae) from the Great Plains were reconstructed using GARP (Genetic Algorithm using Rule-set Prediction) an ecological niche modeling (ENM) program. This is the first use of ENM and GARP in the continental fossil record; the requisite environmental data layers come from a variety of proxies preserved in sediments. The Equinae underwent a dramatic radiation as climate changed from warm and humid in the middle Miocene to cooler and more arid conditions during the late Miocene. Reconstructed distributions of individual species were analyzed in relation to this climate change. Species ranges were predicted for two successive time slices that span from the Mid-Miocene Climatic Optimum into the early Pliocene (14.5-8.5 Ma and 8.5-2.0 Ma). During the initial cooling phase, species with larger predicted ranges were more likely to survive during times of faunal turnover than species with smaller ranges. As climate continued to become cooler and drier in the late Miocene, range size became irrelevant and extinction rates increased. The reconstructed ranges suggest that patchy distributions were more common than continuous distributions in the middle Miocene when speciation rates were high. In contrast, during the late Miocene, when speciation rates were lower, continuous ranges appear to be more common.

68.—MODELLING COMMUNITY PATTERN IN A DISTURBANCE MEDIATED ECOSYSTEM

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Defining the factors influencing vegetation condition in natural systems can be challenging due to the range of potential influences and interactions at various scales. Where there are large numbers of variables, the availability of suitable field measurements can become limiting as model power is reduced. The modelling of group or community properties can assist in simplifying large datasets and can lead to increase predictive power and more robust inferences. This poster presents preliminary results from a landscape-scale study investigating drivers of vegetation change in heathy woodlands in South Eastern Australia. The woodlands are a Mediterranean type environment, exhibiting summer drought, wildfire, low soil nutrients and high floristic diversity. Management of these areas involves landscape-scale manipulation of fire to achieve a range of goals, including ecological and socioeconomic, even when vegetation dynamics are not fully understood. Modelling community response to environmental influence has the potential to maximise the utility of scarce information, help target information collection and assist in optimising management activities. The results presented here are initial outcomes from a project investigating vegetation composition at both a microsite and landscape levels. Key aims are to assess the environmental drivers of abundance for plant species and compare various methods of modelling species and community pattern at a landscape scale. Methods studied include using Generalized Additive Models (GAMs) to model grouped species response to environmental variables, modelling key species individually with GAMs and then grouping, and modelling multiple species concurrently using Multivariate Adaptive Regression Splines (MARS).

69.—THE EFFECTS OF FISHING, HABITAT, AND BIOGEOGRAPHY ON THE STRUCTURE OF ROCKY REEF FISH ASSEMBLAGES

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The reduction of fishing from coastal environments has been shown to have dramatic effects on total fish biomass and community structure. However, basic patterns of habitat availability are also known to affect fish assemblage structure, especially for species that require a diversity of habitats throughout their ontogeny. In this study, we investigate the effects of fishing, habitat availability, and biogeography on the structure of rocky reef fish assemblages within the Tropical Eastern Pacific. We contrast reef fish assemblages within fished regions of the Sea of Cortez with protected assemblages from the remote islands of the Revillagigedo Archipelago. When comparing fish assemblages from boulder and seamount habitats in each region, we find dramatically different effects of protection on fish assemblage structure. In boulder environments where the dominant fishes have complex ontogenies, local habitat diversity (e.g., presence of mangroves and sea grasses) appears to be more important than fishing pressure in determining the total biomass and trophic structure of fish assemblages. On seamounts, fishing pressure has the strongest and most direct effects on fish assemblage structure, likely due to the site fidelity of most species through ontogeny. We discuss supporting patterns in shark and manta abundance, length frequency distributions, and biogeography to understand the general importance of habitat diversity and fishing pressure on rocky reef fish communities.

70.—THE PROJECTED IMPACT OF CLIMATE CHANGE ON MONTANE BIRDS WORLDWIDE

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Montane regions are an important feature of the biosphere containing high biological diversity and high endemism. Montane systems are also projected to be particularly sensitive to climate change. Local and regional investigations have found that montane species typically respond to changing climates by moving up in altitude. Here we model the global impact of climate change for 1106 montane birds in a spatially explicit manner. We measure projected changes in area of occupancy determined by historic altitudinal associations and projected temperature anomalies between two 20-year time periods (1980-99 and 2080-99). We test four biological scenarios defined along a gradient of altitudinal and geographic responses. Across all scenarios, species located in regions with lower mountain ranges are projected to have the most severe losses in area of occupancy. This outcome is particularly pronounced in southern Africa, northern Asia, northern Europe, and North America. High, extensive mountain ranges, such as the Andes and the Himalayas, provide greater opportunities for altitudinal and geographic dispersal, and as a consequence projected losses in area of occupancy for species in these regions are not as extreme. Across all regions, species with larger historical areas of occupancy or broader elevation associations tend to fare better. In most cases, species with lower minimum altitudinal associations tend to experience smaller losses in area of occupancy. Our assessment suggests that, in many regions and under ideal dispersal and habitat conditions, birds will have limited opportunities to maintain their historic climatic associations. Therefore, unless current anthropogenic climate trajectories are moderated or reversed, mountain-top extinctions for birds and other taxa during this century are likely to be extensive.

71.—GLOBAL WARMING, LAVATIONAL RANGE SHIFTS, AND LOWLAND BIOTIC ATTRITION IN THE WET TROPICS

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Many studies suggest that global warming is driving species ranges poleward and towards higher elevations at temperate latitudes, but evidence for range shifts is scarce for the tropics, where the shallow latitudinal temperature gradient makes upslope shifts more likely than poleward shifts. To date, the only published examples of contemporary tropical range shifts are upslope shifts. Based on new data for plants and insects on a 3000-m elevational transect in Costa Rican wet forests, we assess the potential for lowland biotic attrition, range-shift gaps, and mountaintop extinctions under projected warming. Experimental and observational evidence for decreased fitness in lowland tropical species is beginning to accumulate. We conclude that tropical lowland biotas may face a level of net lowland biotic attrition without parallel at higher latitudes (where range shifts may be compensated by species from lower latitudes) and that a high proportion of tropical species soon face gaps between current and projected elevational ranges. The challenges posed by projected elevational range-shift gaps are exacerbated by habitat fragmentation.

72.—CLIMATE CHANGE AND AMPHIBIAN COLLAPSE IN A MEGADIVERSE COUNTRY

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Global changes are occurring rapidly with an enormous effect on biodiversity. Consequently the need of analytical tools that allows us to understand the changes and making predictions for the future of biodiversity is urgent. Based on the close relationship between species distributional range (DR) and beta diversity we propose a simple model to comprehend the effect of climate change on spatial and temporal dynamics of beta diversity. The model proposes three scenarios depending on the response of the range size of species: “Moderate” predicts an increase in the DR of some species, while a decrease in others; “Homogenization” assumes extinction of species with the smallest DR, i.e., the average range size will increase with time; and “Catastrophic” assumes that individual ranges will decrease massively. Depending on the scenarios we expect different response of beta diversity: remaining similar to today, decreasing or increasing (respectively). As an example of the application of the model we use the amphibians of Mexico. Amphibians have been identified as one of the most threatened groups in the world and Mexico is the fourth richest country in amphibians with around 60% of the species being endemics to the country. We modeled the present and the future scenarios using MaxEnt and CCCma B2 predictions for 2020, 2050 and 2080. The results match our Catastrophic scenario, resulting in dramatic decreases in range sizes. Local extinction of amphibians was predicted to be particularly intense in the period 2020–2050, causing (as expected) maximum beta diversity. A collapse of beta was predicted by 2050–2080.

73.—BIVALVE COMMUNITY CHANGE DURING THE PLIO-PLEISTOCENE CARIBBEAN EXTINCTION

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Extinctions have played a major role in shaping the history of life and defining biogeographic boundaries. While the five major extinctions have played key roles in Earth's history, regional extinctions have also directed the evolutionary trajectories of major portions of the globe. Two million years ago an extinction event in the Caribbean and western Atlantic affected groups as diverse as molluscs, corals, foraminifera, and bryozoans, profoundly shaping modern Caribbean communities. However, the cause of this extinction is not well understood. While the formation of the Isthmus of Panama and associated environmental changes certainly contributed to this extinction, a time lag between environmental change and extinction suggests a nonlinear connection. We examined changes in guilds of bivalves from the southwest Caribbean in order to better understand overarching ecological changes during this period. Trends in the life history characteristics of the bivalves show a decrease in the abundance of suspension feeding bivalves, as well as an increase in epifaunal bivalves, especially those that live attached to hard substrates. These responses are consistent with ecological predictions based on decreases in productivity and increases in habitat heterogeneity, which may have driven extinction and faunal turnover. Future work in the northern Caribbean will address whether a similar change in community structure occurs throughout the region, further informing our perception of the causes of this extinction event.

74.—MORPHOMETRIC ANALYSES OF GEOGRAPHICALLY ISOLATED SHREWS OF THE EFFECTS OF CLIMATE AND LAND USE CHANGE ON BIODIVERSITY IN FRAGMENTED BIOGEOGRAPHICAL REGIONS – A REVIEW

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Land use change is the main driver of biodiversity change and biodiversity loss. These changes are caused by new technologies in agriculture and forestry but also by an important increase in urbanization. Climate change itself influences the potentials of land use and leads to adaptations in land use systems. New mitigation methods to climate change have consequences for the land use itself and for land use intensity. A typical example is the intensification of agriculture for biomass production world wide. These present changes influence the size and structure of different habitats and the configuration of habitats in the whole landscape. Land use adaptation to climate change and mitigation methods will have strong consequences for different elements of biodiversity. These changes will have impacts on the landscape matrix, the linear landscape elements/corridors, stepping stone habitats as well as core areas itself. In biogeographical regions in which the degree of habitat fragmentation allows persistence of selected species and the cohesion of habitats is relatively intact, the change and/or shift of species ranges is inhibited, but generally possible. Additionally, these landscapes allow new species to colonize new areas and habitats better than highly fragmented landscapes. In landscapes with a low spatial cohesion of the habitats climate change will impact much more the degree of species loss and will inhibit the range expansion of new species. An increased frequency of extreme weather events will cause local species loss and an overall reduction of the distribution range, particularly in areas with relatively low levels of spatial cohesion. Both, climate change impact and land use change can result in a mismatch of species ranges and increase in species loss.

75.—CONSERVATION DESIGN FOR RARE BIRDS IN THE UPPER MIDWESTERN UNITED STATES

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Conservation design is comprised of five facets. These five elements are landscape characterization and assessment, population response modeling, conservation opportunities assessment, optimal landscape design, and monitoring and evaluation. I will describe my research in these areas for a collection of rare birds occurring in the Prairie Hardwood Transition Bird Conservation Region. The rare birds we focused on included Bobolink (*Dolichonyx oryzivorus*), Savannah Sparrow (*Passerculus sandwichensis*), Grasshopper Sparrow (*Ammodramus savannarum*), Henslow's Sparrow (*A. henslowii*), Eastern Meadowlark (*Sturnella magna*), Sedge Wren (*Cistothorus platensis*), Upland Sandpiper (*Bartramia longicauda*), American Woodcock (*Scolopax minor*), Black-billed Cuckoo (*Coccyzus erythrophthalmus*), Red-headed Woodpecker (*Melanerpes erythrocephalus*), Golden-winged Warbler (*Vermivora chrysoptera*), Cerulean Warbler (*Dendroica cerulea*), and Wood Thrush (*Hylocichla mustelina*). We mapped predicted abundances resulting from hierarchical spatial count models. These mapped results were then assessed relative to the conservation estate to ascertain which areas of peak abundance were outside of the direct management by governmental authorities. We also used these maps to identify ensemble strategies for affecting conservation for this suite of rare birds. Lastly, we have begun exploring means by which we may be able to use these maps of predicted abundance to calculate regional population sizes to assess how and where the population stands relative to regional population goals identified for these species by Partners in Flight.

76.—OPTIMAL GLOBAL SOLUTIONS FOR THE CONSERVATION OF VERTEBRATES

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Irreplaceability analyses provide a mechanism to assess the relative importance of spatial units to the conservation of a set of species. In this poster, we explore the extent to which the global irreplaceability surfaces for terrestrial mammals, birds and amphibians differ from one another and from similar surfaces targeting combinations of these groups. We identify the degree to which global and regional spatial priorities change as the taxonomic scope of conservation action increases. We also investigate the way in which the characteristics of species distributions from different groups act to constrain the overall flexibility of spatial choice available to conservation planners. We present accumulation curves showing the increasing area of minimal sets of cells required to represent species as the number of representations and number of groups considered increases.

77.—MAKING A STAND: COLONIZATION AND RECRUITMENT OF PONDEROSA PINE AT A RANGE MARGIN

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The colonization and recruitment processes involved in geographic range expansion are poorly understood. In view of predictions that ongoing climate change will radically alter species ranges, the dynamics underlying tree colonization and recruitment near range boundaries are critical to understanding the potential impacts of climate change on vegetation distributions. Using ponderosa pine (*Pinus ponderosa*) this study combines dendroecology and molecular genetics to address colonization and recruitment processes. We studied four disjunct populations of ponderosa pine in the Bighorn Basin of north-central Wyoming. These populations range from 70 to 800 individuals and occur between 10 and 100 kilometers from the nearest core populations of ponderosa pine, which are all in the western Bighorn Mountains. All trees in each of the four populations were aged using dendrochronological methods. All four populations were established within the last 500 years. Initial population growth was slow until the mid 1700's when all populations experienced pulses in recruitment. Records of hydroclimatic variability for the region were obtained. Recruitment pulses coincide with average to wet periods through the record; however, other similar periods do not show corresponding recruitment. Seven nuclear microsatellite markers are being used to analyze the genetic structure of the populations. Combined analysis of age and genetic structure will allow assessment of the relative importance of climatic factors versus genetic variability for population growth and viability.

78.—COMPARATIVE PHYLOGEOGRAPHY OF THREE MANGROVE-RESTRICTED AUSTRALIAN BIRDS

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Climatic fluctuations and their effects on distributions of species have played important roles in shaping the global biota. A particularly interesting aspect of the climatic fluctuations, continental aridification, and faunal exchange between Australia and New Guinea is the evolution of a mangrove-inhabiting avifauna. Especially noteworthy are mangrove-specialized birds in Australia, where several clades include species or subspecies restricted to mangroves. Using DNA sequence data derived from mitochondrial markers, I explored the genetic structure of three mangrove forest restricted Australian birds: *Pachycephala lanioides*, *Peneoanthe pulverulenta*, and *Rhipidura phasiana*. Results show all three species exhibiting similar phylogeographic structure across their sympatric range, pointing towards effects of recent, shared historical events throughout their distributions.

79.—CONSERVATION OF PORTUGUESE SIGNAL BRYOPHYTES SPECIES - PROMOTING A SHIFT IN PERSPECTIVE ON CLIMATE CHANGE

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The Portuguese bryophyte flora is estimated to include more than 40% of European bryophytes species and about 45% of Mediterranean liverworts. Portuguese species comprise 65% of all Iberian taxa rendering bryophytes a recognized key group for the maintenance of Iberian Peninsula biodiversity. It is well known that the protection of bryophytes is limited by the complexity of ex situ conservation. Consequently, for in situ conservation of threatened or endemic species, it is essential to know ecological requirements and the most favorable climatic condition to apply management strategies, which aim to guarantee their long-term persistence. On the other hand, the assessment of species' response to climate change scenarios is a key tool in future conservation strategy. In this study, we examine the response of an assemblage of “signal species” whose distributions are well recognized in Portuguese territory. These “signal species” were individually selected based on their vulnerability, contrasting distributions, their ecological traits and geographic singularity. Predictive models were projected using standard climate change scenarios according to IPCC (2007) data. Projections can indicate broad trends in the response of species placed into contrasting biogeographic groups, and can point to the probable adjustment in the spatial distribution of the Portuguese bryoflora. We underline possible pressures to Boreal/Alpine elements as well as to important Mediterranean bryophyte species.

80.—MORPHOMETRIC VARIATION IN THE THREATENED DIANA FRITILLARY BUTTERFLY

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The Diana fritillary, *Speyeria diana*, is a threatened butterfly that once ranged from the Ozark and Ouachita mountains in the Midwest across the southern United States to the Atlantic Ocean. From a comprehensive survey of over 2000 museum and literature records dating back to the 1800s, we found that this species has disappeared from large portions of its range, while expanding into others. Some populations have become isolated and a major disjunction exists between populations in the Ozark and Ouachita mountains and in the Southern Appalachian Mountains. Our goal is to determine if there are differences across the range and between historical and modern populations, using a combination of morphometric and molecular analyses. We have photographed and digitized wing venation landmarks on fore- and hind wings of 197 individuals, representing most of the specimens in major university and museum collections in the USA and Europe. We performed a Procrustes analysis to remove differences in wing size, then performed a principle components analysis to see which landmarks contributed the most variation in shape. A preliminary analysis found that wing shape varied between sexes and between pre-1950 and post-1950 samples. Current work involves the addition of samples from the western populations to allow an East-West comparison. We are also examining mitochondrial sequence data to test for patterns of genetic differentiation across the range of this species, and through the recent decades of change in geographic distributions.

81.—CAUSES OF SPECIES DIVERSITY GRADIENTS IN NORTH AMERICAN FRESHWATER FISHES

Gerald Ray Smith

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North American freshwater fishes are most diverse in large, wet, old, and stable drainages, characteristic of the Mississippi Basin and adjacent areas. Physical factors, especially geologic and climatic stability, have been much more important than biological interactions in causing regional species diversity differences. Multivariate analysis of environmental variables and fish species presence or absence in quadrats of G. G. Simpson's equal area grid produces a model in which geological processes determine relative persistence or extinction of species. Tectonically active continental margins have low freshwater fish diversity because active uplift reduces metapopulation sizes and connectivity while increasing energy demands on individuals. Comparison with Late Cenozoic fossil diversity shows no evidence for different speciation rates in different regions of North America, leaving extinction rates to explain low diversity in the west and north. Demonstrated correlations with simple null models fail to identify mechanisms that cause diversity patterns.

82.—SIZE MATTERS: EXAMINING PATTERNS OF MAXIMUM BODY SIZE OF MAMMALS OVER TIME AND SPACE

Felisa A. Smith, Alison Boyer, James H. Brown, Dan P. Costa, Tamar Dayan, Alistair Evans, Mikael Fortelius, S. K. Morgan Ernest, Larisa Harding, Kari Lintulaakso, S. Kathleen Lyons, Richard M. Sibly, Juha Saarinen, Jessica Theodor & Mark D. Uhen

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Macroecologists often focus on body size as a factor of interest because it serves as a proxy for many different aspects of an organism's biology - size results from a complex and dynamic tradeoff between physiology, life history, environment, phylogenetic constraints, and past geologic and/or climatic history. Nonetheless, certain 'invariant' size-dependent scaling relationships and broad scale distributional patterns are repeatedly observed for mammals and other taxa. Do these patterns arise because of common ancestry, because organisms exist in similar environments, or because they face similar design or life history constraints? To examine these questions, we assembled a database of maximum body size for the major orders found on each continent (North and South America, Africa, Eurasia and Australia) over the evolutionary history of mammals (late Mesozoic to Recent). Maximum size was chosen because of taphonomic issues involved in characterizing minimum or mean/median size. Our temporal resolution is at the epoch or sub-epoch level (e.g., early, mid or late Miocene); data were collected from a number of primary and secondary sources and/or estimated directly from taxon-specific allometric regressions based on measurements of fossil teeth or limbs. Overall, our results clearly demonstrate a rapid increase in the body size morphospace of mammals over the Cenozoic, reflecting the evolutionary radiation that occurred after the extinction of dinosaurs and other groups at the K/T boundary. Patterns on each of the continents show general similarities when examined by trophic structure, although geologic factors influence the distribution of orders among the continents.

83.—BIODIVERSITY CONSERVATION IN THE DEVELOPING COUNTRIES – MORE OR POOR INVESTMENT?

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Recent studies emphasize the importance of considering costs of conservation in global conservation prioritization. Often developing countries appear as conservation priorities due to low acquisition costs and high biological diversity. However, socio-political factors have been shown to affect the effectiveness and long term costs of conservation in those areas. We use data from the Worldwide Governance Indicators research project as an indicator of effectiveness of protected areas. These are used in conjunction with acquisition costs in a complementarity-based conservation planning approach to identify priorities for mammals at a global scale. Our results highlight the importance of investing not only where the conservation benefits will be the greatest but also where the risk of investment is the smallest.

84.—NOT IN MY BACKYARD! GEOGRAPHIC PATTERNS OF ENVIRONMENTALISM IN THE USA

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How do geographic, cultural, economic, and social factors interact to influence human behavior? More specifically, which factors determine how much value people place on the environment and influence them to the extent that they are willing to donate to conservation organizations? It has been argued that examining economic behavior is an accurate way to investigate individuals' values. Here, I used state-level data of donations to conservation organizations as a proxy for the value people place on environmental protection across the USA. I then chose several factors that I felt might influence donations—income, education level, political climate, population density, and housing unit density—and analyzed these factors in a geographic context. Data were derived from the U.S. Census Bureau. I used Pearson's r correlations and a Pearson Chi-squared test to analyze the data. My results suggest that both median income and education level were significantly and positively correlated with the amount donated. Political climate was related to donations, with Democratic (liberal) states having significantly higher donations than Republican (conservative) states. Population density was not significantly correlated with donations, while housing unit density was significantly and negatively correlated with donations, suggesting that urbanization may influence donations. My findings clearly indicate that there is a relationship between geography and environmentalism in the USA. Further examination of individual values and donation level would lead to a better understanding of the factors that contribute to how much value people place on the environment.

85.—BIOGEOGRAPHY OF EXTANT NORTH AMERICAN MAMMALS: SPATIAL TURNOVER IN RELATION TO CLIMATIC AND PHYSIOGRAPHIC VARIABLES

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This study examined spatial turnover of extant North American mammals geographically and in relation to climatic and physiographic variables that were shown to have strong quantitative relationships to richness and ecological structure. The spatial approach to turnover could allow us to predict its magnitude, location, and rates, with possible paleontological and conservation applications. A grid of 150 mi² quadrats was superimposed over North America, and species presence/absence per quadrat was assigned based on range maps. We identified regions with concentrations of range boundaries. The frequency of boundaries per quadrat was compared to climatic variables describing aspects of temperature, moisture, and topography. The Jaccard index, which quantifies similarity of species composition per pair of adjacent quadrats, was compared to the absolute value of the difference in each environmental variable for the quadrat pairs. Calculations were repeated with body size and trophic categories.

The most obvious geographic pattern in the range boundary data is the concentrations of boundaries on the edges of the Great Plains. Pairwise and multiple regressions of Jaccard indices for species and ecological categories on differences in environmental variables do not indicate strong quantitative relationships between turnover and the environmental variables. Some variables (actual evapotranspiration, elevation, maximum temperature) explain more of the variation in Jaccard indices than others. Jaccard indices are generally high and spatial patterns of turnover may be more obvious over longer distances. The environmental variables seem to explain patterns of species and ecological richness better than turnover in composition at the spatial scale of adjacent quadrats.

86.—ASSESSING THE RELATIVE IMPORTANCE OF CLIMATE AND MEGAHERBIVORY ON LATE-GLACIAL NO-ANALOG VEGETATION COMMUNITIES IN EASTERN NORTH AMERICA

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North American pollen records spanning deglaciation (17-12k cal. years BP) have been shown to include vegetation assemblages that lack a modern analog. These unique communities, centered in the Great Lakes region, have previously been linked to orbitally forced climate change. Deglaciation, human arrival, and the North American megafaunal extinction also occur within the same interval, complicating the search for a cause. Biotic controls of community composition (e.g. herbivory) have previously gone untested, largely because fossil scarcity and dating uncertainties have hindered the establishment of precise lead-lag relationships. Spores from the dung fungus *Sporormiella* persist in lake sediments and have a demonstrated abundance in Pleistocene records, but are absent during the Holocene, suggesting they are a suitable proxy for megafaunal presence. Sediments from Appleman Lake, Indiana, were analyzed for changes in vegetation dissimilarity from present, fire regimes, and herbivore presence (inferred from *Sporormiella*) to investigate the response of vegetation to the removal of megaherbivores and the environmental context of the extinction. At Appleman, *Sporormiella* decreased before warming-induced vegetation change, suggesting that habitat loss was not responsible for the megafaunal decline at this site. Immediately afterwards, vegetation dissimilarity peaked due to an increase in *Ostrya/Carpinus* and *Fraxinus*; this may indicate the release of palatable hardwoods following the relaxation of herbivory pressure. Charcoal data indicate low fire frequencies initially, with an increase in accumulation after the no-analog interval. Data are currently being collected from nearby Spicer Lake to see if the same vegetation pattern holds on the regional scale.

87.—PLIO-PLEISTOCENE CLIMATE CHANGE AND GEOGRAPHIC HETEROGENEITY IN PLANT DIVERSITY-ENVIRONMENT RELATIONSHIPS IN EUROPE

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Plio-Pleistocene climate change may have induced geographic heterogeneity in plant species richness–environment relationships in Europe due to greater *in situ* species survival and speciation rates in Southern Europe. We investigated distinct hypotheses on how Plio-Pleistocene climate change may have affected richness–topographic heterogeneity and –water-energy availability relationships using data on the distribution of 3069 species and Geographically Weighted Regression (GWR). Our analyses showed that plant species richness generally increased with topographic heterogeneity (ln-transformed altitudinal range) and actual evapotranspiration (AET). As predicted, we also found evidence for strong geographic heterogeneity in the species richness–environment relationships, with a greater increase in species richness with increasing topographic heterogeneity in Southern Europe. In contrast, the local AET slopes were at most weakly different between the two regions, and contrary to prediction, there was a band of high local slopes across southern-central Northern Europe. We discuss the potential explanations for these contrasting findings, and conclude that Plio-Pleistocene climate change may sometimes affect current species richness–environment relationships via its effects on regional species pools.

88.—SYSTEMATIC CONSERVATION ASSESSMENT FOR THE MESOAMERICA, CHOCÓ AND TROPICAL ANDES BIODIVERSITY HOTSPOTS

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Using IUCN Red List species as biodiversity surrogates, priority areas for Mesoamerica, Chocó and Tropical Andes (MCTA) conservation were identified using systematic conservation planning. Species' ecological niches were modeled from occurrence records using a MaxEnt (maximum entropy algorithm). Niche models for 78 species were clipped to produce geographical distributions. Areas were prioritized for conservation attention using a complementarity-based algorithm implemented in ResNet software package. Targets of representation for Red List species were set at 10 - 90% of the modeled distributions at 10% increments; for the 53 ecoregions, the target was 10% for each ecoregion. Selected areas were widely dispersed across the region, reflecting the wide distribution of Red List species in MCTA, which underscores the region's importance for biodiversity. Existing protected areas were no more representative of biodiversity than areas outside of them. Among the countries, the protected areas of Belize performed best and those of Colombia and Ecuador worst. A high representation target led to the selection of a very large proportion of each country except Colombia and Ecuador (for a 90% target, 83 -95% of each country was selected). Because such large proportions of land cannot realistically be set aside as parks or reserves, biodiversity conservation in MCTA will require integrative landscape management, which combines human use of the land with securing the persistence of biota.

Contributed Paper Session I

REGIONAL AND LOCAL DRIVERS OF ANT COMMUNITY STRUCTURE

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Environmental gradients such as those tracking variation in elevation have been used as natural experiments for decades. Typically diversity along elevational gradients is correlated to abiotic variables such as temperature, productivity or precipitation. But at local scales, biotic interactions, such as competition for resources, might also affect community structure. In order to assess the extent to which environmental variation and local processes interact to determine the structure of local ant communities, we manipulated food availability and microclimatic conditions at 18 sites along a well-studied elevational gradient in southeastern USA. Specifically we predicted that at low elevations, where climatic conditions are mild, local processes should act to structure communities. But at high elevations, where selection should favor those species which are adapted to tolerate cold temperatures, environmental factors should limit local communities. First, we found that ant species density was negatively related to elevation. Second, once the effect of elevation was statistically removed, we found that adding food to a 1m² quadrat increased ant species density, but only when ground temperature was not reduced by our experimental treatments. Third, our results further show that the effect of food addition was independent of elevation: food addition increased ant species density equally at low and high elevation. We conclude that using manipulative experiments along gradients can help tease apart the relative importance of local vs. regional processes in shaping ant communities.

PHYLOGENIES REVEAL THE UBIQUITOUS INFLUENCE OF COMPETITION ON THE STRUCTURE OF REGIONAL CARNIVORE COMMUNITIES

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The importance of competition in determining regional patterns of species coexistence remains controversial. Traditionally, ecologists have compared the distribution of traits within communities to null expectation derived from a wider species pool, making assumptions regarding species' dispersal abilities and biogeographical limits to range extents. However, the sample of traits within a species pool will also reflect phylogenetic affinities. It has long been recognised that closely related species share similar traits, thus species in a community might sample more or less evenly dispersed trait values depending on the evolutionary distances separating them. Using extensive geographic and biological databases for carnivores, we reveal evidence for widespread competition across communities globally. We use species lists from over 800 national parks in 107 countries to identify carnivore communities, and extract the phylogenetic trees that connect them. We generate null expectations for the distribution of traits within each community given their phylogeny and assuming a Brownian motion model of evolution, in which lineages evolve independently in a manner analogous to a random walk. We show that the empirical distribution of traits is more evenly dispersed than phylogenetic expectations, providing strong evidence for competition. Either species are sorted into regional communities based upon their morphology, or ecological character displacement is common, and species traits evolve rapidly to minimize resource use overlap.

TOWARD A GLOBAL BIOGEOGRAPHY OF TRAITS - AVIAN CLUTCH SIZES ACROSS SPECIES AND SPACE

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Traits vary markedly across species and environmental gradients, but have usually been investigated from either a comparative or a geographic perspective, respectively. Here we analyze the global variation in clutch size across 5,290 bird species, excluding brood parasites and pelagic species. We integrate intrinsic (morphological, behavioural), extrinsic (environmental) and phylogenetic effects in a combined model that predicts up to 68% of the interspecific variation in clutch size. We then apply the same species-level model to predict mean clutch size across 2,521 assemblages worldwide and find that it explains the observed eco-geographic pattern very well. Clutches are consistently largest in cavity nesters and in species occupying seasonal environments, highlighting the importance of offspring and adult mortality that is jointly expressed in intrinsic and extrinsic correlates. The findings offer a conceptual bridge between biogeography, macroecology and comparative biology, and provide a global and integrative understanding of the eco-geographic and cross-species variation in a core life history trait.

ECOLOGICAL AND EVOLUTIONARY PROCESSES IN THE ASSEMBLY OF MAMMALIAN FAUNAS

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Modern species density gradients and the fossil record both show that mammalian faunas, adjusted for latitude, reach the highest species densities in topographically complex areas in tectonically active environments. Likewise, tectonically old, stable environments at the same latitude exhibit lower species density. Modern examples include the depauperate eastern versus the rich western North American faunas and the moderately rich Congo Basin versus the richer East African Rift Valley. The ecological structure of mammalian faunas, as represented by body-size structure and trophic structure, varies predictably in relation to climate and topography. Together these patterns suggest a model of tectonic plus climatic controls on evolution and environmental sorting. Tectonically active regions have promoted speciation in excess of extinction of terrestrial mammals over geologic time. Quaternary climatic variations have caused species that originated in highly fragmented landscapes to expand their ranges as habitats become connected during periods of glacial advance. Climatic variations also sort species according to their ecophysiological tolerances into different continental regions. Several predictions of this model are tested with modern phylogeographies and data from the Neogene fossil record.

JANZEN REVISITED: ARE MOUNTAIN PASSES PHYSIOLOGICALLY HIGHER IN THE TROPICS?

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In 1967, Dan Janzen proposed the influential, but largely untested hypothesis that tropical mountains are physiologically higher than temperate mountains. I test his most basic prediction, the one upon which all the others rely: namely, that elevational range sizes of organisms get larger on mountains at increasing latitudes. My analyses use 187 montane gradients spanning 36.5°S to 48.2°N latitude compiled from over 80 years of research and 16,500 species of rodents, bats, birds, lizards, snakes, salamanders, and frogs. In support of Janzen, I find that all vertebrate groups except rodents increase elevational range size with increasing latitude. Further, I find that controlling for mountain height, sampling, and scale effects is necessary to reveal the trend in breeding birds and detect the strength of the trend in other taxa. I document additional lines of evidence for temperature regime variability as a plausible mechanism for vertebrate range size trends by contrasting of ectotherms and endotherms, low- and high-elevations assemblages, degree of dispersal proficiency, and dry and humid mountain climates.

PREDICTING THE PAST DISTRIBUTION OF SPECIES' CLIMATIC NICHES

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Predicting the past distribution of the climatic niches of species, hindcasting, using species distribution models is emerging as an exciting research area. Species distribution models, SDMs, have been applied to examine veiled evolutionary questions about extinctions, locations of past refugia, migration pathways, and to propose hypotheses concerning the past population structure of species in phylogeographical studies. SDMs are sensitive to theoretical assumptions, to model classes and to projections in non-analogous climates. Studies hindcasting the climatic niches of species often make reference to these limitations. However, awareness of the potential limitations without dealing with them is not enough to obtain strong scientific inferences. Here, I review the literature on hindcasting SDMs. I also summarise a set of “minimum requirement procedures” that would allow for more robust hindcasting of the distribution of the climatic niche of species. Many of the studies reviewed do not reach the basic standards that the community working in niche modelling has widely accepted. Those studies: 1) do not test the conservatism of ecological niche conditions along time; 2) only use one model class (80% of the reviewed studies) and one paleoclimatic reconstruction (70%) to calibrate the niche; 3) do not check for the occurrence of non-analogous climates (100%); and 4) do not use independent data to validate the models (70%). Using inadequate methods for hindcasting SDMs may well entail a cascade of errors and naïve ecological and evolutionary inferences. Also, it is difficult to compare studies when there is no unified protocol to hindcast the distribution of the climatic niche of species.

NICHE THEORY AND NEUTRAL THEORY AS EXPLANATIONS FOR BROAD-SCALE DIVERSITY GRADIENTS: A TEST WITH ANTS

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Two bodies of theory have evolved to elucidate what limits the number of species in a local community, and why that number varies among communities. First, niche theory posits that differences among species in their environmental tolerances, niche requirements, and competitive abilities determine coexistence. Second, and in stark contrast to niche theory, the Neutral Theory of Biodiversity (NTB) suggests that all species are functionally equivalent and that community changes arise as a product of drift, dispersal, and random speciation. I tested the predictions of both niche theory and the NTB using data from elevational diversity gradient in ants. Specifically, I asked whether differences among species in their responses to temperature or competitive interactions shape the elevational diversity gradient, as niche theory would predict, or whether purely neutral processes lead to the elevational diversity gradient, as the NTB predicts. Using null models and detailed behavioral observations of species competing for resources, I found that competition does not shape the broad-scale distribution of diversity in this system. Instead, the most likely explanation is that differences among species in their thermal niches shape this elevational diversity gradient. I also found that beta diversity between communities was not related to distance between communities in the way that the NTB predicts. This finding, coupled with the evidence for thermal niches, indicates that there is no support for the hypothesis that drift, dispersal, and speciation shape this gradient. In addition, even in environmentally benign portions of the gradient, there was no evidence for the NTB. Taken together, the results of this study suggest that understanding how individual taxa respond to climate may shed light on the mechanisms that limit the number of species in local communities and lead to variation in the number of species among communities.

GLOBETROTTING: PATTERNS OF SIMILARITY IN MAMMALIAN DISTRIBUTIONS ACROSS CONTINENTS

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What characteristics predispose mammals to be successful migrants? Is there an optimal body size or ecological specialization that facilitates the movement of species across space? Here, using a global database of mammals, we examine the overlap in species distributions across the 5 major continents (North America, South America, Eurasia, Africa and Australia). We include late Quaternary and both volant and nonvolant mammals, but exclude humans and anthropogenic-mediated introductions. Interestingly, less than 5% of the species present in the late Quaternary are found on more than one continent, and only 4 species have distributions that include three continents; no non-introduced mammal is found on all continents except humans. Given the very low taxonomic overlap, we discuss the potential roles that body size, ecology, and phylogeny play in driving observed continental species distributions.

RECENT UPWARD SHIFT IN FOREST PLANT SPECIES' MEAN ELEVATION FROM GLOBAL TO LOCAL SCALE

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There is growing evidence that plant species are shifting their distribution pole-wards and upwards due to the warming climate, especially at their latitudinal and altitudinal extremes. However, many studies have failed to disentangle climate from other possible drivers of species distribution changes. Here, we assess changes in the mean altitudinal distribution of forest plant species spanning the entire elevation gradient covered by forest at three different spatio-temporal scales: ranging from the larger scale of six western European mountain ranges (1905-2005) to the smaller scale of one single mountain range (1989-2007). By using both macro- and micro-ecological techniques and filtering out information through these three spatio-temporal scales we confirmed that climate warming has resulted in a significant upward shift of species' mean elevation. Out of the 87 species studied, 42 species shifted upward, whereas only 9 species shifted downward. Larger shifts were found for species with limited dispersal abilities, suggesting range contraction rather than expansion. We conclude that climate change not only affects the spatial core of the distributional range of forest plant species at a global scale, but also at a more local scale.

ECOLOGICAL NICHE CONSERVATISM: THE DOMAINS AND LIMITS OF CONSERVATISM, CHANGE, AND CONVERGENCE IN ECOLOGICAL DIMENSIONS

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Ecological niche conservatism has been explored quantitatively over the past decade, with diverse results: studies of different taxa, in varied regions, and in different ecological dimensions have variably concluded that niche evolution has been conservative, plastic, or even convergent. As recent discussions in the literature reflect, analytical methodologies have been heterogeneous and synthesis is badly needed: 1) how conservative is niche evolution? 2) under what circumstances is it not conservative? and 3) what are the implications of this conservatism? I review results of studies of conservatism to date across several time scales: 1) immediate – species' invasions and evolutionary change of ecological potential during invasions; 2) short – longitudinal studies between Pleistocene and present; 3) intermediate – comparisons between sister species pairs; and 4) long – phylogenetic comparisons across more distantly related lineages. Although results appear to be conflicting, synthesis is possible: I offer a view of evolutionary change in ecological niche characteristics that is more unified and that can provide a robust basis for predictive understanding of biogeography and other biodiversity phenomena.

Contributed Paper Session II

TESTING BIOGEOGRAPHIC MODELS OF COMMUNITY ASSEMBLY, COLONIZATION AND VICARIANCE WITH COMPARATIVE PHYLOGEOGRAPHIC DATA AND HIERARCHICAL BAYESIAN MODELS

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Knowledge of island biodiversity and the population-level genetic composition of island species can provide insights into the history of how island ecosystems were established and how species within those ecosystems evolved after they were established. This knowledge can then provide insight into how island species and communities respond to climate change, invasions, and the possible outcomes of combining species into communities that have no current or historical analogs. The imminent prospect of reconstructing the ecological and evolutionary history of all species within an island community from “whole ecosystem” phylogeographic data will enable testing controversial and unresolved hypotheses of community assembly including neutral and niche-based models. However, the analysis of DNA sequence data from many multiple individuals of many (i.e., 50 - 500) species presents analytical and computational challenges. Here we present and demonstrate an analytical and computational framework that can handle such large scale data sets while incorporating genetic coalescent variance as well as uncertainty and variability in a suite of important demographic factors that vary in magnitude across taxa (i.e. population sizes, dispersal rates, mutation rates, and island colonization times). This hierarchical approximate Bayesian computation (HABC) framework uses coalescent simulations under a range of demographic models and can yield inferences about colonization patterns across co-distributed island taxa while allowing for demographic differences across these taxa. The HABC approach will be used to test controversial community assembly models by inferring temporal patterns of island colonization and invasion.

A MARINE BIOGEOGRAPHIC BARRIER AT THE MARQUESAS: LIMITED DISPERSAL ACROSS THE SOUTHERN EQUATORIAL CURRENT

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The Marquesas Islands have a relatively impoverished marine fauna and rank third in Oceania in level of endemism in shore fishes (11.6%). The high level of endemism at the Marquesas has been attributed to variable sea water temperature and geographic isolation. Scientific surveys of this area are few due to isolation and expense, and only a handful of genetic studies include the Marquesas. One previous study of a surgeonfish (*Acanthurus triostegus*) shows a phylogeographic partition at the Marquesas, but an angelfish (*Centropyge loriculus*) and a squirrelfish (*Myripristis berndti*) show no genetic break in this area. To evaluate the reputed biogeographic barrier at the Marquesas we present Pacific wide molecular surveys of two snappers, *Lutjanus kasmira* and *L. fulvus*. Based on sequences of mitochondrial cytochrome-b we observed strong overall population structure (*L. kasmira*, $F_{st} = 0.44$; *L. fulvus*, $F_{st} = 0.65$). Pairwise comparisons indicate that both snappers demonstrated strong genetic differentiation of Marquesas populations (*L. kasmira*, $F_{st} = 0.58-0.63$; *L. fulvus*, $F_{st} = 0.64-0.90$). Removing this population from analyses revealed a contrasting pattern of population structure with *L. kasmira* demonstrating no genetic structure in the Pacific ($F_{st} = 0.01$) and *L. fulvus* retaining high levels of structure ($F_{st} = 0.11$). Molecular evidence coupled with oceanographic current data indicate that the Marquesas occupy the fastest flowing portion of the southern equatorial current, isolating the Marquesas from the rest of the tropical Pacific, while allowing for limited dispersal from the Marquesas in a westerly direction.

HISTORICAL BIOGEOGRAPHY OF THE PANTROPICAL CASHEW (ANACARDIACEAE) AND FRANKINCENSE (BURSERACEAE) FAMILIES

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The sister angiosperm lineages Anacardiaceae and Burseraceae are a valuable comparative model for investigating the interplay of key innovations and historical biogeography during cladogenesis. The families comprise ca. 1500 species worldwide; however, the latitudinal range as well as the morphological and ecological diversity of Anacardiaceae considerably eclipses that of Burseraceae. These differences raise the question of how lineages having identical age and equivalent numbers of species could have undergone such contrasting evolutionary trajectories while becoming so widespread. Here we present an analysis of historical biogeography and evolutionary rates that tests two outstanding hypotheses: 1) that Anacardiaceae and Burseraceae diverged in western Laurasia during the Palaeocene or earlier; and 2) that some disjunct lineages of Anacardiaceae expanded their ranges through cold, high-latitude land corridors whereas those of Burseraceae did not. Phylogenetic reconstruction incorporated Bayesian analysis of DNA sequence data from 250 species representing 62 of 82 Anacardiaceae genera, 15 of 18 Burseraceae genera, and diverse Sapindales outgroups. Nine fossil-based ages were used to estimate evolutionary rates and divergence times across the phylogeny. These results were then considered with those from Bayes-DIVA, which incorporates dispersal-vicariance reconstructions with measures of phylogenetic uncertainty, in order to assess the location, rate, and timing of cladogenic events associated with the hypotheses under investigation.

MOLECULAR DATING AND BIOGEOGRAPHY OF *RUTA* L. (RUTACEAE): A CASE STUDY FROM THE MEDITERRANEAN BASIN

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Understanding the origin of island endemics is a central task of historical biogeography. Recent advances in molecular dating techniques (e.g., modelling fossil calibrations) and model-based range reconstruction methods (e.g., incorporation of geological knowledge into the analysis) provide a rigorous framework in which to address important biogeographic questions. This is crucial to determine the relative contribution of different biogeographic processes (e.g., vicariance, geodispersal, long-distance dispersal) to the origin of island endemics. The Mediterranean basin, with its complex but well-known history of micro-plate movements and climatic oscillations, provides the geological backdrop for the diversification of *Ruta*. This genus includes four species with a peri-Mediterranean distribution and five island endemics: *R. corsica* and *R. lamarmorae*, restricted to Corsica and Sardinia, and *R. pinnata*, *R. microcarpa*, and *R. oreojasme*, restricted to the Canary Islands. Phylogenetic, molecular dating, and ancestral range reconstruction analyses were carried out to investigate the extent to which past geological connections and climatic history of the Mediterranean basin explain the current distribution of species in *Ruta*. The origin of *R. corsica* and *R. lamarmorae*, postulated to be of a vicariant nature due to the split of Corsica and Sardinia from the Iberian peninsula during the Oligocene, is better explained by long-distance dispersal. The Strait of Bonifacio, separating these two islands, is suggested to have promoted vicariant speciation between *R. corsica* and *R. lamarmorae*. Finally, the monophyly of the species endemic to the Canary Islands indicates a single origin of the lineage, driven by long-distance dispersal, followed by diversification within the archipelago.

COMPARATIVE PHYLOGEOGRAPHY OF NORTH ATLANTIC INTERTIDAL AND COASTAL MARINE COMMUNITIES: TESTS OF VICARIANCE AND COLONIZATION USING A HIERARCHICAL BAYESIAN APPROACH

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A primary hypothesis in vicariance biogeography is that congruent patterns of divergence across multiple taxa suggest a common (abiotic) cause. In the North Atlantic, recent studies have used genetic evidence to test this hypothesis, although comparison of a larger number of co-distributed taxa is necessary to further explore hypotheses of divergence patterns and processes underlying community assembly. We conducted a statistical phylogeographic analysis of multiple (>20) co-distributed trans-Atlantic taxa, including fishes, crustaceans, and molluscs, among others, using mtDNA sequence data in a coalescent framework (msBayes) to assess biogeographic questions regarding patterns of divergence and colonization across the North Atlantic. More specifically, we asked (1) Is there evidence for simultaneous divergence across the North Atlantic? (2) Are divergence times congruent within and/or across disparate taxonomic groups? (3) Is there evidence for post-glacial colonization of the North American shore from Europe? and (4) Can ecological correlates explain differences in persistence of taxa in North America through the Pleistocene? Simultaneous divergence was rejected for almost all taxon sets; however, shared divergence times suggest Pleistocene glaciations were important mechanisms in shaping North Atlantic communities. Furthermore, analysis of this larger subset of taxa supported the hypothesis that dispersal ability is generally correlated with Pleistocene persistence in North America.

PHYLOGEOGRAPHY OF THE NORTH AMERICAN RED FOX

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The red fox (*Vulpes vulpes*) is the most widely distributed mammalian carnivore in the world, occurring throughout most of North America, Eurasia and North Africa in a diverse array of habitat conditions. Fossil and morphometric evidence suggests that indigenous populations of the red fox in North America were derived from populations isolated in 2 disjunct refugia during the last glaciation: 1 in Beringia and 1 in the contiguous United States. To test this hypothesis, we conducted a phylogeographic analysis of red fox populations from Eurasia and North America. We sequenced 696 bp of the mtDNA genome from 220 red foxes. Phylogenetic analysis of the cytochrome-b gene produced 2 clades (splitting 408 kya); a Holarctic clade (Eurasia, Alaska, western Canada) and a Nearctic clade (North America). Thus, red fox populations that migrated north or into the western mountains of the contiguous U.S. were from the southern refugium and were derived from a colonization of North America during the Illinoian glaciation (300-130 kya), whereas populations that migrated south from the northern refugium represent a subsequent colonization during the Wisconsin glaciation (100-10 kya). In addition we found division within the Nearctic clade, identifying divergent lineages in the East and in the western mountains. Our findings indicate that Nearctic clade red foxes are phylogenetically distinct from their Holarctic counterparts, and reflect long-term isolation in disjunct forest refugia during the Pleistocene. The montane lineage, which is ecologically distinct from all other North American populations and includes endangered populations, may represent an evolutionarily significant unit.

PHYLOGEOGRAPHY OF THE EURASIAN PYGMY SHREW, *SOREX MINUTUS*

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Sorex minutus, the Eurasian pygmy shrew, is the most widespread species of the Holarctic genus *Sorex*. It is present in the three European Mediterranean peninsulas: Iberia, Italy and the Balkans, considered as Quaternary southern refugia. The geographical distribution of the pygmy shrew prompts interesting questions about its genetic diversity, phylogeographical patterns and postglacial colonization history. Here, we continue and expand the previous research on *S. minutus*, with particular emphasis on the genetic diversity and differentiation among Mediterranean refugial areas. Using cytochrome-b data from 202 individuals, we provide further understanding of the genetic lineages that are found in Europe. As expected, the phylogenetic analysis revealed three distinct phylogroups for the Mediterranean peninsulas, and a fourth independent Northern-Central Europe phylogroup. Haplotypes found in individuals collected from the Mediterranean peninsulas were not found in Northern-Central Europe, reflecting that the Mediterranean region is an area of endemism. Also, the Northern-Central Europe phylogroup carries a signature of recent population expansion, and we consider possible sites from which this expansion originated (the likely refugial area for this phylogroup). Furthermore, a highly distinctive Southern Italian phylogroup has been found, as well as a widespread Pyrenean clade. The phylogeographic analyses show that the pygmy shrew is a mosaic of distinctive genetic lineages with a complex postglacial history of differentiation.

PHYLOGENY AND BIOGEOGRAPHY OF ORIOLIDAE (AVES: PASSERIFORMES)

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The understanding of oscine passerine dispersal patterns out of their Australian area of origin is still hampered by paucity of robust phylogenies. We construct a phylogeny of one of the families of oscines, Oriolidae, which is distributed from Australia across the Old World. We assess direction and timing of dispersal and whether dispersal can be linked with the well-documented movements of geological terranes in the Indonesian Archipelago. We sampled all 30 species of Oriolidae as well as some subspecies of *O. chinensis*. Two nuclear (GAPDH and ODC) and two mitochondrial (ND2 and ND3) genes were used to construct a phylogeny of Oriolidae. The sequence data were analysed using Bayesian inference, and Maximum Likelihood. We also used a Dispersal-Vicariance analysis to assess areas of origin for Oriolidae. A robust phylogeny of Oriolidae confirms the overall sub-groupings as proposed by earlier systematists. *Oriolus chinensis* is polyphyletic and should probably be divided into three species. The DIVA analysis suggests an Australian origin for the group. We find distinct and well supported clades according to classic systematics. Our study demonstrates that Oriolidae has its origin in the Australo-Papuan region from where it dispersed in the first place to Asia and then onwards to Africa, the Philippines and back into the Indonesian Archipelago.

PHYLOGEOGRAPHY AND NICHE PARTITIONING OF THE WESTERN JUMPING MPMOUSE (*ZAPUS PRINCEPS*) DETECTS DEEP, CRYPTIC LINEAGES IN THE SOUTHWESTERN UNITED STATES

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Geographic variation was assessed for the western jumping mouse (*Zapus princeps*), a species that is associated with the highly disjunct montane and mesic habitats of western North America. Nine of 11 subspecies of *Z. princeps* were examined using the mitochondrial cytochrome-b gene and two nuclear genes. Three other species, *Z. trinitatus*, *Z. hudsonius*, and *Napeozapus insignis*, were included as outgroups. Phylogeographic relationships of *Z. princeps* revealed 5 distinct and reciprocally monophyletic lineages (Boreal, Uinta, Southern Rockies, Northern Sierras, and Mid-Sierras). Divergence estimates among these major lineages were about 10% and comparable to interspecific differences often observed among sister species in other rodents. Two lineages detected in the Sierra Nevada of California (Northern Sierras and Mid-Sierras) were more closely allied to *Z. trinitatus* than to other populations of *Z. princeps*. Four lineages have relatively limited geographic distributions in the southwestern United States and occur in habitats that are critically threatened by anthropomorphic and environmental modifications such as livestock grazing, development, and drought. Finally, ecological niche partitioning, using Maxent, revealed significantly segregated habitats between each of the lineages of *Z. princeps*.

BAT FAUNA OF THE EASTERN MEDITERRANEAN: HISTORICAL BIOGEOGRAPHY VS. MACROECOLOGICAL EXPLANATIONS

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Based on a complete database of faunal records of bats in the Eastern Mediterranean (7800 items, essentially contributed from our field studies in all countries of the region summarized in a series of monographs) we analyzed distributional status of particular species and chorologic patterns of bat fauna throughout the region. With current additions the species list consists of 64 species. For 58 of them the Eastern Mediterranean represents either the range margin or the very center of their West Palearctic range. We estimated localization and structure of range margins in that region, and in several model taxa analyzed patterns of geographic variation in morphological and molecular traits. There are clear congruences in the distribution of range margins within particular chorologic groups, but not in the taxa endemic to the region. Climatic and environmental variables related to productivity and aridity were found to be robust explanatory variables in most instances. Geographic plots of residuals of the respective relations, mapping the regions in which faunal patterns cannot be explained by ecogeographic variables, show conspicuous congruence with zones of major phylogeographic shed along the Zagros and Talysh mountains, which were also identified with the aid of other techniques. A core of faunal diversity of the Eastern Mediterranean is in the Levant region (Lebanon in particular), apparently for paleogeographic reasons.

Contributed Paper Session III

RANGE SIZE HERITABILITY MAY FORM CURRENT RANGE SIZE DISTRIBUTIONS

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The geographic ranges of species are fundamental units of macroecology, and their size and location influences patterns of species richness and modulates community interactions. The determinants of geographic range sizes themselves are a subject for discussion, although likely candidates are ecological traits such as the degrees of resource specialization and climatic tolerance, as well as historical events. However, range size is an emergent trait that exists at the species level, and it has been argued that it may largely be determined by inheritance from ancestral species; it would thus be a candidate for a trait undergoing genuine species-level selection. We employed a computer simulation to test whether species-level heritability of range sizes is consistent with the range-size frequency distributions of extant assemblages. The simulation models a branching process, in which the range size of each new species is determined by the range size of its ancestor plus a random term, emulating the assumptions of linear ancestor/descendant regressions (“Jablonski Plots”) that are frequently employed to describe range size heritability. We employed an inverse modeling approach, where we tested a large range of parameter values. The results of simulations were sensitive to the exact assumptions of the Jablonski Plots; however, simulations incorporating range size heritability consistently generated RSFDs with a better fit to an empirical dataset of the bird distributions in South America. These results indicate that range size heritability is consistent with extant RSFDs, and may play an important role in generating current patterns of range sizes.

EVOLUTIONARY FACTORS IMPORTANT TO THE FORMATION OF RANGE LIMITS AND SPECIES DISTRIBUTIONS

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Patterns of species diversity in tropical communities have been intensively studied and are well documented, but mechanisms that determine the distributions and ranges of individual species within these communities are a catalog of case studies. A tribe of butterflies, the Pronophilini (Lepidoptera, Nymphalidae, Satyrinae), in the northern Andes of South America provides an ideal system for studying patterns of diversification and the evolutionary component of range limits. Pronophilines have a unique pattern of allo- and parapatric distributions. Species ranges are allopatric along the Andes where deep valleys act as dispersal barriers. Within each part of the range, lower-flying species are replaced parapatrically at higher elevations, often by species that are endemic to a specific part of the Andean range. I have developed a species-level phylogeny for the Pronophiline genus, *Lymanopoda*, which is composed of approximately 60 species. A multilocus dataset was created and maximum parsimony, maximum likelihood, and Bayesian methods were used to determine the most suitable tree. The resulting phylogeny was then used to test geographical mechanisms of speciation—speciation across elevational gradients and speciation within elevational bands. Results suggest that speciation occurs primarily within elevational bands. Occasionally speciation events crossed elevational gradients and there was subsequent radiation into higher elevations. Ancestral clades are composed of low elevation species. Within clades composed of species inhabiting different elevations, ancestral species maintain lower elevational range limits than more derived species.

TAXONOMIC AND REGIONAL UNCERTAINTY IN SPECIES-AREA RELATIONSHIPS AND IMPLICATIONS FOR CONSERVATION BIOGEOGRAPHY

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Species-area relationships (SARs), the change in species numbers with increasing area, are an essential tool for conservation biogeography. They are used, for example, to estimate broad biodiversity patterns, to compare species richness when regions differ in area, and to predict extinction rates following habitat loss. In the main, applications of SARs have assumed the classical form of a power function, $S = cAz$. If this assumption of a universal power SAR is released and if the underlying form of SARs actually differs markedly between biomes and between major taxonomic groups this would be of particular concern for ecology. Here, we used data on the species richness of vascular plants and vertebrates across the world's terrestrial ecoregions to conduct global scale and intra-biome SARs analyses. We quantified the probabilities of different models to best describe the SAR and determine whether those probabilities vary systematically across taxa and regions. Our results reveal a general high degree of uncertainty in the best-fitting SAR model. When comparing the results of conservation applications and biogeographical studies taking into account this uncertainty with those arising from classical analyses assuming the power SAR model, we highlight major issues with the assumption of a power SAR. In conclusion, we show that both empirical and theoretical analyses that do not account for the uncertainty in the relative fit of different SAR models may well lead to conclusions and conservation prioritizations that are at odds with real patterns of spatial variation in species richness.

COMPARISON OF TRAIT STRATEGIES OF CO-OCCURRING NATIVE AND EXOTIC PLANTS: IMPLICATIONS FOR PREDICTING SUCCESSFUL INTRODUCTIONS

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Understanding what makes an introduced species successful has been one of the priorities of invasion biology. Determining the syndrome of traits an exotic must possess to survive and flourish has been the common approach to address this problem. Here, an alternative method was used to address the problem. Using a global dataset (529 communities) of co-occurring native and exotic species, the level of between-group trait similarities was established. For this, three physiologically relevant traits (specific leaf area—SLA, seed weight—SWT, and maximum canopy height—Hmax) were compared. Comparisons of co-occurring native and exotics showed exotics having 9% higher SLA, 13% Hmax and 49% smaller SWT. Comparisons of the trait composition and ecological distances pointed out significant differences between plant groups. Based on these differences in a multidimensional trait space, successful exotics are believed to exhibit a fundamentally distinct trait composition when compared to co-occurring natives. In summary, exotics species express a strategy of greater growth rates and larger seed production (both overall and per unit seed mass) compared with natives. This study provides the first global examination of the differences in trait composition between native and exotic species.

LATITUDINAL COINCIDENCE BETWEEN BIOGEOGRAPHIC REGIONALIZATION AND DIVERSITY PATTERNS: THE PRECISE BOUNDARY BETWEEN PALAEARCTIC AND ORIENTAL REALMS IN EAST ASIA AS A CASE STUDY

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In this study, I analyzed the latitudinal biogeographic patterns of 379 reptiles in East Asia. I tested the power of geometric constraint to explain the reptiles' latitudinal richness patterns. I also tested whether there was a significant Rapoport's effect along this latitudinal gradient. Three data sets used were subject to three spatial ranges—the range limit of Oriental Realm, the range limit of Palaearctic Realm and the overall terrestrial range of East Asia. Cluster analysis integrating a bootstrapping technique, the program 'Mid-Domain Null', the relationship between latitudinal range extent and mean latitude and canonical correspondence analysis were used to test the patterns for each data set. My results indicated that: 1) the latitudinal band 34°N was the delimitation line for Palaearctic and Oriental Realms in East Asia; 2) there were mid-domain effects both in the boundary of Oriental and Palaearctic Realms, while within the range of Oriental Realm the mid-domain effect was stronger. However, the mid-domain effect was not detected at the whole range of East Asia; 3) Rapoport's rule was fully not supported for reptilian fauna in East Asia for all three spatial extents; and 4) annual precipitation and minimum annual air temperature were the two major factors to explain reptilian latitudinal patterns in East Asia. In conclusion, biogeographic region is an essential spatial extent for studying macro-ecological patterns. Environmental factors, not geometric constraint, are most consistent with reptilian latitudinal richness in East Asia.

CATASTROPHIC EXTINCTION DEBT ON OCEANIC ISLANDS

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Habitat destruction is generally considered to be the major cause of species extinction in terrestrial environments. However, there is normally a time-lag between habitat loss and extinction because small remnant populations often survive, temporarily, in remnant habitat fragments. These 'surviving but ultimately doomed' (acheronian) species represent an 'extinction debt.' Many oceanic islands provide valuable model systems for investigating the dynamics of extinction debts as they typically combine high endemism and a recently documented history of habitat destruction. Here we are assessing the magnitude of extinction debts by taking into account regional-specific and taxon-specific information. Specifically, we predict the magnitude and taxonomic distribution of the extinction debt in forest-dwelling endemic arthropods on the Azores by using ecologically adjusted species–area projections taking into account the sequential reduction of native forest since human colonization and current densities on islands differentially affected by forest destruction and fragmentation. The results reveal a dramatic extinction debt and suggest that past and current forest conservation management strategies are inadequate.

ECOLOGICAL PATHWAYS TO EXTINCTION IN MAMMALS

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The 2008 Global Mammal Assessment estimates that one quarter of all mammals are in danger of extinction, and over half of all mammal populations are in decline. As such, a major priority for conservation science is to understand not only the key causes of extinction, but also the interactions among ecological traits that make certain species more vulnerable to extinction than others. Here, using a newly compiled database of nearly 5000 mammal species and the 2008 IUCN Red List we use decision tree models to quantify the multiple interacting factors associated with extinction risk. We identify the unique pathways to extinction for species with different lifestyles and sets of traits, and show that species of all body sizes have a non-zero risk of extinction depending on their specific ecologies. Moreover, while extinction risk increases exponentially with body size, a size-selective signature is not simply a function of the absolute size of a species, but its size relative to species with otherwise similar ecologies. These new insights into extinction processes, and the simple rules of thumb generated by the decision tree model, should increase the ability of conservation scientists to identify those species at greatest risk due to their specific suites of ecological traits.

RICHNESS-CLIMATE RELATIONSHIPS IN WOODY PLANTS ARE CONSISTENT THROUGH THE HOLOCENE

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Many hypotheses have been proposed to account for global scale gradients of taxonomic richness. The hypothesis that climate determines richness (by some unspecified mechanism) predicts that spatial variation in richness should correlate with climate, and that when climate changes, richness should change accordingly. Richness-climate relationships have been extensively documented for a wide range of taxa and environments. Moreover, it has been shown that richness-climate relationships are very similar in different regions of the planet, and that they persist as seasons change, i.e. over time. However, it is not known whether these relationships also persist as climate warmed since the Last Glacial Maximum. We tested this prediction of the richness-climate hypothesis by analyzing reconstructions of woody plant distributions and temperature for the last 14,000 years in North America (north of México). We found that richness-temperature relationships remained constant during the Holocene. However, during the late Pleistocene, richness at intermediate temperatures (~8-15°C) was higher than the Holocene would predict. These results suggest that richness tracked climate during periods of moderate climate change. During the rapid warming following deglaciations, richness increased rapidly and subsequently relaxed to an apparent steady-state.

WHERE WERE REFUGIA FOR AFRICAN BIRDS AND MAMMALS DURING THE LAST GLACIAL MAXIMUM?

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Refuge theory holds that the distribution of forest and non-forest biomes changed continuously during the Quaternary, breaking up into isolated blocks and again expanding and coalescing under the varying arid and humid climatic conditions. Pollen-based reconstruction of past biomes corroborate the existence of forest refugia in tropical Africa during the last glacial maximum (LGM, 21ky ago). However, no consensus exists with regard to where exactly refugia for African vertebrates occurred, and whether these were common for different taxa. By applying hindcasting niche modelling, we model climatically suitable areas for birds and mammals endemic to sub-Saharan Africa, using climate reconstructions for the LGM. We found several species-rich areas that may represent LGM refugia, the most prominent ones being the Congo Basin and Mount Cameroon. We also randomised the position of the LGM distributions in order to simulate species richness occurring by chance alone. Even after accounting for chance, 'refugia' for birds and mammals were highly concordant. This study represents the first cross-taxonomic study exploring the refugia theory at a continental scale, and lends support the hypothesis that African birds and mammals adjusted their distributions and persisted in common 'refugia' during the LGM.

A TALE OF TWO CONTINENTS: BODY SIZE, ECOLOGY, AND THE GREAT AMERICAN BIOTIC INTERCHANGE

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South America was an island continent from the end of the Cenozoic until 2.7 million years ago, when the Isthmus of Panama connected South America with North America, leading to the most dramatic biotic interchange in the fossil record. The interchange was not balanced between the two continents; half of modern South American mammals are of North American decent, but only ten percent of modern North American mammals are of South American decent. Hypotheses to explain this pattern include phylogenetic superiority of North American mammals, easy invasion of South America due to its long isolation, and differential timing of dispersal north during glacial minima and dispersal south during glacial maxima. We examined the body size and ecological characteristics of mammals that descended from participants and non-participants in the interchange. We found that body size varies significantly between descendents of dispersers and non-dispersers from each continent, and that descendents of South American dispersers tend to have larger body size than descendents of North American dispersers. Because large body size made species less likely to survive the Pleistocene extinction, South American species may have been affected more strongly than North American species by this event, leading to dominance of North American species. We are using various modeling methods to examine relationships between dispersal and ecological characteristics of mammals from both continents.

POSTER SESSION V: POSTER AWARDS

A specially appointed committee of the Board will select the best posters from the previous poster sessions (I—IV).

These posters will be on display in the Central Garden from 12:30—2:00 pm during the buffet lunch.

AUTHOR LIST

- Abalo, M., 116
 Aburto-Oropeza, O., 41, 111
 Aceves G., 20
 Aguiar, C., 42
 Aguilar-Ortigoza, C., 34
 Aguilera, M., 86
 Aguilera-Gómez, L., 34
 Altieri, A. H., 44
 Amorim, I., 42
 Andelman, S. J., 97
 Anderson, J. M., 97
 Anderson, K., 139
 Anderson, R. P. 83, 85, 86
 Andras, J. P., 51
 Ángel Rodríguez, M. Á., 79
 Angulo, O. J., 20
 Aranda, I., 103
 Araújo, M. B., 19, 37, 85, 103, 143
 Arita, H. T., 32, 81, 84, 87
 Armitage, G., 62
 Arponen, A., 118
 Aubry, K. B., 133
 Azuma, H., 74
 Badgley, C., 119, 124
 Baird, K., 71
 Ball, S., 102
 Ballard, H. E., 76
 Balslev, H., 80
 Barber, P., 28
 Barnosky, A. D., 109
 Barreiro, R., 36
 Barton, H. D., 53
 Baselga, A., 76
 Bedolla-Guzmán Y. R., 41
 Behrens, M. D., 54
 Bell, L. J., 42
 Bell, T. L., 110
 Belmaker, J., 39
 Benda, P., 135
 Bergamini, A., 43
 Bini, L. M., 76, 79
 Bird, C. E., 43
 Błachowiak-Samołyk, K., 102
 Blaus, L., 52
 Bogonovich, M., 89
 Böhning-Gaese, K., 81, 101, 124
 Boeiro, M., 42
 Borchardt, P., 100, 104
 Borges, P. A. V., 37, 39, 42, 141
 Borregaard, M. K., 139
 Bowe, S., 54
 Bowen, B. W., 26, 40, 131
 Bowie, R. C. K., 134
 Boyd, D., 90
 Boyer, A. G., 96, 117, 142, 143
 Brehm G., 112
 Brown, J. H., 117, 126, 142
 Brown, S. K., 38
 Bruno, J. F., 63
 Brush, T., 106
 Buck, B. J., 91
 Burgiel, S., 54
 Burnside, W., 89
 Cabeza, M., 118
 Campbell, K., 98
 Campbell, M. L., 73
 Campos, J. M., 28
 Cardelús, C. L., 112
 Cardoso, P., 42
 Castoe, T. A., 17
 Ceballos, G., 142
 César Garcia, C., 44
 Chang, L., 119
 Chen, Y., 141
 Cheng, S., 28
 Christidis, L., 134
 Cody, S., 15
 Collins, L. S., 16
 Colwell, R. K., 112
 Conti, E., 132
 Cook, A., 63
 Cook, J. A., 23, 135
 Correa-Sandoval, F., 41
 Costa, A., 40
 Costa, D. P., 117
 Couceiro, L., 36
 Cowling, S., 106
 Crawford, D. L., 22
 Crawford, P. H. C., 56
 Cristobo, J., 40
 Cully, J., 53
 Cunha, A., 40
 Cunniffe, N., 63
 Cunningham, C. W., 133
 Currie, D. J., 142
 Daly, D. C., 132
 Daszak, P., 49, 50, 54
 Davidse, G., 33
 Davidson, A. D., 142
 Davies, T. J., 50, 123
 Davis, R., 53
 Dawson, M. N., 23, 42
 Dawson, N., 23
 Dayan, T., 117

- Daza, J., 17
de Nascimento, L., 37
Delgado, J. D., 37
DeMuria, J., 76
Denslow, M. W., 55
Dhondt, A. A., 52
Diniz-Filho, J. A. F., 76, 79
Distler, T., 33
Doadrio, I., 30, 31
Domínguez-Domínguez, O., 30, 31
Donlan, C. J., 98
Downie, S. R., 75
Dransfield, J., 80
du Feu, D., 102
Duff, T. J., 110
Dunn, R. R., 57
Early, R., 58
Eble, J. A., 40
Echavarren, I., 78
Ecker, K., 43
Edwards, T. C., 109
Eernisse, D. J., 31
Eichhorn, M., 90
Eklund, J., 118
Engel, M. S., 58
Ericson, P. G. P., 32
Ernest, S. K. M., 117
Erwin, D. H., 95
Estrada, A., 104
Evans, A., 117
Felger, R. S., 21
Feng, C., 69
Feria Arroyo, T. P., 58, 61
Fernández, J. A., 19
Fernández-Palacios, J. M., 37
Field, R., 90
Figueira, R., 116
Fine, P. V. A., 132
Fjeldså, J., 134
Fløjgaard, C., 27
Flores-Villela, O., 112
Forister, M. L., 59
Fortelius, M., 117
Fox, D., 119
Fox, L., 53
Francisco, F. L., 44
Funk, V., 71
Gabriel, R., 141
Gaither, M. R., 131
Gallardo, M., 24
García, C., 116
García-Barros, E., 78 (two)
García-del-Rey, E., 37
García-González, R., 34
Garrido-Olvera, L., 32
Gaspar, C. S., 39, 42
Gaston, K. J., 90, 140
Gaubert, P., 60
Ge, S., 75
Gégout, J.-C., 127
Gibson, J. R., 109
Gilbert, F., 102
Gill, J. L., 119
Gillespie, E., 71
Gilligan, C. A., 63
Gillings, S., 102
Gilman, A. C., 112
Gimenez, O., 140
Glazier, A., 62
Goldblum, D., 105
Golubov, J., 61
Gómez, J., 20
Gomez-Dagliom L., 23
González-Barba, G., 34
Gotelli, N., 139
Gough, L., 90
Graham, A., 33
Graham, C. H., 33, 81, 92
Gregory, A., 99
Grenyer, R., 114
Greve, M., 101
Griffin, D., 92
Guevara, L., 35
Guilhaumon, F., 140
Guisan, A., 105
Gutiérrez, E. E., 86
Gwiazdowski, R., 61
Hadly, E. A., 30
Hafner, D. J., 18
Hafner, M. S., 19
Hamilton, M. J., 142
Hansen, D., 98
Harding, A. M., 103
Harding, L. E., 117, 126
Harris, N. C., 57
Harris, W. K., 69
Harris, W., 88
Harvell, C. D., 51
Hawkins, B. A., 76
Heard, M. J., 63
Hernández-Martínez, J., 34
Hewitt, C. L., 73
Hickerson, M. J., 131, 133
Himes, C., 24
Hinojosa-Díaz, I. A., 58, 59
Hoagland, B. W., 56
Hochachka, W. M., 52
Hof, C., 85

-
- Horacek, I., 135
Horn, S. P., 91
Hortal, J., 37, 76
Hull, P. M., 111
Hulva, P., 135
Humanes, M., 40
Hunter, R. D., 63
Ilves, K. L., 133
Irestedt, M., 134
Jackson, J. B. C., 113
Jackson, S., 115
Jakubas, D., 102, 103
Jenkins, D. G., 77
Jetz, W., 25, 111, 124
Jezkova, T., 21
Jiménez, I., 33, 69, 70
Johnson, K. R., 95
Jones, K. E., 50
Jones, O. R., 37
Jønsson, K. A., 134
Jørgensen, P. M., 33
Jud, N. A., 72
Kar, D., 107
Karnovsky, N. J., 103
Kenagy, J., 24
Kennedy, L., 107
Kidawa, D., 103
Kilias, G., 41
Kissling, W. D., 25
Klicka, J., 16
Klossa-Kilia, E., 41
Klotz, S., 113
Kron, K., 71
La Sorte, F. A., 111
Ladle, R. J., 36, 141
Lane, C. S., 91
Larson, K., 22
Laube, I., 81
Lavers, C., 90
Lavin, M., 15
Laybourn, A. J., 22
Lenoir, J., 127
Leonard-Pingel, J., 113
Lessard, J.-P., 123
Lesser, M., 115
Levinsky, I., 143
Levy, M., 50
Li, D.-Z., 72
Li, R., 74
Lilly, E., 62
Lilly, L., 60
Lindsey, E. L., 109
Lintulaakso, K., 117
Liu, K.-B., 107
Lobo, J. M., 76
Lockwood, J., 57
Long, C. D., 62
Longino, J. T., 112
Loomer, P., 62
López, L., 36
Lopez, M., 82
Lopez-Fernandez, M.-L., 82
Lu, J.-M., 72
Lucan, R., 135
Luís, L., 43
Lyons, S. K., 96, 117, 126
MacDonald, S., 23
Maguire, K. C., 110
Malaney, J., 135
Mandujano, M. C., 61
Marano, N., 54
Marín-Cardona, D., 35
Márquez, A. L., 104
Martens, J., 24, 35
Martimianakis, S., 41
Martin, J. T., 118
Martin, L. E., 42
Martin, T. E., 108
Martínez, I., 103
Mast, J. N., 99
Mathys, B., 57
Matzke, N. J., 82
McCain, C. M., 125
McCloskey, T., 107
McGuire, J. L., 83
McInnes, L., 108
McLaurin, B. T., 91
McNew, L., 99
Medley, K. A., 55
Meentemeyer, R. K., 63
Mehltreter, K., 89
Meiri, S., 77, 123
Mendonça, E. P., 141
Meng, Y., 74
Merkler, D., 91
Midgley, G., 97
Miller, J. A., 60, 86
Mora, F., 112
Morrone, J. J., 17
Mouillot, D., 140
Moyle, R., 134
Mulligan, M., 88
Mundt, C. C., 49
Munguía, M., 19
Munguia-Vega, A., 20
Muñoz-Saba, Y., 29
Murguía, M., 79
Murrell, Z. E., 55

- Mylonas, M., 38
Nájera, A., 91
Nakazawa, Y., 27
Neilson, R., 107
Newbold, T., 102
Nie, Z.-L., 74
Nogués-Bravo, D., 76, 103, 125, 143
Norman, J., 134
Normand, S., 27, 105
Normark, B. B., 61
Novillo, A., 26
Nyári, Á. S., 115
Ochoa-G., J., 86
Ochoa-Ochoa, L., 112
Ohlson, J. I., 32
Ojeda, A. A., 25
Ojeda, R. A., 26
Olalla-Tárraga, M. Á., 79
Oiff, H., 140
Olival, K. J., 51
Olivero, J., 104
Ordonez, A., 140
Orme, C. D. L., 114
Otto, R., 37
Overgaard, A. B., 80
Owen, J., 102
Päckert, M., 24, 35
Palardy, J. E., 44
Papes, M., 60
Parham, J. F., 87
Parkinson, C., 17
Patris, S., 42
Patten, M. A., 100
Pedersen, A. B., 50
Pedersen, N. C., 38
Pedraza-Lara, C., 30
Pell, S. K., 132
Pennington, R. T., 15
Pereira, F., 42
Pérez-Ponce de León, G., 30, 31, 32
Perrine, J. D., 133
Peterson, A. T., 127
Phillips, Z., 89
Piwczynski, M., 75
Planes, S., 131
Price, J. P., 45
Primo, C., 73
Pulido, F., 103
Qiu, Y.-L., 74
Quicke, D. L. J., 37
Radosavljevic, A., 85
Rahbek, C., 85, 139, 143
Randin, C., 105
Rangel, T. F. L. V. B., 80
Reader, T., 102
Real, R., 104
Ree, R., 67, 132
Rego, C., 42
Relman, D., 62
Ribeiro, S. P., 39, 42
Ricklefs, R. E., 69, 70
Riddle, B. R., 15
Rigg, L., 105
Rios, P., 40
Rivas-Manzano, I., 34
Rizzo, D. M., 63
Robertson, D. R., 131
Rodríguez, M. Á., 76
Rodríguez, P., 112
Rodríguez-Zaragoza, S., 79
Rogers, B. M., 107
Romero-Morales, H., 21
Rominger, A. J., 30
Romo, H., 78
Ruiz, J. M., 36
Rull, V., 15
Runquist, E. R., 59
Rypien, K. L., 51
Saarinen, J., 117
Sacks, B. N., 38, 133
Salvo, G., 132
Sánchez-Ortiz, C., 41
Sandercock, B., 99
Sanders, N. J., 123, 126
Sandin, S. A., 111
Santos, A. M. C., 37
Savage, M., 99
Sawyer, Y., 23
Sax, D. F., 58, 63
Schickhoff, U., 100, 104
Schloegel, L. M., 54
Schmidt, M., 100
Schumm, P., 54
Schwager, M., 101
Schwartz, M. W., 29
Schweizer, P. E., 76
Scoglio, C., 54
Searle, J. B., 134
Sekercioglu, C. H., 124
Sérgio, C., 44, 116
Serrano, A., 42
Severinghaus, L. L., 35
Seymour, C., 101
Sfenthourakis, S., 38, 41
Shapiro, A. M., 59
Shapiro, B., 68
Shcheglovitova, M., 83
Shroat-Lewis, R. A., 73

-
- Sibly, R. M., 117
Silva, I., 42
Silva, N., 33, 92
Simison, W. B., 84
Sim-Sim, M., 43, 44
Šizling, A. L., 90
Šizlingová, E., 90
Skillings, D. J., 43
Skov F., 27
Smith E. N., 17
Smith, B., 106
Smith, B. T., 16
Smith, C. J., 16
Smith, F. A., 96, 117, 126, 143
Smith, G. R., 117
Smith, K. F., 54
Smith, S. A., 69
Smith-Patten, B. D., 100
Snell, R., 106
Solari, S., 29, 35
Soley, M., 86
Sorte, C. J. B., 56
Sotka, E., 36
Soukup, D., 91
Spalik, K., 75
States, S. L., 52
Statham, M. J., 53, 133
Steen, H., 103
Stempniewicz, L., 102, 103
Stigall, A. L., 110
Storch, D., 90, 135
Sumrall, C. D., 73
Sun, Ha., 74
Sun, He., 91
Sun, W.-B., 74
Sun, Y-H, 24
Svenning, J-C., 27, 80, 101, 103, 105
Sydney, A., 54
Tavera, J. J., 34
Taylor, Z. P., 91
Theodor, J., 117
Thogmartin, W. E., 114
Thomas, D. M., 85, 86
Tonkyn, D., 116
Toonen, R. J., 40, 43, 131
Töpfer, T., 35
Treier, U. A., 105
Trejo Barocio, P., 84
Trejo-Cantwell, T., 26
Triantis, K. A., 36, 37, 38, 141
Turmelle, A. S., 51
Ugland, K. I., 39
Uhen, M. D., 117
Valente, M. J., 91
Valesquez, J., 33
Valladares, F., 103
Van Soest, R., 40
Vazquez, E., 73
Vázquez-Domínguez, E., 87
Vázquez-Rivera, H., 142
Vega, R., 134
Verhelst, J., 88
Viers, J. H., 29
Villalobos, F., 81
Vittoz, P., 105
Wagner, W. L., 45
Wahlert, G. A., 76
Wang, X.-Q., 68
Wares, J. P., 133
Weeks, A., 132
Weeks, A., 71, 132
Welcker, J., 103
Wells, C., 116
Wen, J., 67, 70, 71, 72, 74 (two), 75
Weyandt, S., 45
Whiteman, S. B., 143
Whittaker, R., J., 36, 141
Wilder, B. T., 21, 22
Williams, A. J., 91
Williams, J. N., 29
Williams, J. W., 119
Williams, S. L., 56
Wing, S. L., 72
Wisely, S. M., 28, 53 (two), 54, 99, 133
Witman, J. D., 44
Wojczulanis-Jakubas, K., 102, 103
Wolf, J., 64
Woodworth, C., 116
Wright, I., 140
Xavier, J., 40
Xiang, Q.-Y., 69, 88
Xu, X.-W., 75
Yao, C-T., 35
York, A., 110
Youberg, K. M., 126
Zambrana-Torrelío, C. M., 22
Zambrano-González, L., 32
Zimmer, E. A., 74
Zimmermann, H., 61
Zuccon, D., 32

