

Conference Program and Abstracts

7 - 11 January, Irakleio Crete GREECE



5th International conference
of the International
Biogeography Society



Fifth biennial conference of the
INTERNATIONAL BIOGEOGRAPHY SOCIETY
an international and interdisciplinary society
contributing to the advancement of all studies of the geography of nature
Irakleion, Crete, Greece
7 – 11 January 2011



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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

Friday 7 January 2011

Field trips & Pre-conference workshops

Room 1

09:00 SAM workshop (3.5 hrs)

12:30 Lunch (in town)

14:00 PAM workshop (3.5 hrs)

18:00 IBS board meeting - 2 hrs

Room 2

CB workshop (3.5 hrs)

Saturday 8 January 2011

08:00 Opening Ceremony

08:15 *Mylonas Moissis* Brief introduction to the Biogeography of Crete

Symposium 1 Mediterranean biogeography: where history meets ecology across scales

conveners: *S. Sfenthourakis / J.-C. Svenning*

08:50 Conveners Introductory Remarks

09:00 *Comes H.P.* Plant speciation in the Mediterranean area

09:30 *Finlayson C.* Lost worlds: Biogeography of the Genus *Homo* in the Plio-Pleistocene

10:00 *Tzedakis T.C.* Museums and cradles of Mediterranean plant biodiversity

10:30 Coffee

11:00 *Rackham O.* Human Activities and the Distribution of Mediterranean Plants, Especially Island Endemics

11:30 *Santos-Gally R. et al.* Insights into Neogene Mediterranean Biogeography Based on Phylogenetic Relationships

11:45 *Palombo M. R.* Palaeobiogeography of the Western Mediterranean Insular Faunas

12:00 Conveners Closing remarks

12:10 Lunch (on venue) and poster session

Symposium 2 Comparative phylogeography: new perspectives, integrative approaches & challenges

conveners: *A. Carnaval / M. Hickerson*

14:00 Conveners Introductory Remarks

14:10 *Moritz C. et al.* Evolutionary biogeography: Prediction and relevance of phylogeographic diversity

14:40 *Gillespie R.* Predictability of Long Distance Dispersal: Comparative Phylogeography of Multiple Pacific Lineages

15:10 *Riginos C.* Comparative Landscape Genetics – Global Patterns in Benthic Fishes

15:40 Coffee

16:10 *Baird S.* Spatial Coalescent Methods and Phylogeography

16:40 *Reynolds H.T. et al.* Surprising Dispersal Events in the Phylogeographic History of the Stag Truffle Family

16:55 *Robin V.V. et al.* A Phylogeographic Paradigm for the Indian Subcontinent

17:10 Conveners Closing remarks

17:20 Poster session + cash bar

Even-numbered posters attending

18:30 Grad student discussion - for 1 hour

Poster session continues at same time

19:30 Welcoming reception - for 1½ hour

Sunday 9 January 2011

Symposium 3 Biogeography and Ecology - two lenses in one telescope

conveners: *R.E. Ricklefs, D. Jenkins*

- 08:00 *Jenkins D.* Introductory remarks
08:10 *Chase J.* Disentangling the Importance of Niches for the Maintenance of Species Diversity at Local and Regional Scales
08:35 *Wiens J.* Ecological Niches and Large-Scale Biogeography
09:00 *Poulin R.* The Comparative Ecology and Biogeography of Parasites
09:25 *Smith F.* Macroecology and Body Size: an Ideal Match?
09:50 *Weiher E.* Advances, Challenges, and Critical Tests of Ecological Community Assembly Theory
10:15 *Emerson B.* Phylogeny, Phylogeography and Community Assembly
10:40 Coffee
11:10 *Chiarucci A.* Old and New Challenges in Using Species Diversity for Assessing Biodiversity
11:35 *Davies J.* Deviations between Mammalian Phylogenetic Diversity and Species Richness Provide a Signature of the Evolutionary and Biogeographic Histories
12:00 *Ricklefs R.E.* Synthesis

12:15 Lunch (on venue) and poster session

Symposium 4 Analytical advances in macroecology and biogeography

conveners: *A. Diniz-Filho, C. Rahbek*

- 14:00 *Diniz-Filho A.* Introduction: Key themes and directions
14:10 *Purvis A.* Linking Macroevolutionary Analysis with Macroecological Questions
14:40 *Peres-Neto P.* Old Trends, Current Methods and Alternative Views on Spatial Analyses in Ecology
15:10 *Colwell R.* Stochastic Simulation Models in Biogeography
15:40 Coffee
16:10 *Phillimore A.* Macroecology meets Quantitative Genetics
16:40 *Cardillo M.* Phylogenetic Structure of Mammal Assemblages at Biogeographic Scales
16:55 *Ree R. et al.* Phylogenetic Inference of Reciprocal Effects Between Geographic Range Evolution and Diversification
17:10 *Rahbek C.* Synthesis
17:20 Poster session + cash bar **Odd-numbered posters attending**
18:30 Grad student discussion - for 1 hour **Poster session continues at same time**
18:30 National Environmental Observatory Network (NEON) (presentation by S. Scheiner)

Monday 10 January 2011**Room 1****Contributed papers 1 Island Biogeography**

chair: K.A. Triantis

- 08:30 *Rosindell J. & Phillimore A.B.* A Unified Model for Species Richness, Abundance and Origin on Islands
- 08:45 *Tjørve E. & Tjørve K.M.C.* What is the Shape of Species-Area Relationships in Island Archipelagoes?
- 09:00 *Economou E. & Samat E.* Revisiting the Ants of Melanesia and the Taxon Cycle
- 09:15 *Carstensen D.C. et al.* Historical and Contemporary Drivers of Biogeographic Modules and Island Roles
- 09:30 *Boyer A.G. & Jetz W.* Extinctions and the Loss of Ecological Function in Island Bird Communities
- 09:45 *Aranda S. et al.* Bryophyte Species Richness Patterns in Macaronesia

10:00 Coffee**Contributed papers 3. Conservation biogeography**

chair: C. Graham

- 10:30 *Winter M. et al.* Between Loss of Uniqueness and Increased Diversity: Biotic Homogenization
- 10:45 *Ordóñez A. & Olff H.* Spatial Components of Native-Alien Functional Differentiation
- 11:00 *Roderick G. et al.* Dynamic Biogeography of Agricultural Plant/Insect Communities
- 11:15 *Harris N. & Dunn R.R.* Species Loss Alters Spatial Patterns of Zoonotic Risks
- 11:30 *Villalobos F. et al.* Range Diversity Plots for Conservation Planning
- 11:45 *Ochoa-Ochoa L.* Not All That Glitters Is Gold

12:00 Lunch (on venue)**Contributed papers 5. Marine biogeography**

chair: M. Dawson

- 14:00 *Renema W.* The Dynamics of Biodiversity: Range Shifts and Areas of Origin
- 14:15 *Tellier F. et al.* What Originated Speciation and What Presently Maintains the Species Integrity and Their Geographic Distribution?
- 14:30 *Wedding L. et al.* Extending Terrestrial Spatial Pattern Metrics to the Marine Realm
- 14:45 *Tyberghein L. et al.* Inferring Marine Macroecological and Biogeographical Patterns Using Bio-Oracle
- 15:00 *Davidson A.D. et al.* Determinants of Global Extinction Risk in Marine Mammals
- 15:15 *Tittensor D. & Worm B.* Range Changes in Large, Highly Mobile Oceanic Predators

Room 2

Contributed papers 2. Climate Change Biogeography

chair: J.-C. Svenning

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| 08:30 | <i>Brown C.D. & Johnstone J.F.</i> | Degradation of Treeline Forest by Fire |
| 08:45 | <i>Feeley K.J. et al.</i> | Extinction Risks of Amazonian Plants |
| 09:00 | <i>Vázquez-Domínguez E. et al.</i> | Distributional Area and Phylogeographic Uniqueness Loss |
| 09:15 | <i>Hof C. et al.</i> | Standing Still in Running Waters |
| 09:30 | <i>Sandel B. et al.</i> | Climate Change Velocity Since the Last Glacial Maximum and Its Importance |
| 09:45 | <i>Rodriguez-Castañeda et al.</i> | Winners and Loser in Bird Species Richness Between Genera: the Role of Climatic Fluctuations |

10:00 **Coffee**

Contributed papers 4 Palaeoecology

chair: J. Williams

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| 10:30 | <i>Stigall A.</i> | Using Ecological Niche Modeling to Evaluate Niche Stability in Deep Time |
| 10:45 | <i>Munguía-Carrara M. et al.</i> | Differential Dispersal Response of Mammals During the Great American Interchange |
| 11:00 | <i>Williams J. et al.</i> | Apparent Niche Shifts and No-Analogue Climates |
| 11:15 | <i>Gavin D.G. & Herring E.M.</i> | Reconstructing a Putative Cryptic Northern Mesic Refugia |
| 11:30 | <i>Westergaard K.B. et al.</i> | Glacial Survival May Matter After All |
| 11:45 | <i>Cheddadi R.</i> | Revisiting Reid's Paradox by Integrating Genetic and Topographic Information |

12:00 **Lunch (on venue)**

Contributed papers 6 Hot Topics in Biogeography

chair: V. Funk

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| 14:00 | <i>Graham C. et al.</i> | Untangling the Influence of Ecological and Evolutionary Factors on Trait Variation |
| 14:15 | <i>Kissling W.D. et al.</i> | The Phylogenetic Structure of Palm Assemblages Worldwide |
| 14:30 | <i>Linder H.P. et al.</i> | What Constrains Long Distance Colonization? |
| 14:45 | <i>Silva S. et al.</i> | Divide to Conquer: Is There An Atlantic Forest Vertebrates' Longitudinal pattern of Distribution? |
| 15:00 | <i>Hoorn C. et al.</i> | Andean Uplift as Driver of Biodiversity in Amazonia |
| 15:15 | <i>Storch D. & Šizling A.L.</i> | Limits to Species Ranges and Diversity Patterns |

15:30 **Coffee**

16:00 **IBS business meeting and Awards ceremony**

16:30 **President introduces Wallace Awardee**

16:45 **Closing keynote by Wallace Awardee**

17:30 **Close of meeting**

18:00 **IBS board meeting - 2 hours**

20:30 **Conference dinner**

Tuesday 11 January 2011

Field trips

THE BIOGEOGRAPHY OF CRETE AND ITS SATELLITE ISLANDS

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Crete, the biggest Aegean island that is situated in the South Aegean Island Arc, is characterized as a very peculiar island with more than 20 islets and three mountainous areas with peaks that exceed 2000 m. The western part is more humid while the east is dry and sunny. Shrubs, maquis and phrygana predominate in the island, where the main cultivation is olive trees and goat grazing is intense. The paleogeography of the region is very complicated. Until middle Miocene it was part of an extended land mass. A sea transgression, 12-9 Mya, caused the separation of Crete first from Anatolia in the east and then from Cyclades in the north. It became permanently isolated before 5 Mya. Until early Pleistocene the area was an archipelago of islands. An extensive uplift during Pleistocene rejoined most of the islands, created the high mountains and formed Crete more or less as we know it today. The biogeography of Crete has been approached through many plant and animal taxa, such as angiosperms, terrestrial molluscs, insects, arachnids, centipeds and reptiles. The species area relationship, the phylogeography of native and alien species, the influence of climatic and geological changes on their current distribution, and the intense human history are among the main interests of the biogeographers for the region. Although, endemism among plants and invertebrates is impressively high, the biodiversity of Crete is characterized by the extinction of several characteristic species of the Miocene, Pliocene and Pleistocene epochs. Very few relicts are still present. The rapid geographic and climatic changes in relation to the isolation of the island are responsible for the impressive unbalanced fauna and flora. Human activities drastically fill the gaps.

Symposium I

**Mediterranean Biogeography:
Where History Meets Ecology Across Scales**

PLANT SPECIATION IN THE MEDITERRANEAN AREA: DO TEMPORAL COURSES OF DIVERSIFICATION AND MODES OF ORIGIN DIFFER IN THE AEGEAN ARCHIPELAGO?

COMES Hans Peter

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This talk addresses some of the concepts involved in the analysis of the temporal course of diversification of Mediterranean plant taxa and their underlying modes and mechanisms of speciation, including (1) rates of diversification through time; (2) the role of geography in speciation regarding the relative frequency of allo-/parapatric vs. sympatric modes; and (3) the distinction between supposedly competing hypotheses of ‘ecological’ (adaptive) vs. ‘non-ecological’ (non-adaptive) mechanisms of speciation. There can be little doubt about the important role of ecological and geographical speciation in Mediterranean and/or Alpine plant radiations. By contrast, the genus *Nigella* is a purported example of non-adaptive plant speciation by genetic drift in the Aegean Archipelago based on data from neutral genetic markers. In contrast to other Mediterranean and/or Alpine plant groups, showing constant, two-phased, or declining rates of diversification, the accelerated rate of speciation in Aegean *Nigella* is plausibly related to increased opportunities for allopatric speciation afforded by the palaeogeographical complexity of the archipelago combined with Late Pleistocene changes in climate and sea-level. Work is presently underway to test whether in this *Nigella* island system there is a positive correlation between genetic distance and (partial) intrinsic post-zygotic reproductive isolation, as would be expected if intra-genomic conflicts (‘Dobzhansky-Muller incompatibilities’) had evolved as by-products of the divergence of genomes in allopatry and via drift. Very few direct empirical studies of reproductive isolation evolving via drift exist, and it remains an open question *whether accelerated rates of speciation via drift is the norm in the Aegean Archipelago*.

LOST WORLDS: BIOGEOGRAPHY OF THE GENUS *HOMO* IN THE PLIO-PLEISTOCENE – THE MEDITERRANEAN AS PART OF A LARGER BIOGEOGRAPHICAL ENTITY

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Biogeography is incomplete when viewed in three dimensions. This work is an exercise in 4-d ecology and biogeography. It examines the deep history of the mid-latitude belt (MLB), a zone roughly delimited in the south by the 30th and to the north by the 50th parallels. The Mediterranean Basin is the western end of this wide latitudinal belt. Compared with Temperate, Boreal and Arctic zones to the north, which are fairly continuous and unfragmented across the Palaearctic, the MLB is highly patchy as a result of the impact of Africa, Arabia and India into the Eurasian land mass. It is argued that the MLB once formed a belt of continuity of a similar nature to those to the north. Evidence is provided that this belt was dominated by temperate and sub-tropical savannahs and wetlands that were occupied by species of these habitats, including early hominins. The protracted break-up of this belt, caused by the build-up of major mountain masses and the uplift of the Tibetan Plateau intensified in the Miocene and Pliocene and generated new ecologies. The diversification and expansion of genera and species adapted to rocky and arid habitats was one consequence. Birds and hominins will be used as examples of taxa that exploited the new opportunities. It will be argued that the Quaternary (to the present) pattern of distribution of genera and species of birds and mammals, including hominins, across the MLB (including the Mediterranean – the Far West) has been a composite of vicariant arrangements and subsequent radiations and dispersals of taxa that assimilated the new conditions of the Plio-Pleistocene. The geographical distribution of the genus *Homo*, including the extinction process of the Neanderthals, will be examined in the context of these larger processes in time and space.

HUMAN ACTIVITIES AND THE DISTRIBUTION OF MEDITERRANEAN PLANTS, ESPECIALLY ISLAND ENDEMICIS

RACKHAM Oliver

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What makes islands special? Mediterranean islands tend to differ from the mainland in various ways, both in their natural histories (most of them had peculiar and unbalanced faunas in the Pleistocene) and in their human histories. This contribution will examine the interactions of island plants with various aspects of human history and prehistory: extermination of the native mammals; introduction of domestic animals and plants and mainland animals; introduction of exotic wild plants (mostly from very different climates); people's recognition of island endemic plants and their uses, especially medicinal. Future threats to island endemics will be considered, especially globalization of plant diseases and global warming.

MUSEUMS AND CRADLES OF MEDITERRANEAN PLANT BIODIVERSITY

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An attempt is made to examine the palaeoecological record for presence of tree populations in the circum-Mediterranean region during the Last Glacial Maximum. Despite the limited evidence, different types of refugia are discernible in terms of physical characteristics and species composition. These refugia may represent areas of long-term environmental stability, where local conditions provided a wide diversity of microhabitats, mitigating the effects of climatic extremes. The richness of the Mediterranean flora with its unusually high endemism is, in part, a reflection of its geographical position and geological history, as well as the extent to which Tertiary species managed to survive the effects of climate variability. However, long-term buffering from extreme environmental effects together with genetic isolation may have not only led to reduced extinction rates, but also provided an opportunity for lineage divergence to proceed. Mediterranean refugia may therefore have acted both as 'museums' for the conservation of diversity and 'cradles' for the production of new diversity.

INSIGHTS INTO NEOGENE MEDITERRANEAN BIOGEOGRAPHY BASED ON PHYLOGENETIC RELATIONSHIPS OF MOUNTAIN AND LOWLAND GROUPS OF *NARCISSUS* (AMARYLLIDACEAE)

SANTOS-GALLY Rocío, VARGAS Pablo & ARROYO Juan

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To explain current lineage distribution of daffodils we reconstruct the phylogenetic relationships, estimate the temporal diversification and reconstruct the migration patterns of *Narcissus* focusing on the lowland subgenus *Hermione* and mountain section *Apodanthi*. Finally, we performed phylogeographical analysis of wide-ranging *N. tazetta* to examine microevolutionary differentiation. Plastid (trnT-L, trnL-F and ndhF) sequences were obtained from 23 species of *Narcissus* and combined with published data. Phylogenetic relationships and dating were inferred by Bayesian inference. A dispersal-extinction-cladogenesis analysis was performed using maximum likelihood methods to infer ancestral geographical distributions, and phylogeographical reconstruction was performed using coalescence analysis. Results suggest that the ancestor of *Narcissus* originated in the Iberian Peninsula far earlier than the onset of the Mediterranean climate. Lineage range eastward expansion proceeded from the western Mediterranean and involved colonization of mountain ranges in northern Africa. The phylogeography of *N. tazetta* revealed a widespread distribution of certain haplotypes. Three key historical events in *Narcissus* diversification: the Messinian Salinity Crisis, tectonic shifts of the Alboran Domain, and the establishment of the Mediterranean climate followed by repeated glaciations periods. Diversification of section *Apodanthi* probably resulted from allopatric speciation while subgenus *Hermione* may have shown more sympatric speciation and high dispersal, despite lack of apparent long-distance dispersal adaptations. Wide-spread colonization is best exemplified by the presence of both ancestral and recent haplotypes of *N. tazetta* and relatives across the Mediterranean.

PALAEOBIOGEOGRAPHY OF THE WESTERN MEDITERRANEAN INSULAR FAUNAS DURING THE LATE CENOZOIC

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The Western Mediterranean Basin is a hotspot for biogeographic, paleogeographic and evolutionary studies, revealing an exceptional level of biodiversity and a high rate of regional endemism both in the present and in the past. A complex geological history, characterized by orogenic processes and widespread extensional tectonics, caused repeated separations/connections of microplates and isolations/connections of insular and mainland territories, leading to peculiar faunal evolution. Palaeobiological studies are of outstanding importance both as a support of geodynamic models and as a basis for an understanding of the complex Cenozoic palaeobiogeographical history, which led to the modern biodiversity. The population histories of the main insular realms (Balearic, Sardinia and Sicily islands, and Tusco-Sardinia and Abruzzi–Apulia palaeobioprovinces) are here critically revised. Each one of these insular areas, which belong to different tectonic domains, has a peculiar biogeographical history. For instance, the early isolation of the Balearic Islands from the mainland allowed the establishment of an endemic fauna since the Miocene (MN5?). While, since the Eocene, Sardinia has had an extraordinarily complex, but still imperfectly known history of isolation phases, temporary connection with mainland or other insular areas, such as Maritime Tuscany, with which formed the so-called Tusco–Sardinian paleobioprovince. In the Late Miocene, a palaeoarcipelago, characterised by faunas with clearly endemic features, was located on the Adriatic side of Apennines (paleobioprovince). At the same time Sicily, an island since the Late Pliocene, as well as Southern Calabria, were parts of a mainland, extending at the northern border of the African plate.

Symposium II

**New Perspectives on Comparative Phylogeography -
Novel Integrative Approaches and Challenges**

EVOLUTIONARY BIOGEOGRAPHY: PREDICTION AND RELEVANCE OF PHYLOGEOGRAPHIC DIVERSITY

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Phylogeographic analyses reveal that the majority of low-dispersal species, as recognized by current taxonomy, are comprised of multiple genetically divergent lineages. These lineages, often morphologically cryptic, represent terminal branches on the tree of life and are relevant to understanding evolutionary processes in relation to environmental change. To the extent that they represent genealogically divergent, or reproductively isolated lineages, they also warrant consideration in strategies for conservation. With some exceptions, evidence from multilocus analyses of phylogeography and contact zones support this contention and highlight the importance of non-adaptive, allopatric divergence in speciation. The prediction that narrow-range phylogeographic lineages will be concentrated in climatically stable landscapes is supported by spatial modeling and phylogeographic evidence of rainforests and their fauna from Australia and Brazil. This result aligns with emerging consensus on the need to protect present climatic refugia in the context of rapid global warming. Thus, we have the means to predict and protect this prevalent component of biological diversity.

PREDICTABILITY OF LONG DISTANCE DISPERSAL: COMPARATIVE PHYLOGEOGRAPHY OF MULTIPLE PACIFIC LINEAGES

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Long distance dispersal is generally considered insufficiently predictable to allow generation of testable hypotheses for how organisms colonize remote localities. However, current detailed understanding of wind and storm patterns, ocean currents, and migratory routes, now provides sufficient information to formulate hypotheses, while detailed molecular phylogeographies presents the opportunity to test these hypotheses. The three primary mechanisms of long distance dispersal are: (1) rafting over water; (2) attachment to migratory birds; and (3) aerial dispersal. Based on our knowledge of vector routes in the Pacific, and the known response to selection on colonists, we predict the following: (1) Taxa that cross the ocean by rafting should colonize remote islands sequentially by means of stepping-stones. The habitat that they colonize will likely be coastal strand, with the presence of lineages at higher elevation requiring shifts in habitat. (2) Taxa that disperse on birds should follow migratory routes. Such taxa may lose adaptations for bird-associated dispersal upon colonization, and differentiate within the newly colonized landmass. (3) Taxa that disperse aerially by wind are predicted to colonize remote sites directly from a mainland source, with selection again acting to reduce their ability for long-distance dispersal upon colonization. The habitat that they colonize is likely to match that whence they originated. We will examine these predictions using multiple lineages of animals and plants from remote Pacific islands.

COMPARATIVE LANDSCAPE GENETICS – GLOBAL PATTERNS IN BENTHIC FISHES

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Landscape genetics holds the promise of examining within-species disjunctions and connections in a spatially explicit manner. A challenge for inferring biogeographic processes from observed patterns is that replication across species is low or non-existent. Data mining of published data sets can provide replication across species, allowing statistical evaluation of landscape features and species traits in a comparative framework. Using these “free” data, however, introduces additional complications and mitigating factors to consider. Drawing on data from benthic marine fishes, I illustrate how we can estimate the effects of geographic features such as distance and transitions between biogeographic regions on population subdivision. I also show that a coarse dichotomy describing modes of parental investment (i.e. fishes laying large benthic eggs that are typically guarded by the male versus fishes releasing pelagic eggs directly into the water column with no parental care) significantly predicts population subdivision and species diversity at the taxonomic family level. Benthic-egged families have significantly greater mean within-species genetic differentiation and species richness as compared to pelagic-egged families. Finally, I will discuss some preliminary attempts to visualize patterns of genetic diversity across species in the tropical Indo-Pacific and correlate these patterns to potential causative factors.

SPATIAL COALESCENT METHODS AND PHYLOGEOGRAPHY

BAIRD Stuart J.E.

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The recent adoption of the population genetic coalescent (PGC) into phylogenetics illustrates how population-level process can benefit phylogenetic inference, at least at the near-species level. The PGC is non-spatial, naturally limiting its application to phylogeography. However, the PGC effective population size parameter does have a spatial equivalent: effective density, which, varying through space, describes effective ranges. GIS habitat suitability retrodictions are natural priors for such ranges. Spatial genetic coalescence (SGC) parameterised by effective density might therefore seem a more natural candidate than PGC for adoption into phylogeography. Progress in this direction is currently limited because, while PGC is mature technology, SGC is not. I present a simple SGC based on Kimura’s stepping stone model, and describe its application to recent range expansion of the cane toad. I use this simple case to illustrate a more general approach to SGC, and discuss future prospects for SGC in phylogeography: information to be gained, hypotheses to be compared, and likely limitations arising from either simplifying assumptions or computational load.

SURPRISING DISPERSAL EVENTS IN THE PHYLOGEOGRAPHIC HISTORY OF THE STAG TRUFFLE FAMILY ELAPHOMYCETACEAE

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Truffles are an ecological guild of fungi that form underground fruiting bodies. Most truffles are ectomycorrhizal and are dispersed by mammalian mycophagists attracted to their scent. Because of their apparent dispersal limitation, a general hypothesis for truffles is of limited species ranges and relatively rare long distance dispersal. A phylogeographic study of a broadly distributed truffle family, the Elaphomycetaceae (Eurotiales) indicates instead frequent long-distance dispersal and expands the known geographic ranges of common Northern Hemisphere species. The Elaphomycetaceae are a family consisting of two ectomycorrhizal genera: the false truffle *Elaphomyces* and the above-ground genus *Pseudotulostoma*. *Elaphomyces* has been found in all continents save Africa and Antarctica, in temperate to subtropical forests and on numerous host genera. *Pseudotulostoma*, a recently discovered genus, has been found so far only in Guyana and Japan. We conducted a multi-gene phylogenetic study of over 60 species of the Elaphomycetaceae collected from its known range from several hosts. The study uncovered 4 major morphological clades of *Elaphomyces*, each with a broad distribution. We further studied a Northern Hemisphere species complex and found a mixture of broadly distributed species found from Central America to Asia and some species with apparently restricted ranges in western North America.

A PHYLOGEOGRAPHIC PARADIGM FOR THE INDIAN SUBCONTINENT

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While phylogeographic patterns in temperate regions have been relatively well studied, India, despite its biodiversity, lacks a phylogeographic paradigm. Absence of strong physical barriers within the subcontinent, a relatively small area, and relatively recent colonization by most mammalian groups, suggest that phylogeographic patterns are driven by differences/similarities in the species' ecology. We investigate this hypothesis using genetic data from seven species (leopards, tigers, leopard cats, jungle cats, bonnet macaques, Arunachal macaques and white-bellied shortwings) distributed across the Indian subcontinent. Our results reveal that for relatively large-bodied species like leopards and tigers, phylogeographic pattern is driven by differences in body size. For smaller felids like jungle cats and leopard cats, small differences in habitat preference are responsible for phylogeographic pattern. Additionally, niche models for leopard cats support the possibility of a small, isolated population in Southern India that potentially mandates conservation attention. The two primate species (Arunachal macaque and bonnet macaque) reveal patterns driven by differences in sex-biased dispersal. Finally, data from a high elevation bird in the Western ghats reveals the impact of biogeographic divides and potential population expansion following the last glacial maximum. Taken together, our results provide the beginnings of a paradigm for the Indian subcontinent, and illustrate the relative importance of geography and ecology in this understudied region.

Symposium III

**Biogeography and Ecology:
Two Lenses in One Telescope**

DISENTANGLING THE IMPORTANCE OF NICHES FOR THE MAINTENANCE OF SPECIES DIVERSITY AT LOCAL AND REGIONAL SCALES AMIDST A GAUNTLET OF STOCHASTIC AND BIOGEOGRAPHIC PROCESSES

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The foundations of modern-day community ecology arise from Hutchinson and MacArthur's classic works on species' niches, trade-offs, and coexistence. More recently, owing to the influence of Ricklefs, Hubbell, and others, there has been an increasing recognition of large-scale biogeographic processes, including history, phylogeny, dispersal limitation and ecological drift in driving patterns of coexistence and diversity in local communities. However, comparisons of these approaches are difficult, owing to the widely divergent scales at which these processes are studied. Here, we take one step in comparing the two approaches by examining how the relative importance of niche processes is influenced by variation in the strengths of local and regional filters (e.g., disturbances, dispersal), as well as variation in biogeography/history (e.g., size of the regional species pool). By devising a series of null-modeling approaches, we can begin to discern how the relative importance of niche-related factors for local and regional coexistence varies with changing local, regional, and biogeographic processes. We present approaches for disentangling niche versus stochastic processes, as well as biogeographic/historical processes, using examples from observational and experimental studies on pond invertebrates, terrestrial herbaceous communities, and forest trees.

ECOLOGICAL NICHES AND LARGE-SCALE BIOGEOGRAPHY

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This talk will address the importance of the concept of the niche to the field of biogeography. First, I will review different niche concepts, especially as they relate to species interactions vs. range limits. I will argue that the field of biogeography has often ignored both ecology and the niche. I will give examples of biogeographic patterns that seem to be generated by ecological tolerances (i.e., the niche); these include trivial examples (e.g., oceans as a barrier to terrestrial taxa) and non-trivial examples (e.g., borders between biogeographic provinces within continents, elevational turnover). I will then review the aspects of the niche that may be most important in creating biogeographic patterns. There seems to be abundant evidence for the importance of abiotic tolerances (e.g., salinity, climate) and somewhat less evidence for the importance of biotic factors (e.g., competition, predation) in biogeography. Nevertheless, the integration of biotic and abiotic factors over time (i.e., niche pre-emption) may be important in creating many biogeographic, ecological, and macroevolutionary patterns, but is not well-studied yet. Finally, I will talk about new areas for research at the intersection of biogeography and the niche.

THE COMPARATIVE ECOLOGY AND BIOGEOGRAPHY OF PARASITES

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Comparisons between different species have been a powerful heuristic tool in the development of ecological thought. They can both provide a testing ground for macroecological hypotheses and inform biogeographical research. Comparative ecology can only operate within a phylogenetic context, given the evolutionary (and statistical) non-independence of species. Controlling for phylogenetic influences in comparative analyses is particularly challenging for host-parasite interactions, since a given trait may be either a parasite trait, a host trait, or a property of the coevolved association rather than of one participant only. This talk will discuss the challenges of using comparative approaches in studies of parasite biogeography and how to overcome them. These issues will be illustrated by examples in which parasite species traits and host species traits are linked with biogeographical patterns. First, two fundamental properties of parasites, their niche breadth (= host specificity) and the nature of their life cycle, will be used to explain interspecific and latitudinal variation in the sizes of their geographic ranges. Then, the influence of a key host trait, i.e. their vagility or dispersal ability, on rates of decay in the similarity of parasite communities as a function of increasing distance, will be discussed. Overall, the concepts and examples presented here will illustrate and strengthen the ties between comparative ecology, macroecology and biogeography.

MACROECOLOGY AND BODY SIZE: AN IDEAL MATCH?

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Macroecology is a big picture, statistical approach to the study of ecology. By focusing on broadly occurring patterns and processes operating at large spatial and temporal scales rather than focusing on localized and/or fine-scaled details, macroecology aims to uncover general mechanisms operating at organism, population, and ecosystem levels of organization. Here we briefly review the history of macroecology and use the body size of mammals as a case study to highlight current developments in the field, including the increasing linkage with biogeography and other disciplines. We use body size because of its obvious ecological and evolutionary importance. Previous work has shown that the distribution of modern mammals is remarkably similar across the different continents. This extends even to the ordinal level with the statistical moments of clades being statistically equivalent on different continents. Here, we expand that analysis to ask: a) how the differing evolutionary and geological histories of continents play into patterns and b) whether the overall distribution and the relative contributions of the different orders were changed as a result of the end-Pleistocene megafaunal extinction. Our results illustrate not only how the reproductive strategies of mammals influence their ecological roles and distributional patterns, but also highlight how our interpretations of modern ecology are influenced by anthropogenic events of the past.

ADVANCES, CHALLENGES, AND CRITICAL TESTS OF ECOLOGICAL COMMUNITY ASSEMBLY THEORY

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The ecological approach to community assembly has tended to emphasize the interplay between neutral processes, niche-based environmental filtering, and niche-based species sorting in an interactive milieu. Over the past few years, notable progress has been made in terms of assessing how trait-based community functional parameters differ from neutral expectation and how traits are filtered and sorted along environmental gradients. The development of community phylogenetics has forged common ground between ecologists and biogeographers and has also led to notable advances. Community phylogenetics provides a way to avoid functional traits, but traits are required for mechanistic understanding and therefore a purely phylogenetic approach may not lead to mechanistic or causal understanding. We suggest two principal challenges are involved in advancing community assembly: developing predictive mechanistic theory and more firmly linking causal mechanisms to observable outcomes. Our recent experiments provide causal evidence for the role of biotic interactions (competition) in shaping community functional parameters in accordance with theory, however the degree of species checkerboarding did not increase with competition intensity. We also estimated the relative importance of dispersal history, abiotic filtering, biotic sorting, and neutral processes on community functional parameters within a large-scale experiment in order to move from a scientific mode focused on demonstrating the existence of causal linkages to a comparative mode focused on relative influence of multiple causal pathways.

PHYLOGENY, PHYLOGEOGRAPHY AND COMMUNITY ASSEMBLY

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There has been much recent interest and progress in the characterisation of community structure and community assembly processes through the application of phylogenetic methods. To date most focus has been on groups of taxa for which some relevant detail of their ecology is known, for which community composition is reasonably easily quantified, and where the temporal scale is such that speciation is not likely to feature. Here I explore how we might apply a phylogenetic approach to investigate community structure and assembly at broad taxonomic and geographic scales, where we have little knowledge of species ecology, where community composition is not easily quantified, and where speciation is likely to be of some importance. I explore these ideas using the class Collembola as a focal group. Gathering molecular evidence for cryptic diversity suggests that the ubiquity of many species of Collembola across the landscape may belie greater community complexity than would otherwise be assumed. However, this morphologically cryptic species level diversity poses a problem for attempts to characterise diversity both within and among local species assemblages. Recent developments in parallel sequencing technology provide an advance that can bring together the fields of phylogenetic and phylogeographic analysis to bear on this problem. Such an approach can be standardised for analyses at any geographic scale for a range of taxonomic groups to quantify the formation and composition of species assemblages.

OLD AND NEW CHALLENGES IN USING SPECIES DIVERSITY FOR ASSESSING BIODIVERSITY

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Although biodiversity is a major natural resource, it is heavily threatened and it is urgent to standardize the methods for its assessment and monitoring. Species diversity is one of the most widely adopted methods for assessing patterns and processes of biodiversity, under both the ecological or biogeographical perspective, even if differences exist because of the type of data and questions. Unfortunately, despite the existence of a deep theoretical background shared by the international scientific community, standardized methods for measuring species diversity are still lacking, especially at the scales needed to monitor biodiversity for conservation and management purposes. In the present paper we review a series of concepts in relation to the use of species diversity measures for conservation and management purposes. In particular, we review the concepts behind the metrics which are used for measuring species diversity, the applicability of methods that differently weight species richness and evenness and the methods which include the phylogenetic linkage among species to weight the species diversity measures. We then analyzed the major pitfalls and problems which are associated to the quantitative measurement of species diversity in ecological systems, discussing some potential solutions and proposing a few basic points for the future research agendas. The main issues are associated to the censusing of complete species lists for getting complete richness data, the difficulties in collecting adequate abundance data to be used for evenness calculation and, finally, the problems associated to the taxonomic changes and the proper identification of species. We finally provide some suggestions about the next research agenda for maturing our capacity of measuring species diversity in ecological systems.

DEVIATIONS BETWEEN MAMMALIAN PHYLOGENETIC DIVERSITY AND SPECIES RICHNESS PROVIDE A SIGNATURE OF THE EVOLUTIONARY AND BIOGEOGRAPHIC HISTORIES THAT UNDERLIE PRESENT-DAY DIVERSITY GRADIENTS

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Phylogenetic diversity (PD), the summed branch lengths on the evolutionary tree of life, represents the shared ancestry of species and their evolutionary divergences. Regionally, PD frequently co-varies closely with species richness; however, variation in speciation and extinction rates and/or the biogeographic history of lineages can result in significant deviation. Locally, these differences can be pronounced. Rapid recent speciation or high temporal turnover of lineages can result in low PD but high richness. In contrast, rare dispersal events, for example, between biomes, can elevate PD but have only small impact on richness. To date, environmental predictors of species richness have been well studied but global models of PD are lacking. Here, we contrast the global distribution of PD versus species richness for terrestrial mammals. We show how that an environmental model of lineage diversification can predict well the discrepancy in the distribution of these two variables in some places but not others. Our results identify both global centres of evolutionary diversification and biogeographic melting pots. By prioritizing the preservation of PD in addition to species richness we may maximize options in an uncertain future.

Symposium IV

**Analytical Advancements in Macroecology and
Biogeography**

LINKING MACROEVOLUTIONARY ANALYSIS WITH MACROECOLOGICAL QUESTIONS

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Large-scale patterns in the diversity of life are the results of evolutionary ecology played out over large areas and long periods of time. From this perspective, it is clear that macroecological and macroevolutionary research should be more closely linked than they often have been. In this talk I use two very different systems – mammals and planktonic foraminifera – to outline (1) how macroevolutionary analysis can shed light on macroecological patterns like latitudinal diversity gradients and species-area relationships, and (2) how macroecological considerations in turn help us to understand macroevolutionary patterns like phylogenetic imbalance and temporal changes in taxonomic richness.

OLD TRENDS, CURRENT METHODS AND ALTERNATIVE VIEWS ON SPATIAL ANALYSES IN ECOLOGY

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Organisms, along with their environments, present remarkable patterns of variation across space. Unravelling the multiple mechanisms behind the myriad, yet complex patterns that dominate in nature, is one of the most important intellectual challenges in the science of ecology. Much as astronomers cannot perform planetary experiments, ecologists cannot easily manipulate most biodiversity patterns because these patterns occur at many different scales, from a few centimeters to thousands of kilometers. Therefore, in a way similar to astronomers, ecologists need to use spatial models to understand the processes that structure biodiversity patterns such as species richness and species co-occurrence across space. Although spatial models can provide great insights into these processes, ecologists tend to see spatial autocorrelation as a nuisance rather than an interesting property to be studied. Beyond the standard nuisance viewpoint, an alternative and less acknowledged perspective is that the spatial legacy of ecological data can help us challenge models and improve our understanding of ecological phenomena. In this presentation, I provide an account of these two issues for the interpretation of ecological patterns, present methods that can tackle these two issues and suggest alternative views about when spatial models should be considered and how they should be interpreted.

STOCHASTIC SIMULATION MODELS IN BIOGEOGRAPHY

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The realization that chance events and contingency play a key role in evolution (e.g. mutation, drift, founder effects, exaptation) and in ecology (e.g. alternate stable states, chaotic dynamics, lottery competition) has long stimulated modeling in these fields. In biogeography, no one doubts that chance events, acting within the constraints of evolution, ecology and earth history, have left their signature on biogeographical patterns, but we have been slower to find ways to incorporate stochasticity and contingency into biogeographical models. The emergence of null models in biogeography, beginning with Maillefer's card-deck draws in 1928, aimed to weigh the relative contributions of mechanism and chance in producing the biogeographical patterns that we observe or infer. Process and agent-based models that explicitly incorporate stochastic variation share this objective with null models, while focusing on outcomes in relation to empirical patterns, a pattern-oriented approach. Within this conceptual and historical framework, we trace the development of increasingly realistic stochastic simulation models that incorporate speciation and phylogeny, adaptation and niche conservatism, range shifts and extinctions in spatially and temporally explicit dynamic environments. We will argue that such models have the potential not just to mimic, but to help us understand biogeographical patterns in the past, present, and future.

MACROECOLOGY MEETS QUANTITATIVE GENETICS

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Macroecologists are often interested in the intraspecific correlation between an environmental variable, such as temperature, and geographic variation in phenotype. Such correlations will arise due to the combined effects of phenotypic plasticity and local adaptation. Knowing the contributions of temperature mediated plasticity and local adaptation to geographic variation is key to predicting the likely effects of climate change on population fitness and persistence. Unfortunately, standard macroecological approaches are unable distinguish the contributions of phenotypic plasticity and microevolution. Quantitative geneticists usually partition the plastic and adaptive component of geographic variation using logistically challenging transplant experiments. However, by applying a statistical approach that borrows from quantitative genetics, it is in fact possible to estimate temperature-mediated plasticity and local adaptation from spatiotemporal phenotypic data. An advantage of this statistical approach over transplant experiments is that it can be applied to abundant existing data and to species for which transplants are difficult. Applying this approach to spawning dates of common frogs (*Rana temporaria*), we found that, although all populations exhibited a plastic response to temperature, spawning earlier in warmer years, between-population differences in first spawning dates were mainly the result of local adaptation. There is considerable potential to extend this approach further and to scale-up other quantitative genetic ideas to a macro-scale.

PHYLOGENETIC STRUCTURE OF MAMMAL ASSEMBLAGES AT BIOGEOGRAPHIC SCALES: LINKING PHYLOGENETIC COMMUNITY ECOLOGY WITH MACROECOLOGY

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Phylogenetic community ecology seeks to explain the processes involved in the formation of species assemblages by analyzing their phylogenetic structure, and to date has focused primarily on local-scale communities. Macroecology, on the other hand, is concerned with the structure of assemblages at biogeographic scales, but has remained largely non-phylogenetic. Analyzing the phylogenetic structure of large-scale assemblages provides a link between these two research programs. I ask whether we should expect large-scale assemblages to show significant phylogenetic structure, by outlining some of the ecological and macroevolutionary processes that may play a role in assemblage formation. As a case study, I then explore the phylogenetic structure of carnivore assemblages within the terrestrial ecoregions of Africa. Many assemblages at these scales are indeed phylogenetically non-random (either clustered or overdispersed). One interpretation of the observed patterns of phylogenetic structure is that many clades underwent rapid biome-filling radiations, followed by diversification slowdown and competitive sorting as niche space became saturated.

PHYLOGENETIC INFERENCE OF RECIPROCAL EFFECTS BETWEEN GEOGRAPHIC RANGE EVOLUTION AND DIVERSIFICATION

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Geographic characters - traits relating to the spatial distribution of a species - may both affect and be affected by processes associated with lineage birth and death. This is potentially confounding to comparative analyses of species distributions because current models do not allow reciprocal interactions between the evolution of traits and the growth of phylogenetic trees. Here we introduce a likelihood-based approach to estimating region-dependent rates of speciation, extinction, and range evolution from a phylogeny, using a new model in which these processes are interdependent. We demonstrate the method with simulation tests that accurately recover parameters relating to the mode of speciation and source-sink dynamics. We then apply it to the evolution of habitat occupancy in Californian plant communities, where we find higher rates of speciation in chaparral than in forests and evidence for expanding habitat tolerances.

Contributed Paper Session I

Island Biogeography

A UNIFIED MODEL FOR SPECIES RICHNESS, ABUNDANCE AND ORIGIN ON ISLANDS

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The colonisation of Krakatau and diversification of species in the Galapagos illustrate two ways in which islands have captured the imagination of ecologists and evolutionary biologists. Island biogeography has been advanced by theories modelling species on either nearby islands based on immigration, or isolated islands where speciation dominates. In reality, however, there is a continuum in island isolation. Here we present a parsimonious model of speciation and dispersal, which predicts the species richness, abundance, age and origin on islands across the complete spectrum of isolation. We find the predictions generated by our model to be consistent with a broad range of patterns in empirical data and existing theory. Our work also highlights the importance of studying largely neglected phenomena, such as the abundance and age of island species about which the model makes new predictions. The success of our model suggests dispersal and speciation are the dominant forces in assembling island communities. Other factors must either be less important or their influence will only be visible if we look beyond the classic patterns of island biogeography.

WHAT IS THE SHAPE OF SPECIES-AREA RELATIONSHIPS IN ISLAND ARCHIPELAGOES?

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A search on ISI Web or Knowledge reveals close to 1000 hits on species-area relationship(s) (SARs), species-area curve(s), and species-area model(s). Most of these (about 800) also mention “islands” or “island archipelagoes”. It is a common assumption that the power law ($S=cA^z$) is appropriate for both sample-area (mainland) SARs and isolate (island) SARs. We argue that neither of these SARs consistently conforms to the power law, and that isolate SARs are not even monotonically decelerating in arithmetic space when the finest scales are included, but are actually sigmoid. Further, recent mechanistic approaches based on “first principles”, which typically aim at explaining why SARs are power law, have compounded this oversight. A large number of candidate curve models have been suggested or fitted to species-area data, but very few exhibit the expected shape of island SARs, that is, sigmoid with no upper asymptote. We thus propose a new model that separates out the effect of species minimum-area requirements (MAEs). MAEs are ultimately caused by resource restrictions and are expected to depress the isolate (island) SAR more at fine scales than at coarse scales, making it diverge from the sample-area (mainland) SAR. The new model performed well on four broad-scale data sets (on birds, isopods, and plants) of different island archipelagoes, compared to (three) other candidate models, including the power model. Proponents of mechanistic modelling have argued that we should be looking for mechanistic explanations for species distributions and diversity rather than wasting time “tweaking” a well known phenomenological pattern that is widely accepted to be power law. We maintain that this fine-tuning is far from trivial because it is essential to consider (or separate out) the effect of MAEs in mechanistic modelling of isolate diversity as well.

REVISITING THE ANTS OF MELANESIA AND THE TAXON CYCLE

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In synthesizing his field and taxonomic studies on the Melanesian ant fauna, E.O. Wilson proposed a hypothesis for the dynamics of faunal development in space and time - the taxon cycle. The ideas initiated paradigm shifts in biogeography and ecology and have been usefully applied in other systems and geographic areas. However, the original evidence for a taxon cycle in ants was very limited. Here, for the first time since Wilson's landmark studies, we test predictions of a historical Melanesian taxon cycle with a new dataset on habitat distributions of the entire Fijian ant fauna (183 spp.) and a community phylogeny for the genus *Pheidole*. We revisit the system in the midst of an ongoing invasion of exotic ants into the Pacific islands, and ask how both these recent arrivals and the native fauna are organized across habitats in the island landscape. We find that as lineages progress to deeper levels of endemism, there is clear evidence of shifts from marginal to interior primary habitats, from ecological generalism to specialization, and from high to low population density, in universal agreement with a historical taxon cycle. Interestingly, exotics are following a similar pathway to these older natural invasions and now dominate the marginal habitats that historically facilitated dispersal and colonization across the Pacific. We propose this invasion has ended the regional Melanesian taxon cycle, and may be the first phase of an incipient global taxon cycle in ants.

HISTORICAL AND CONTEMPORARY DRIVERS OF BIOGEOGRAPHICAL MODULES AND ISLAND ROLES: A CROSS COMPARISON OF WALLACEA AND WEST INDIES

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To compare biogeographical patterns, we adopted a network approach to detect biogeographical modules (sub-regions of islands compartmentalized on the basis of a common avifauna) and island topological roles in Wallacea and West Indies. In both archipelagoes we could explain these biogeographical modules with a combination of historical and contemporary factors such as geological origin, past connections, current geographical position, and island area. Each island was given two coordinates, l (localized topological importance), and r (regionalized topological importance), placing it in a two dimensional l-r space. This designates the biogeographical function or role of an island and can be used as a way to characterize and compare its importance for the local and regional fauna. The relative influence of island characteristics and species richness were tested as predictors of l and r. In both Wallacea and West Indies, island area, maximum elevation, and species richness were strongly correlated with l, while two measures of isolation correlated positively, although not strongly, with r. Large, mountainous, and species-rich islands were thus highly connected within modules and responsible for the conglomeration of modules, while islands distant from the mainland and locally isolated could behave as sinks and stepping stones for dispersing species. We discuss islands in different positions in the l-r space and their significance for the regional avifauna, while comparing islands with similar roles in Wallacea and West Indies.

EXTINCTIONS AND THE LOSS OF ECOLOGICAL FUNCTION IN ISLAND BIRD COMMUNITIES

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The combination of ecological traits exhibited by species and the resulting functional diversity (FD) is a key component of biological diversity and its decline may severely affect ecosystem services. Yet, the way observed species extinctions change communities and result in loss of function at biogeographic scales is not well understood. Here we quantify the distribution of FD in 45 pre-historic island bird communities and document its loss due to species extinctions over the past 3500 years. FD is a decelerating function of community species richness with species-rich communities harboring greater functional redundancy and putative extinction resilience. Observed declines in FD reject the idea of extinction biases toward functionally unique or redundant species and do not deviate strongly from those expected under random extinction ordering. Thus, observed loss FD is highly predictable from the pre-extinction composition of communities with island age and isolation as secondary determinants. Our findings highlight the dramatic loss of community function incurred by species extinctions, especially in low-richness communities (such as isolated islands) which exhibit particularly low resilience.

BRYOPHYTE SPECIES RICHNESS PATTERNS IN MACARONESIA: DISENTANGLING THE ROLE OF GEOGRAPHICAL VARIABLES, GEOLOGICAL AGE AND CLIMATE

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According to the classical equilibrium theory of island biogeography (ETIB), larger and less isolated islands support more species while in equilibrium, due to higher immigration and lower extinction rates. This simple and general theory needs further improvement, to account for the covariation of area with environmental heterogeneity (habitat and climatic diversity), and the role of historical processes (e.g. island ontogeny and geological age) on diversification patterns. Here we investigate the effects of area, isolation, geological age and climate on bryophyte species richness in Macaronesia, identifying their pure and shared effects. A model including all variables explained 74% of data variability. Partial regressions indicated that climate and ETIB account for 73% and 21% of between-island species richness variations, respectively, with a negligible effect of island age. Temperature seasonality was the most explanatory climatic variable. Our results indicate that bryophyte species richness on Macaronesian islands is mainly determined by the presence of favourable climatic conditions, for annual temperature oscillations can be associated with the phenotypic seasonality of bryophytes. The high dispersal capacity of this group may explain the lack of relevance of island age and isolation on species richness patterns, while the moderate independent effect of area may be due to local extinctions processes in small islands and/or the higher habitat diversity of large islands.

Contributed Paper Session II

Climate Change Biogeography

DEGRADATION OF TREELINE FOREST BY FIRE: AN INDIRECT EFFECT OF CLIMATE CHANGE

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Treeline forests occupy areas on the extremes of species tolerance limits, and are likely to be sensitive to direct climate effects. Species distributions are expected to shift northward with increased temperatures. In the boreal forest of northwestern North America, the bottleneck to forest establishment is recruitment, which is strongly mediated by reproductive output and disturbance effects. Fire frequency in many areas of the boreal forest is expected to increase as the climate warms. Northern black spruce require several decades to become reproductively mature; therefore a reduction in the fire return interval (FRI) may interrupt their typical cycle of post-fire self-replacement. Our objective was to investigate how an altered FRI can drive ecosystem shifts in black spruce forests near the treeline. We hypothesized that a shortened FRI results in forests with lower post-fire black spruce seedling density than occurs under the typical FRI. We compared both seed availability and seedling establishment in stands of varying FRI. Recruitment was drastically reduced following two closely timed fires. However, on-site germination experiments demonstrated that black spruce recruitment is limited by seed availability, not substrate. Increases in fire activity may thus lead to a degradation of treeline forests in some areas, rather than the increased tree density and forest extent predicted with climate warming.

EXTINCTION RISKS OF AMAZONIAN PLANTS DUE TO DEFORESTATION AND/OR CLIMATE CHANGE

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Estimations of the number, and preferably identity, of species that will be threatened by land-use change and habitat loss are an invaluable tool for setting conservation policies and priorities. We used geo-referenced herbarium collections data to generate spatially explicit distributions for over 40,000 vascular plant species from the Amazon basin (representing over 80% of the estimated Amazonian plant diversity). Using the resultant distribution maps we then estimated the rates of habitat loss under various future land-use and climate change scenarios. We predict that over the next 50-100 years, deforestation alone will reduce the area of habitat available to Amazonian plant species by an average of approximately 12 to 24%, significantly less than previously estimated due to the incorporation of biogeographic data and species ranges. If temperatures increase by +4°C over the same period, we predict that species will lose a median of 97% of habitat area and most of the Amazon will experience complete biotic attrition, i.e., “die back”. If Amazonian plant species are able to tolerate and/or adapt to rising temperatures then habitat loss will be reduced to a median of just 38%. These results highlight the importance of incorporating biogeographic data, the potential dangers of deforestation and/or climate change for the future of Amazonian diversity, and the need to better understand the factors that determine species distributions now and in the future.

DISTRIBUTIONAL AREA AND PHYLOGEOGRAPHICAL UNIQUENESS LOSS AS A CONSEQUENCE OF CLIMATE CHANGE IN *ORYZOMYS COUESI*

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Our aim was to evaluate the impacts of climate change on the distribution of the rice rat, *Oryzomys couesi*, and to predict the associated potential genetic diversity and phylogeographical loss. We used 69 sampling localities, 19 bioclimatic variables and the GARP and MaxEnt modelling approaches to model the species potential distribution. We also projected its distribution under three climate change scenarios (2010, 2050, 2080). We corrected potential and future projections using land-use maps to include only areas where adequate habitat for the species is actually present. We used 129 samples from 77 localities encompassing the entire species geographic distribution and nine microsatellite loci to estimate genetic parameters. We found high genetic variability and significant structure and detected 3-6 main phylogeographical groups, in accordance with prime geographical barriers. Modelling results showed a drastic distribution reduction, 80% by 2080, and distributional shifting towards higher altitude areas. Associated to the predicted climate change impact, significantly unique genetic and evolutionary lineages disappear. We show that climate change severely impacts both species and genetic diversity.

STANDING STILL IN RUNNING WATERS: HABITAT STABILITY AFFECTS SPECIES' ABILITY TO TRACK CLIMATIC CHANGES

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The habitat shapes life history traits and ecological characteristics of species. The persistence of habitats should influence the dispersal of species, selecting for stronger dispersal in habitats of lower temporal stability. As standing freshwater bodies (lentic habitats) are on average less persistent over time than running waters (lotic habitats), lentic species should show a higher propensity for dispersal than lotic species. Assuming that climatic conditions are an important determinant of species distributions, we hypothesize that the distributions of lentic species should be closer to equilibrium with current climatic conditions and that lentic species should more rapidly track climatic changes. We tested these hypotheses using two datasets (from 1988 and 2006) of European dragon- and damselfly distributions and the according climatic data. Species distribution models showed that range filling (the ratio of realised vs. potential range size) was consistently higher for lentic than for lotic species. When using data from 1988 to model distributions in 2006, models consistently overpredicted the ranges of lotic species, and more strongly so than for lentic species. These results confirm the proposed hypotheses, lending support to the assumption that habitat persistence shapes the evolution of dispersal. Further, we conclude that lentic species may be more successful in tracking climate change.

CLIMATE CHANGE VELOCITY SINCE THE LAST GLACIAL MAXIMUM AND ITS IMPORTANCE FOR PATTERNS OF SPECIES RICHNESS AND RANGE SIZE

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Contemporary patterns of species distributions are influenced by both current and historical conditions. Historically unstable climates can lead to reductions in species richness, when species go extinct because they cannot track climate changes, when dispersal limitation causes species to fail to fully occupy suitable habitat, or when local diversification rates are depressed by local population extinctions and changing selective regimes. Locations with long-term climate instability should therefore show reduced species richness with small-ranged species particularly missing from the community. We used a novel measure of climate stability, climate change velocity, which combines information on temporal and spatial gradients in climate to describe the rate at which a particular climate condition is moving over the surface of the Earth. Climate change velocity since the Last Glacial Maximum is likely to be a more biologically meaningful measure of climate stability than the previously used simple climate anomaly, because it scales climate change relative to local variation in climate, capturing the potential for topographic refuges to buffer species from climate change. We tested these predictions using global data on mammal and amphibian distributions. Consistent with our predictions, richness of small-ranged species of both groups was negatively associated with velocity. Velocity generally explained more variation in richness than did the simple climate anomaly. Climate velocity appears to capture an important historical signal on current mammal and amphibian distributions.

WINNERS AND LOSERS IN BIRD SPECIES RICHNESS BETWEEN SISTER GENERA: THE ROLE OF CLIMATIC FLUCTUATIONS AND PERSISTENCE IN CLIMATICALLY STABLE AREAS

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Most species have climatic constraints that, in combination with dispersal ability and biotic interactions, determine their current distribution. However, climatic conditions have changed drastically since the Last Glacial Maximum (LGM, 21,000ybp). Previous studies evaluating species richness in bird lineages found that dispersal ability and breeding range size explained most of the variation in species richness, but the role of climatic fluctuations has not been considered. We identified 140 bird sister genera, mapped their current distribution and modeled their distribution during the LGM. We then tested if the degree of climate-driven range dynamics can explain contrasts in species richness between sister genera. Specifically, we ask if persistence in climatically stable areas (i.e. climatic refugia) and subsequent range expansion are good predictors of species richness. The extent of climatically stable areas was one of the most important predictors of bird species richness. Moreover, the amount of stable area of a genus was positively correlated with greater habitat expansion since the LGM. Climatically stable refugia likely lowered extinction rates and provided the opportunity for diversification through vicariance. Range expansions out of refugia might also enhance divergence among lineages. We conclude that the combination of location and extent of climatic refugia are crucial for differences in species richness and range size among bird lineages.

Contributed Paper Session III

Conservation Biogeography

BETWEEN LOSS OF UNIQUENESS AND INCREASED DIVERSITY: BIOTIC HOMOGENIZATION OF SPECIES, TRAIT AND PHYLOGENETIC COMPOSITIONS

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Human activities have altered the composition of biota by influencing two fundamental processes: extinction of native species and introduction of alien species, which can lead to increased (homogenization) or decreased similarity (differentiation) of formerly distinct communities globally. Here, we discuss our recent findings about biotic homogenization of vascular plants and vertebrates on three different compositional levels of species communities and spatial scales:

- (i) Introduced species lead to increased similarity of species compositions among and within North America and Europe.
- (ii) The interplay of species' introductions and species extinctions leads to increased similarity of phylogenetic compositions within Europe.
- (iii) Introduced species lead to increased similarity of trait compositions at a regional scale.

Generally, as a result of species losses and introductions, numbers of species in European and North American floras and vertebrate faunas increased within the last 500 years. Moreover the results show a loss of functional, taxonomical and phylogenetic distinctness at various spatial scales. However, climatic differences and large geographic distances seem to form still existing natural barriers against a total biotic interchange.

SPATIAL COMPONENTS OF NATIVE-ALIEN FUNCTIONAL DIFFERENTIATION: LINKING PATTERNS TO MECHANISMS

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One of the main goals of invasion ecology has been identifying determinants of invasiveness by comparing attributes of co-occurring native-alien species; nonetheless we don't know how these differences change across ecological scales. In this work we aim to evaluate the scale effect on the native-alien trait-differentiation patterns, by evaluating its variance partitioning across five nested scales (species, plot, locality, area, region) using a global database of three key functional traits (Specific leaf area, Typical maximum canopy height, and Specific seed weight). All traits showed an unbalanced variance composition with almost all the variance captured by species scale (68 to 93%); while the plot, area, locality or regional scales capturing the remaining variability (0 to 14%). These results were consistent for all contrast criteria (alien to all, closest phlegmatically or mean co-occurring native) and comparisons in multi-trait space. Overall, the small contribution of the plot to region scales aligns with the idea that trait-based environmental filtering has an important role in invasive species success, but local scale dynamics shape the ultimate invasive species distribution. Our work shows how the comparison scale should be considered when evaluating the drivers of alien species success.

DYNAMIC BIOGEOGRAPHY OF AGRICULTURAL PLANT/INSECT COMMUNITIES IN THE MEDITERRANEAN: SPATIAL AND TEMPORAL INTERACTIONS AMONG INDIGENOUS, DOMESTICATED, AND INVASIVE SPECIES

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Because of its complex and well-studied history, the Mediterranean region is a natural laboratory for studying the assembly and dynamics of biological communities. Here, we investigate the historical biogeography of multiple trophic levels associated with several domesticated crops of the Mediterranean, including olive, tomatoes, and related the *Prunus* species plum, almond, peach, and apricot. Molecular population genetics studies show that historical associations of these crops and their herbivorous pests and natural enemies are dynamic in space and time and represent assembly in a series of historical episodes. Some herbivores, such as the olive fly, *Bactrocera oleae*, were present in the region before crop domestication, as were many natural enemies. Some species were associated with early crop domestication, including aphids associated with *Prunus* species. Other herbivores, including *Bemisia tabaci* whiteflies have a history in the Mediterranean associated with early movements of domesticated crops, but also include populations that have invaded more recently. Many species, including the red tomato mite, *Tetranychus evansi*, are only recent invaders. These studies and others can help inform decisions concerning both pest management and conservation of indigenous biodiversity.

SPECIES LOSS ALTERS SPATIAL PATTERNS OF ZONOTIC RISKS

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The loss of species and subsequent spatial patterns of diversity can have cascading effects throughout the environment; though some consequences of species loss are more conspicuous than others. For example, a recent review on coextinction dynamics showed that the composition of parasites in carnivores became dominated by viruses due to the loss of hosts (Dunn et al. 2009). Carnivores are a useful model group to explore spatial patterns of diversity and impacts on human health because the order Carnivora includes species that vary in their geographic extent as well as their rarity/abundance. As a consequence, the parasites of carnivores comprise both abundant species with potential as zoonotic vectors (e.g., raccoons and rabies) and parasites likely to be in need of conservation. We used a coextinction model to explore how the loss of 29 carnivore species in North America could vary human risks to zoonotic parasites. Additionally, we expanded this model by incorporating species distribution projections of parasites based on known host associations. We found that the ratio of zoonotic vs. nonzoonotic parasites increased with the loss of carnivore hosts for several parasite taxa including for viruses, which are the most problematic for human and wildlife health. The loss of carnivore species also altered risks of humans by creating a more homogenous pattern of zoonotic diversity across North America. Our findings demonstrate an added benefit of carnivore conservation for human health.

RANGE-DIVERSITY PLOTS FOR CONSERVATION PLANNING: USING RICHNESS AND RARITY IN PRIORITY SETTING

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Current claims of biodiversity crisis call for immediate conservation actions. These require the identification of priority sites for conservation. Patterns of species richness are crucial such endeavor. Rarity, measured by the size of species' geographical ranges, is often used as a single or complementary criterion. For instance, hotspots for conservation have been defined using either one or the other criterion. We introduce a new tool, range-diversity plots, which simultaneously analyze species richness and range size identifying distinctive types of species assemblages. We applied this tool to the Mexican avifauna and show how it can be readily used to inform conservation practices. Also, we evaluated the representation of different assemblages in the national reserve system. We built a presence-absence matrix from the birds range maps overlaid by an equal-area grid and recorded the number of species and the average range size for assemblages present at each site within Mexico. Mexican birds show congruent patterns between richness and range size, richer sites harbor small-ranged species. These sites are poorly represented in the national reserve system. We show that patterns of congruence between diversity and distribution can be easily identified and interpreted using range-diversity plots based solely on a presence-absence matrix, providing a transparent, robust and explicit application for conservation planning.

NOT ALL THAT GLITTERS IS GOLD

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In the past two decades there has been a change in discourse among global and environmental agendas, tightly linked to the golden toad story (*Bufo periglenes*), and these changes were reflected in the media. The period 1987 to 1992 witnessed something of a shift in the United Nation's focus, from "poverty reduction in developed countries" to "biodiversity crisis", including climate change, biodiversity and forests. Climate change became one of the main issues during the United Nations Conference on Environment and Development in 1992; after the new "paradigm" among conservationists. Even though climate science has advanced at gigantic steps there is much uncertainty about future climate projections and little is known about most of living organisms' adaptation capability/resilience or moving capability. We focused on the case of golden toad, because it has been one of the most important flagships for conservationists and scientists to fight against climate change as declared by WWF "Global warming has already claimed its first species, with Costa Rica's golden toad believed to have become extinct." We explored and compared the representation of the "golden toad" in the media (internet and newspapers), and the academic literature (peer-reviewed journal articles). We also explored the changes in the discourse in both "media", in order to emphasize the hidden danger in distanciation processes and politics of "despair" for conservation.

Contributed Paper Session IV

Palaeoecology

USING ECOLOGICAL NICHE MODELING TO EVALUATE NICHE STABILITY IN DEEP TIME

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Many analyses of species' response to exotic species introductions or climate change in modern ecosystems assume that species conserve the parameters of their ecological niche when faced with changing environmental conditions. This assumption, however, is rarely tested directly, due partly to the limited temporal duration available when studying exclusively extant taxa. Because the fossil record preserves members of the same species at multiple temporal horizons, it is possible to assess how local populations or entire species responded to shifting environmental conditions (biotic or abiotic) using GIS-based tools such as ecological niche modeling (ENM) to reconstruct the parameters of a species' ecological niche before, during, and after an environmental shift. New Maxent analyses for Late Ordovician brachiopod species of eastern North America specifically examine niche stability across an extrabasinal immigration event, the Richmondian Invasion, which provides an opportunity to determine whether species altered parameters of their ecological niches in response to species invasions and ecosystem turnover. Results from these analyses suggest that the degree of niche stability varied through time; stability was highest pre-invasion, lowest during the invasion interval, and intermediate post-invasion. These species, therefore, apparently responded to invasion pressure through niche modification. Results from these analyses are compared with results from ENM analyses of Neogene horses and Devonian brachiopods to examine the generality of the Late Ordovician results.

DIFFERENTIAL DISPERSAL RESPONSE OF MAMMALS DURING THE GREAT AMERICAN INTERCHANGE

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After the Panaman Isthmus in America was established 2.7 mya, a great number of mammalian genera crossed the land-bridge joining the northern and southern subcontinents. This mixing of faunas is known as the Great American Biotic Interchange (GABI). One of the interesting features of the GABI is that it was asymmetrical: a much greater number of mammals from North America successfully colonized South America than the reverse. We tested this proposition by modelling climatic niches for 33 genera in America during the Miocene, the Pliocene, the Pleistocene and Recent times. We asked whether: (1) there were differences in two climatic-niche attributes (area and connectivity) for North American and South American taxa; (2) attributes changes in time; and (3) mammals that dispersed and failed to disperse exhibited differences in their climate niche attributes that were independent of their origin. Genera from North America showed a significant increment of their suitable area in South America from 8 mya to 2.95 mya and from 115 kya to 21 kya ($P < 0.001$). In contrast, South American genera showed a significant decrease of suitable areas in North America ($P < 0.01$). It was also found that successful dispersers had suitable climate niches available for colonization at shorter distances than unsuccessful dispersers ($P < 0.001$). Our results provide support for the proposition that asymmetry in dispersal during the GABI was associated with: (1) greater area of suitable climate niche for mammal colonization in South America, and (2) longer distances required for colonization of suitable climate niches in North America.

APPARENT NICHE SHIFTS AND NO-ANALOGUE CLIMATES IN EASTERN NORTH AMERICA DURING THE LATE QUATERNARY

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For many species, portions of their fundamental niche lie outside the contemporary climate domain. By combining contemporary and fossil occurrence data, one can more fully capture the fundamental climatic niche for species, and thereby enable more robust modeling of species responses to 21st-century climate change. As a first step, we analyzed eastern North American fossil and contemporary pollen records, obtained from the Neotoma Paleocommunity Database, for evidence of apparent niche shifts over the last 21,000 years. These pollen records were cross-referenced with transient climate simulations from the CCSM global climate model. The apparent niche shifts for many taxa are substantial, and are driven primarily by species expanding into late-glacial climates with no modern analogue and secondarily by within-niche shifts in relative pollen abundances. Uncertainty in climate simulations is likely also important. These apparent niche shifts cause species distribution models (boosted regression trees) to perform relatively poorly when training and test datasets are drawn from different time periods versus when drawn from the same time period. Predictive performance decreases with increasing temporal distance. The cross-temporal predictive performance by SDMs varies widely among plant taxa, and is consistently low for the tree taxa most associated with the late-glacial no-analogue climates in eastern North America (*Fraxinus*, *Ostrya*, *Populus*, and *Ulmus*).

RECONSTRUCTING A PUTATIVE CRYPTIC NORTHERN MESIC REFUGIA: PALEOCLIMATE RECONSTRUCTIONS AND TOPOCLIMATIC DOWNSCALING

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The interior wet belt (IW) cedar-hemlock forest of northern Idaho (USA) and eastern British Columbia (Canada) is characterized by steep river canyons, inland fjords, and high environmental heterogeneity, supporting dozens of species that are disjunct by > 150 km from their main coastal distributions. Different biogeographic approaches have led to two alternative explanations for the development of the distinct IW biota. Phylogeographic studies of plants and amphibians suggest the existence of stable refugia in multiple river canyons since the late-glacial period. Furthermore, 53 of 116 disjunct vascular plant species, and six endemic species, are distributed entirely south of the glacial limits in the IW. In contrast to this evidence for refugia, paleoecological and paleoclimatic studies indicate mesic conditions developed only within the last 3000 years, though the nearest such records occur outside of the putative refugia. Here, we present new pollen records from within the putative refugia. We show that the major mesic-adapted tree species, including western hemlock, western redcedar, and mountain hemlock, are registered in the pollen record only within the last 2000 years, and in some cases much more recently. Using both pollen-based paleoclimate reconstructions and GCM simulations, we downscaled climate estimates for the glacial maximum and deglacial time intervals using methods that account for cold air drainages and seasonal lapse rates. Species distribution models generated for mesic-adapted taxa show that they were highly unlikely to have persisted within the region. These results challenge both phylogeographic and phytogeographic interpretations.

GLACIAL SURVIVAL MAY MATTER AFTER ALL

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Biogeographers claimed for more than a century that arctic plants survived glaciations in ice-free refugia within the limits of the North European ice sheets. Molecular studies have, however, provided overwhelming support for postglacial immigration into northern Europe. For the first time we can present molecular evidence strongly favouring in situ glacial persistence of three species, the rare arctic-alpine pioneers *Arenaria humifusa*, *Sagina caespitosa* and *Carex rufina*. All belong to the 'west-arctic element' of amphi-Atlantic disjuncts, having their few and only European occurrences well within the limits of the last glaciation. Two very distinct and partly diverse genetic groups, one East and one West Atlantic, were detected in each species based on amplified fragment length polymorphisms (AFLPs), excluding postglacial dispersal from North America as explanation for their European occurrences. Patterns of genetic diversity and distinctiveness indicate that glacial populations existed in East Greenland and/or Svalbard (*A. humifusa*) and in southern Scandinavia (*S. caespitosa* and *C. rufina*). Despite their lack of long-distance dispersal adaptations, all three species show considerable dispersal abilities. Thus, it is no longer necessary to presume that such abilities are conflicting with possible in situ glacial survival.

REVISITING REID'S PARADOX BY INTEGRATING GENETIC AND TOPOGRAPHIC INFORMATION: *ABIES ALBA* (MILL.) - A CASE STUDY

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The fact that limited dispersal abilities of Northern Hemisphere trees are at odds with the rapid rates at which they seem to have re-colonized during the Holocene has been termed Reid's paradox. Since one and a half decades, considerable effort has been dedicated to resolving this paradox mainly by improving tools for modeling seed dispersal. On the other hand, however, concern has also been raised that the simulated rates by these improved dispersal models have been overestimated. Empirical evidence supporting such concerns stems from molecular analyses that suggest the existence of cryptic glacial refugia not detectable in the fossil record which limits the area that has potentially been re-colonized from populations surviving in southern refugia. To contribute to this debate, we used an interpolated fossil pollen dataset using a spatially explicit approach that includes topography along with genetic data of a European species: *Abies alba* (Mill.). Topography is aimed to constrain the rates and routes during the migration process and the genetic data are expected to detect potential long-distance dispersal. We obtained much lower migration rates (50 to 150 m/year) than previous estimates (102 to 103 m/year). One explanation is that the long distance dispersal and/or the presence of cryptic glacial refugia appear to have not contributed to the process of recolonization of *Abies alba* in Europe.

Contributed Paper Session V

Marine Biogeography

THE DYNAMICS OF BIODIVERSITY: RANGE SHIFTS AND AREAS OF ORIGIN

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The causes of large-scale biodiversity patterns are widely debated, and frequently a single process is seen as dominating their origination. Discussions have focused on macroecological processes such as the contributions of migration, speciation, extinction, and environmental variables to structuring biodiversity patterns. These studies are usually based on cohort analyses, focusing on the behavior of the total species pool and not the individual species contributing to the pattern. In this study I describe the variation in spatio-temporal distribution and morphological change in a single genus of large benthic foraminifera, *Cycloclypeus*. I found that depending on the lineage allopatric, parapatric and sympatric speciation is documented. For the single extant species, *C. carpenteri*, it is argued that its area of origination is outside the current range of the genus. Morphological evolution was constant over large geographical areas in most time intervals. An example of inhomogeneous rates of morphological change within the geographic range shows that, while looking within the centre of its distribution, replacement of a species by its successor appeared to be punctuated, yet in a marginal area the same replacement was a gradual anaphyletic trend. An early attempt to relate this finding to past biodiversity hotspots is provided.

WHAT ORIGINATED SPECIATION AND WHAT PRESENTLY MAINTAINS THE SPECIES INTEGRITY AND THEIR GEOGRAPHIC DISTRIBUTION? A COMPARATIVE STUDY OF TWO MARINE TAXA ALONG THE CHILEAN COAST

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A biogeographic transition zone has been described at 30°S of latitude along the Chilean coast. The factors that originate and maintain this pattern remain poorly known. Here, we present a comparative and multi-disciplinary study of two taxa with low dispersal potential that inhabit contrasting habitat: the exposed rocky shore macroalga *Lessonia nigrescens* (kelp) and the beach dwelling isopod *Excirolana hisuticauda*. We performed a comparative phylogeographic study with 400-1000 individuals/taxa covering >2,500 km of coastline, using DNA sequences and microsatellite data. With robust results we found two cryptic species within each taxon. The edge of the geographic distribution of the species found within each taxon is at 30°S, i.e. in concordance with the biogeographic break. Additionally, we focused on the mechanisms that may be maintaining the species integrity and the geographic distributions: (i) Marked differences in ecological niches among the two kelp species were revealed by field and lab experiments, (ii) The two isopod species presented morphological divergence, particularly on an important reproductive feature.

EXTENDING TERRESTRIAL SPATIAL PATTERN METRICS TO THE MARINE REALM

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Spatial pattern metrics are routinely applied to characterize and quantify terrestrial landscapes, and they have demonstrated great utility in landscape ecology and conservation planning. Increasing awareness of the importance of considering seascape structure in ecology and management combined with recent advances in marine remote sensing technology have led to an increase in the application of spatial pattern metrics in the marine environment. Given the relatively new interest in seascape ecology and the paucity of guidelines on utilizing and implementing landscape metrics in the marine environment, we wanted to assess the application of spatial pattern metrics to seascapes. To do this, we reviewed the marine literature over the 30-year period from 1980-2010 to identify the metrics used to quantify seascape structure. We identified seventeen unique spatial pattern metric studies that characterized seascape structure. Twelve studies quantified spatial patterns using a two-dimensional patch-mosaic model, and five applied a continuously varying three-dimensional surface model. Of the twelve two-dimensional studies, all applied standard metrics used in terrestrial studies with no marine-specific metrics. Because relatively few studies have been conducted on seascapes, we place our results in context of current landscape ecology concepts of spatial, temporal and thematic resolution as well as statistical techniques for handling multiple metrics. Seascape ecology is a relatively new sub-discipline that is in the process of forming its theoretical basis, and identifying useful metrics for the marine environment represents a critical next step in understanding the link between pattern and process in the ocean.

INFERRING MARINE MACROECOLOGICAL AND BIOGEOGRAPHICAL PATTERNS USING BIO-ORACLE, A GLOBAL MARINE ENVIRONMENTAL DATASET

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We present Bio-ORACLE (Ocean Rasters for Analysis of Climate and Environment), a global marine environmental dataset designed for species distribution modeling. This dataset offers an array of geophysical, biotic and climate data at a spatial resolution of ca. 9.2 km and is freely available online. We illustrate the utility of this dataset for macroecological and biogeographical applications using two case studies of recent macroalgal speciation in the Indian Ocean: the *Halimeda discoidea* and *Codium duthieae* species complexes. These species complexes consist of two and three cryptic species, respectively, and each of the sibling species is geographically disjunct from the others. Species' niches are predicted using environmental characteristics derived from "Bio-ORACLE" in association with occurrence localities for a given species. Remarkable shifts of the climatic niche were observed between the different sibling species of both species complexes. In conclusion, we recall that biogeographical studies benefit from the use of ecological niche models and show that Bio-ORACLE has the potential to serve as a robust environmental dataset for marine biogeographers.

DETERMINANTS OF GLOBAL EXTINCTION RISK IN MARINE MAMMALS

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The world's oceans have undergone profound changes over the last century as a result of human activities. However, the consequences of escalating human impacts on marine mammal biodiversity remains poorly understood. Currently almost 40% of all marine mammals are considered data deficient by the IUCN Red List, and the potential impacts of climate change on marine mammals are only beginning to be understood. With the number and extent of human impacts on the marine environment expected to increase with projected human population growth in coming decades, a growing number of species will be subject to these threats. Predictive models of species at risk are key to informing present and future conservation needs, yet such models have not been explored for marine mammals. We developed predictive and spatially explicit models of marine mammal extinction risk using machine learning approaches coupled with spatial analyses of habitat productivity and human impacts, including climate change. We show that the speed of life history is overwhelmingly the most important predictor of extinction risk in marine mammals. Other top predictors of risk include small social group size and small geographic ranges. In general, intrinsic traits are more important predictors of extinction risk than extrinsic variables for marine mammals, as they measure the intrinsic susceptibility of species to human impacts. We also show that nearly 40% of all marine mammals, including many data deficient species, are predicted to be at risk of extinction, and identify global hotspots of marine mammal risk.

RANGE CHANGES IN LARGE, HIGHLY MOBILE OCEANIC PREDATORS

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In the past decade, substantial declines in both the abundance and diversity of large pelagic predators such as tunas and billfishes have been documented at a global scale. In terrestrial systems, such changes can often be accompanied by a decline in species range sizes. Yet it is not known whether this is also the case in the oceans, given the differences in dispersal patterns and mobility. Here we combine two global datasets over a four-decade period (1960-1999) to examine whether we can detect a difference in the range sizes of tunas and billfishes. We then relate our results back to species life-history characteristics, and assess possible mechanisms.

Contributed Paper Session VI

Hot Topics in Biogeography

UNTANGLING THE INFLUENCE OF ECOLOGICAL AND EVOLUTIONARY FACTORS ON TRAIT VARIATION ACROSS HUMMINGBIRD ASSEMBLAGES

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Community assembly theory predicts that at a given site a series of nested processes whose importances vary across spatial and temporal scales will influence local community composition. Evaluating this theory requires integration of historical processes associated with trait evolution and dispersal limitation, how functional traits vary across environmental gradients and how biotic interactions might influence trait spacing in local communities. Here we investigate patterns of morphological variation in 286 hummingbird assemblages (125 species) across an elevational gradient from tropical lowlands to the high Andes (0-4500 m) using information about 1) the relatedness among co-occurring species, 2) trait-environment relationships for four traits whose functional roles have been clearly established in the literature, and 3) evolutionary trait lability. Trait means, variation and range varied across the gradient indicating that filtering was prevalent especially at high elevations. Across the gradient traits were more evenly spaced than expected by chance, indicative of niche differentiation potentially driven by biotic interactions. Taken together, our results provide strong evidence for filtering and potentially biotic interactions in structuring morphological variation across assemblages. Further, we show that patterns of morphological variation cannot be directly predicted from measures of phylogenetic structure and trait lability emphasizing the need to conduct analyses that integrates various types of data. We suggest that our predictive framework combining evolutionary and ecological information will provide new insight into processes influence assemblage structure.

THE PHYLOGENETIC STRUCTURE OF PALM ASSEMBLAGES WORLDWIDE

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The recent increases in the availability of phylogenetic and species distribution data open up new avenues for examining the structure of ecological assemblages. Here, we examine for the first time the phylogenetic structure of palm (Arecaceae) assemblages globally by using presence-absence data of all 2445 palm species and a dated genus-level phylogeny. We calculate the net relatedness index (NRI) as a measure of how strongly the mean pair-wise phylogenetic distance of palms in a given assemblage deviates from null model expectations (applying different sampling pools). In all analyses, we only find significant clustering but no significant overdispersion. Biogeographic regions show pronounced differences in the degree of phylogenetic clustering with palm assemblages in the New World (particularly in the Neotropics) being significantly more clustered than assemblages in the Old World. Most palm assemblages in Africa as well as many countries at the northern range limits of present-day palm distributions show neither significant clustering nor significant overdispersion. Further, a number of islands and island systems stand out with remarkably high clustering, notably Madagascar (which has the highest NRI value globally), but also e.g. New Caledonia, Hawaii, and Cuba. Our results suggest an important role of evolutionary history and past climate change in structuring palm assemblages worldwide.

WHAT CONSTRAINS LONG DISTANCE COLONISATION? EXPLORING THE LIMITS TO THE WANDERINGS OF THE DANTHONIOID GRASSES

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We explored the constraints to colonisation in the globally distributed grass subfamily Danthonioideae. We used an almost completely sampled, well-resolved phylogeny to reconstruct the ancestral area, found to be in Africa, probably southern Africa. From this area, the Danthonioideae colonised Australia, New Zealand, South America, North America, and finally Europe and Asia. We postulate some 32 overland and overseas colonisation events across barriers that are at least 1500 km wide, in addition to very numerous shorter-distance colonisation events. We used a niche modelling approach to locate potentially suitable habitat, which the clade may not yet have reached, and determined that the only suitable vacant habitat is in SE Asia, specifically Japan and SE China. Molecular dating allowed us to calculate the colonisation rate across each barrier. The most important constraint on colonisation is the width of the barrier. There is a hyperbolic relationship that reflected a rapid reduction in the colonisation rate between 1500 and 5000 km, after which there is no more a detectable drop in the rate. We detected no West Wind Drift effect, and in the Southern Hemisphere easterly and westerly colonisation is equally frequent. We also did not detect any difference between overland and overseas colonisation, except that most south-north colonisation is overland, and east-west colonisation is overseas. However, we detected a very strong contingent effect, with colonisation direction almost always towards suitable, unoccupied, habitat.

DIVIDE TO CONQUER: IS THERE AN ATLANTIC FOREST VERTEBRATES' LONGITUDINAL PATTERN OF DISTRIBUTION?

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In the last decade several studies on Atlantic forest (Af) vertebrates report distinct north and south groups within the biome. This led authors to believe in the presence of a longitudinal pattern of distribution across the Af. Nevertheless, there is some inconsistency between the groups' range boundaries, questioning the pattern's veracity. Thus, we conducted a literature survey focusing a principal question: does the distribution of vertebrates' in the Af represent a common pattern? We divided this main question in two secondary topics. Firstly, we examined the most cited endemic areas. Secondly, we focused on distribution differentiation studies. We analyzed geographical data with panbiogeographic tools. This is the first time that panbiogeography is applied to the Af. We found two dozen studies reporting longitudinal differences. From these, 15 references could be analyzed, comprising 16 taxonomic groups (genus and species), divided in 40 taxonomic subgroups (species, subspecies, populations or lineages), represented by 375 occurrence records. Our results confirmed the existence of a general longitudinal pattern of vertebrate distribution in Af, with greater complexity than a simple north/south organization. Ten generalized tracks could be converged in seven nodes. Four of them overlapped with the most consistently cited endemic areas of Pernambuco, Bahia and São Paulo. Additionally, we found evidence for three other important areas, namely Rio Doce, Paraná and Rio Grande do Sul. We also found evidence indicating that likely different events were involved in the formation of each region. A biogeographic history can only be deciphered considering its heterogeneity and dividing the biome in its components.

ANDEAN UPLIFT AS DRIVER OF BIODIVERSITY IN AMAZONIA

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The relationship between geological history and biogeographical patterns has long been recognized. Recent advances in the fields of geology and biology now provide new insights into the origin of present biodiversity in Amazonia. We propose that mountain building in the Andes was the driving force behind speciation in this region. Amazonia was relatively stable for many millions of years, but since the Neogene (c. 23 million years ago) large paleoenvironmental and paleogeographical changes took place. The landscape changed from predominantly fluvial to a wetland with shallow lakes, while from 10 Ma the Amazon River connected Andes and Atlantic. This all formed the basis for the present geography and landscape that is characterized by flooded forests (varzeas) of the Andean rivers, and the new mosaic-type, Andean substrate in Western Amazonia. The newly formed Andes and Amazon River with its floodplains created new habitats that were open for colonization. At the same time as being conduits that bridged previously disconnected areas, Andes and Amazon also constituted barriers that split the floral and faunal populations. The latest geological and palynological data further suggest that over time different factors have played a role in driving speciation. In the Paleogene high temperatures and moist were the most important causes. Nevertheless, during the late Neogene temperatures dropped and diversity remained high. During this time mountain building and its effect on climate (raising precipitation rates) and erosion seemed to have been the overruling factors.

LIMITS OF SPECIES RANGES AND DIVERSITY PATTERNS: RAPOPORT'S RULE, LATITUDINAL GRADIENTS AND GEOMETRY

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Diversity patterns are tightly related to patterns in species ranges. Latitudinal diversity gradient has been related to Rapoport's rule, i.e. decreasing latitudinal extent of species ranges towards equator. According to this theory, species can have narrower tolerances in more stable climates, leading to smaller ranges and allowing coexistence of more species. The problem is, however, that observed patterns only indirectly reflect ideal principles assumed to lie behind them. Using a simple geometric model, we show several unexpected relations which could not be revealed without explicit discrimination of theoretical principles from the patterns we observe. (1) The postulated decrease of species potential range sizes towards the tropics would itself lead to a latitudinal gradient opposite to that observed, whereas an increase in extent of potential ranges towards the tropics would lead to the observed diversity gradient. (2) In the presence of geographic barriers constraining actual species ranges, Rapoport's rule emerges if the latitudinal trend in extents of potential ranges (as defined by climatic tolerance) is opposite to that postulated or if variability in potential range extents decreases towards the poles. (3) A strong implicit latitudinal diversity gradient (i.e. higher concentration of midpoints of species' potential ranges in the tropics) produces both observed macroecological patterns without the contribution of any latitudinal trends in species climatic tolerances or in potential range sizes. Our model is supported by data on global distribution of species range sizes and provides a way how to evaluate the role of species tolerances and dispersal boundaries on diversity patterns.

Posters

1. INFERRING THE FACTORS THAT SHAPE SPECIES' RANGES

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Why some species are widespread while others are very restricted geographically is one of the most basic questions in biology, although it remains basically unanswered despite the sustained interest from ecologists, biogeographers and evolutionary biologists. A variety of ecological and evolutionary explanations for the observed range size variation have been suggested, including differences in niche breadth or environmental tolerance, body size, population abundance, latitude, environmental variability, colonization and extinction dynamics, and dispersal ability. However, there are still unresolved fundamental questions, best exemplified by the fact that closely related species often display dramatic differences in range size for completely unknown reasons. Tests of these differences remain relatively scarce, have been performed for examples of very few taxa, and generally fail to address the potentially confounding effects of the phylogenetic relatedness of species. Here, we used a set of ten lineages of western Palearctic aquatic Coleoptera for which comprehensive phylogenies were available with the aim to investigate the role of different ecological, biogeographical and historic factors on the size of the geographic range of species. The geographic position of the range emerged as the main factor determining range-size differences, with more northern and eastern species having the largest ranges. Main habitat type (lotic or lentic) was also significantly related to range-size in those lineages with both lotic and lentic species, with lentic species displaying larger distributional ranges than lotic ones.

2. DELIMITING THE EXTENT OF THE STUDY AREA IN SPECIES DISTRIBUTION MODELLING

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Recent studies have shown that the extent of the study area can have important effects on the results of species' distribution models (SDMs), but no objective criterion for its delimitation has explicitly been assessed yet. Our objective is to propose and assess an approach to delimit the extent based on the 'trend surface analyses' (TREND). A TREND was run using the occurrences of the species, and the outputs were considered to delimit extents of different sizes for further training of SDMs. We compared the results obtained using TREND with those obtained after applying a minimum convex polygon and similar criteria for extent delimitation. Using data of four well-known wild ungulate species, we studied the effects of the extent size on model calibration and discrimination, and on the tendency of the models to predict environmental potential when they are projected to a new scenario. Our results showed that the models with the best discrimination power and the highest capacity to forecast environmental potential were obtained using TREND. In general, discrimination significantly increased and calibration decreased as extent size was enlarged. When models trained in small extents were transferred outside, they showed a tendency to predict higher environmental potential for the species (that was in accordance with expert knowledge) than those models trained in large extents.

3. MAMMOTH AND MASTODON GEOGRAPHIC RANGE SHIFTS IN THE GREAT LAKES REGION DURING THE TERMINAL PLEISTOCENE

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Since the nearly global acceptance of climate change, many studies have attempted to understand how 'global warming' may affect geographic ranges. However, as stated by the principle of uniformitarianism, understanding the geographic range shifts of the past may provide greater understanding for the range shifts of the future. Such studies have utilized FAUNMAP, a database produced by the Illinois State Museum documenting the late Quaternary distributions of mammal species. While FAUNMAP may be useful, it has been found lacking and the studies utilizing it have focused on communities as a whole rather than individual species. Previous studies have shown a Gleasonian response to climate change but few have actually studied an organism's individual response. Mammoths and mastodons (Order Proboscidea) are some of the most widely studied organisms of this time period, but no one has attempted to understand their response to glacial retreat spurred by climate change. Using all known site locations for three species (*Mammuthus jeffersonii*, *Mammuthus primigenius*, and *Mammuthus americanum*), geographic ranges were determined for the Great Lakes Region (Minnesota, Wisconsin, Illinois, Indiana, and Ohio) for four different time periods between 18,000 and 10,000 years ago. Additionally, since no one has attempted to understand the habitats of such organisms utilizing geographic information science (GIS), the hope exists to associate each site location with vegetation data. With knowledge of the geographic ranges and vegetation, future identification of unknown proboscidean species may be possible.

4. VEGETATION ANALYSIS OF THE FARASAN ARCHIPELAGO, RED SEA, SAUDI ARABIA

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The coral islands of the Red Sea are regarded as having a high national and international conservation value because of the diversity of marine and terrestrial habitat. However, urban development, pollution and increasing pressures of commercial and recreational use of resources pose serious threats to the biodiversity of these habitats. In the present study, the species composition, vegetation structure and several environmental factors were investigated for 210 stands on twenty coral islands of Farasan at the Red Sea of Saudi Arabia. Multivariate statistical analysis techniques in the terms of classification (Cluster Analysis) and ordination (Determined Correspondence Analysis - DCA, and Canonical Correspondence Analysis - CCA) were employed to identify vegetation types and their relevance to the underlying environmental gradients. A total of 191 flowering plants that belong to 53 families and 129 genera were recorded. Geophytes and chamaephytes dominate the saline habitats, while climbers, therophytes and hemicryptophytes dominated the sandy formations and rocky plains. The cluster analysis and DCA ordination resulted in the recognition of twelve vegetation groups, each of definite floristic composition and environmental characteristics, and could be linked to a specific habitat. The main environmental variables controlling the separation of the vegetation groups on the first two axes of CCA were soil salinity and elevation. The results of this study indicated that the flora of the study area has a transitional character where the Saharo-Arabian Desert, Sudanian and Tropical vegetation interact. These findings should guide conservation efforts to maintain species diversity, which is threatened by anthropogenic activities and invasion by the exotic invasive tree *Prosopis juliflora*.

5. NICHE MODELING OF COASTAL MEDITERRANEAN FISHES UNDER CLIMATE CHANGE SCENARIO SIMULATED BY THE NEW NEMOMED8 MODEL: EXPECTED BIODIVERSITY LOSS AND SPECIES TURNOVER

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The Mediterranean Sea is a hotspot of biodiversity, and global warming is expected to have a significant influence on fish species distributions and the composition of fish assemblages. Here, we projected the potential future climatic niches of 339 Mediterranean coastal fishes based on a global warming scenario (IPCC, scenario A2) implemented with the new Mediterranean model NEMOMED8. Fish distributions were compiled from the atlas of Fishes of the Northern Atlantic and Mediterranean and corrected by the bathymetry of each species. This atlas is based on regional data sets and expert knowledge; it provides the only available basin-wide information on the geographic ranges of all Mediterranean Sea fishes. Since there is still uncertainty in the modeling of climatic habitats that determine species geographic distributions, we implemented an ensemble forecasting method according to the most recent methodological developments. Through these analyses we explored the difference (i) in sea surface temperature under climate change scenario, (ii) in coastal fish richness (iii), and in fish composition within coastal assemblages (β diversity) between now and two time periods (2040-2059 and 2080-2099). As a result, by 2070-2099, the average surface temperature of the Mediterranean Sea was projected to warm by 2.9°C. Projections for 2041-2060 and 2070-2099 suggest that 21 and 60 species, respectively, were expected to become extinct.

6. TIMING AND GEOGRAPHY STRUCTURE HEAT WAVE AND DROUGHT EFFECTS ON AVIAN COMMUNITY DYNAMICS

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Climate warming and increased variability in temperature and precipitation are expected to produce more intense heat waves and droughts in the 21st century. We sought to elucidate fundamental effects of these extreme weather events on avian communities across the conterminous United States. Specifically we explored how avian abundance varied in response to: 1) timing and duration of heat wave and drought events, 2) whether events occurred jointly or individually, 3) nest location and migratory habit, and 4) ecogregion. Using mixed effects models, we quantified the effects of heat waves and droughts on US avian communities based on 2000-2008 data from the North American Breeding Bird Survey, the remote sensing instrument MODIS, and a network of precipitation measurements. We found large changes in avian abundances related to 100-year extreme weather events occurring in both breeding and post-fledging periods. We also found that jointly, rather than individually occurring heat waves and droughts were more predictive of abundance changes. Declines in avian abundance following heat waves and droughts were largest in the arid southwest, and among ground-nesting birds and Neotropical migrants. In addition to indicating the importance of functional traits, timing, and geography, these results suggest that increasing drought and heat wave conditions may have important consequences for avifaunas.

7. COMPARATIVE PHYLOGEOGRAPHY OF AMPHIBIANS AND PALEOECOLOGICAL MODELLING SUPPORTS THE PLEISTOCENE PERSISTENCE OF SOUTHERN BRAZILIAN ATLANTIC FORESTS

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We compare paleoecological distribution models for six amphibian species endemic to the Brazilian Atlantic forests with historical inferences of diversification derived from phylogeographic data. In contrast to recently proposed scenarios derived from paleoecological modeling, the distributions of all species are predicted to have persisted in the southern part of the Brazilian Atlantic forest biome since the Last Interglacial (c. 135,000 years ago). The phylogeography of at least three of the species (mitochondrial and nuclear gene data) are generally concordant with paleodistribution scenarios, with species persistence indicated by the presence of phylogeographical breaks south of the previously proposed limit for the forest distribution in the Last Glacial Maximum (c. 20,000 years ago). Multi-species comparisons with coalescent isolation-migration models suggest the persistence and divergence of several geographical units within species across the Brazilian Atlantic forests since the Pliocene. The geography of divergence across species is concordant with recognized biogeographic boundaries. Divergence time estimates at each phylogeographic break reveal both old and more recent diversification events, suggesting continuous and perhaps idiosyncratic diversification processes in these distinct forest-dependent amphibians.

8. TESTING THE HUTCHINSONIAN FRAMEWORK FOR SPECIES DISTRIBUTIONS: CARIBBEAN ANOLIS LIZARDS, CLIMATIC NICHE AND THE GEOGRAPHY OF SPECIES INTERACTIONS

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The general theoretical framework for species' geographical distributions, built upon the Hutchinsonian niche concept, is well established in biogeographical thought. It posits that species' potential distributional limits are set by their fundamental environmental niches. Species are predicted to inhabit only a subset of their potential distributions due to factors such as dispersal barriers and/or biotic interactions. Predicting a priori where species will be absent from their potential distributions, especially due to interspecific interactions, has proven difficult due to the lack of widely applicable geographical indices of potentially occurrence-limiting ecological interactions. Here, by integrating trait-based ecology and ecological niche modelling, we develop the concept of the species-interaction landscape (SIL). A species' SIL quantifies the strength of potential interactions through geographical space, based on ecomorphological similarity of potentially co-occurring species. We build on a long history linking *Anolis* lizard morphology to micro-habitat use, competitive interactions, and fitness to construct SILs for species on Cuba and Hispaniola. Then, we combine these SILs with climatic variables and null modelling to predict species distributions on these islands using multivariate adaptive regression splines. This approach allows us to evaluate the influence of phenotypic-based interactions and environmental variables on species' potential and realized geographical distributions.

9. PLANT COMMUNITY STRUCTURE AND DIVERSITY IN MEDITERRANEAN EVERGREEN FORESTS: THE USE OF LIDAR IN CONSERVATION MAPPING

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Using very high frequency pulses of near-infrared energy, airborne LiDAR is an active remote sensing technique which can be used to characterise the structure of plant communities. The intensity and timing of return pulses from interceptions with vegetation and ground can help discriminate different tree species and forest communities, and provide structural information such as heights, crown diameters and gap locations. This is illustrated for the cork oak forests of the Algarve, Portugal – important for their biodiversity as well as economic values, yet threatened by changing land-use practices, fire and other disturbances. We show how LiDAR can be used to distinguish them from pine and eucalyptus plantations, and characterise their sub-canopy plant communities. LiDAR can be used to model their habitat quality and map areas of conservation importance in remote and steep terrain with poor access for ground surveys. The LiDAR-derived models of canopy and understorey vegetation of these forests can help assess how they change over gradients of disturbance and climate. Thus LiDAR serves as an analytical tool to bridge the gap between landscape and finer scales of conservation interest.

10. DIVERSITY AND COMPOSITION OF PALM COMMUNITIES (ARECACEAE) IN QUINTANA ROO, MEXICO

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We compared the composition and diversity of palm (Arecaceae) communities in three forest types along a gradient from dry deciduous, over intermediate to wet evergreen forest in Quintana Roo, Mexico. In forty-nine 5×500 m transects, we counted 52,612 individuals representing 14 species in 11 genera. Within the 49 transects we found monodominance in six. The most abundant palms were *Cryosophila stauracantha*, *Thrinax radiata* and *Coccothrinax readii* and the least abundant were *Bactris major* and *Gaussia maya*. *Thrinax radiata* was the most abundant species in the northern deciduous and central intermediate forests and *Cryosophila stauracantha* was the most abundant palm in the evergreen rain forest to the south. *Chamaedorea seifrizii* and *Sabal yapa* were the most frequent palms in the sample. Combining all individuals in the three forest types 29% were seedlings, 59% juveniles, 1% subadults and 10% were adults. As expected, the Shannon index confirmed that the southern evergreen forest was the most diverse. Because the Yucatan Peninsula has been recognized as biotic province, and palms have ecological and economic importance, our results could be relevant for conservation and contribute to understanding diversity changes along gradients. Both species richness and overall palm abundance increased from north to south, which correlates with higher precipitation, deeper soils, fewer ground rocks and a higher forest cover.

11. THE BRAZILIAN ATLANTIC FOREST BIODIVERSITY HOTSPOT: LAND PLANARIANS AS MODEL ORGANISMS FOR FINE-SCALE PHYLOGEOGRAPHIC STUDIES

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The Brazilian Atlantic Forest is one of the richest biodiversity hotspots, as well as one of the most damaged by human activities. In recent years, with the aim to preserve the small remaining forest fragments, the Brazilian authorities have supported the creation of protected areas based on biodiversity studies of this region. Some paleoclimatic modeling studies have predicted two stable regions in the central part of the Atlantic Forest while southern regions might have suffered strong instability during glaciations. Molecular phylogeographic and endemism studies show, nevertheless, contradictory results: some data support these predictions, while other indicate that paleoclimatic models fail to predict areas with stable rainforest in the south. Most of these studies however, have been conducted using species with relatively high dispersal rates, whereas taxa with lower dispersion capacity will likely be better predictors of habitat stability.

Here, we have used two land planarian species as model organisms to analyze the patterns and levels of nucleotide diversity on a locality in the Southern Atlantic Forest. We find, in both species, high levels of genetic variability without the molecular footprint of recent colonization or population expansions. The results reflect, therefore, a long-term habitat stability scenario for this region. This result gives support to the existence of stable areas, maybe glacial refuges, also in the southern Atlantic Forest, and at the same time show the suitability of land planarians to understand current patterns of biodiversity.

12. MOLECULAR ANALYSIS OF THE TERRESTRIAL PLANARIAN *MICROPLANA TERRESTRIS* MULLER, 1774 FROM THE NORTH OF THE IBERIAN PENINSULA

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Terrestrial flatworms (Tricladida, Continenticola, Geoplanidae) form a little known group of free-living flatworms including little more than eight hundred species described at the moment. They are triclads with an auxiliary ventral nerve plexus and a distinct creeping sole. Although they are poorly known, especially in Europe, they have interesting features that make them good bioindicators. In a previous work on the diversity of terrestrial planarians in the Iberian Peninsula, this was found to be higher than expected, uncovering the presence of at least 15 species, some of them new to science, and, except one, all belonging to genus *Microplana*. In this study we focus on *Microplana terrestris* Muller, 1774, a species that was found to present a wide distribution in the northern part of the Peninsula. By combining morphological data (both external and internal anatomy) and molecular analyses (using the mitochondrial cytochrome oxidase I gene) we intend to evaluate the status of this species in the Peninsula as well as to estimate its evolutionary and biogeographic history through a population study. Our preliminary results show a clear separation between two big clades, corresponding with the eastern and western part of the north of the Peninsula. At present we are analysing the possible causes of this separation (geographical barrier, recent speciation event, etc) that will be discussed.

13. THE EFFECT OF SPECIES RANGE ESTIMATION METHODS ON RICHNESS AND PHYLOGENETIC DIVERSITY ESTIMATES: A COMPARISON OF FOUR METHODS USING AUSTRALIAN MARSUPIALS

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Biodiversity assessments are a fundamental tool in biogeographical and macroecological studies. Nevertheless, the methods used to estimate species distribution may affect the maps' outcome. With the aim to analyse the effect of using different approaches to estimate species ranges, we elaborated richness and phylogenetic diversity (PD) maps across Australia. The first approach 'Range-wide occurrences' is related to museum records, and the geographic records count as presence. This method underestimated the presence of species, and therefore had low richness and PD scores. 'Marginal Occurrences' (MO) is generally an expert drawn distributional map. Despite its coarseness, the assessments derived from this approach had intermediate richness and PD scores. The third, 'Statistical Modeling' (SDM) combines geographic records and environmental data to predict species occurrence. This approach overestimated the richness and PD estimates, by mapping the species fundamental niche. In order to reduce the false presence from SDM approach, we used a last approach which we called 'Combined' (Co), because it is a combination of both SDM and MO. We conclude that biodiversity assessment may vary depending on which method used to estimate species distribution. The Co approach showed a finer level of detail than MO, making it potentially useful for regional and smaller scale studies. Because of its coarseness, 'Marginal Occurrences' should be considered when geographical data is not available, for example when research is done at continental or global scales.

14. DIVERSIFICATION ON MACARONESIAN ARCHIPELAGOES: MOLECULAR PHYLOGENIES OF BEETLES AND BUTTERFLIES OF THE AZORES, MADEIRA AND THE CANARY ISLANDS

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The Macaronesian islands, given their location, range of geological ages and high levels of endemism, are a good system to investigate evolutionary and biogeographical questions. However, most studies concern species on single islands or archipelagoes, and studies addressing multiple islands on several archipelagoes are scarce. *Tarphius* beetles and *Hipparchia* butterflies, insects with distinct dispersal abilities, colonized and underwent extensive speciation on the Macaronesian islands, providing an excellent opportunity to study patterns and processes of diversification. We used mitochondrial and nuclear molecular markers to estimate phylogenetic and phylogeographic relationships amongst populations from the Azores, Madeira and Canary Islands, and putative continental sources of colonists. Phylogenetic reconstructions for both groups support inter and intra archipelago structure, and that colonization of the most remote of the Macaronesian archipelagoes, the Azores, is a rare event. For the low vagile *Tarphius*, data suggest a colonization event to the Macaronesian islands followed by dispersal and speciation; for *Hipparchia*, several colonization events from mainland can account for the closest relatives of Madeiran and Canarian specimens being different continental lineages. The roles that geological age, habitat diversity, area, and isolation of islands, and dispersal ability of the study groups may play as diversification drivers, as well as their explanatory power for the phylogeographic patterns inferred are discussed.

15. HISTORICAL BIOGEOGRAPHY OF EUROPEAN HARES: INSIGHTS FROM MITOCHONDRIAL DNA VARIATION

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European hares (*Lepus europaeus*) constitute an important faunal element in open areas and are of great socio-economic importance, yet little is known regarding the species' biology, including its phylogeography and population structure. In an attempt to unravel the evolutionary history of the species and to determine its micro and macro-geographical genetic structure, information from partial control region (D-loop) sequences of mitochondrial DNA from European hare populations distributed in the eastern Mediterranean was assessed. The studied samples exhibited high variability and a remarkable spatial genetic structure despite various restocking practices that have taken place in the study area. The produced phylogenetic relationships coupled with paleogeographic, paleoclimatic and paleontological data allowed us to propose a phylogeographic hypothesis according to which the species colonized Balkans during Pleistocene. The proposed scenario explains the existence of the two highly divergent phylogenetic clades present today in Balkans indicating that they reached Europe by two distinct dispersal routes.

16. ANALYSIS TECHNIQUES IN HISTORICAL BIOGEOGRAPHY. APPLICATION TO THE ANAGA'S LAUREL FOREST (TENERIFE, CANARY ISLANDS, SPAIN)

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Historical biogeography has among its objects of study how the geography of vegetation has been conditioned by human activity. The interpretation of the historical vegetation dynamics of a landscape needs to be addressed by synthesizing information using a variety of analytical approaches from different disciplines. Phytogeographical study of Anaga's laurel forest demonstrated the important imprint of the forest exploitation from sixteenth century to the later twentieth century, and allowed deduction of changes in use over this period. This poster shows that assessment of this hypothesis requires detailed knowledge of the socioeconomic history of the area, as well as soil and archaeological evidence of anthropogenic soil processes. More specifically, it underscores the utility of studying historical documents, and of soil analyses such as biomineralization, organic matter and granulometry.

Spanish National Plan I+D. MCINN. CSO2009-14116-C03-03. Transformaciones históricas de los paisajes forestales de montaña. Los Parques Rurales de Anaga y Teno. Tenerife. Islas Canarias.

17. DO MICROBES HAVE BIOGEOGRAPHY? CASE STUDY OF MARINE BENTHIC CILIATES

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World-wide diversity and distribution of marine benthic ciliates have been studied using the comprehensive database (1342 species, over 350 sources). Twenty six percent of species have been found in a single region only; whereas 44 % have wide geographical distribution covering both hemispheres. Only 5-7 % of regional faunas are endemics, which is much lower than for macro-organisms. Regional diversity depends neither on total area nor coastline length and does not show any latitudinal trends, but highly correlates with investigation effort expended in a region and (negatively) with average salinity. Comparison of species composition reveals more or less distinct differences between Arctic Area (the White, Barents and Kara seas), Laurasian Area (North Atlantic, North Pacific and European seas), Gondwanian Area (Southern Ocean), and Antarctic. No clear geographical correlates are found in faunistic composition on genera or families levels. There is the tendency to narrowing the occupancy ranges for species found at high latitudes, as contrasted with the opposite pattern for macro-organisms (Rapoport rule). We suggest that marine benthic ciliates demonstrate some patterns that are in general agreement with the “Moderate endemism” model (Foissner 2004, 2008) but consistently contradict the regularities commonly obtained for multi-cellular taxa. Thus, even if ciliates have biogeography, it is very specific and quite differs from those for macro-organisms.

18. DATING THE ORIGIN AND LOCATING THE DIVERSIFICATION CENTRE OF APOIID UMBELLIFERS (MAGNOLIOPHYTA, APIACEAE SUBFAMILY APIOIDEAE)

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The angiosperm family Apiaceae comprises mostly herbaceous and temperate holarctic members, whereas its sister group, Araliaceae, and the basal Apiales are predominantly woody and tropical. The order is probably of Gondwanan origin. Locating the ancestral area and dating the diversification time of the major branch of the subfamily Apioideae will therefore contribute to the understanding of the origins of the northern hemispheric temperate flora. We performed phylogenetic analyses of nearly 1200 nrDNA ITS sequences of umbellifers, calibrated the phylogeny with fossil pollen, and inferred the ancestral range using parsimony and Bayesian methods. The results suggest that the core apioiid umbellifers originated and started to diversify in central and eastern Asia about 60 million years ago. Its sister group, tribe Bupleureae, is of Mediterranean origin.

19. BIOGEOGRAPHY OF SNAKES IN THE BRAZILIAN ATLANTIC FOREST: DIVERSITY AND ENDEMISM AREAS

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The Brazilian Atlantic Forest harbors one of the highest species diversity and endemism. Among the vertebrate groups of Atlantic Forest, snakes are well represented in scientific collections, allowing studies of evolutionary patterns of distribution as well as historical relationships among areas. We aim to identify areas of endemism by means of distributional congruence of snakes endemic to the Atlantic Forest. We overlapped 90 one degree quadrats with an Atlantic forest shapefile, and records from 4,195 snakes belonging to 80 species. We employed a Parsimony Analysis of Endemicity (PAE) to determine areas of endemism. We registered 80 endemic species from the Atlantic Forest. PAE analysis was performed with PAUP 3.1.1, resulting in 20 equally parsimonious trees (339 steps, consistency index = 0.23; retention index = 0.55). The strict consensus indicates 15 areas of endemism throughout the Atlantic forest, in which three major clades observed: the first from Pernambuco state to southern Bahia state; the second from southern Bahia to southern Espírito Santo state; third, from northern Rio de Janeiro state, crossing São Paulo and Paraná states, up to northern Santa Catarina state. The observed patterns are congruent with those from other vertebrate groups, like mammals and birds, indicating a single causal biogeographical event.

20. DISTRIBUTION ATLAS VS. RANGE EXTENTS FOR DETERMINING CHOROLOGICAL RELATIONSHIPS BETWEEN SPECIES: THE CASE OF MAMMALS IN WESTERN EUROPE

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Distribution atlases represent species distributions as presences and absences on a spatial grid, usually UTM squares. Undetected presences and even non-surveyed localities are depicted as absences, hence atlases often underestimate species distributions. Conversely, range extent maps outline the areas encompassing the records of species presence. Non-surveyed localities within these areas are usually depicted as presences, so range maps often overestimate species distributions. To assess how much these errors can affect the chorological relationships encountered between species - i.e. their patterns of distributional overlap - we classified terrestrial mammals according to their distributions in Western Europe using, on the one hand, the distribution atlas published by Societas Europaea Mammalogica and, on the other, the range extent maps published by the World Conservation Union. Species were classified according to their presence or absence at UTM 50x50-km squares, and grouped hierarchically into dendrograms. We analyse and discuss the differences between the chorological relationships obtained from atlas data and from range extent maps, and how the type of data can affect the results of such analyses.

21. CHANGES IN SPECIES AND COMMUNITY SPECIALIZATION AT A LARGE SPATIAL-SCALE

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Ecological and functional homogenizations of communities are two major sources of biodiversity loss linked to global changes. They are often described as resulting from winners-losers dynamics, in which generalists benefit from resource fragmentation and from relaxed competition with specialists. However, this community-scale approach hides the possibility that species specialization itself may vary over short time scales. In addition, species differ in their sensibility to processes that underline biotic homogenization at various spatial scales. For instance, species may have different sensibilities to local habitat degradation and to land use changes at a landscape scale. Considering bird specialization on several habitat gradients, we explore these sources of variability and discuss their implications in biotic homogenization monitoring. First, we show that species' habitat specialization experiences a short term temporal variability which affects a community-levels trend towards generalization in addition to the well known winners-losers dynamics. Second, we argue that expressing specialization over explicitly-defined habitat gradients, and accounting for species' preference over the gradients, would be a significant improvement to the understanding of homogenization, which has been shown to express heterogeneously between types of habitats. We conclude that homogenization results from an interaction between intra-specific processes and species' distribution over gradients of habitats, which contribute to create heterogeneity in the winner-losers dynamic response to global changes.

22. A CLOSE RELATIONSHIP BETWEEN SPECIES LATITUDINAL AND LONGITUDINAL RANGES REVEALS NON-CLIMATIC CONTROLS OF SPECIES DISTRIBUTIONS

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Understanding what determines species ranges is a fundamental, but unresolved question in ecology. We show for a wide variety of taxa and regions across the world that species generally have very similar latitudinal and longitudinal ranges; this shows that ranges have a general tendency for being near-circular rather than elongated. The major competing hypotheses explaining species distributions emphasize dispersal or climatic determinism. Using a novel methodology, we show that neither neutral models assuming random, but spatially constrained dispersal, nor models assuming pure climatic control of species distributions describe range shapes adequately. The general relationship between latitudinal and longitudinal dimensions of species ranges falls between the predictions of these competing models, and we propose that this pattern arises from the combined effect of intrinsic dispersal limitation and macroclimate. Accurately projecting climate change impacts on species ranges will require a solid understanding of how climate and dispersal interact to control species ranges.

23. THE SPECIES RICHNESS-ENERGY RELATIONSHIP AT MULTIPLE SCALES

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Understanding how spatial pattern and scale contribute to observed species richness patterns is necessary to provide insight into the underlying mechanistic processes and help generate hypothesis for future testing. We present a novel method for analyzing the effect of scale on irregularly sampled data in two dimensions and use it to systematically explore the relationship between avian richness from 1990 - 2005 and four energy-associated variables [evapotranspiration, net primary production, temperature and precipitation] across the contiguous United States. First, wavelet lifting was used to create orthogonal scale specific decompositions of each dependent and independent variable. Next, wavelet coefficient regression was applied to determine how the richness-energy relationship changes with scale and identify at what scale (or scales) these four energy forms contribute to the observed pattern of avian richness. We find that different energy-associated variables show up as significant predictors at different spatial scales. Net primary production is the best predictor of species richness at both relatively small (< 200 km) and large (300 to 2000 km) spatial scales. The positive relationship between net primary production and species richness is the strongest at 350 km scale explaining 41% of the variation. Mean annual temperature and precipitation are significant predictors of species richness only at large spatial scales. Temperature is inversely related to avian richness while precipitation is positively related.

24. REGIONAL POOLS AND ENVIRONMENTAL CONTROLS OF VERTEBRATE ASSEMBLAGES

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The composition of local communities is controlled by the presence of species in the regional species pool and the filtering processes that preclude some of them from immigrating locally. These filters affect community assembly and are a critical mechanism behind local species diversity. Environmental filtering is predicted to be strongest when local productivity, heterogeneity and environmental similarity with the region are low. Here we evaluate the strength of environmental filters in sub-setting extensively surveyed local assemblages of birds, mammals and amphibians worldwide from their respective regional pools. Regional influences on local richness were strong and only a relatively small amount of additional variance was explained by environmental gradients. This finding highlights the importance of regional-scale processes rather than environmental filters for local richness. Local productivity or heterogeneity did not moderate the influence of regional on local richness, but environmental similarity environments did. We suggest that relative rather than absolute local environmental conditions are prime determinants of local richness.

25. DISTRIBUTION OF TREE DIVERSITY ON CONTINENTAL ISLANDS OF SOUTHEASTERN BRAZIL

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The Brazilian Atlantic forest is a complex biome with extraordinary diversity and high endemism. It harbors 13,708 species of Angiosperma with 49% endemics. The vegetation and plant species diversity of continental islands in this biome is poorly known. We explore the distribution of tree species diversity in continental islands, and if stochastic or deterministic processes are related to community structure. We sampled four continental islands that ranged in area from 2.2 to 43 ha, and were 0.4 to 35 km from the mainland. We recorded the following species richness rarefied to 34 individuals: 24 (95% IC = 6), 19 (6), 14 (3), and 2. Null models were employed to test for non random patterns of species co-occurrence and distribution of species abundances. The observed C-score did not differ from those expected by chance, indicating a random pattern of species co-occurrence. Both indices of niche partitioning, employed to explore patterns of species abundances, were higher than expected by chance, indicating that tree abundances are not evenly partitioned among islands. Our results indicate stochastic processes structuring island tree assemblages, i.e. each island flora may be a random subset of the mainland. Future analysis must explore mainland assemblages in order to understand the role of potential colonialists from the species pool in structuring island communities.

26. PATTERNS OF DIVERSIFICATION IN *HARPACTOCRATES* GROUND SPIDERS OFFER INSIGHTS INTO THE ORIGINS OF MEDITERRANEAN TERRESTRIAL BIODIVERSITY

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The Mediterranean basin is one of the 25 biologically richest hotspots on Earth. Tertiary tectonics and climatic oscillations are key factors contributing to the generation of this outstanding biodiversity. The ground-dwelling spiders of the genus *Harpactocrates* provide an excellent model to test the role of historical factors in the diversification of Mediterranean biota. The genus includes thirteen species distributed throughout the mountain ranges of the Iberian Peninsula, the Alps and the northernmost Apennines. They are most often found at high elevation, temperate and moist forests, suggesting a preference for cool and humid environments. Here, we investigate the evolutionary history of *Harpactocrates* at two different levels. First, we conduct multilocus phylogenetic analyses of most *Harpactocrates* species and a broad sampling of outgroups and, second, we conduct phylogeographic analyses of 3 closely related species restricted to the Iberian Sistema Central (ISC) mountain range. Using relaxed clock models and including fossil and biogeographic calibrations, we infer a temporal framework for the genus diversification. Our results support monophyly of Western Mediterranean Dysderinae genera and suggest that their split from Eastern relatives predated Alpine orogeny. In addition, the Alps and the Apennines were colonized from the Iberian Peninsula. The time of diversification of the main evolutionary lineages of the genus can be traced back to the Tertiary period, whereas deeper population structure in the ISC species dates to around the Plio-Pleistocene epoch. Our results suggest the existence of several glacial refugia in the ISC.

27. OUT OF SARDINIA: GLACIAL RANGE EXPANSION IN THE ENDEMIC TREEFROG *HYLA SARDA*

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The Corsica-Sardinian block is a well known hotspot of Mediterranean biodiversity, and a major area of endemism for many taxonomic groups. In spite of this importance, still little is known about the population history of species endemic to this area, particularly how they have coped with the Pleistocene climatic oscillations. We investigated the evolutionary history of *Hyla sarda*, a treefrog endemic to the Corsica-Sardinian block and the surrounding islands, through the analysis of its population genetic structure. Our results showed the occurrence of two main lineages, one restricted to south-eastern Sardinia, the other widespread throughout the species range. Historical demographic analyses indicated a long-term demographic stability for the first lineage. On the contrary, for the widespread lineage a sudden demographic expansion was inferred, lasting most of the Late Pleistocene and leading to a (re)colonization of Corsica and the other minor highlands from northern Sardinia. These inferences were also supported by the paleogeographic scenario, indicating glaciation-induced widening of coastal plains and the formation of wide and persistent land bridges among the major islands during the Late Pleistocene. Thus, our results revealed that, while both demographic and range dynamics of *H. sarda* were strongly influenced by Pleistocene climatic oscillations, such influence did not lead to a pattern of glacial retreat and interglacial expansion of populations, as usually observed in mainland species, but rather the opposite.

28. PALEOBIOGEOGRAPHICAL HISTORY OF GREEN TOADS *BUFO VIRIDIS* S.L. (AMPHIBIA, ANURA) AT THE WEST OF ITS CURRENT DISTRIBUTION IN WESTERN MEDITERRANEAN: STATE OF THE ART

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Bufo viridis s.l. corresponds today to a widespread group of closely related species with a range that extends from eastern France and Italy to central Asia, including northern Africa and numerous Mediterranean islands. Because of the high morphological variability of the green toad, several forms, as species and subspecies, have been described within its extensive range: *Bufo balearicus* (Apennine Peninsula, Corsica, Sardinia, and Balearic Islands), *Bufo siculus* (Sicily), *Bufo boulengeri* (North Africa), *Bufo viridis* sensu stricto (central and eastern Europe) and *Bufo variabilis* (the Balkans, Anatolia) mainly based on molecular data. In the fossil record of Western Europe (west of its current continental distribution area) the *B. viridis* group is reported since the Early to Middle Miocene to the Pliocene of Spain and France. Recently three Spanish Early Pleistocene sites [Barranco León D (Granada), Cueva Victoria (Murcia) and Almenara-Casablanca 3 (Castellón)] have delivered abundant remains that document the presence of a green toad. The youngest recorded occurrence of the *B. viridis* group outside but very near to the current westernmost limit of its distribution area has been made in the Middle Pleistocene of Terra Amata, southeastern France. Occurrence and extinction of green toads in Western Europe is discussed in relation to palaeobiogeography and palaeoecology. Molecular and palaeontological scenarios are compared.

29. PHYLOGENETIC AND BIOGEOGRAPHIC HYPOTHESIS OF THE GREY MULLET (MUGILIDAE; ACANTHOPTERYGII)

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The Mugilidae (grey mullets) comprise some 72 species, representing a single family within the order Mugiliformes. Grey mullets occur in marine coastal, brackish and freshwater habitats in all temperate and tropical seas of the world. Due to their conserved morphology, classical taxonomy of grey mullets has proven complex and difficult at both generic and specific levels. Recently, a number of scattered molecular studies have addressed particular questions that have improved our understanding of the relationships among some species and genera. However, a broad study including all available representative taxa has not yet been carried out. Information about their origin and the historical factors accounting for their current diversification and distribution is very scarce. We applied a Bayesian MCMC analysis combining all available sequenced representatives of the family for the mitochondrial 16S and 12S ribosomal RNA gene. Our study provides the first phylogenetic hypothesis calibrated with fossil data for this family. We relate this tree with biogeographical data and advance a preliminary hypothesis on the evolutionary history of species of *Liza* and allied genera within the Mugilidae. Our preliminary results suggest an Indo-Pacific (Tethys Sea) origin of these genera and rapid vicariance speciation of the Mediterranean species during the Messinian Event.

30. EVOLUTIONARY TRENDS IN MEDITERRANEAN SEEDS AND FRUITS

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As Raunkiaer documented long ago, the Mediterranean region is distinguished by its great diversity of annual plant species. Predominance of annuals is greatest in those parts with the most “Mediterranean” climate, i.e., most pronounced alternation of winter rain and summer drought. Botanists have discussed some aspects of seed and fruit (diaspore) evolution in Mediterranean annuals, and pointed to the extreme nature of the diversification. Ehrendorfer pointed out that Turkish annuals of the Rubiadeae exhibit a greater diversity in fruit morphologies than is found in the remainder of the tribe globally. Similar statements would apply to several families characteristic of temperate herbaceous associations, such as the Poaceae, Brassicaceae, Papilionaceae, and Apiaceae. Certain evolutionary trends in diaspores can be identified, namely towards heterocarpy; synaptospermy; seed gigantism; dimorphism for seed size, dormancy, and/or dispersal; and fruits that are peculiar for their phyletic group. These trends are also visible in other Mediterranean or semi-arid climate regions, particularly in the Asteraceae, but nowhere are they nearly so pronounced as in the Mediterranean itself. While existing explanations for these patterns have merit, they seem incomplete. The apparent correlation with soil structure in genera such as *Avena*, *Triticum/Aegilops*, and *Medicago* suggests that Harper’s notion of “safe site” is relevant, and that many of these annual species are adapted to germinating in the same location year after year, rather than seeking scattered, disturbed, open sites as in the case of perennial-dominated vegetation.

31. BIODIVERSITY AND ENDEMICITY PATTERNS OF BEETLES (COLEOPTERA: CARABIDAE, STAPHYLINIDAE AND CURCULIONIDAE) ASSOCIATED TO MADEIRAN LAURISILVA HABITATS

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Madeira Island is considered a biodiversity hotspot due to the high number of species and the uniqueness of its flora and fauna. The beetle fauna of Madeira Island is one of the richest in Macaronesia, although it is still poorly known. With this work we aim to compare the biodiversity associated to each forest site and between habitats within each forest site for three beetle groups. Forty nine species were identified: 25 Carabidae (22 endemics), 12 Staphylinidae (3 endemics) and 12 Curculionidae (11 endemics). The sites with higher species richness also had the higher number of endemics. The three beetle groups showed higher biodiversity values in different sites. Beta diversity was highest for Curculionidae ($\beta=4,77$) and lowest for Staphylinidae ($\beta=3,92$). Ground beetles were strongly associated with the leaf litter, but a considerable number of species was also recorded on dead and living trees. Rove beetles occurred with similar values of species richness on dead and living trees and in the leaf litter. Weevils were strongly associated to the leaf litter and, in a lesser extent, to dead and living trees. Principal component analysis highlighted the distinctness of the assemblages of Carabidae, Staphylinidae and Curculionidae of all three major habitats.

32. BRYOPHYTES ON TRAVERTINE DEPOSITION IN TUSCAN “NATURA 2000” SITES

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There is considerable scientific interest in plant communities on travertine depositions. According the Council Directive 92/43/EEC, Annex 1, on the conservation of natural habitats, hard water springs with active formations of travertine, namely “petrifying springs included in the phytosociological alliance *Cratoneurion commutati*”, are priority habitats in EU due to their sensitivity water pollution and their specialized biota. In Tuscany petrifying spring are restricted to a few localities. In the province of Siena there several sites showing presence of water springs with active formations of travertine. The present study was undertaken to investigate the distribution data of the plant communities, of this particular habitat in the province of Siena, with special attention to bryophytic vegetation, in order to obtain basic ecological and biogeographical data to be used for conservation and management purposes.

33. A SPECIES BOUNDARY WITHIN *PETROSPONGIUM RUGOSUM* SENSU LATO (ECTOCARPALES, PHAEOPHYCEAE): NEW INSIGHTS FROM MOLECULAR EVIDENCE

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The relative scarcity of morphological differentiation in marine macroalgae has resulted in underestimation of species diversity. Recent molecular studies have revealed cryptic species in marine algae, suggesting that marine algal diversity is much higher than previously recognized. *Petrospongium rugosum* is a brown crust alga that occurs in the Pacific Ocean region, yet its taxonomy, biogeography, and evolution are poorly known. Here, we presented plastid *rbcL* and two mitochondrial genes (*atp6* and *cox1*) sequence and found four distinct clades within *P. rugosum*. Although these clades are very similar in morphology, each of four clades is allopatric in distribution: Clade I from Baja California, Mexico to Oregon, USA, Clades II on the southern coasts of Korea, and Clade III mostly in Jeju, Korea, and Clade IV in Santa Catalina and San Clemente Islands, USA. We consider these four clades as separate species. The present results suggest their divergence events as early as the glacial period, consistent with the formation of well-recognized barriers to gene flow among them. Considering that many countries remain unsampled, e.g., Japan, Hong Kong, New Zealand, and Australia, four is probably a modest estimate of the number of species within *P. rugosum* sensu lato.

34. MOUNTAIN PASTURES AND GRASSLANDS IN THE SW TIEN SHAN, KYRGYZSTAN

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We addressed the following questions in selected summer pastures in the walnut-fruit forest region of southern Kyrgyzstan, Middle Asia: Can the vegetation of southern Kyrgyzstan's mountain pastures be classified in distinctive community types? Which site factors exert the greatest influence on the differentiation of the vegetation? Which phytogeographical distribution types are predominant? To what extent do human land use and land degradation affect the differentiation of the vegetation? Species composition was classified by cluster analysis; underlying environmental gradients were explored using DCA. A dataset of 395 relevés was used for classification and ordination as well as for phytogeographical and ecological analyses. A subset of 79 relevés was used in a second DCA to analyze the correlation between vegetation, environment, and grazing impact. Southern Kyrgyzstan's pastures were classified into four distinctive plant communities. The site factors altitude, inclination and grazing impact were found to be the major determinants of the vegetation pattern. The DCA#1 axis explained 65.2% of the variation, and showed a significant overlap between floristic composition and structural and spatial properties. DCA#2 revealed a high impact of grazing and soil parameters on the floristic differentiation. The majority of the species pool consisted of Middle Asian endemics and Eurosiberian species. However, disturbance-tolerant species played a significant role with respect to species composition and coverage of the herbaceous layer in vast areas of southern Kyrgyzstan's mountain pastures. Considering the intense grazing impact on species compositions and structural variables of the plant communities, it is indispensable to adopt appropriate pasture management strategies.

35. HEAVEN OR HELL: A PORTRAIT OF THE CONSERVATION OF THE AZOREAN ARTHROPODS' DIVERSITY

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Arthropods are the most diverse of all the terrestrial biota from the Azores. In addition, they are also the richest group in endemic taxa. Currently we have spatial data on the distribution and abundance of Azorean arthropods in different scales in native forests: islands, protected areas within islands, sites within protected areas, habitats within sites. In addition, we have data on the occurrence of arthropod species in other habitats (*Cryptomeria japonica* exotic forest, semi-natural pasture and intensive pasture) for four islands (Terceira, Faial, Flores and Santa Maria). Within the bigger context of a standardized sampling program for epigeal insects and spiders we want to find out which species are truly rare and which are pseudo-rare species in the Azores. Two dimensions of rarity were measured: abundance and habitat specialization. Two domains of rarity were identified: “among habitats” and “geographic”. Some interesting patterns emerged. The high dispersal abilities of many insect and spider species together with the fact that many species from islands tend to be generalists imply that many species tend to be vagrants in several habitats and consequently are locally habitat pseudo-rarities. Truly regionally rare species are those that are habitat specialists and many of them are threatened endemic species or recently introduced exotic species. Although this study demonstrates the important role of the native forest in arthropod conservation in the Azores, it also shows that unmanaged exotic forests have provided alternative habitat suitable for some native species of forest specialist arthropods, particularly saproxylic beetles.

36. PATTERNS OF COLONIZATION AND SPECIES DISTRIBUTION FOR AZOREAN ARTHROPODS: EVOLUTION, DIVERSITY, RARITY AND EXTINCTION

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Here we address a list of questions based on long-term ecological and biogeographical studies performed in the Azores, a remote volcanic oceanic archipelago composed by nine islands. The target group is Arthropoda, and the main habitat Laurisilva, the Azorean native forest. Diversification of Azorean arthropod species is affected by island age, area and isolation. However, results obtained for over a decade show that distinct groups are differently affected by these factors, which has led to the extreme diverse distribution patterns currently observed. Spatial distribution of arthropods in each island may be interpreted as caused by a typical “mass effect”, with many species following a “source-sink” dynamics. Truly regionally rare species are those that are habitat specialists, many of them being threatened endemic species. Although various endemics persist as sink populations in human-made habitats (e.g., exotic forests), more than half of the original endemic forest arthropods may already have vanished or may eventually be driven to extinction in the recent future. These species which have evolved in, and are mainly found in association with the native forest, are dramatically affected by hitherto unrecognized levels of extinction debt, as a result of extensive destruction of native forest. We argue that immediate action to restore and expand native forest habitat is required to avoid a future of disastrous extinctions of a biologically unique fauna with an unique evolutionary history.

37. HOW ARE TREE SPECIES DISTRIBUTED IN GEOGRAPHIC AND CLIMATIC SPACE? SURPRISINGLY SIMPLY

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Many different factors (abiotic, biotic, historical, etc.) undoubtedly influence species' distributions. We have investigated, for 482 North American trees, 1) whether the bulk of the variation in geographic distributions relates to climate; 2) the shape(s) of the response (we tested hypothetical responses inferred by theory and literature); and 3) whether observed climatic niches are conserved across dispersal barriers. We found that:

1. The probability that a tree species occupies a geographic area is generally a bivariate normal function of temperature and precipitation, with no interaction between the two variables. This model explains, on average, 82% of the variance in the probability that a species will occupy a given region.
2. Species' distributions in climate space neither have strong thresholds (i.e., we reject the hypothesis that unfavourable climates exclude species, but species may or may not be present in favourable climates), nor are they systematically skewed towards mild conditions (i.e., we reject the hypothesis that abiotic factors determine range limits in extreme climates, versus biotic factors in benign climates).
3. Species' climatic niches are largely conserved between regions but how fully a species occupies that climatic niche is not strongly conserved.

We conclude that, despite the vagaries of individual species' histories and biologies, their distributions relate strongly to climate, in similar ways for nearly all species.

38. DISCORDANT PATTERNS OF MORPHOLOGY, ADVERTISEMENT CALLS, AND GENETIC TRAITS IN A BRAZILIAN BROMELIAD TREEFROG

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Scinax perpusillus includes a complex of bromeliad treefrog species endemic to the Atlantic forest of southeastern Brazil. We examined if patterns of variation in morphology, calls and genetic structure are concordant across geographically distinct populations. We analyzed morphological characters, advertisement calls, and genetic structure in 62 individuals representing 10 populations including the type-locality and four coastal islands. We found deep genetic divergences among a population on Alcatrazes Island and one in Rio de Janeiro based on mtDNA sequences. Other haplotypes grouped into two clades in northern and southern São Paulo state. We found discordance in the evolutionary diversification of character types, including cases where population were different at all characters, and other where genetically-similar populations differed significantly in morphology and/or calls. We also found populations that showed high genetic divergence but were very similar in morphology and calls. Vocalizations are often important pre-zygotic isolating mechanisms for frog species and those behavioral characters may evolve faster than population genetic parameters.

39. LONG-TERM ECOLOGY OF A RAMSAR WETLAND, SOUTH AFRICA: A 10,500 YEAR PALAEOECOLOGICAL RECORD OF VEGETATION DYNAMICS

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Wetlands are among the world's most productive environments. Conservation and management of wetlands, their biodiversity, and their role in water provisioning, have been identified as a priority for action in international conventions and regional policies. Knowledge of wetland responses to environmental and climatic variability is required in order to conserve these ecosystems. We present the ecological history of a Ramsar wetland in the Mpumalanga Province of South Africa, reconstructed from a sedimentary sequence spanning 10,500 years. A wetland-grassland mosaic has been in place for the last 7000 years, obtaining its current form around 4000 BP. Prior to this, open grassland dominated the site. Climate appears to be the principle mechanism driving vegetation change, though changes in site hydrology have been important in the development of the wetlands. The vegetation has always contained a mixture of C3 and C4 grasses, though their proportions have varied, as have those of tall and short C4 grasses. Changes in grass composition, fire regimes and nutrient availability have implications for current and future management of this Ramsar wetland. So too does the finding that the resilience of the ecosystem to environmental change appears to have declined throughout the Holocene.

40. THE ECOLOGY AND BIOGEOGRAPHY OF SUSTAINABILITY

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A new discipline of sustainability science is emerging in response to concerns of natural and social scientists, policymakers, economists, and lay people about whether the earth can continue to support population growth and economic prosperity. Socioeconomic activities depend on human-environment interactions; these interactions occur at multiple scales from local to global. Thus, human ecology and biogeography are central to sustainability science. Unfortunately, however, rigorous applications of ecology and biogeography are largely missing from sustainability science. Here we focus on three fundamental principles of ecology and biogeography: 1) the conservation laws that govern the flows of energy and materials between human systems and the environment, 2) the effects of scale and embeddedness on these flows, and 3) the constraints at the global scale that ultimately limit the flows at all smaller scales. A rigorous science of sustainability must take account of these ecological and biogeographic principles, which affect all human activities.

41. COMPARATIVE PHYLOGEOGRAPHY OF TWO SPECIES OF MOSAIC-TAILED RAT (*MELOMYS* SPP.) IN AUSTRALIA

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The phylogeographic structure of *Melomys burtoni* and *M. cervinipes* (Rodentia: Muridae) was assessed using mitochondrial DNA markers. While both species co-occur along the north-east coast of Australia, *M. burtoni* is restricted to grassland habitats while *M. cervinipes* is only found in closed rainforest. Analyses revealed that the phylogeography of *M. burtoni* has been influenced by Pleistocene sea level fluctuations which have allowed gene flow between Australia and New Guinea via grassy land bridges either side of Lake Carpentaria. Four biogeographic barriers were identified including 1) the Wet Tropics rainforest region, 2) the Kimberley-Arnhem Land barrier, 3) an unidentified barrier between western and eastern Northern Territory and 4) the Gulf Plains region, which prevented secondary mixing at the south end of the lake as *M. burtoni* expanded from New Guinea into Australia. Conversely, the distribution of *M. cervinipes* spans a number of potential biogeographic barriers to closed-forest restricted taxa including 1) the Black Mountain Corridor, 2) the Burdekin Gap, and 3) the St. Lawrence Gap. Analyses revealed three divergent lineages within *M. cervinipes* corresponding to northern, central and southern clades. Unexpectedly, however, these divergent lineages did not correspond directly to the aforementioned potential barriers to gene flow and the highly divergent (~2.1% 16S) northern and central lineages occur in sympatry in a narrow suture zone, suggesting a more complex evolutionary history within the archipelago of closed forest present along Australia's north-east coast.

42. WHY HOTSPOTS OF INTRASPECIFIC GENETIC DIVERSITY ARE SO HOT? INSIGHTS FROM THE ITALIAN PENINSULA

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Hotspots of genetic diversity have been observed in most species within areas of putative glacial refugia. Their occurrence has thus mostly been viewed as the product of long-term stability of refugial populations. However, growing evidence shows that genetic diversity is often not only higher within refugial areas, but also deeply structured, suggesting the involvement of microevolutionary processes other than long-term demographic stability. We investigated the contribution of these processes to current patterns of genetic diversity in four species endemic to peninsular Italy, three amphibians and one mammal, whose southern populations invariably showed the highest levels of genetic diversity. Population genetic, phylogeographic and historical demographic analyses, indicated that populations of these species cyclically underwent allopatric differentiations within the refugial range in southern Italy, followed by secondary admixtures. Furthermore, paleogeographic evidences support this scenario, suggesting that these cycles of population divergence and admixture were driven by the glacio-eustatic oscillations of the sea level, which led to the cyclical formation of a paleoarchipelago in southern Italy. Thus, our results suggest that long term persistence of populations in refugial areas could have been a necessary but not always sufficient condition for the rising of intraspecific hotspots of diversity, and argue for the need of a reappraisal of the role of gene exchange in this process.

43. WHAT MATTERS THE MOST FOR THE PERFORMANCE OF ECOLOGICAL NICHE MODELS: ECOLOGICAL NICHE CHARACTERISTICS OR DATA STRUCTURE? AN EVALUATION USING HYPOTHETICAL SPECIES

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In recent years, Ecological Niche Modelling (ENM) has proven useful in a wide array of basic and applied questions in biogeography, ecology, evolution, and conservation biology. However, despite several explorations regarding the performance of different modelling methods, most of them have been made using data from real species from which characteristics of their ecological niches and sample data are incomplete, thus limiting our understanding to learn which models perform better under what circumstances. Herein, we evaluate the performance of a number of niche modelling methods to produce geographical distributions using hypothetical species for which we have full control over their ecological niche characteristics and data structure, with the aim to determine strengths and limitations of modelling approaches. Our results have implications in applications of ecological niche models, conservation and biogeography (e.g., identification of areas of endemism).

44. BIOCLIMATIC AND ENVIRONMENTAL SUITABILITY FOR ASSESSING THE POTENTIAL RECOLONIZATION OF AN EXTINCT SPECIES: THE CASE OF THE OTTER IN SWITZERLAND

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The geographical distribution of species is determined by different ecological factors that act at different spatial scales. This is particularly relevant for wide distributed species like the Eurasian otter, one of the widest distributed Palearctic mammals. The otter underwent a severe decline in Europe during the years 1970-1990 and the species went extinct in several countries. Now the otter is gradually recovering in its former range, but in a large part of central Europe. However, it is still not occurring in Switzerland. The role of Switzerland for the recovering of the otter in Europe is important due to the central geographic position of the country. Nowadays, it is of crucial importance to evaluate if the conditions to sustain otter populations on the long term are still present in Switzerland both in the case of a natural recolonization from adjacent populations, as well in the case of human-designed reintroduction. For this purpose, we assessed the habitat suitability of the otter in Switzerland by jointly investigating the bioclimatic and the environmental niche of the species. The bioclimatic suitability was fitted at the European scale to capture the entire bioclimatic niche of the species, while the environmental suitability was fitted in Austria at a finer scale resolution. The two types of suitability were projected to Switzerland. Finally, we evaluated the potential role of PCBs pollution in the Swiss freshwater for this recolonization. This integrated approach developed at different scales allows us to assess which are the ecological factors at different scales that influence the distribution of the species. We believe it is a useful approach that helps identifying the areas where the species could persist in the future.

45. TRACING THE HISTORY OF SOUTH-AMERICAN NEOTROPICAL SEASONALLY DRY FOREST: EVIDENCE FROM THE PHYLOGEOGRAPHY OF *TABEBUIA IMPETIGINOSA* (BIGNONIACEAE)

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The Neotropical Seasonally Dry Forests (SDF) are tree-dominated ecosystems that occur in disjunct areas of fertile soils throughout the Neotropics. The hypothesis of vicariance of a formerly continuous seasonal woodland formation, which may have reached its maximum extension during a dry-cool period 18,000–12,000 BP (the LGM), has been raised to explain the disjunct distribution. We are interested in testing this hypotheses using the genus *Tabebuia* as a model. Here, we present the results based on the phylogeography of *T. impetiginosa*. At least 16 individuals from 12 populations were sampled and sequenced for three chloroplast intergenic spacers (1635bp). Our results strongly support the theory that the disjunct distribution of *T. impetiginosa* may be derived from vicariance and that long-distance gene flow is unlikely, since we found a deep genealogy with allopatric lineages and a remarkable differentiation among populations (AMOVA). Nevertheless, we have no evidences of a recent connection of SDF in the LGM. Coalescent analyses showed that *T. impetiginosa* populations probably originated at ~9 Myr BP, with the divergence of two major clades corresponding to the forests from the Southeast and to an ancestor which spread throughout the fertile soils of central, west and northeast Brazil at ~6-5 Myr BP. Hence, we hypothesize that the isolation of an ancient forest due to the uplift of the Brazilian Central Shield during the Late Miocene is responsible for the disjunct distribution of SDF.

46. THE INVENTORY OF THE ALIEN FLORA OF CRETE: STATE OF THE ART

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The island of Crete, lying between Greece and Libya, is the most southerly region of Greece and Europe. As generally recognised, the potential damage caused by invasive species to biodiversity on small and isolated islands is usually greater than on the mainland. Islands have a high proportion of endemic species which are jeopardised by displacement by alien invasive species and because remote islands typically lack competitors and predators which are present in the native range of alien invasive species. The aim of this study, which was started in 2005 and is on-going, is to carry out the first comprehensive inventory of the alien flora of Crete and map the distribution of the main invasive alien species. Data from literature and field observations were used to develop a preliminary information database for the inventory that currently includes 277 alien taxa, 82 of which are naturalized and 21 are invasive. For each species the following information has been collected: origin, status, distribution, life form, phenology, habitat preferences, altitudinal range, and introduction pathway. Spatial data has been stored in a geodatabase using GIS software, and preliminary analysis of the main features of the Cretan alien flora will be presented.

47. ESTIMATING INTRASPECIFIC DIVERSITY AT DIFFERENT GEOGRAPHIC SCALES IN THE MEDITERRANEAN SEA: THE CASE OF *SPONGIA OFFICINALIS* (PORIFERA: DEMOSPONGIAE)

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Identifying spatial patterns of intraspecific variation of marine sessile invertebrates is crucial for the establishment of comprehensive conservation strategies, particularly given the threat of recent climate change effects on their coastal Mediterranean habitats. The harvested bath sponge *Spongia officinalis*, having recently undergone several mass mortality incidents, is a model species in this context since it is distributed throughout the Mediterranean. A sample set from three distinct regions of the Mediterranean was analyzed, corresponding to its main biogeographic zones (eastern - western Mediterranean and the Alboran Sea), thus allowing for the identification of barriers to gene flow occurring along the basin. A supplementary network of sampling locations inside each region, separated by a distance range of 10 to 500 kilometers was additionally surveyed for fine-scale estimation of diversity patterns. Variation was evaluated with partial mitochondrial cytochrome oxidase subunit I sequences, along with a set of high-resolution polymorphic microsatellite loci we recently developed for the species. While mitochondrial markers distinguished individuals only between the main Mediterranean basin and the Alboran Sea, microsatellites showed a more complex pattern, providing evidence for additional separation across the biogeographic zones, and revealed considerable structuring at the level of different geographic locations.

48. SPECIALIZATION IN HUMMINGBIRD-PLANT NETWORKS: THE ROLE OF ASSEMBLAGE SIZE, CLIMATE AND CLIMATE CHANGE

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Biotic specialization is implicated as a driver of speciation and species coexistence and, hence, may determine biodiversity patterns, such as the latitudinal species richness gradient. Despite its importance, large-scale geographic variation in specialization and the underlying drivers remain to be determined. Hence we related specialization in plant-hummingbird networks sampled at 31 localities across the Americas to latitude and a series of putative historical and contemporary drivers. There is a trend toward increased biotic specialization at lower latitudes and favorable contemporary climates, mainly high precipitation. However, strong specialization is primarily associated with diverse assemblages and areas that have experienced relatively high spatiotemporal climatic stability during the Late Quaternary. As expected from their abilities to track changing climates, relative climatic stability affects plants more than hummingbirds. Our results are consistent with theories claiming that climate-driven range dynamics diminish local adaptations.

49. GENE FLOW AND COMMUNITY SIMILARITY PARALLEL ENVIRONMENTAL CONNECTIVITY

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Reconstructing the evolutionary history of lineages and biotas are parallel themes in phylogeography and biogeography. Biological diversity at genetic and species levels is expected to respond similarly to environmental influences. Dispersal should increase gene flow and community similarity; geographic isolation and natural selection should increase population differentiation and community dissimilarity. We investigated the extent to which genetic structure (in 6 species of macro-invertebrates) and community composition (of 389 macrophytes and macroinvertebrates) parallel oceanographic connectivity and environmental variation at 30 sites along the California mainland and adjacent California Channel Island array. As predicted by theory, levels of gene flow increase with increasing pelagic larval duration. Low and medium dispersal species showed significant population genetic structure providing an empirical null hypothesis against which to compare patterns of community similarity. Bray-Curtis similarity calculated from species presence-absence data was significantly correlated with gene flow. These results suggest that environmental connectivity, as a composite of physical and environmental separation, influences population genetic and community ecological processes in parallel.

50. CLIMATIC HISTORY PREDICTS EVOLUTIONARY RELATIONSHIPS ACROSS THREE SOUTHEAST ASIAN BIODIVERSITY HOTSPOTS

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A number of mechanisms have been proposed to act as drivers of diversification in one of the global “hotspots”, the archipelagos of southeast (SE) Asia. We examined phylogenetic and population genetic patterns across three genera of co-distributed freshwater halfbeak fishes from the region, to test between competing hypotheses of diversification. We assessed morphometric and mitochondrial variation, and developed markers and screened for novel anonymous nuclear variation. We tested these data against several a priori models of diversification, within an Approximate Bayesian Computation (ABC) framework incorporating palaeo-drainage models of the study region. The halfbeaks radiated within the Pleistocene, with the data consistent with a Pleistocene climatic ‘species-pump’ model of diversification. For much of the Pleistocene when sea-levels were lower than today, a number of SE Asian islands (e.g., Borneo, Sumatra, Java) were conjoined to the SE Asian mainland, forming a vast landmass – ‘Sundaland’. The relationships among fish populations and taxa across the three genera of halfbeaks mirror past connections via Sundaland palaeo-drainage basins. The halfbeak phylogeny reflects incipient allopatric speciation after sea-levels rose at the end of the Last Glacial Maximum.

51. NEW PALAEOECOLOGICAL DATA FROM THE CANARY ISLANDS: A JUMP TO LA GOMERA

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The Canarian Archipelago (Spain), with over 30% endemic plant species, is one of the world's biodiversity hotspots. Relatively little is known about ecosystem baselines and the natural variability of the vegetation prior to human activities and how the ecosystems responded to climate change. Another important question is the extent of the anthropogenic impact on the landscape following the arrival of the first humans (around 2000 years ago). In order to address these questions, we have initiated a palaeoecological analysis of lake sediments from La Gomera Island, which contains one of the most extensive and well-preserved Canarian laurel forests. The sequence is the oldest studied in the Archipelago to date (spanning 8600 years cal. BP). Preliminary results showed the dominance of laurel forest, represented by *Myrica*, *Erica*, *Viburnum*, *Ilex* and *Salix* tree species. Pollen from *Pinus canariensis* has also been detected in the pollen record; however, its low percentage in comparison to that detected from La Laguna (de Nascimento et al. 2009) cannot rule out an exogenous origin. An increase in grasses and other herbaceous taxa towards the end of the sequence, together with the concentration of charcoal, indicates the first contact of humans with the forest. The first palaeoecological results from La Gomera will improve the understanding of long-term vegetation dynamics previously known from the Island of Tenerife.

52. NEOGENE CLIMATE CHANGE, THE EVOLUTION OF EARTH'S NEOBIOMES, AND THE SHIFT TOWARDS MAMMALIAN MICROHERBIVORY

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As the world climate cooled since the end of the Eocene, mammalian herbivore lineages suffered a major shift in faunistic composition. While these faunistic changes are well known, published material revolves around the downfall of brachydont lineages and the surge of hypsodont herbivores. This view remains central in the study of Neogene herbivores, but other important phenomena have not received proper attention: from a world dominated by dicot leaf eaters, mostly forest dwellers, a much less diverse assemblage of grass eating, savanna adapted lineages emerged; at the same time there was an explosion of microherbivory, the diversification of rodents. Overall, medium to large ungulate herbivores had their taxonomic diversity diminished from 49 families at the end of the Eocene to 14 of today. Rodents have followed the opposite trend, diversifying from 17 families to 27. Here I propose that this shift has been caused by two distinct and independent factors, both directly related to the increasingly cooler climates of the Neogene: a) a marked decrease in the area occupied by tropical climate biomes around the world, replaced by temperate and cold climate neobiomes at high latitudes and savanna neobiomes in the tropics causing herbivore lineage extinction; and b) the increasingly more seasonally variable world climate which favored lineage life histories such as those of rodents.

53. EFFECTS OF EXPERIMENTAL RAINFALL EXCLUSION ON A DIVERSE ANT ASSEMBLAGE ALONG AN ELEVATIONAL GRADIENT IN THE ECUADORIAN ANDES

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Models of global climate change predict higher rainfall variability, with more intense rainfall events separated by extended drought periods. We integrated experimental and gradient approaches to study the effects of prolonged droughts on a diverse ant assemblage in a mountain rainforest of Ecuador. The experiment was designed to test three predictions. (1) Prolonged drought will lead to declines in species richness and abundance. (2) Declines will be more marked at higher elevations where ants are adapted to moist conditions. (3) Soil-nesting species will be less affected than species nesting in dead wood or in leaf litter because the moisture decrease will be more important aboveground than underground. Three 3x3 m experimental tents and three controls were installed at three elevations (1000, 1500 and 2000 m a.s.l.). Ants were collected six months after the experiment started. Total species richness was not significantly affected by the experiment but abundance increased and assemblage composition was modified. Changes differed according to microhabitat. *Camponotus* in dead wood, and *Dacetini* in leaf litter, were more frequent underneath tents. At the opposite, *Pheidole* species seemed to prefer moist conditions. Ant response was globally consistent over the elevational gradient. It appears that moisture limits the production of a majority of Andean ant species, maybe by causing a physiological distress and/or limiting nesting site quantity.

54. COMPARATIVE PHYLOGEOGRAPHY OF AFROMONTANE MAMMALS: INTEGRATING CLIMATIC HISTORY AND GENETIC VARIATION

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In African montane forests, the expansion and contraction of habitats may have played an important role in shaping the diversity of mammalian communities. More specifically, centers of taxonomic and genetic diversity are predicted to be coincident with areas that acted as persistent forest refugia during glacial maxima. My study utilizes species distribution models that are integrated with molecular genetic data to investigate how geographic and climatic processes have driven these evolutionary processes. An array of spatio-temporal population genetic hypotheses are tested using a model-based statistical phylogeographic approach based on wide sampling of five co-distributed rodent and shrew species groups in the Eastern Afromontane region. Questions addressed include whether and by what processes taxa are continuing to diverge and how historical scenarios shaped current patterns of lineage and genetic diversity. The Eastern Afromontane region is ideally suited for combining climatic/landscape modeling and new approaches in genetic data analysis in order to study the evolutionary processes that have shaped variation within a megadiverse and ecologically threatened region.

55. IS THERE REALLY AN AZORES DIVERSITY ENIGMA? INSIGHTS FROM THE PHYLOGEOGRAPHY OF THE HEATHER *ERICA SCOPARIA* S.L.

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The Azorean flora, in contrast to that of other archipelagos, is characterized by a paucity of evolutionary radiations and widespread distribution of most endemics. Several hypotheses, including isolation from the continent, recent age, ecological homogeneity, and limited paleoclimatic variations, have been proposed to account for this pattern. These hypotheses are tested here within the context of the molecular phylogeography of the heather *Erica scoparia* s.l., a Mediterraneo-Atlantic species complex distributed across Macaronesia, North Africa and southwestern Europe. The marked molecular radiation of this species in the Azores, including an array of single-island endemics, suggests that the apparent homogeneity of the Azorean flora might, in fact, conceal undetected patterns of endemism that are similar to those observed in the Canarian flora for morphological data. Haplotype richness was higher in the Azores than in the Canaries and extensive dispersal mediated allopatry is apparent at the molecular level. The Azores were colonized at least twice independently by *E. scoparia*, whereas the Canarian haplotypes are monophyletic, suggesting that the greater distance between the Azores and the continent does not necessarily hamper the chances of successful colonization.

56. EVOLUTIONARY SIGNIFICANCE AND TRADE-OFFS IN LIFE-HISTORY TRAITS ASSOCIATED TO ECOLOGICAL SPECIALIZATION AND MATING SYSTEMS IN THE LIVERWORT GENUS *RADULA* DUMORT

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Shifts in mating systems are amongst the most common and important transitions in plants and are correlated with a suite of life-history traits. The evolution of mating systems and their relationships to gametophyte size, sexual reproduction, formation of asexual diaspores, and ecological specialization, is examined here in the leafy liverwort genus *Radula*. From a molecular phylogeny of the genus and using comparative methods, we assessed the sequence of trait acquisition, as well as the phylogenetic correlations between those traits. Shifts in mating system in *Radula* have been directional and recurrently occurred from dioecy to monoecy, suggesting that the transition to monoecy is adaptive in liverworts, i.e., allows them to produce spores and disperse more effectively. Shifts to monoecy have been dependent on habitat specialization but, in contrast to expectations from life-history theory, occurred more frequently within ecologically generalist lineages. Obligate epiphytes do not tend to produce asexual gemmae more frequently than facultative ones and we hypothesize that, due to the extreme habitat conditions on the tree, epiphytes tend to disperse by whole gametophyte fragments, which have a higher establishment rate than spores or gemmae in unstable conditions. This strategy indicates that epiphytes are rather poor dispersers, rendering them sensitive to habitat disturbance.

57. DISTRIBUTIONAL VARIATION OF COLUBRID SNAKES IN SOUTH AMERICA: A STUDY OF THE ECOLOGICAL COMPONENTS OF REPRODUCTIVE MODE

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Relating ecological niche modeling and communities under a comparative approach provides an appropriate link between ecology and biogeography. We propose to describe broad-scale distributional interspecific patterns of South American snakes assemblages and to explore whether reproductive mode is determined by environmental conditions. We also discuss possible processes underlying these patterns. For this purpose, we consider the Xenodontini and Tachymenini clades within the Colubridae family. We generated a dataset of 14 species, which included species presence data and reproductive mode. We used Maxent to model species geographical distributions with environmental predictors (precipitation, temperature and topography at 10 km x 10 km resolution). We processed the distribution maps of the snakes to analyze interspecific spatial variation of reproductive mode and identified the environmental variables responsible for these patterns. We performed simple and multiple regressions to identify the set of models best supported by the data. Geographical variation in reproductive mode in South American snakes is complex. While some species show a consistent association of reproductive mode with environmental variables, other species do not. The inconsistent associations of reproductive mode with environment at regional scale in colubrid snakes are discussed, taking into consideration the dissimilar evolutionary histories of these closely-related clades.

58. EARLY PERSISTENCE OF DIVERGING LINEAGES – A NEGLECTED COMPONENT OF SPECIATION WITH BIOGEOGRAPHIC IMPLICATIONS

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The mechanisms behind variation in diversification rates among lineages remain elusive. We argue that an important component of diversification has been generally neglected: Persistence of recently diverged gene pools. Studies on mechanisms leading to speciation focus almost exclusively on factors promoting gene pool separation, but lineage persistence through the entire speciation process is of course also required. This neglect has consequences for our perception of how different factors affect diversification and thus how biogeographic patterns in species diversity are interpreted. We introduce a framework distinguishing how traits of organisms and lineages as well as environmental factors affect initial lineage splitting from how they affect lineage persistence during speciation. Some traits may have opposite effects on lineage splitting and persistence. For example, specialization may promote splitting and simultaneously reduce gene pool persistence. Such traits could therefore have positive or negative net effects on speciation in different situations, depending on the relative strengths of the promoting and hindering processes. Environmental factors also affect persistence. For example, climate change may initiate splitting by isolating gene pools in refugia and by providing novel environments with vacant niches. Recurrent climate change may also hinder speciation by causing extinction or merging of diverging gene pools before speciation is complete. Acknowledging the role of early lineage persistence will make discussions on controls of speciation and diversification clearer and more productive.

59. PHYLOGENETIC TURNOVER AND COMMUNITY ASSEMBLY OF NEW WORLD PALMS (ARECACEAE)

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Recent advances in palm phylogenetics allow new insights into the ecological and evolutionary processes structuring the diversity of this group in tropical and subtropical ecosystems worldwide. Phylogenetic turnover methods allow disentangling the effects of dispersal limitation, niche conservatism, adaptation and competition on the composition of assemblages. We study palm community assembly across scales by combining a new, dated genus-level supertree covering all palms with a) a dataset including >340,000 palm individuals in 430 transects in the Western Amazon, and b) a set of gridded distribution maps for all New World palm species (n=550). On a continental scale, we identify seven regions of in situ diversification (biogeographic regions). This pattern is strongly driven by a combination of phylogenetic niche conservatism and dispersal limitation. Niche conservatism with respect to temperature seasonality and extremes emerges as an important determinant of palm species and clade distributions. On a regional to local scale, preliminary results show phylogenetic overdispersion of palm communities. This implies that community composition is influenced by competition (conserved alpha-niche) and/or divergent beta-niche evolution along environmental gradients. Our findings indicate that the impact of environmental factors on palm diversity patterns can be understood much better in the light of phylogenetic history.

60. RELATIVE IMPORTANCE OF WARMING-DRIVEN RANGE FRAGMENTATION AND NICHE SPECIALISATION OF SAXIFRAGA SPECIES IN EUROPE

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This study focuses on reconstructing the potential distribution of suitable habitat during the Pleistocene for a rare perennial herb, *Saxifraga rosacea* Moench. This weak competitor is a supposed glacial relict species with a highly fragmented distribution in central Europe. The few remaining populations of this species are confined to mainly open rocky habitats in mountains of middle elevation (“Mittelgebirge”) in Central Europe. Two alternative scenarios could explain the actual distribution of *S. rosacea* populations. Scenario one: the species was widespread during glacial periods, but suffered warming-driven fragmentation during Quaternary interglacials due to direct (climate) and indirect (competitive exclusion by woody plants) factors. Scenario two: the populations have been isolated throughout the glacial-interglacial cycles due to strong association with rocky habitat and their sizes were rather constant. These hypotheses are addressed by combining species distribution modelling (SDM) and hind-casting SDM to reconstruct the past structure of *S. rosacea* populations, and will furthermore be tested with coalescent simulations and empirical genetic data. As two different ploidy levels were detected within the species *S. rosacea*, in accordance with taxonomically defined subspecies, the alternative hypotheses were also tested independently on both subspecies and compared to the results for the species as a whole.

61. HYLOGEOGRAPHIC ANALYSIS OF MONKEYPOX STRAINS

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Monkeypox virus is a poxvirus closely related to variola virus, the causative agent of smallpox. The virus occasionally infects humans in western and central sub-Saharan Africa, sometimes with severe consequences. Phylogenetically, monkeypox virus is divided into two clades; one more virulent form circulating in the central Congo region (DRC, ROC, etc.) and one less virulent form circulating in the western part of the continent (Sierra Leone, Liberia, etc.). Additionally, some genetic variation exists within these major clades. This diversity can be explained by a variety of scenarios including isolation by distance, vicariance, or simply genetic drift. This study conducts phylogeographic analyses of monkeypox virus clades using GIS and genetic data to examine the distribution of intra-clade genetic mutations. Monkeypox virus genomic data collected from isolates across the known range of both monkeypox clades are compared to identify geographic barriers acting within and between Central and Western African monkeypox virus isolates.

62. BIOGEOGRAPHIC HISTORIES WITHIN THE FLOWERING PLANT FAMILY ANNONACEAE: FROM STEADY DIVERSIFICATION AND BOREOTROPICAL GEODISPERSAL TO RAPID SPECIATION

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Rain forest-restricted plant families show disjunct distributions between the three major tropical regions: South America, Africa and Asia. The pantropical plant family Annonaceae is used to test alternative hypotheses for this distribution (the museum hypothesis, Indian rafting and boreotropical geodispersal). Early diversification within Annonaceae fits a museum model of tropical diversification. Present day distribution of species within the two largest clades of Annonaceae is the result of two contrasting biogeographic histories (geodispersals via the boreotropics and several more recent long distance dispersal events versus one dispersion into Asia via the boreotropics with limited further dispersal).

At the generic level boreotropical dispersal and rapid speciation is important. For instance, the largest Annonaceae genus *Guatteria* (c. 250 species) migrated via the North Atlantic Land Bridge during the Eocene and estimated node ages are in line with the southward movement of megathermal forests from the Middle Eocene onwards. Its ancestors reached Central America just before the northern climate became too hostile. Because of extinction, a phylogenetically and taxonomically isolated genus remains.

63. BIOCLIMATIC VARIABLES TO PREDICT ANIMAL SPECIES DISTRIBUTIONS

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Bioclimatic variables have been applied basically to explain plant distributions. We aim to test if bioclimatic variables are useful to predict animal species distribution. We modelled breeding areas of Bonelli's eagle in peninsular Spain with variables related to the categories of ombrotypes, thermotypes, bioclimates-variants and isobioclimates. We performed five models, one for each category, and a combined model with all the variables. We also performed a combined model for other mountain species, i.e., Baetic midwife toad, Lataste's viper and Iberian wild goat. Models obtained had a reasonable discrimination capacity of the distribution of the species. We compared the discrimination capacity of the bioclimatic models with models performed with common climatic variables. Three species showed higher discrimination in the climatic models, but Lataste's viper for which bioclimatic models presented better discrimination. Thus, we showed that bioclimatic variables, although originally designed for plants, can be applied also to predict animal species distributions. This is especially relevant at a time when the scientific community and the general public are worried about the possible consequences of a hypothetical climate change on biodiversity.

64. DRIVERS OF SNAKE RICHNESS DIFFER GEOGRAPHICALLY

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Temperature is considered to be the most important factor affecting reptile richness. Large-scale analyses of the relationship between different climatic variables and snake species richness, however, are scarce. I studied the effect of temperature, precipitation, elevation range and environmental productivity on snake species richness in different parts of the world: Australia, North America (Mexico to Canada) and the Middle East (Israel, Egypt, Jordan and Arabia). In all regions the best model (inferred using AIC weights) included all the candidate variables, but the amount of variance explained by the models differed between regions, being much higher in North America than elsewhere. Furthermore, the relative effects of different variables were region-specific. Temperature was by far the most important factor explaining the richness of North American snakes, while its effect on the richness of Australia and Middle Eastern snakes was minor, and richness actually decreased with increasing temperature in the Middle East. In Australia precipitation was the single most important factor, and was positively correlated with richness, while this factor was weakly correlated with North American snake richness. Elevation range was the strongest single variable affecting Middle Eastern snake richness. Snake species richness is thus driven by different factors in different parts of the world, a point to consider when drawing inferences from global models.

65. THE MILLIPEDE GENUS *MEGAPHYLLUM* VERHOEFF, 1894 (DIPLOPODA: JULIDAE) IN THE BALKAN PENINSULA: SPECIES RICHNESS, TAXONOMIC PROBLEMS AND PRELIMINARY BIOGEOGRAPHICAL ANALYSIS

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We provide the first contemporary review of the millipede genus *Megaphyllum* in the Balkan Peninsula, one of the species-richest and most diverse millipede genera in South-east Europe, with special reference to the Greek fauna. The poster summarizes the current knowledge on the taxonomic status of the currently known species and outlines their general distribution. With a total number of 42 species the Balkans seem to represent a center of origin and diversification for the genus in Europe. So far, 30 species are known from Greece, with 70% of them being hitherto known only from the country. A more thorough approach focusing on the island fauna could be used as a model for understanding the processes of origin, colonization or vicariance of each species group in the mainland and the Greek islands. The lack of phylogenetic criteria in comparing the gonopodial structures, the sole characters hitherto used to define the subgenera in *Megaphyllum*, as well as the absence of synapomorphic characters have led to a number of taxonomic problems and uncertainties in the genus. We also discuss the biogeographical patterns among the Balkan *Megaphyllum*, and the arguments for some changes in the status of certain species and subspecies respectively. This review is part of long-term projects of E.L., I.F and B.V. aiming at establishing the phylogenetic relationships among the genera of *Brachyiulini* and the species of *Megaphyllum* and their biogeographic applications.

66. COMMUNITY COMPOSITION CHANGES IN FOREST ECOSYSTEMS IN TURKEY DUE TO CLIMATE CHANGE

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The community composition of forests may affect spatial temperature patterns and related services to terrestrial animals including humans. Understanding and predicting the climate-vegetation cause and effect relation is important. Dynamic vegetation models are now one of the most useful tools for representing this relationship. LPJ-GUESS is one of the most tested, well-documented and developed modeling framework in this area, in which the simulated biological units can be plant functional types or species. The model was applied over a window covering the entire landmass of Turkey and its region at a resolution 0.5° longitude and latitude with climate data (temperature, precipitation, insolation), CO₂ data and soil type data as input. As an output, the model gives the spatial distribution of each plant functional type in terms of net primary production and carbon biomass. In this context, the changes in the community composition of forest ecosystems are simulated for Turkey. The ecosystem model represents current ecosystem distribution fairly under modern mean climatic and atmospheric CO₂ conditions (1969–1998). The results predict future shifts in climatic zones and associated changes in species distribution and community composition for major tree species of natural Turkish forests. Increasing CO₂ concentrations and temperatures cause Mediterranean needleleaved evergreen types to expand northwards, boreal types to emigrate from Turkey and a change from deciduous to conifer dominance in southern Turkey.

67. THE EXISTENCE OF WINDOWS OF OPPORTUNITY IN DISPERSAL OR HOW TO RETRO-COLONIZE IBERIA AND NORTH AFRICA FROM MACARONESIA

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Recently published coupled-model simulations for the Last Glacial Maximum (LGM) result in a shift of the peak westerlies in the Northern Hemisphere toward the equator. In the same line of argumentation, it has been asserted that the Westerlies wind regime have been dominant across the Madeiran-Canarian latitudes (25-30° N) during the glacial periods in the Pleistocene, due to the southwards shift of the Azores high because of the pressure exerted by the North Polar Front. Dune fields in several Canary Islands and Maghrebian areas cannot have been formed with the present wind regime provide support for this hypothesis. On the other hand, during glacials the Macaronesian region was larger (almost double as large as today), higher (ca. 120 m higher) and less isolated from the African mainland (just 60 km away) archipelagoes, than in the interglacial periods, like the Holocene. Furthermore, an important array of emerged seamounts have appeared repeatedly and likely facilitated dispersal among archipelagos and between archipelagos and the mainland. The biogeographical consequences of such events are of high importance, because westerlies may have enhanced the back-colonizations from Macaronesian lineages of the African mainland. Today we know that several Macaronesian lineages have representatives in the African and European continents and several recent phylogenetic studies have located Macaronesian taxa as basal to continental lineages. Such back-colonization events have been denominated “boomerangs”.

68. SPATIAL CONGRUENCE OF FUNCTIONAL AND PHYLOGENETIC ASPECTS OF BIOLOGICAL DIVERSITY

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Spatial variation in biological diversity is a main subject in biogeography since its establishment as a science, but the focus has been on species richness as the diversity measurement. Alternative metrics that take into account biological processes may provide good insights regarding the mechanisms of species diversification and reveal patterns that are not readily available by species richness. The objective of this study was to describe the spatial variation of two diversity measurements that reflect ecological (functional distinctness) and historical (phylogenetic distinctness) processes and contrast them with the spatial patterns reported to species richness. To accomplish this, we assembled a database on the geographic distribution, ecological traits and phylogenetic information of 1,642 non-aquatic mammals in continental America (3115 cells, 110 km by side each). Species richness was defined as the number of species in each cell and functional and phylogenetic distinctness were estimated based on functional attributes and phylogenetic distance matrices. Functional distinctness decreased towards tropical regions. It was negatively related to species richness and possibly associated to ecological processes related to niche-assembly mechanisms, which operate in local scales. On the other hand, phylogenetic distinctness was not related to species richness and its spatial pattern was idiosyncratic overall, reflecting the unique evolutionary history of American mammals.

69. IMBALANCED DIVERSIFICATION OF TWO MEDITERRANEAN SISTER GENERA (*BELLIS* AND *BELLIUM*, ASTERACEAE) WITHIN THE SAME TIMEFRAME

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The only representatives in the Mediterranean basin of the worldwide-distributed Astereae (c. 100 genera; Asteraceae) are two small sister genera of daisies: *Bellis* (14 spp), and *Bellium* (5 spp.). From habitat-specific to ubiquitous, the species of *Bellis* and *Bellium* occur as frequent elements in the Mediterranean vegetation. We estimated divergence times and lineage diversification rates of the *Bellis/Bellium* complex using nuclear (ITS) and plastid (*rbcL*, *ndhF*, *matK*) DNA sequences. This, in combination with the biogeographical analysis performed, allowed us to place and time the major lineages of this complex. Unlike many other plant Mediterranean colonization events which have an inferred African origin, our results suggest that the colonization of the Mediterranean basin by the Astereae was from Eurasia some 10 Myr ago. A Messinian early divergence of the *Bellis/Bellium* complex (6.7-6.3 Myr ago), followed by a four million year delay for the within-genera diversification, (2.8-2.5 Myr ago) was inferred. This scenario suggests an interesting correlation between the diversification of the *Bellis/Bellium* complex and the evolutionary history for the establishment of both the Mediterranean climate and Mediterranean vegetation during late Miocene and Pliocene. We conclude that the onset of the summer drought ca. 2.8 Myr ago is important in the diversification of the Mediterranean daisies and resulted in an imbalanced number of species in the two genera.

70. THE UNEVEN BIOGEOGRAPHY OF *ERODIUM* (GERANIACEAE)

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The genus *Erodium* (Geraniaceae) is a common feature of Mediterranean-type climates throughout the world, but the Mediterranean Basin has significantly higher diversity than other areas: 22 endemic to west Mediterranean and 10 endemic to east Mediterranean. Seventy-eight new nrITS sequences were incorporated with existing plastid data to explore the phylogenetic relationships and biogeography of the 74 species of *Erodium* using several reconstruction methods. Divergence times for major clades were calculated and contrasted with other previously published information. Furthermore, topological and temporal diversification rate shift analyses were employed using these data. Biogeographical reconstructions point to Asia as the ancestral arsea of *Erodium*, arising approx. 18 mya, after the divergence from its sister *California macrophylla*. Four incidences of intercontinental dispersal from the Mediterranean Basin to similar climates are demonstrated. Increases in diversification were present in two independent *Erodium* lineages concurrently. Two bursts of diversification (3 mya and 0.69 mya) were detected only in the Mediterranean flora. Two lineages diverged early in the evolution of the genus *Erodium*: (1) subgenus *Erodium* plus subgenus *Barbata* subsection *Absinthioidea* and (2) the remainder of subgenus *Barbata*. Dispersal across major water bodies, although uncommon, has had a major influence on the distribution of this genus and is likely to have played as significant role as in other, more easily dispersed, genera. Establishment of Mediterranean climates has facilitated the spread of the genus and been crucial in its diversification. Two, independent, rapid radiations in response to the onset of drought and glacial climate change indicate putative adaptive radiations in the genus in the Mediterranean Basin.

71. CONSTRAINTS ON THE DISPERSAL OF AN INVASIVE CRYPTOGENIC SEA ANEMONE

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The cryptogenic sea anemone, *Anemonia alicemartinae* (n. sp Häussermann & Försterra 2001) is a well-documented case of range expansion on the coast of Chile. Since its identification in northern Chile (18°S) in 1975, this species has invaded intertidal and subtidal habitats towards the south, now covering over 1900 km of the coast, and crossing frequent biogeographical barriers for coastal marine species between 30 and 33°S latitudes. Researchers have suggested that *A. alicemartinae* undergoes asexual reproduction and is capable of non-larval dispersal through a detachment-reattachment strategy. The successful establishment of this species could be explained by its use of a wide variety of substrata (e.g. rock, algae, living invertebrates, plastic bags), nevertheless, although substrate is available at its current southern range limit (36°S), abundances suddenly drop to zero. We evaluated three abiotic factors that could explain the constraint on dispersal: sand accumulation, temperature and salinity. Abundances of *A. alicemartinae* were low in areas with high accumulation of sand. Laboratory experiments showed that sand reduced adhesion to substrata, high temperature increased detachment, and low salinity increased detachment and reduced survival of anemones. We suggest that the current southern limit to the distribution of *A. alicemartinae* is due to the presence of extensive sandy beaches and a high volume river, which likely constitute biogeographical barriers for this invader.

72. ENVIRONMENTAL CONTROL IN FRUCTIFICATION IS RESTRICTING THE EFFECTIVE RANGE OF SOME SPECIES OF PALMS IN A CENTRAL AMAZONIAN TERRA FIRME FOREST

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Species distribution pattern could be determined by environmental factors or by dispersal limitation. The aim of this study was to determine how environment (e.g. topography, distance to water and soil nutrients) limits fructification of nine palm species. We sampled in 30 permanent plots of 250 x 40 m in Central Amazonia, Brazil. The proportion of fruiting individuals and the mean number of fruits per individual were related to clay and phosphorus contents, except for *Oenocarpus bacaba* and *O. minor*. The fruit production of *Geonoma aspidiifolia*, *Iriartella setigera*, *Euterpe precatoria*, *O. bacaba*, *O. minor* and *Attalea microcarpa* followed the distribution patterns of the adults. However, the fruit production of *O. bacaba* and *Attalea attaleoides* were restricted to one part of the soil gradient occupied by adults, which suggests an environmental limitation for the establishment of functional adults and that dispersion creates a wider distribution pattern. It suggests that these populations behave as metapopulations with a source/sink dynamics. To determine the effects of environmental gradients in the occurrence and capacity to produce fruits could be important to define protected areas which hold enough environmental heterogeneity to conserve viable populations.

73. DENDROCHRONOLOGICAL ANALYSIS OF *ZELKOVA ABELICEA* (LAM.) BOISS. (ULMACEAE), A THREATENED TREE ENDEMIC TO CRETE

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Demographical data is of vital importance for the definition of conservation strategies for rare and threatened species. In plants, these data are generally difficult to obtain. However, in woody plant species, dendrochronological methods provide a potentially powerful tool to address this problem. Additionally, the analysis of increment cores can give insights into the climatic history and geomorphic processes of a given site and therefore help to define management strategies. The extraction of increment cores from rare and threatened trees is limited, as this technique is invasive. Broadleaved trees such as *Zelkova abelicea* are especially vulnerable, as they do not normally produce resin to fill up boreholes as conifers do. Therefore, apart from extracting increment cores of living trees, we also took samples of dead trees. Altogether we determined the age of over 100 *Zelkova* individuals distributed across 14 populations throughout the whole range of the species. All habitat types and morphological forms (tree or shrub) of the species were included as well. We hypothesize that the age of an individual can be predicted when knowing its habit, habitat and diameter and discuss the value of our approach for conservation purposes.

74. THE CONSEQUENCES OF MIGRATION ON AVIAN COMMUNITY METABOLISM ACROSS NORTH AMERICA

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Every year, an estimated 5 billion New World birds migrate away from the equator in order to take advantage of the fleeting surge in productivity occurring at higher latitudes where they will breed. Using low estimates, this equates to the mass movement of 56,000 metric tons of biomass occurring twice annually. This influx of migrant biomass must play a pivotal role in forming avian community structure and determining community dynamics, yet little has been done to quantify the metabolic contribution of migrants to avian communities. Using allometric scaling relationships of body size and field metabolic rates, I calculate relative energy consumption of migrants to residents for 213 communities across North America by latitude during summer breeding. An increasing proportion of summer productivity entering the avian community is allocated to migrants relative to residents with increasing latitude. Migrant birds are increasingly important contributors of biomass and consumers of energy during the breeding season with increasing latitude. This technique has further potential to differentiate the magnitude of contributions to this pattern by various taxonomic or trophic groups. While this pattern prevails in North America, perhaps due to its higher proportion of landmass concentrated in northern latitudes, future studies may determine how strong this pattern holds on other continents.

75. AMPHIBIAN PHYLOGENETIC DIVERSITY IN SPACE

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The phylogenetic diversity underlying the species richness in an area can provide information about the history of its species, adding an evolutionary angle to the macro-ecological study of species-richness patterns. We examined global patterns of amphibian species richness and phylogenetic diversity (PD) by combining distribution maps for 6110 species with a new global phylogeny collated from molecular studies. Due to their capturing of different phylogenetic aspects, we explored four different measures of PD and their relationship with species richness across grid cells. We then identified areas with unusually low and high PD relative to their richness. Many island faunas had low PD for their richness, indicating that they consist of radiations of very few lineages. Areas with unusually high PD for their richness were in areas of faunal transition in Central America and southern China. Our results emphasise the importance of dispersal for species-richness patterns and their underlying evolutionary history.

76. HOW UNCERTAIN ARE PROJECTIONS OF AFRICAN SPECIES RANGE SHIFTS UNDER CLIMATE CHANGE?

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Assessing the potential impacts on biodiversity of future climate changes often relies on bioclimatic envelope models (BEM). Multiple BEMs and an increasing number of 21st century climate projections and greenhouse gas emission scenarios are available. Each of these tools or model outputs has the potential to generate markedly different projections of species range shifts. We examine climate and BEM uncertainties in ensemble forecasting of more than 2,500 mammal, bird, amphibian and snake species' future distributions in sub-Saharan Africa. Climate uncertainties are treated a priori by grouping co-varying projections, whereas BEM uncertainties are explored through the use of alternative consensus methodologies and the examination of non-analogue climates. We show how alternative climate assumptions and consensus methodologies affect assessments of climate change impacts on African biodiversity. Our analysis represents the most extensive treatment of uncertainties in predictions of climate change impacts on biodiversity hitherto performed for the continent.

77. REFINING PREDICTIONS OF IBERIAN PLANT DISTRIBUTION: LESSONS FROM *P. NIGRA* AND *P. SYLVESTRIS* PALAEOECOLOGICAL-BASED HABITAT SUITABILITY MODELS

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In recent years, challenged by the climate scenarios put forward by the IPCC and its potential impact on plant distribution, numerous predictive techniques -including the so called habitat suitability models (HSM) - have been developed. Yet, as the output of the different methods produces different distribution areas, developing validation tools are strong needs to reduce uncertainties. Focused in the Iberian Peninsula, we propose a palaeo-based method to increase the robustness of the HSM, by developing an ecological approach to understand the mismatches between the palaeoecological information and the projections of the HSMs. Here, we present the result of (1) investigating causal relationships between environmental variables and presence of *Pinus sylvestris* L. and *P. nigra* Arn. available from the 3rd Spanish Forest Inventory, (2) developing present and past presence-predictions through the MaxEnt model for 6 and 21 kyr BP, and (3) assessing these models through comparisons with biomized palaeoecological data available from the European Pollen Database for the Iberian Peninsula.

78. BIOGEOGRAPHICAL PROJECTION OF GROWTH AND MAINTENANCE COSTS IN *QUERCUS ILEX*. A TEST OF THE CORE-PERIPHERY PARADIGM

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The notion that there are strong relationships between the biogeographical location of the populations, their resistance to stress, and the use that individuals make of energy, has become a topic in biogeographic research. Owing to the higher overall levels of stress in populations native to the boundaries of their area of distribution, evolution seems to have favored more abundant defensive biochemical endowments in these populations; with the result of individuals inherently more resistant to stress. The synthesis and operation of greater defensive endowments should result in both, higher tissue growth and maintenance costs. In order to test this hypothesis, we collected acorns from six populations of *Quercus ilex* (a Mediterranean evergreen tree) in the range of North Spain and Southern Morocco. Acorns were grown in homogeneous conditions and seedlings were considered for comparison. Our results show no differences in leaf growth cost (1.23 g glucose g⁻¹) between populations. However, maintenance costs were significantly higher in the leaves of the plants native to the two peripheral localities (60.5 versus 40.3 mg glucose g⁻¹ day⁻¹), indicating that boundary populations expend more energy in processes other than growth and reproduction. Also, results so far suggest a higher resistance of both photosynthetic rate and growth rate to a generic stress factor (ozone treatment) in these populations.

79. HARPACTICOID FAUNA OF THE BLACK AND ADJACENT SEAS FROM BIOGEOGRAPHICAL POINT OF VIEW

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The Black Sea fauna is traditionally considered as a depauperate part of the Mediterranean and formed mainly by recent migrants. However, our data show that harpacticoid fauna of Ponto-Caspian region are very close together and far from the Mediterranean fauna. The Black Sea harpacticoid fauna in comparison with the other European seas (and in particular to the Mediterranean) has several specific features: (1) deep-sea fauna is absent, (2) there are no tropical families, and (3) family Canthocamptidae is "overrepresented" owing to a large number of freshwater and brackish species. At the present, the Ponto-Caspian fauna numbers 291 species, of which 178 were also reported from the Mediterranean Sea and 202 from the North or Central Atlantic. Among these species, 33 are found in both the Ponto-Caspian and Mediterranean seas but do not penetrate into Atlantic; whereas 57 species are presented in both the Ponto-Caspian basin and Atlantic Ocean but not in the Mediterranean Sea. Moreover, most of Ponto-Caspian harpacticoids are widely distributed. Nine species has been found in all 4 seas of the region (Black, Azov, Caspian and Aral), and all of them are euryhaline cosmopolites. Presumably, they represent the ancient elements of Sarmatic basin. The boreo-atlantic species therefore contribute more to the modern Ponto-Caspian fauna than the Mediterranean species do.

80. SPATIO-TEMPORAL PATTERNS OF LATE-GLACIAL MEGAFUNAL COLLAPSE, NO-ANALOGUE PLANT COMMUNITIES, AND FIRE REGIMES IN THE MIDWEST, USA

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The Pleistocene-Holocene transition was marked by widespread biotic upheaval, including the extinction of 33 megafaunal genera, the emergence of novel plant assemblages, and changes in fire activity. We present evidence that these phenomena may be linked. Paleoecologists have long recognized pollen assemblages with high dissimilarity from present; these "no-analogue" communities are characterized by the coexistence of boreal conifers (e.g. spruce, larch) with temperate hardwood taxa (e.g. ash, hop-hornbeam), and low abundances of pine, alder, and birch. The North American megafaunal extinctions coincided with these novel plant communities; while the causes of the late Quaternary megafaunal extinctions have been widely studied, the ecological consequences of those extinctions are poorly understood. Identifying the absolute timing of vegetation change and local megafaunal declines has been hampered by dating uncertainties and the poor spatiotemporal and taxonomic resolution of fossil data. Previous hypotheses for the cause of the no-analog communities have focused on abiotic drivers such as increased seasonality or wetter-than-present conditions. Spores from the dung fungus *Sporormiella* preserved in lake sediments have been shown to be coincident with megafaunal presence and absence in a range of environments, allowing for the direct interpretation of vegetation change in the context of local megaherbivory. We present several multi-proxy (pollen, charcoal, and *Sporormiella*) records in a northwest-southeast transect in the Great Lakes region that suggest that the loss of keystone megaherbivores may have altered ecosystem structure and function through the release of palatable hardwoods from herbivory pressure and a shift in fire regimes due to increased fuel loads.

81. ENVIRONMENTAL DETERMINANTS OF TREE SPECIES DISTRIBUTIONS IN CENTRAL ONTARIO, CANADA

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The ability to accurately model forest distributions in light of anthropogenic disturbance requires a thorough understanding of how trees respond to their physical and climatic environment. The primary objective of this study is to determine how four environmental variables (elevation, latitude, slope angle, and slope aspect) affect the distribution of seven common tree species (*Acer saccharum*, *Betula alleghaniensis*, *Betula papyifera*, *Abies balsamea*, *Picea glauca*, *Thuja occidentalis* and *Acer spicatum*) using both regression tree analysis (RTA) and canonical correspondence analysis (CCA) techniques. In general, within the study area, *Acer saccharum*, *Abies balsamea* and *Thuja occidentalis* abundance was controlled by elevation and latitude, while the other species showed limited response to the measured environmental variables. While CCA and RTA showed similar patterns, RTA allowed for a more nuanced evaluation of species-environment interactions. Reflecting that the study area encompasses *Acer saccharum*'s northern limit *Abies balsamea*'s response to environmental conditions depended on the presence or absence of *Acer saccharum*.

82. CLIMATE CHANGE, BIOGEOGRAPHY AND PALEOECOLOGY OF THE SHARKS AND BATOIDS FROM THE EOCENE-OLIGOCENE TRANSITION IN BAJA CALIFORNIA SUR, MEXICO

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The Eocene-Oligocene climatic transition from a greenhouse to an icehouse effect left behind a good biostratigraphic sequence in Baja California Sur, Mexico, including the Tepetate and Bateque formations (Eocene) and the El Cien and San Gregorio formations (Oligocene), with a relative complete Eocene-Oligocene succession that yields selachian remains throughout. There are four abundant and diverse shark and batoid faunal assemblage for the Ypresian, Lutetian-Priabonian, Rupelian and Chattian stages, consisting mostly of teeth, caudal spines, vertebrae and dermal denticles, coming from neritic deposits with tropical and temperate climatic zone-, and benthic and pelagic zone-affinities. Tethyan elasmobranch assemblages from Europe, Africa, Middle East, Asia, Oceania and Antarctica, include a good number of cosmopolitan species with high vagility that can be used as a fossil index, have been recorded, and represent broad-scale biostratigraphic correlations. Benthic small sharks and batoids with low vagility and high endemism are very important, especially from sieved or screened microvertebrate specimens, because they are rather provincial in their distributions. The analysis of their distributional patterns in conjunction with the closing and opening of seaways may reveal evolutionary patterns in the Pacific Basin. Some of the recorded genera have no extant representatives in the area, and some are restricted to the Caribbean or Western Atlantic and the Indo-Pacific.

83. COMPARING THE RELATIVE CONTRIBUTIONS OF BIOTIC AND ABIOTIC FACTORS AS MEDIATORS OF SPECIES DISTRIBUTIONS

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One of the most important goals of ecology is to characterize and quantify the ecological niche of species by identifying which factors affect and limit their ranges and then predict their distributions. However, the full ecological niche depends on a myriad of factors, both biotic and abiotic, that correspond to completely different data types. In this paper we present a modeling framework within which different data types, representing both abiotic and biotic factors, can be integrated into predictive niche models. To illustrate the efficacy of the approach we used a mammal *Lynx rufus* as case study. We determine and quantify the relative importance of biotic versus abiotic factors in the niches of this species using climatic, land cover and point collection data. We show that including in different factors not only leads to a fuller, more comprehensive understanding of the niche but also leads to more accurate prediction models. In analogy with the concept of a fitness landscape, we discuss the concept of a “niche landscape” where the height function is a measure of the probability of finding the species – high regions corresponding to suitable niche areas and low regions corresponding to unsuitable “anti-niche” areas.

84. MODELING HABITAT SUITABILITY CHANGE FOR A GRASSLAND SPECIALIST AS A FUNCTION OF INCREASING HUMAN LAND USE AND GLOBAL CLIMATE CHANGE ACROSS THE U.S. GREAT PLAINS

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Worldwide, the extent and integrity of grassland systems are declining due to anthropogenic pressures and climate change. Landscape Conservation Cooperatives are US Fish and Wildlife service partnerships between landscape managers and research scientists to get scientific knowledge about global climate change and other stressors to land managers. The Great Plains Landscape Conservation Cooperative (GPLCC) encompasses portions of eight states: South Dakota, Nebraska, Kansas, Oklahoma, Texas, New Mexico, Colorado, and Wyoming. Greater Prairie-Chicken (GPC; *Tympanuchus cupido*) is a grassland lek-breeding grouse native to the GPLCC. GPC is a charismatic species of conservation concern due to their economic value, status as a grassland specialist, and large home range requirements. Using lek location data provided by GPLCC state agencies and publicly available land cover data, we modeled lek habitat suitability across the GPLCC using a hierarchical Bayesian model selection procedure and Program MaxEnt. We then used eco-forecasting models predicting GPLCC land cover changes over 70 years and re-ran our analyses on putative future landscapes. We found a 4% reduction in landscape quality, a 27-40% reduction in areas suitable for GPC lek habitat, and a reduction in the number of suitable lek habitat patches from 200 to 120. We also detected 137 km southeastern shift of the center of GPC habitat distribution. Such findings are concerning to land managers because GPC is considered an umbrella species as conservation of blocks of grassland habitat for GPC enables conservation for numerous other grassland species.

85. DETERMINANTS OF VEGETATION DISTRIBUTION AT CONTINENTAL SCALE: THE CONTRIBUTION OF NATURAL AND ANTHROPOGENIC FACTORS

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It has long been debated what determines the distribution of vegetation types, though this has rarely been tested at continental scale. We thus aimed to determine which vegetation types are most accurately predicted by natural environmental factors, and which of these factors best predict current vegetation distribution across Africa. Vegetation types were extracted from the Global Land Cover Map for the year 2000, and the distribution of vegetation types modelled in terms of climate, soil and topography. Annual precipitation was the best predictor of the distribution of all vegetation types, and response curves showed that, at lower rainfall levels, an increase in precipitation brought on vegetation types with greater woody cover, though this pattern disappeared at higher rainfall levels. Subsequently, the influence of current and historic human impacts on the distribution of vegetation types was also assessed, and found to be of some importance for most vegetation types. We conclude that, in addition to including environmental variables in predicting vegetation distribution, it is essential that human impact be considered, also in future climate change scenarios.

86. FLOWERING PLANT BIODIVERSITY GRADIENTS IN EASTERN NORTH AMERICA, 21,000 BP TO PRESENT

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Contemporary latitudinal diversity gradients are well-described for many extant taxa, and reconstructions from the marine bivalve fossil document gradients extending back to the Paleozoic. In this study, I use fossil pollen data to investigate the development of contemporary diversity gradients in eastern North America over the past 21,000 years. Using data from the North American Pollen Database, I calculated palynomorph diversity for 1,000 year time steps and summarized diversity values in 1 degree latitudinal bands. Peak diversity increases and the gradient's slope decreases between 21000 BP and 6000 BP. However, scaled to the maximum diversity and latitudinal values, the shape of the gradient remains relatively constant through time. This suggests a consistent relationship between available taxa and controls on diversity as vegetation assemblages organized themselves in response to postglacial environmental changes.

87. A BENCHMARK FOR ENSEMBLE FORECASTING OF SPECIES RANGE SHIFT UNDER CLIMATE-CHANGE

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Investigating climate-change impacts on biodiversity mainly relies on bioclimatic envelope modeling (BEM), where current associations between species ranges and environmental factors are estimated and used to forecast shifts in the potential ranges of species under climate-change scenarios. Numerous statistical techniques exist for fitting BEM and recent studies have demonstrated that projections by alternative techniques can be as very variable as to leading to substantial uncertainties in the outcomes of forecasts. To overcome these limitations, ensemble forecasting has been proposed. This approach accounts for inter-model variability and combines the outcomes of different techniques so as to generate a consensus. Although a limited number of empirical tests have been undertaken to evaluate the performance of ensemble forecasting methodologies, the limitations associated with empirical data prevent a general understanding of the strengths and limitations of the approach. Here, we investigate the performance of ensemble forecasting vs. individual forecasts that constitute the ensemble using artificially generated data. To simulate a wide breadth of responses of species to environmental gradients we simulated species with symmetrical, left and right-skewed response to environmental gradients using Europe as a geographical and environmental template. We examined the performance of the ensemble forecasting vs. the individual forecasts that integrate the ensemble under different plausible scenarios regarding sampling biases (random, geographically- and environmentally-biased sampling) and degree of equilibrium of species with their environment (i.e., range filling). The analysis demonstrates the usefulness of artificially generated data for testing and improving understanding of the algorithmic and ecological uncertainties of BEM under climate change.

88. IMPORTANCE OF THE SMALL RIVER VALLEYS IN DISTRIBUTION OF DRY GRASSLAND VEGETATION IN THE ZEMGALE LOWLAND, LATVIA

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Some major functions of riparian areas are to provide migration routes and refugia for flora and fauna, as well as to maintain biological diversity. Riparian areas have special importance in territories intensively used for agriculture. Several studies have been made on biogeographical processes in central and eastern Europe's large river valleys, but few about small rivers. The aim of this study is to find out the importance of small river valleys in the distribution of dry grassland species in the intensive agricultural landscape. The study took place in the Zemgale Lowland (Latvia), where 50-80% of territory is used for agriculture. Valleys of 14 rivers were inspected and 64 localities of dry grassland vegetation described. The localities of the species belong to the grassland vegetation classes *Festuco-Brometea* and *Trifolio-Geranietea*. 47% of localities maintain a large diversity of dry grassland species (10-21 species per relevé), but in other relevés less species were found, in some just two species (mostly in *Trifolio-Geranietea* communities). All described communities are affected by processes of ruderalization and overgrowing. Riparian corridors of the Lowland are fragmented by dams, roads and arable lands, but grassland habitats also by woodlands and bushlands. Migration of dry grassland species can take place only very locally. River valleys in the Zemgale Lowland are still important for the distribution of dry grassland species and serve as refugia and hotspots of biodiversity, but, because of fragmentation of riparian corridors and grassland habitats, their importance for species migration is decreasing and migration of dry grassland species can occur only locally.

89. MAMMALIAN DIVERSIFICATION AND RANGE DYNAMICS IN THE FACE OF QUATERNARY CLIMATE CHANGES

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Throughout the Quaternary, the flux of glaciers across American landscapes altered climates and created refugial pockets where species persisted, often in isolation. Glacial patterns have changed significantly since the late Pleistocene, and mammals have responded to shifting climates in various ways. Often, vicariant processes and differences in dispersal ability are invoked to explain variation in geographic distributions and divergence of lineages while the effects of stable areas on diversity are largely ignored. Here, we use the contemporary distributions of related lineages (i.e., sister genera) to model climatically suitable habitats for each during the late Quaternary (21 kbp) to examine the effects of stable climatic refugia on diversification. Specifically, we compare the amount of stable area from the last glacial maximum to the present-day for each genus to see whether it can explain current species diversity within genera. Furthermore, we include the possible effects distinct biogeographic barriers have exerted on diversification. We focus on the Americas since they represent higher connectivity through the Mesoamerican isthmus and contain a myriad of distinct habitats influenced by tectonic dynamism and topography. When combined, the influence from these barriers and information about shared areas of stable climate (or shared refugia) across genera may do much to reveal information that can be used to interpret historical scenarios about the diversification of mammalian lineages across the Americas.

90. COMPARATIVE PHYLOGEOGRAPHY OF BENTHIC MARINE INVERTEBRATES ACROSS A BIOGEOGRAPHIC BREAK IN THE SOUTH EAST PACIFIC COAST

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We hypothesize that the widely recognized biogeographic break at 30°S in the Chilean coast corresponds to a historical break. Consequently, that there will be a coinciding phylogeographic break in species with relatively low dispersal potential (DP), while in highly dispersing species, the signatures of the break have been erased by gene flow. The phylogeography of the mitochondrial gene COI is being analyzed in eight benthic marine invertebrate species that have an ample range of distribution along crossing the biogeographic transition zone. Results obtained up to date suggest that three species, two with moderate and one with low DP, have a phylogeographic break along the study area. Further sampling and analyses will reveal the exact latitude at which these genetic breaks occur. None of the species with high DP show signs of a strong genetic break along studied area, although they do display different interesting genetic diversity. The results validate the proposed historic origin of the biogeographic break at 30°S, and the importance of life history traits and the evolution of the lineages of species in the geographic distribution of the genetic diversity.

91. OCEANIC ISLANDS, SPECIES RICHNESS, AND ENDEMISM: A CAUTIONARY TALE

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Oceanic islands are the focus of great interest because of their levels of species richness and endemism and attendant implications for long-term biogeographical dynamics. We have conducted surveys since 2000 on a “well-known” mammal fauna on Luzon Island, Philippines, a large (105,000 km²), geologically old and complex plate-margin island. Our surveys were guided by a simple, predictive model: areas of highland habitat separated by intervening lowlands constitute unique areas of endemism. Estimates prior to 2000 included 31 species of native, non-flying mammals, with 20 (65%) single-island endemics (SIEs) among them. Our current conservative estimate has at least 54 species present, with 43 SIEs (80%), and these may rise to 60 species and 49 SIEs, nearly twice the number of species known in 2000. Most of the 20 “new” species have been discovered in previously unrecognized subcenters of endemism. In 2000, 3 such areas were recognized on Luzon; we now estimate at least 8 subcenters, and ca. 40 (75%) of the SIEs are confined to only one subcenter. We suggest that on large, complex oceanic islands 1) the diversity of even “well-known” taxa may be severely underestimated; 2) the number of subcenters of endemism may be far higher than previously estimated; 3) the number of SIEs may be particularly underestimated; and 4) a large percentage of SIEs may have far smaller areas of distribution than a “single island”.

92. EVOLUTIONARY CONSEQUENCES OF CLIMATE-DRIVEN PHENOLOGICAL SHIFTS

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Contemporary climate change is shifting the phenology of many species across the world. However, the evolutionary consequences of these shifts remain largely unknown. Here, we present a conceptual framework and theoretical overview of the potential evolutionary outcomes of phenological shifts for individual species. We suggest that phenological shifts are likely to increase reproductive connectivity among some populations while also increasing reproductive isolation among others. Together, these changes in the degree of reproductive isolation have the potential to alter patterns of gene flow resulting in both short and long-term consequences for the persistence of individual species. Short-term consequences may include changes in genetic diversity within populations, which can alter reproductive fitness, and disrupt local adaptation. In the long-term, consequences may include speciation and extinction, which have important implications for global biodiversity. As a result of these potential outcomes, predicting the direction of phenological shifts will become increasingly important for conservation biologists and land managers in the future. Our findings highlight the complex ways in which the climate change predicted for the coming decades may influence the evolution of species and presents a number of new research topics that we recommend be examined.

93. BIOME SHIFT, TREE COVER CHANGE AND CLIMATE-DRIVEN UNCERTAINTY FOR 2050 IN WEST AFRICA

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Africa is expected to face severe changes in climatic conditions affecting biomes and tree cover. Thus, our objectives: (1) to model trends and extent of future biome shifts by 2050; (2) to model a trend in tree cover change, while accounting for human impact; and (3) to evaluate uncertainty in future climate projections. We modeled the future spatial distribution of major biomes in West Africa by using six bioclimatic models, while tree cover change was analyzed with Generalized Additive Models. We used climate data from 17 General Circulation Models (GCMs). Consensus projections were derived via weighted average to: 1) reduce inter-model variability and 2) describe a trend from the different GCM projections. Climate change most strongly affects grassland, resulting in a northern expansion of its bioclimatic envelope in the magnitude of 2 million km². Savanna is projected to lose area in the south ($54 \pm 22 \times 10^4$ km²) while deciduous and evergreen forest are expected to expand ($64 \pm 13 \times 10^4$ km² and $77 \pm 26 \times 10^4$ km²). Higher tree cover is projected for large parts of Benin, Burkina Faso, Cote d'Ivoire, Ghana and Togo (1-10 %), whereas decrease is expected in coastal areas (1-20 %). Furthermore, human impact negatively affects tree cover and even inverts the climate-driven increase of tree cover to a decrease. Despite considerable GCM-based uncertainty we extracted trends of future vegetation change in West Africa. Simulations indicate a climate-driven greening trend by 2050. However, human impact may invert this trend by reducing vegetation cover which is enforced by positive feedbacks.

94. GEOGRAPHICAL PATTERNS OF BUTTERFLY SPECIES DIVERSITY IN THE SUBTROPICAL RYUKYU ISLANDS: THE IMPORTANCE OF A UNIDIRECTIONAL FILTER BETWEEN TWO SOURCE ISLANDS

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We examined the relative influences of historical and current factors on geographical patterns of butterfly assemblages in the Ryukyu Islands by evaluating species richness and rarity, dissimilarity between islands, and dissimilarity to two source islands. The Ryukyu Islands is an arc of continental islands located between two source islands, Kyushu and Taiwan, and categorised into three regions separated by the Tokara and Kerama Gaps. Butterfly assemblages comprising 184 species (five families) were examined on 59 islands. In this study, the roles of historical and current factors were identified. The gaps and island area determine species richness and rarity of butterflies in the islands, whereas altitude and isolation regulate the dissimilarity of butterflies between islands. The contributions of the two source islands to the assembly of island butterflies are different; the establishment of immigrants from Kyushu is facilitated in islands farther from Kyushu while immigration from Taiwan is inhibited in islands farther from Taiwan. The disproportionate roles of the two source islands indicate that a unidirectional filter characterises the geographical patterns of butterfly species diversity in the Ryukyus.

95. THE RELATIVE ROLES OF CLIMATE AND OCEAN CIRCULATION PATTERNS IN ESTABLISHING THE RANGE LIMITS OF MARINE INVERTEBRATES AT POINT CONCEPTION, CALIFORNIA

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Climate is often assumed to be the major factor in defining the limits to species' distributions, but ocean circulation patterns may further confine the distributions of marine species by limiting dispersal of larval stages. A large number of marine invertebrates have northern limits to their distributions at Point Conception, California, a region with a steep gradient in seawater temperatures as well as eddy circulation that may limit the northward dispersal of marine larvae. Here I present data on the response of marine snail survival and feeding to decreasing water temperatures, as well as patterns of larval abundance within and beyond the natural geographic range of selected marine invertebrates (snails, mussels and lobster). Laboratory experiments indicate that marine snails with northern range limits at Point Conception have lower survival and feeding rates in cold seawater than their northerly relatives. Relative levels of larval abundance indicate whether the eddy limits northward dispersal of these species and contributes to establishing the northern range boundaries. Understanding the mechanisms that define species' ranges is crucial for predicting how these distributions will respond to changes in climate.

96. GEOGRAPHIC DISTRIBUTION OF HIGH LATITUDE SPECIES IN THE FACE OF FUTURE CLIMATE CHANGE

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The threat of a further changing climate has been recognised as one of the main drivers behind (future) extinctions. The arctic region is expected to be especially affected. Evidence shows that species respond to climate change by adjusting their geographic distributions. The large expected impacts of future climate change in the arctic region make species in areas like the Barents Region particularly vulnerable. In response of expected climate change and subsequent effects on biodiversity, we use species distribution modelling to assess the capacity of existing protected areas in the Barents region to safeguard their current biodiversity under different climate change scenarios (CCCMA, HADCM3, emission scenarios A and B) in the future. Currently, the spatial distributions of over 60 mammalian species have been modelled for current and future situations, and we are continuing with other taxa. We conclude that the climatic conditions are expected to improve in the Barents Region for many mammalian species in the future. More warm and less wet conditions allow a considerable number of species to expand their distribution range. However, various species (especially Carnivora and Rodentia) are expected to contract their ranges over time. Furthermore several new species are predicted to be able to invade the region, altering community composition and biotic interactions in ways difficult to anticipate.

97. CURRENT CLIMATE, CLIMATE CHANGE SINCE LAST GLACIAL MAXIMUM AND DIVERSITY GRADIENTS THROUGHOUT EUROPE

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Species distributions are related to both present and past climate. However, the relationship of current diversity gradients with these factors varies in space. We evaluate the relative importance of the association between species richness and both current climate and the variation of climate since Last Glacial Maximum, for nine taxa (mammals, birds, amphibians, reptiles, butterflies, dung beetles, Brassicaceae, Caryophyllaceae and trees) throughout Western Europe. We implemented Partial Geographically Weighted Regressions to partition the relationship between richness and current and past temperature and precipitation while accounting for spatial non-stationarity. In all cases, non-stationary models outperformed global OLS models. Our results show that richness is generally more strongly associated with long-term variations in climate than with current climate in many parts of Europe, and that the location of these areas is consistent among groups.

98. COMMUNITY SIMILARITY ACROSS ONE MILLION YEARS OF GLOBAL CHANGE: LATE PLIOCENE PHYTOPLANKTON IN THE NORTH ATLANTIC

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Fossils record the ecology and evolutionary response of species to abrupt, global change, and provide a baseline for understanding the present biotic crisis. For instance, terrestrial pollen records have detailed the individualistic response of plants to past climatic and environmental change, resulting in ancient communities with no modern analog (no-analog communities). With this paleo perspective on community composition, it is predicted that no-analog terrestrial communities are likely to develop in response to the novel environments of the next century. Considerably less is known about marine community similarity across past climatic oscillations, or about the dynamics of communities comprised entirely of now-extinct species. Here, we investigate the presence of no-analog paleocommunities (no-analogpaleo) in a group of calcareous marine phytoplankton (discoasters) in five sites across the north Atlantic. These temporally highly resolved records capture 1-million years of change in community structure across major climatic events, like the onset of North American glaciation, and terminate in the global extinction of all discoaster species. We use methods developed in terrestrial analyses to analyze community dissimilarity through time and across the north Atlantic, and to quantify the rate and cyclically of changes in community dissimilarity.

99. PLANT PATTERNS OF ENDEMISM IN THE ROMANIAN CARPATHIANS. CAN PALEODISTRIBUTION MODELS OFFER MORE INSIGHTS?

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The current distribution of species is the result of numerous historical events and ongoing processes of vicariance, dispersal and extinction. In many cases the use of data on endemic species provides strong insight into these processes, as observed biological entities are tightly linked to the history of occupied biogeographical units. Although there is no “magic bullet” approach to elucidating this history, several techniques can contribute to unveiling these phenomena. Starting from the assumption of niche stability over time, we used species distribution models (SDMs) and parsimony analysis of endemism (PAE) to delineate geographic and ecological barriers. Our dataset is comprised of literature data, historical herbarium collections and field surveys covering the Romanian and Serbian part of the South-Eastern Carpathians. Through the use of paleoclimatic data and state of the art statistical techniques implemented in R software (BIOMOD), we reveal geographical shifts and conservatism during postglacial times.

100. SEEING THE FOREST FOR THE TREES: UNDERSTANDING THE LATITUDINAL DIVERSITY GRADIENT BY READING PHYLOGENIES OF MANY TAXA

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Most plant and animal taxa increase in diversity from the equator towards the poles. Even though many hypotheses have been proposed to explain this phenomenon, tests evaluating different hypotheses still remain scarce. Higher tropical diversity may be caused by more time for accumulation of lineages (tropical conservatism hypothesis), higher diversification, or higher capacity for local coexistence. Information from phylogenies may be used to distinguish between the first two mechanisms. We sampled information from phylogenies of mammals, birds, amphibians, insects and plants (in cases where the phylogenies provided a phylogram, included lineages from both tropical and temperate regions and at least 50% of all known taxa were sampled to construct the phylogeny) to address this question. We found strong support for the tropical conservatism hypothesis, with most clades being most diverse in their climatic zone of origin, and most originating in the tropics. In contrast, 30-39% of lineages switched between tropical and temperate latitudes at each node in the tree, not supporting strong conservatism of geographic ranges. Contrasts in diversification in tropical versus temperate lineages were highly variable depending on taxa and level of taxonomic resolution. We conclude that the latitudinal diversity gradient is maintained by a complex interaction between tropical originations and bursts of high tropical diversification, counteracted by a relatively high frequency of transitions between climatic zones.

101. THE PARADOX OF THE PLANKTON, TESTED IN TIME AND BIOGEOGRAPHIC SPACE

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Hutchinson (1961) hypothesized that multiple plankton species coexist because the time for competitive exclusion approximates the time for significant environmental change. Temporal overlap of populations is central to this hypothesis but could not be tested until recently, when a new algorithm (Rosario) and software (TimeOverlap) were developed – we used this approach in a meta-analysis of rotifer data. Hutchinson's hypothesis predicts that significant temporal partitioning among rotifer populations should be rare. Also, we hypothesized that temporal partitioning may increase with: (a) greater latitude or altitude if shorter growing seasons force competition, (b) smaller lake area that may limit habitat heterogeneity, and (c) species richness if “species packing” drives niche partitioning. We obtained 79 data sets distributed over 38 degrees latitude, 2 km altitude, and 25,000 km² lake area. Only 5% of the data sets (4/79) exhibited significant or marginal temporal partitioning, while 51% (40/79) were not significantly different from random, and 44% (35/79) had more temporal overlap than expected at random. Also, temporal overlap patterns were not significantly related to latitude, altitude, or area, and more speciose data were actually less likely to exhibit significant temporal partitioning. Hutchinson's Paradox of the Plankton is largely supported with temporal overlap among rotifers in diverse lakes; multiple mechanisms may explain these widespread patterns.

102. SOUTHERN IBERIA AS A REFUGE FOR THE LAST NEANDERTHAL POPULATION

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This paper evaluates the role of glacial refugia in the survival of the last known Neanderthal populations in Europe. This evidence is found at Gorham's Cave, Gibraltar, which contains Middle Palaeolithic deposits dated to c. 28,000 years ago. We developed a new methodology using biogeographical principles to model past climate scenarios of southern Iberia. Present day temperature and rainfall maps of southern Iberia were generated using data from 338 weather stations. The maps were subjected to incremental falls in temperature and rainfall and redrawn within a GIS framework. Cool and dry climate models were created and combined to provide a representation of climate conditions in southern Iberia during the last glacial period. The modelling showed that four refugial environments were present: cool/humid, cool/dry, warm/humid and warm/dry. 165 Middle Palaeolithic sites were examined with respect to these environments to evaluate the relationship between Neanderthal occupation patterns and climate. Many sites correlated well within the two types of refugial environments that were governed by high levels of rainfall. Notably, a large warm/humid refugium extended from the slopes of the Cadiz-Malaga sierras to Gibraltar and the Atlantic and Mediterranean coasts, and a smaller cool/humid refuge was located in the uplands of Córdoba and Granada provinces. The results suggest that rainfall was a key factor in the late survival of Neanderthal populations in the area.

103. SOME THOUGHTS ABOUT THE AREA UNDER THE ROC CURVE

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The area under the ROC curve (AUC) is a widely used statistic to evaluate species distribution models (SDMs). Its main advantage is its threshold-independence, so that the potential arbitrariness associated with the selection of a cut-off is avoided. The ROC analysis has also been modified to deal with scenarios in which no absence data is available. Here, the x-axis of the traditional ROC curve (1-specificity) is replaced by the proportion of the background locations falling above the threshold for all possible thresholds. I used simulated and real data to examine the interdependence of the AUC and threshold-dependent discrimination measures derived for the application of a threshold. I also discuss and exemplify with simulated data the application of the AUC when no absence data is available. There was a strong relationship between the AUC and the sensitivity and specificity yielded after the threshold that makes these two measures equal was applied, suggesting that the independence of the AUC from the threshold selection may be irrelevant in practice. On the other hand, the AUC derived from the modified ROC curve penalizes the models that estimate potential distributions and favours those that estimate realized distributions. Thus, the AUC is only truly informative when the realized distribution – not the potential one – is the goal of the research.

104. FOSSIL EVIDENCES OF INSECT-PLANT ASSOCIATION: A PRELIMINARY STUDY OF PALEOENVIRONMENTAL CHANGE IN MIOCENE SEDIMENTS, KOREA

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Insects make up most of Earth's biodiversity, and almost half of insect species are herbivores. Consequently, understanding how plant-insect associations respond to climate change is a vital component of global environmental change research. For example, insect-damaged leaf fossils from American and European continents of the Paleogene sediments have provided deep insight on patterns of climatic changes. A great amount of insect-damaged leaf fossils were found from the Geumgwangdong Formation (ca. 21Ma; total 292 specimens) and the Duho Formation (ca. 13Ma; total 397 specimens) of the Pohang Basin situated in southeastern Korean Peninsula, and each represents a unique view into Neogene freshwater ecosystems and marine sedimentary environments. The leaf assemblages are dominated by deciduous broad-leaved elements in inland mountainous region and by deciduous/evergreen broad-leaved elements from coastal land area. The total percentage of damaged leaves for the Geumgwangdong and the Duho Formation is 36.3%, 47.4% respectively. External foliage feeding types (e.g., margin feeding, hole feeding and skeletonization) have the highest frequency and there was minimal damage from other feeding types (e.g., galling and mining). Analysis of damaged fossils in the record show higher frequency of damaged fossils in the middle-Miocene Duho assemblages than that in the early-Miocene Geumgwangdong assemblages, which suggests the Duho Formation may have been deposited under a warmer climate condition than in the Geumgwangdong Formation. This is well correlated with results of a recent quantitative climatic study of the two formations. In addition, a higher occurrence of galling (14.6%) in the Duho Formation than in the Geumgwangdong Formation (6.5%) may indicate a more humid environment in the Geumgwangdong Formation, because wet environments, in general, select against gallers by facilitating predator attacks and pathogen growth.

105. CONSERVATION OF LOCAL ENDEMIC PLANTS OF PENTADACTYLOS RANGE (CYPRUS)

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The mountain range of Pentadactylos is located in the northern part of Cyprus and hosts 64 endemic plant taxa of the island, out of which 17 are local endemics. Several anthropogenic activities, as well as climate change, pose severe threats for the persistence of these species. Therefore, the implementation of both in situ and ex situ conservation measures is considered of utmost importance. This work presents the main results of a project that focused on the conservation of the local endemic plants of Pentadactylos. The project collected information on the geographical distribution of these taxa, the environmental conditions (temperature, humidity, light) prevailing at their locations and the specific threats that each species is experiencing. Laboratory work included the investigation of the seed germination ecophysiology of each species. The information resulting from this investigation was correlated to the geographical distribution, the habitat characteristics and generally the survival strategy of each species. This work provides useful information for both in situ and ex situ conservation of these taxa. Information on seed germination in relation to their survival strategy is critical in optimizing the timing of in situ conservation efforts. Regarding ex situ conservation, the knowledge of seed germination behaviour is of utmost importance for the conservation of the targeted taxa in a seed bank, as well as for producing new plants and creating living collections within botanical gardens.

106. CONSERVATION OF THE ENDEMIC ORCHID OF CYPRUS *OPHRYS KOTSCHYI*

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Ophrys kotschyi, an endemic orchid of Cyprus, is listed as a priority species in Annex II of the Directive 92/43/EEC. It is widely distributed in the island, occupying a variety of habitats at altitudes 0-900 m. *O. kotschyi* usually occurs in small subpopulations of less than 50 individuals each. The entire population amounts at least 1800 individuals. However, only 7 out of 30 locations are within protected areas such as Natura 2000 sites or state forest lands. Most of the *O. kotschyi* subpopulations occur close to inhabited areas and some of them have already become extinct due to land development, thus decreasing the species geographical distribution and extent of occurrence. In order to improve the conservation status of the species, a Plant Micro-Reserve (PMR) has been established at Mitsero area, within the framework of LIFE+ project "Establishment of a Plant Micro-Reserve Network in Cyprus for the Conservation of Priority Species and Habitats – LIFE 08/NAT/CY/000453". The PMR comprises the largest subpopulation of *O. kotschyi* and the project adopts sound in situ conservation measures, aiming at protecting and enriching the natural population of the species. The present work presents these measures and information relating to their effectiveness.

107. A SCALE BASE STUDY OF *CYMODOCEA NODOSA* AND *ZOSTERA NOLTII* COEXISTENCE AT BOUNDARIES OF THEIR GEOGRAPHICAL DISTRIBUTION (N. AEGEAN, GREECE)

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The species *Cymodocea nodosa* and *Zostera noltii* often coexist in the N. Aegean, Greece (Mediterranean Sea) coastal waters at the limits of their northern and southern distribution boundaries, respectively. The morphological (leaf length and width), structural (shoot density, leaf and rhizome-root biomass) and dynamic (leaf area index, % of broken-grazed leaves) metrics were studied in a shallow (2.5-3.5 m) meadow of Epanomi, outer Thermaikos Gulf. The aim was (1) to establish basic line knowledge for the spatial growth pattern of the species, (2) to estimate the meadow degradation due to industrial, agricultural and urban sewages using CymoSkew index. Twenty quadrates (25 x 25 cm) were destructively sampled by scuba diving means in summer 2010. All data have been analyzed using nested ANOVA in two spatial scales (100's of meters-site, 10's of meters-area). Both species showed statistically significant differences ($p < 0.05$) or not in their morphological, structural and dynamic features at different spatial scales indicating that their growth pattern is patchy. CymoSkew index (2.96), a quantitative expression of *Cymodocea nodosa* leaf length asymmetry, indicated the meadow as moderately degraded. This result is in accordance with the local perturbation pattern.

108. COMPARING ISLAND BIOGEOGRAPHIC PATTERNS BETWEEN THE AEGEAN AND IONIAN ARCHIPELAGOS OF GREECE

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We examined the relationship between biogeographic factors and plant diversity in two archipelagos of Greece (Aegean in the east and Ionian in the west of the country). We estimated endemism at two scales (i.e. species that are endemics to Greece and species that are endemics to a single island). The Aegean archipelago includes considerably more islands than the Ionian, and also a greater range of island sizes, and altitudes. Also, the Aegean archipelago is surrounded by mainland in the east, north and west; while in the Ionian archipelago the mainland is located only on the eastern side. Our analysis showed that some patterns hold on both archipelagos while others differ. In both cases total species richness is most strongly correlated to island area followed by maximum elevation, with only weak correlations to other biogeographic factors, like isolation. In the Ionian, the endemic species richness correlation to biogeographic factors follows, a similar pattern as that for total species richness, while in the Aegean, endemic species richness is primarily associated to an island maximum elevation and only then to island area. We discuss possible explanations for the observed differences in endemic diversity patterns between the archipelagos.

109. PHYLOGEOGRAPHY OF A HABITAT SPECIALIST TERRESTRIAL ISOPOD IN GREECE

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The genus *Trachelipus* comprises of stenoeocious animals living in habitats generally threatened by human activities, such as humid forests and riparian habitats. Five endemic species have been reported from Greece, but species-level taxonomy is still under debate, mainly after the application of molecular markers for their phylogeny reconstruction. Nevertheless, in most part of the Greek mainland and central-south Aegean islands the genus is represented by a clade of morphologically very similar populations that traditionally are considered as two separate and allopatric species, *T. kytherensis* and *T. aegaeus*. Herein we investigate the phylogeography of a large number of *Trachelipus* populations from both the mainland and insular Greece, using two mtDNA markers (COI and 16S rRNA), aiming to identify possible geographic structure in their divergence and to evaluate the effects of habitat fragmentation on the genetic structure of these animals. The results reveal very large amounts of genetic differentiation even among neighbouring populations, and a geographic pattern that is not congruent with current taxonomy and established palaeogeography. The occurrence of more than one clade in mainland Greece raises the possibility of repeated episodes of clade expansion/contraction during Pleistocene glaciations. Nevertheless, several new questions are raised for further research, especially regarding the insular clades. In any case, it is evident that in these relatively sedentary animals, habitat fragmentation promotes population divergence at a very high rate. In fact, the genetic distances recorded herein among closely related populations are comparable with those reported for different genera in other isopods and arthropods.

110. PHYLOGEOGRAPHY OF A SAHARO-SINDIAN GENUS: *MESALINA* (SAURIA: LACERTIDAE)

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Mesalina is a widely distributed lacertid genus occurring throughout the Saharo-Sindian region. It belongs to the tribe Eremiadini that, according to previous studies, is thought to have originated in the Middle East during the mid-Miocene. The genus has undergone a series of taxonomical revisions, mainly based on morphological characters, resulting in the identification of 14 species. In the current study we explored the phylogenetic relationships among 12 species of the genus based on two mitochondrial loci and proposed a phylogeographic scenario. The retrieved phylogeny differs from the accepted taxonomy, implying the need for revision. The phylogeographical scenario proposed reveals that dispersal–vicariance events between North Africa and southwest Asia throughout the Miocene, Pliocene, and Pleistocene resulted in the present distribution of the species of *Mesalina* under study. Key geological events for the understanding of the phylogeography of the genus are the Atlas range formation and the movement of the Arabian plate that led to the shaping of Middle-East (formation of the mountain ranges of Iran, opening of the Erythrean sea) and permitted the faunal exchange between Eurasia and Africa. The dramatic climatic changes that occurred in the area since the mid-Miocene seem to have played a great role in the further diversification of the genus.

111. BODY SIZE PATTERNS IN TERRESTRIAL ISOPODS

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Ecogeographical rules are among the oldest but still vivid research fields in biogeography. The majority of studies concerning the most commonly investigated rules are based on vertebrates. Nevertheless, invertebrates can provide useful insights in the shaping of such general patterns. Moreover, ectotherms that use some kind of behavioural or other indirect form of thermoregulation are expected to conform to temperature-related rules, such as Bergmann's. Herein, we use sex-specific body size data on some 600 species of terrestrial isopods worldwide in a search of global patterns, using latitude and climatic factors (based on temperature or on the combination of humidity and temperature) as predicting variables. Terrestrial isopods are behavioural thermoregulators and generally known to be constrained by humidity. We do find evidence for compliance to Bergmann's rule, with larger species generally found in higher latitudes. We also find some evidence for an inverted geographical version of Rensch's rule, since females exhibit greater body size variation in response to latitude. The patterns exhibited by terrestrial isopods are strongly influenced by the joint effect of precipitation and temperature.

112. GENETIC MONITORING OF THE RED DEER POPULATION (*CERVUS ELAPHUS*) OF MOUNTAIN PARNITHA

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Until the middle of the 19th century, the red deer (*Cervus elaphus*) was widespread in continental Greece with large populations mainly in North and Central Greece and in Euboia areas. However, in recent years, its populations have suffered a major range decline in our country with the exception of Parnitha's National Park where, due to the protected status of the area and the lack of natural enemies, the red deer population has increased significantly. However, little information is available on the origins and the genetic structure of this population. For this reason, non invasive methods were used to collect biological material from 80 samples. The analysis of the mitochondrial DNA control region indicated the existence of three discrete mitochondrial haplotypes. Comparison with similar European studies supported the Balkan origin of this population while there was no evidence of central European haplotypes present on mountain Parnitha. Microsatellite analysis of 14 loci revealed high heterozygosity values which are comparable to other European populations. The effect of landscape features on the gene flow of red deer within mountain Parnitha is also investigated.

113. THE PUZZLING PHYLOGEOGRAPHIC HISTORY OF THE EUROPEAN ANCHOVY (*ENGRAULIS ENCRASICOLUS*)

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The phylogeographic pattern of the European anchovy is characterized by the presence of two mitochondrial phylogenetic clades, A and B, with disjointed frequency distributions in different marine basins: clade A predominates in the Black Sea and the North Aegean, as well as in the Atlantic from Portugal to Senegal, and clade B in most of the Mediterranean, the north-east Atlantic north of Portugal and the Benguela upwelling system. Nevertheless, these findings, based on mitochondrial DNA RFLP data, have not been sufficient to elucidate the phylogeographic history of anchovy. In this study, we analyzed samples that represent almost the entire distribution range of anchovy, including samples from areas that have not previously been analyzed. The samples were sequenced for two mitochondrial genes (cytb and control region) and some of them were also genotyped for 10 microsatellite loci. The sequencing data revealed a subtler phylogenetic structure for clade B than previously recognized, with 4 subclades that display heterogeneous geographical distributions. The estimated ages of these clades suggest a link to the Milankovitch cycles. The genetic structure revealed by the microsatellite data was generally congruent with the mitochondrial DNA structure, with the exception of the Black Sea. The latter, although dominated by clade A, like some areas of the Atlantic, was genetically more similar to the Mediterranean at the nuclear level. From phylogeographic, demographic and other analyses of the genetic data, as well as paleoclimatic evidence, we attempt to elucidate the phylogeographic history of anchovy by identifying the potential refugia and expansion routes that shaped the present genetic structure of anchovy.

114. TWELVE YEARS AFTER THE INTRODUCTION OF THE CRAB *PERCNON GIBBESI* (H. MILNE EDWARDS, 1853) IN THE MEDITERRANEAN: CURRENT DISTRIBUTION AND INVASION RATES

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The distribution of the alien crab *Percnon gibbesi* in the Mediterranean Sea was assessed using new data from four independent surveys in Albania, Montenegro, Tunisia, Libya, and Crete (Greece), other personal observations of the authors and a thorough compilation of existing information. The species is reported herein for the first time from Albania, Algeria, Cyprus, Israel, and Lebanon. *P. gibbesi* rapidly increased its spatial distribution in the Mediterranean after its introduction in 1999. At present, twelve years after its introduction, *P. gibbesi* is established in most Mediterranean coasts, especially in middle latitudes. It is absent from the Adriatic Sea (except from its southern limit in the Albanian part of the strait of Otranto), the Ligurian Sea, the Corsica Island, and the northern Aegean Sea, possibly because of the low winter temperatures in these areas. In the North African coasts, *P. gibbesi* has not yet been observed in Egypt, Morocco and Gibraltar. After its initial introduction, its spread in the Mediterranean basin seems to be primarily by natural dispersal via larval transport by currents. The invasion rate of *P. gibbesi* was assessed in the Kaş – Kekova Marine Protected Area in southern Turkey, based on a time series of monitoring data from 2002 to 2010. Its occupancy reached 23% (probability of presence in 500-m length of coastline) within four years from its first sighting. Its abundance increased exponentially with an intrinsic rate of increase $r = 0.79$, corresponding to more than doubling of its population each year.

115. PATTERNS OF BETA DIVERSITY AND BIOGEOGRAPHIC REGIONALIZATION IN EUROPE: WHAT DRIVES SPECIES TURNOVER AND HOW UNIQUE ARE THE SPECIES-RICH AREAS IN THE SOUTH?

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Within the EU FP7 SCALES project we studied patterns of beta-diversity in various taxa across Europe and across various spatial scales. We used high-quality gridded datasets to evaluate the effects of the distance between grid cells on species turnover (beta diversity; measured as Beta-sim index) and partitioned this effect into climatic, habitat and pure spatial differentiation. We also performed a cluster analysis based on the values of species turnover between all grid cells. We found that the main driver of beta diversity at the pan-European scale is geographic distance, with distinctly lesser contribution of climatic and land-cover dissimilarities. We also found that, in the north, European biota forms few geographically large and coherent clusters of similar species composition. However, the further we move down to the south, the clusters become smaller, more numerous and diversified. We point out the important role which dispersal limitations could have played in shaping the patterns of beta diversity and uniqueness of the south-European areas.

116. AFRICAN ADDERS AND AFROMONTANE ISLAND PHYLOGEOGRAPHY: THE GREAT ESCARPMENT AND CAPE FOLD MOUNTAINS AS A SPECIATION HOT-BED FOR DWARF BITIS (SERPENTES: VIPERIDAE)

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Stretching 5000 km around the perimeter of southern Africa, the Great Escarpment (GE) is the world's third longest mountain range, and to the south the nearby Cape Fold Mountains (CFM) form an integral feature of the Cape Floristic Region global biodiversity hotspot. Several dwarf members of the adder genus *Bitis* are endemic to these mountains, occurring as a fragmentary series of 'island' populations. We illuminate the contentious systematics of these snakes and investigate their biogeographic history using DNA sequences from two mitochondrial and two rapidly-evolving nuclear genes. Results indicate that montane populations form two non-sister species complexes. The *Bitis atropos* complex comprises six basal evolutionary lineages consistent with geographic distribution, diversifying between 5.0 and 0.6 Ma in a northeast to southwest direction. The *Bitis rubida-inornata-albanica* complex comprises four such lineages radiating first southwards then west to east, between 1.0 and 0.4 Ma. Many of these lineages represent cryptic species. Flux of montane habitats with tectonic uplift in the late Miocene and climatic oscillations in the Pleistocene have probably driven adder speciation by both vicariance and dispersal. Thus, the GE and CFM have been and will likely remain a speciation hot-bed for dwarf *Bitis* and co-distributed organisms.

117. NO-ANALOG PREDICTIONS OF BUTTERFLY SPECIES RESPONSES TO GLOBAL CHANGE

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Climate and land use changes have elicited widespread biological responses and are poised to accelerate extinction rates. Predicting how species will respond to the challenges posed by global change is likely to be a necessary component in strategies intended to minimize negative outcomes. Considerable effort has focused on the development of species distribution models to predict future responses to anticipated climate changes, although these models are known to be susceptible to an array of errors. Here, we test whether historical calibration of species distribution models can influence their predictions regarding how species are affected by climate change in particular. Using an extensive assembly of 20th century butterfly observations from Canada, which covers an extensive area in which anthropogenic climate change began relatively early, spatial models linking each species observation against its contemporary environment was used to project changes in spatial distribution through the recent past. It is clear that the historical calibration of species' responses to observed, modern-day climate changes can reliably predict temporal shifts in the distribution of species: species have begun to shift in directions and extents predicted by models. These shifts include areas of apparent range collapse as well as range expansion and are not simply poleward. It is equally clear that some species have responded to the advent of non-analog climates in surprising ways, risking ecological extinction. Climate change impacts on species distributions are demonstrated quantitatively: model predictions fit direct species observations closely across space and through time. This historical calibration of species distribution models may assist in predicting species' future responses, but the advent of no-analog climates presents a dangerous risk that models will sometimes fail when projected into the future.

118. GENETIC STRUCTURE AND PHYLOGEOGRAPHY OF THE *GELIDIUM ELEGANS* (GELIDIALES, RHODOPHYTA) BASED ON THE MITOCHONDRIAL COX1 HAPLOTYPE

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Gelidiales are important marine resources for producing agar for food and bacterial growth media. Recently Korean companies produced high quality pulp from endofibers of the gelidioid species. *Gelidium elegans* Kützing, previously named as *G. amansii*, is the most common species in the Gelidiales in northeast Asia and is harvested for agar production in May in Korea. We collected more than 200 samples on the west and south coast of Jeju and the east coast in Korea from seven localities in Japan and four localities in China. We analyzed plastid *rbcL* and mitochondrial *cox1* genes in order to elucidate diversity and phylogeny of the species. Both data sets were congruent in topology. However, eight haplotypes of *rbcL* were found in 57 specimens, while 38 haplotypes of *cox1* occurred in 203 specimens. The same *cox1* haplotypes occurred in Korea, China and west of Japan. The haplotype diversity was 0.734 ± 0.031 and the nucleotide diversity was 0.00093 ± 0.00007 . It is interesting that western Korean populations had high haplotype diversity ($h=0.746 \pm 0.060$) and southern Korean populations had high nucleotide diversity ($\pi=0.00104 \pm 0.00013$). On-going analysis of the remaining specimens will give us a better understanding of the distribution pattern of *G. elegans*.

119. PHYLOGENY OF *DUSSIA* (LEGUMINOSAE-PAPILIONOIDEAE) ILLUMINATES THE AFFINITIES OF THE CHOCÓ AND THE INFLUENCE OF THE ANDEAN UPLIFT AND CLOSURE OF THE PANAMA ISTHMUS

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Dussia is a small, taxonomically complex, neotropical tree genus growing in rain forests spanning the Andes and throughout Central America. This distribution makes it a good paradigm taxon to address two key issues of neotropical biogeography: the influence of the orogeny of the Andean mountains and the closure of the Panamá Isthmus. Furthermore, with endemic species in the Chocó biogeographical region of north-west South America, *Dussia* is ideal to examine the relationships of the Chocó biogeographical region. This area of hyper-wet rain forest is isolated on the Pacific coast of South America by the Andes, has excessively high species richness and endemism, but has been poorly studied biogeographically. A phylogeny for *Dussia* species based on nuclear ribosomal ITS and chloroplast DNA sequences was dated using Bayesian approaches and demonstrated that: (i) the uplift of the Andean mountains created a biogeographical barrier to migration; (ii) migration between South America and Central America occurred before the closure of the Panamá Isthmus indicating that for *Dussia* the Pacific Ocean was less of a barrier than the Andes; (iii) the biogeographic affinities of *Dussia* species from the Chocó biogeographical region lie with Colombian Inter-Andean valleys and Central America.

120. PHYTOGEOGRAPHICAL RELATIONSHIPS AMONG MT PANACHAIKON AND THE NEIGHBORING MOUNTAINS OF PELOPONNESE AND STEREA ELLAS

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Mount Panachaikon is located in the north-western part of Peloponnese, Greece, east of the city of Patras. It is characterized by a complex relief, with several peaks, the highest reaching an altitude of 1926m. Mt. Panachaikon is also has a variety of geological substrates and soil types. The vascular flora comprises 610 taxa, 65 of which are Greek endemics. In this work we present information on life forms, chorological data and species habitats. The floristic affinities between Mt. Panachaikon and the neighboring mountains of Peloponnese (Erymanthos, Kyllini) and Sterea Ellas (Vardousia, Oiti, Tymfristos, Parnitha, Geraneia, Pateras) were examined using the Sørensen coefficient. The strongest phytogeographical relation is between Mt. Panachaikon and Mt. Erymanthos, followed by Mt. Kyllini, in the Peloponnese. As far as Sterea Ellas is concerned, Mt Panachaikon shows greater affinity to Mt. Vardousia and Mt. Tymfristos. Multivariate analysis techniques applied to endemic taxa were used to reveal floristic similarities between the areas involved, in order to identify centers of endemism. The largest number of Greek endemic species on all mountains examined is found above the forest zone (1500m), at steppe-grasslands. More specifically, regarding Mt. Panachaikon, steppe-grasslands host most of its Greek endemic species, followed by calcareous cliffs.

121. PHYTOGEOGRAPHICAL DISTRIBUTION PATTERNS OF THE METHANA PENINSULA FLORA

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The Methana peninsula, located in the northwestern part of the South Aegean Volcanic Arc in the Saronic Gulf, is the youngest peninsula in the region, aged ca. 0.9 m.y.a. It covers an area of ca. 58 km² with a rocky and hilly relief, the highest peak reaching an altitude of 740 m. The substrate is mainly volcanic, though the southern part of the peninsula consists of limestone, and some limestone outcrops are also present at the NW coast. The floristic composition of the Methana peninsula consists of 621 taxa, 38 of which are Greek endemics. In order to illuminate the phytogeographical affinities of the peninsula with other areas of Greece, we compared its flora with that of 20 other (ecological or actual) islands. Two of the above-mentioned islands lie in the Saronic Gulf and several others are scattered throughout the Aegean Sea, belonging to different phytogeographical areas. Results using Sorensen's coefficient show that Methana peninsula is more closely related with Serifos, an island belonging to the phytogeographical region of Kyklades. Three more islands from the same complex (Syros, Naxos, and Paros) seem to have strong phytogeographical affinities with the study area. It was expected that the Methana peninsula, which is part of the phytogeographical region of Peloponnese, would show higher floristic affinities with islands belonging to that region. On the contrary, islands like Poros, the nearest island to Methana, or Salamina, an island in close proximity to the study area, seem to be less related to Methana peninsula than the islands of the Kyklades. This contradicts Rechinger's line (the phytogeographical barrier between Kyklades and Peloponnese) which was believed to be solid, and may be partly explained by the similar climatic conditions prevailing in these areas.

122. DISENTANGLING LOCAL VERSUS REGIONAL CONTROLS OF β -DIVERSITY ALONG LATITUDINAL GRADIENTS

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One of the most striking patterns in ecology is that species richness declines systematically with increasing latitude, though our understanding of this gradient remains in flux. Differences in β -diversity, a measure of compositional turnover among samples, have been used to make inferences about possible mechanistic differences along gradients, including variation in range size, dispersal abilities, and the strength and form of various community assembly processes.

We show that tree diversity at α -, β -, and γ - scales increases along a latitudinal gradient towards the equator in large-scale plant survey dataset. However, using a simple simulation, we show that β -diversity is expected to increase monotonically with γ -diversity in the absence of any ecological process. Applying a simple null model that corrects for this relationship between β - and γ -diversity to the plant dataset, we find that there is higher β -diversity than expected at all latitudes, likely reflecting widespread intraspecific aggregation and nonrandom interspecific co-occurrence patterns. Critically, however, there is no trend in γ -corrected β -diversity with latitude, suggesting that any ecological processes that generate woody plant β -diversity do not vary in intensity across this gradient.

123. SPECIES-STABILITY AND GEOGRAPHIC VARIATION IN ECOLOGICAL PROPERTIES OF PARASITES

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The expression of any trait depends, on the one hand, on species-specific limits of variation and, on the other hand, on the external environment. Any population of any species is characterized by ecological properties such as abundance and niche breadth. However, these properties may vary greatly among populations of the same species. Consequently, a question arises: is the observed manifestation of an ecological trait a species attribute subjected to natural selection, or is it merely a reflection of the local effects exerted by a variety of both biotic and abiotic ecological factors? In this talk, we consider species-specific stability and spatial variation in abundance and host specificity (niche breadth) of two taxa of arthropod ectoparasites (fleas and mesostigmatid mites) exploiting small mammals. Using extensive data collected from more than 60 regions of the Palaearctic we show that, on the one hand, these properties represent genuine species attributes, but, on the other hand, they also parallel to some extent the responses of parasites to their local external environment. In addition, we discuss two geographic patterns of variation in parasite abundance and host specificity, namely the “abundance optimum” and latitudinal gradients, in light of our previous findings.

124. TOWARDS A QUANTITATIVE BIOGEOGRAPHIC REGIONALIZATION OF TERRESTRIAL VERTEBRATES

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Biogeographic regionalizations represent fundamental concepts in biogeography, and classifications of the world's biota into meaningful geographical units for analysis are central to many basic and applied questions in ecology, evolutionary biology, and conservation. First global biogeographic regionalizations have been proposed some 150 years ago by Sclater and Wallace based on qualitative evidence, but the lacking quantitative support has set constraints on their generality and utility and has led to ongoing debates about where to draw boundaries. In order to bridge this gap, we developed a methodological framework for species-level biogeographical regionalizations at global scales that takes advantage of the increasing availability of global species range maps, multivariate techniques, and computational power. We explore biogeographic relationships of three major groups of terrestrial vertebrates (amphibians, birds, mammals) covering a total of 19,269 species and define biogeographic regionalization using UPGMA cluster analyses. We observe great similarities among the primary biogeographic divisions across the three vertebrate classes. At higher smaller geographic scale, however, biogeographic associations are less congruent but for all groups mainly reflect geology (e.g. continents, subcontinents, mountain ranges, island groups). At lower hierarchical levels, biogeographic regions strongly reflect the distribution of major biomes within continents reflecting contemporary constraints on species distributions. Quantitative biogeographical regions exhibit both striking similarities and differences to the classic biogeographic divisions. We argue that quantitative methods applied to global-scale distribution range map data will likely offer opportunities for more rigorous inference in ecological and historical biogeography.

125. GENETIC CONSTITUTION OF MOUNTAIN SPECIES IN THE FRENCH MASSIF CENTRAL – GENERAL PATTERNS AND THE SITUATION OF *SOLDANELLA ALPINA* (PRIMULACEAE)

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High genetic diversity is generally regarded as one prerequisite for organisms to evolve and react well in relation to environmental changes. Given the pressure of global change phenomena on organisms populating (sub)alpine habitats, conservation plans might therefore ask for their genetic constitution. The French Massif Central (MC), although reaching only 1885m a.s.l. altitude (Puy de Sancy), represents an important mountainous region in-between the European Alps and the Pyrenees. Therefore, the present paper asks for the general biogeographical relationships of MC mountain plants and their genetic diversity with respect to neighbouring high mountain ranges. In addition, an isolated MC population of *Soldanella alpina*, the Alpine Snowbell, was analysed using 365 polymorphic AFLP fragments. This species shows three phylogroups with a strong among-region component (AMOVA: 33.17%) corresponding to the three mountain ranges analysed. This pattern fits with the biogeographical hypothesis of successive vicariance, i.e. a postglacial sequence of retreats into those mountain ranges. Given the high genetic diversity values observed in the MC *Soldanella*, this population is not only characterised by an independent postglacial history, but also indicates a high conservation priority.

126. LINKING ECOLOGICAL AND EVOLUTIONARY PROCESSES IN THE FORMATION OF TREE SPECIES DIVERSITY IN THE JAPANESE ARCHIPELAGO

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We examined the importance of in situ evolution, i.e., adaptive radiation, in shaping species diversity of coniferous, deciduous broad-leaved and evergreen broad-leaved trees in the Japanese Archipelago by relating the geographical patterns of phylogenetic beta diversity to historical barriers (Tsugaru and Tokara straits). The Japanese Archipelago that ranges from subtropical, temperate to hemiboreal zones provides a unique setting to examine the effects of biogeographical events on geographical patterns of the tree species diversity. The tree flora has been repeatedly fragmented due to eustasy and concurrent sea-level changes, and repeatedly coalesced through discrete colonisation windows due to landbridge connections by past climate changes. In this study, we used phylogenetic beta diversity of the tree floras to identify historical effects. For conifer and evergreen broad-leaved species, the dependencies of phylogenetic beta diversity on historical gaps and geographic distance were remarkably weak, in comparison with that of taxonomic beta diversity. This indicates that the northward expansions of conifer and evergreen broad-leaved species were limited by fragmentations during interglacial periods and that these species rapidly radiated in response to the reduction of land area within the same biogeographic regions.

127. QUANTITATIVE RECONSTRUCTION OF HOLOCENE CLIMATE ON SICILY

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Pollen records with evidence of vegetation change were not available until very recently from Sicily. New profiles provide evidence of pronounced vegetation changes during the Holocene, which are apparently the result of climatic and land-use changes. Reconstructing climate of the Mediterranean and in particular Sicily using pollen data is a challenge, for which the long human-impact history is a major reason. Trials with the modern analogue technique, often applied as standard procedure for quantitative climate reconstructions using pollen, yielded unexpected results. No-analogue situations could be identified as likely reason for this. As an alternative, a substantially different, relatively recently developed method has been applied. This method, termed ‘pdf method’, is a probabilistic indicator taxa approach which until now has been applied to central European cores. Characteristics of the method are that it is quite robust to anthropogenic vegetation changes, that the most climate-sensitive taxa have the strongest influence on the reconstruction and that a quantitative error estimation is provided. Here we present for the first time reconstructions of Mediterranean Holocene climate with this method. The quantitative reconstructions from the two records are in agreement with qualitative expectations derived from ecological interpretation.

128. FACTORS DETERMINING THE NORTHERN RANGE BOUNDARY OF A SPECIALIST MARINE LIMPET

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Understanding how species range boundaries are set is one of the most fundamental questions in biogeography. This area of research has received increased attention in recent years because it is also central to predicting species’ responses to future climate change. There is a critical need to understand what factors maintain current range boundaries and how these determinants may be altered in the face of climate change. We are testing whether the current northern range boundary of a specialist marine limpet *Lottia insessa*, found exclusively on the kelp *Egregia menziesii*, is constrained by (1) its physiological intolerance of the temperatures found beyond the range boundary, (2) the lack of suitable habitat (i.e., its host kelp), and/or (3) more frequent disturbances and local population extinctions beyond the range boundary. Data from field experiments and laboratory studies suggest that these three ecological factors may not be the primary determinants of this species’ range limit, and that dispersal barriers owing to oceanographic processes and long stretches of unsuitable sandy habitat may be the most important mechanism. We are developing a two-dimensional advection-diffusion model to address the dispersal barrier hypothesis, and to explore how climate change (warming temperatures and ocean acidification) may alter the dispersal potential and range boundary of this species.

129. CONSERVATION BIOGEOGRAPHY OF THE U.S.-MEXICO BORDER: A TRANSCONTINENTAL RISK ASSESSMENT OF BARRIERS TO ANIMAL DISPERSAL

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Humans have dramatically transformed landscapes along the U.S.-Mexico border. We aim to assess the risk of barriers that may significantly impede animal migrations within this ecologically sensitive region. We examined the intersection of current and possible future barriers along the border with the geographic ranges of 313 amphibian, reptile, and non-volant mammal species. We considered areas of intensive human land-use and ~600 km of pedestrian fence as current barriers along the border. We evaluated the impacts of two scenarios of dispersal barriers - continuation of existing and construction of new barriers - on species vulnerable to global and local extinction. Three border regions: California, Madrean archipelago, and Gulf coast, emerge as being of particular concern. These regions are characterized by high total species richness and high richness of species that: 1) have small sub-ranges resulting from barriers; 2) have large proportions of their border range occupied by barriers; 3) are near range edges; and 4) are listed as threatened. Forty-nine of these species were identified as most at risk from current barriers, species meriting further study to determine impacts of border dispersal barriers. New barriers would increase the number of species at risk, especially in the three identified regions, which should be prioritized for mitigation of the impacts of barriers.

130. NICHE AVAILABILITY IN SPACE AND TIME: MIGRATION IN SYLVIA WARBLERS

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The rapid development and increasing sophistication of species distribution modelling methods has sparked a renewed focus on the niche concept in ecology. Generally, the underlying environment and the niches quantified with species distribution modelling have been treated as static entities. However, in reality, the environmental conditions available to a particular species are spatially and temporally dynamic on a variety of scales (e.g. circadian, weather, seasons, climate change). Organisms have two basic options for coping with this variation in environmental conditions: they can track suitable conditions spatially or they can stay in one place and tolerate the change in occupied niche, i.e. their fundamental niche has to encompass the environmental variation. Migration is one fascinating example of the strategies organisms evolve to deal with spatially and temporally dynamic environments. We evaluate migratory behaviour in the bird genus *Sylvia* with the goal of increasing our understanding of the complexities of dynamic niches. *Sylvia* warblers vary greatly in their spatial response to changing conditions and include residents that endure a variety of environmental conditions to long-distance migrants. We explore how variation in spatial movement relates to characteristics of their breeding and wintering niches and to the availability of suitable environmental conditions across continents and seasons.

131. PLEISTOCENE CLIMATE AND PHYLOGENY PREDICT 21ST CENTURY CHANGES IN RATTLESNAKE DISTRIBUTIONS

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The global climate is changing, with mean annual temperature expected to increase anywhere from 1.1 to 6.4 °C by this century's end. Species must respond by tracking suitable habitat, adapting to the changing conditions, or becoming extinct. We combined current climate data, paleoclimate models, stable oxygen isotopes, species distribution models, and phylogenetic relationships to produce paleophylogeographic models through the last 320 ky of interglacial-glacial climate cycles. We predict that the centers of suitable habitat for eleven species of rattlesnake will shift on average 38.31-217.49 km in the next century and their areal extents will change by 133,783-799,963 km². We show that past non-anthropogenic climate change probably moved the centers of suitable habitat by an average of 34.93 km/°C of surface mean annual temperature and changed their areal extents by 121,591 km²/°C. The annual rate of displacement is likely to be 2 to 3 orders of magnitude greater over the next century (0.43-2.42 km/yr) than it has been on average for the past 320 ky (0.0023 km/yr). Our models suggest that adaptation has not played a substantial role in the strategies these species have used to cope with the changing climate. Our models illustrate the dramatic extent to which past global climate change has modified the distribution of species, and indicate that even more dramatic responses will soon be required for these species to escape extinction.

132. GENETIC PATTERNS ACROSS MULTIPLE INTRODUCTIONS OF THE GLOBALLY INVASIVE BROWN ALGA *COLPOMENIA PEREGRINA*

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The Asian brown alga *Colpomenia peregrina* is one of the world's most successful aquatic invaders, having established populations on every continent with temperate shores. Here we describe patterns of genetic diversity across both the native and introduced ranges of *C. peregrina*. The global data set includes a combination of mitochondrial DNA sequence data from two regions (cytochrome c oxidase subunit III; *cox3*, ATP synthase F0 subunit VI; *atp6*) to trace the invasive history of *C. peregrina*. High levels of genetic variation were detected, with 18 haplotypes present in the species' native range in Asia and 14 of all found in introduced populations. These invasive populations displayed a high level of geographical structuring of haplotypes. Combined phylogeographic and population genetic analyses clarify the global colonization history of *C. peregrina*, providing evidence of multiple invasions to Europe, secondary invasions to Atlantic North America. Successful *C. peregrina* invasions vary broadly in the degree to which they retain genetic diversity, although populations with the least variation typically derived from secondary invasions or from introductions that occurred more than 100 years ago.

133. DO SALT LAKE ISLAND ASSEMBLAGES CONFORM TO ISLAND BIOGEOGRAPHY PREDICTIONS?

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Island biogeography theory forms a powerful framework for understanding the patterns and processes influencing insular populations and biodiversity in general. Small islands, however, have been anomalous despite the relative simplicity of their biotic and abiotic characteristics. Habitat islands may also be less predictable because of their diffuse boundaries. In this study, we investigated whether the biotic assemblages of ephemeral salt lake islands in the Australian arid zone conform to island biogeography theory predictions. Specifically, we analysed whether the taxonomic richness of two types of biota – perennial vascular plants and ants – correlated with island area and isolation, or if the small island effect over-rides these parameters. Plant species, generic and family richness, and ant subfamily richness, were found to be significantly associated with island area but not influenced by island isolation. In contrast, ant morphospecies and generic richness correlated neither with island area nor isolation but with plant species richness. However, while plant richness was similar in island and mainland quadrats, ant taxa were more diverse in mainland sites. Overall, salt lakes represent a differential barrier to the dispersal of arid zone ant and plant species. The influence of island area as a direct or indirect predictor of taxonomic richness and the incidence of a small island effect depends on the taxon being investigated.

134. THE EVOLUTION OF THE FAUNA OF GREECE FROM THE PREHISTORIC TO THE BYZANTINE PERIOD

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The fauna of Greece has changed significantly during the past 25.000 years, on one hand because of the intense changes in environmental conditions and on other because of human disturbance. This study presents the evolution of the fauna as it appears from archaeological and anthropological excavations that have taken place in many parts of Greece. The data analyzed include only terrestrial and freshwater species. It is evident that the majority of finds include wild animals that are used as food or as worship items. It is interesting to note that some animals, such as the red deer, the fallow deer, the roe deer, the wild boar, the hare, the bear, the wolf and others, have a continuous presence in Greece. Some species have a continuous limited presence, such as the wild goat and some have disappeared in historical times, such as the lion or earlier such as the ibex. The changes in the fauna correlate well with changes in physical geography, climate, vegetation and human activities.

135. GLOBAL-SCALE PATTERNS AND PROCESSES OF FRESHWATER FISH BETA DIVERSITY

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Beta diversity is a crucial facet of biodiversity that has important implications for both fundamental and applied issues in ecology. Yet patterns and processes of beta diversity have received less attention on macroecological scales and the influence of history of place have never been explicitly considered in global-scale analyses of beta diversity. Here we explore a uniquely comprehensive database of freshwater fish species distributions. Specifically, we employ an additive partitioning framework to disentangle the contribution of spatial turnover and nestedness to beta diversity patterns in the global freshwater fish fauna. We expect that disentangling spatial turnover and nestedness patterns should permit strong inferences about the roles of historical vs. contemporary environmental factors in shaping present-day patterns of freshwater fish beta diversity. Based on our results, we argue that quantifying the relative roles of historical and ecological factors in explaining present-day patterns of beta diversity requires considering the different processes generating these patterns and not solely the overall level of beta diversity. This represents a crucial issue given the current debate on whether historical and evolutionary hypotheses can be tested with current species distributions. In addition, our study provides evidence that future conservation studies should disentangle spatial turnover and nestedness patterns as whether beta diversity patterns are caused by nestedness or turnover imply opposite conservation strategies.

136. CLIMATIC AND EVOLUTIONARY DRIVERS OF PHYLOGENETIC SIGNAL IN THE STRUCTURE OF ANT COMMUNITIES

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While examining the determinants of community structure, macroecologists tend to focus on the effects of climatic variation over broad geographic provinces often ignoring local factors. Alternatively, community ecologists tend to focus on the role of species interactions in a single locality or on a set of geographically clustered localities, often ignoring historical context. If combined, these approaches might prove to be powerful in identifying the key determinants of community structure and how they vary in space. Here, we examine how the phylogenetic structure (i.e. mean phylogenetic relatedness) of local ant communities varies along climatic gradients. In addition, we assess whether changing the definition of the source pool affects patterns of phylogenetic community structure. We conclude that considering various definitions of the source pool allows for disentangling the relative contribution of contemporary ecological and evolutionary processes in driving geographic variation in the phylogenetic structure of communities.

137. GEOGRAPHIC VARIATION IN CRANIAL MORPHOMETRICS OF THE COMMON HAMSTER (*CRICETUS CRICETUS*) IN GERMANY

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The common hamster was very common historically, but is now considered critically endangered in eight European countries. The major decline started between 1960 and 1970 and only scattered populations occur today in Germany. To explore the craniometric variability within and geographic differences between populations of *Cricetus cricetus* we studied samples from Thuringia, Saxony-Anhalt, Saxony, Brandenburg and Rhineland-Palatinate. Eighteen linear variables were measured on adult skulls. Principal Component Analysis was used to determine which variables contribute most to cranial morphometric variability. Subsequently, these variables were used in Discriminant Analysis to assess if geographic groups separate by cranial morphology. The sample from Rhineland-Palatinate was well separated from the others along factor 1, which mainly represents length of upper tooth row. The samples from Thuringia and Saxony-Anhalt were slightly separated along factor 2, which mainly represents mandible length and coronoid height. The specimens from Rhineland-Palatinate were larger for several cranial variables. A possible small western subspecies *C. s. canescens* has been discussed, but further studies are necessary to address its existence.

138. THE ROLES OF LONG-TERM CLIMATIC CHANGE AND GLACIAL REFUGIA IN THE BIOGEOGRAPHY OF THE *ABIES* GENUS (PINACEAE) IN THE MEDITERRANEAN BASIN

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The genus *Abies* exemplifies plant diversification related to long-term climatic, geological, and evolutionary changes. The Mediterranean firs contain nine species and one natural hybrid. *Abies* fossils from the western Mediterranean indicate a wide Tertiary circum-Mediterranean distribution of the *Abies* ancestor. Palaeogeographical data also suggest a single eastern Mediterranean Tertiary ancestor. Following the Miocene to Pliocene climate crisis and marine transgressions, the ancestor of the northern Mediterranean firs is hypothesized to have separated into two eastern groups, one on the Balkan Peninsula and the other in Asia Minor. However, land bridges may have permitted gene flow at times. A southward migration of *A. alba* to refugia areas, where older fir species would have remained isolated since the Miocene, could explain recent findings indicating that distant species that are more closely related than expected based on morphological classification. The *Abies* genus appears to have undergone significant morphological differentiation that does not necessarily imply reproductive isolation. That is, long-term Mediterranean Basin dryness along a SE to NW gradient may have caused an initial Miocene–Pliocene speciation sequence. Pleistocene glacial cycles probably forced migrations to occur, leading to repeated contact between fir species in glacial refugia.

139. CAN BIOCLIMATIC MAPS BE DRAWN FROM IPCC FORECASTS?

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Bioclimatic maps provide useful biogeographic information and they can add an extra value to the climatic ones. The IPCC climatic forecasts claim to be useful for environmental and biodiversity conservation politics. Bioclimatic maps produced with the IPCC forecast information illustrate in a geographically explicit manner the possible changes that will influence life on Earth. In this study, maps representing wet-dry climate gradients –ombrotype maps – have been drawn, based on the Atmosphere-Ocean General Circulation Model (AOGCM) CGCM2 and the special report on emission scenario (SRES) B2 for the periods 2011-2040, 2041-2070 and 2071-2100. The maps produced are compared among themselves as well as with the ombrotype map for Peninsular Spain and Balearic Islands that was published in 2008, based on information provided by 3400 weather stations.

140. BIOCLIMATIC PATTERNS FOR PLANTS: DOES THE SCALE MIND? VERY LOCAL ENDEMIC AND WIDELY DISTRIBUTED SPECIES

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A relationship between Bioclimatic Variables and geographic distribution of plant species in Spain is established. In ArcView, maps of Macrobioclimate, Bioclimate, Thermotypes, Ombrotypes and Isobioclimate can be overlaid on the distribution map of any plant species, and thus, it is possible to know the bioclimatic amplitude of the species, that is, its Bioclimatic Pattern. It is also possible to calculate the % of the potential bioclimatic amplitude, which is really occupied by the species. Bioclimatic Patterns of very local Alicante Province, Spain, endemics -such as *Teucrium carolipai* subsp. *carolipai*- and widely distributed species, -such as *Taxus baccata*, are compared and discussed.

141. FIRST EVIDENCE OF AN ANCIENT “INTERGLACIAL REFUGIUM” IN THE PYRENEAN REGION

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A refugium is generally understood as an area where temperate species survive cold periods, such as the Iberian, Italian or Balkan Peninsulas in Europe. Strictly speaking, this definition refers to what is known as a glacial refugium. However, there are various types of lesser-known refugia such as the interglacial refugium, which denotes a mountainous region at low latitudes, such as the Pyrenees, where species adapted to the cold survive during interglacial periods. The small-vertebrate association from the sequence of Cova Colomera, which is located on the southern face of the Pyrenees and covers the final cold spell of the Late Pleistocene and the beginnings of the temperate period in which we currently find ourselves (the Holocene), may constitute the first fossil evidence of such an interglacial refugium.

142. TESTING SCENARIOS OF INTRASPECIFIC DIVERGENCE *CYANUS TRIUMFETTII* USING APPROXIMATE BAYESIAN COMPUTATION

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It has become a paradigm in phylogeography that the population structure of widespread temperate plant species is determined by range shifts during the most recent Pleistocene climate oscillations. In fact, processes forming species genetic structure likely acted much earlier. We investigate *Cyanus triumfettii* (Asteraceae), an herbaceous plant broadly distributed in the southern European mountains with characteristics in between genuine mountain plants and widespread Submediterranean elements. Using intron sequence data from protein encoding nuclear genes we find as much as six evolutionary lineages and conduct coalescent simulations in an Approximate Bayesian Computation framework to evaluate different models of population divergence and jointly estimate demographic parameters. We test whether different lineages originated by vicariance or by colonization starting from a small bottleneck population. The best fit model suggests that the youngest population splits among Alp, Tatra and Balkan lineages had occurred approximately 200,000 years before present suggesting that the last glaciation has had only a minor influence. Regarding the origin of the European flora, the present study is among the first to infer complex patterns of intraspecific diversification on the basis of multiple nuclear sequences.

143. ANALYSIS OF SPATIAL POPULATION STRUCTURE IN BUFF-BREASTED SANDPIPERS (*TRYNGITES SUBRUFICOLLIS*) ACROSS ITS GLOBAL MIGRATORY ROUTE

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A historically abundant animal, the Buff-breasted Sandpiper (*Tryngites subruficollis*) is an example of a global migratory shorebird that has been declining since the late nineteenth century. The goal of this study was to understand the biogeography, site fidelity and patterns of gene flow of this species across its global distribution. To this end, we conducted a genetic survey of Buff-breasted Sandpiper populations at their Arctic breeding sites from 2006-2009 to infer genetic structure within and among Nearctic breeding grounds. An initial analysis of 3 polymorphic microsatellite loci developed for this species (n=94, K=4, using a Bayesian clustering approach) indicated that cryptic population structure was present despite finding no pattern of site fidelity or structure in capture and resight data in the breeding grounds. Using mitochondrial DNA (approx. 400 bp of cytochrome b and 400 bp of the control region), we examined phylogeographic structure across the breeding range to infer historical processes shaping genetic structure. Initial analyses of breeding site populations indicated substantial population structuring into haplogroups with no apparent correlation with sampling site or time. Future analyses will increase the number of polymorphic microsatellite loci and expand sampling sites to flyway and overwintering sites.

144. PHYLOGEOGRAPHY OF THE RAINFOREST-DWELLING PADEMELONS (*THYLOGALE*) IN NEW GUINEA

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Complex geological beginnings including progressive terrane accretion and recent orogeny are thought to have greatly influenced biodiversity in New Guinea. Glacial cycles of the Plio-Pleistocene period may have also influenced the current distribution of inter- and intra-specific genetic diversity. This is due to changes in habitat distribution and intermittent land-bridge connections with surrounding continental islands. Pademelons (*Thylogale*) are rainforest-dwelling macropods found in both the lowland and high montane forests of New Guinea. Therefore, current genetic structuring within and among pademelon species might be expected to reflect the biogeographic history of New Guinea. We used an extensive collection of museum specimens to sample representatives of the three *Thylogale* species from across New Guinea. Data from the mitochondrial control region and cytochrome b gene show two major clades corresponding to western and far eastern New Guinea. Genetic structuring within the clades is congruent with geographic region, but not with current morphological species designations. Low levels of genetic divergence among species may indicate either recent dispersal into new habitats, or, recent hybridisation due to changes in habitat distribution during the Pleistocene glacial cycles. In addition, it is hypothesised that two isolated populations of *T. calabyi* have evolved independently from lowland *T. brunii* to exploit the montane subalpine grasslands.

145. HISTORY OF TREE POPULATIONS IN THE CENTRAL MEDITERRANEAN REGION OVER THE LAST 1.5 MA

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In the last few years a number of long pollen records have been studied in Italy, enabling a reconstruction of the vegetation history during the last 1.5 Ma, which shows that the behaviour of tree populations is highly variable. A number of tree taxa have disappeared from the Italian territory (e.g. *Tsuga*, *Cedrus*, *Cathaya*, *Liquidambar*, *Parrotia*, *Carya*, *Pterocarya*). Their disappearance is spread out through time. The local extinctions of these taxa occurred generally later than in Italy than in the rest of central-western Europe. Many tree taxa show considerable stability in their geographical distribution, being permanently present in Italy since the beginning of the Quaternary. During the Quaternary no native tree genera were recorded in Italy that were absent in previous time periods. During the Middle Pleistocene Revolution (0.9-0.6 Ma) the Italian and Greek pollen records show a slow and progressive change from forests dominated by *Quercus*, *Liquidambar*, *Carya*, *Tsuga*, and *Picea* to forests dominated by *Quercus*, *Abies*, *Carpinus*, and *Fagus*. The importance of extending the observation of tree taxa behaviour to the time scale of the whole Quaternary is highlighted. This extension is necessary in order to explain the modern distribution of species and populations and to reach a better understanding of evolutionary processes.

146. MACROECOLOGY OF SOCIAL SPIDERS - ON THE LINK BETWEEN SOCIALITY AND NICHE WIDTH

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Social spiders occur in tropical and subtropical habitats worldwide. The convergent ecological niche these spiders occupy is shaped both by abiotic factors and biotic interactions. Across the spider phylogeny convergent evolution of life history traits such as elimination of pre-mating dispersal, regular inbreeding and female-biased sex-ratios have evolved multiple times independently. Permanent sociality invariably implies competition for resources, and limited prey availability to sustain groups has been hypothesized to restrict the social spiders' distribution ranges. To counter resource competition, cooperative prey capture should also allow social species to increase their dietary niche relative to solitary foragers. The genus *Stegodyphus* (Eresidae or family spiders) has 3 independently derived social species and 18 solitary congeners. They are distributed across the Mediterranean basin, African continent, Middle East and Southeast Asia. In this study we quantify continental-scale habitat niche of *Stegodyphus* spp. using species distribution modelling. Moreover, we determine the local-scale dietary niche of 2 social and 2 solitary species to assess if cooperative foraging in social spiders is linked to an increase in dietary niche. We show that social *Stegodyphus* occur in habitats with higher amount of rainfall than those of solitary congeners. Solitary species geographically overlap with social species, furthermore expanding their habitat range beyond the limits of social spiders. Comparing prey availability and dietary niche among one social and one solitary *Stegodyphus*, prey abundance in the social spiders' habitat was lower compared with the solitary species, however, the social species captured relatively larger prey and showed a wider dietary niche than the solitary species. We propose that sociality in spiders is associated with a narrower habitat niche, but broader dietary niche.

147. PHYLOGENETIC ANALYSIS OF A SOUTH ATLANTIC KELP: *LAMINARIA ABYSSALIS*

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The aim of this study is to analyze the phylogeny of Brazilian species of *Laminaria* (*L. abyssalis* and *L. brasiliensis*) and contribute to the discussion of the biogeography of kelps based on its molecular, morphological and ecological parameters. The study of two Brazilian *Laminaria* populations and their temperature habitat indicated that the studied populations are composed by just one *Laminaria* species: *L. abyssalis*. Furthermore, despite the fact that some morphological characters were usually used to discriminate different taxa of the order Laminariales, morphological varieties described as distinct species for Brazilian *Laminaria* were related to the upwelling frequency/intensity. The molecular analysis of plastidial, nuclear and mitochondrial genes confirmed not only the genus *Laminaria* for the Brazilian kelp, but its close phylogenetic relationship with *L. hyperborea* and *L. digitata*. Based on this analysis and latest hybridization experiments we can reinforce the hypothesis that *L. abyssalis* is a phylogenetic link between kelps of Northern and Southern Hemisphere and between the American and African continent. Its ancestor possibly migrated from the Northern Hemisphere Pacific through the Bering Strait, and crossed down from West Africa along African, then American coast during the Pleistocene.

148. ASSESSING INFLATED AND OBSCURED EFFECTS OF CLIMATE ON SPECIES DISTRIBUTION

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Mountain species are fast responders to global warming, so they are especially useful for studying the possible effect of climatic change on future species distribution. We obtained favourable areas for four mountain species in Spain (*Alytes dickhilleni*, *Vipera latasti*, *Aquila fasciata*, *Capra pyrenaica*). By using variation partitioning and weighting the effect of climate in relation to non-climatic factors we evaluated the relative contribution of climate in these favourable areas. We assessed the apparent and the pure effects of the climatic factor and then projected the models to the future. We used two Atmosphere-Ocean General Circulation Models (AOGCMs) and two special reports on emission scenarios (SRESs). We calculated the pure effect of the climatic factor (PCF), the pure non-climate factor (PNCF), the shared climatic factor (SCF) and the proportion of pure climatic factor in relation to whole climatic factor for each species and combination of AOGCM-SRES. We found that there are remarkable differences in the areas forecasted as favourable for a species if we consider the apparent climatic effect or the pure climatic effect on the favourability model projected to the future, because the apparent effect of the climatic factor can be either inflated or darkened by other factors.

149. DEVELOPING A SPATIAL INDEX FOR CONFLICT AREA IDENTIFICATION

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Over the last century, predator populations have suffered severe declines, which is partly due to direct persecution. Illegal use of poisoned baits has had dramatic effects on many predator species. Currently, the highest number of poisoned events in Spain has been recorded in Andalusia, an important hunting region and a biodiversity hotspot. In the present work, two raptor species were selected, i.e., the black vulture and the black kite, because they are the threatened raptor species most affected by poisoned baits in the study area. We chose other two species of carnivores: the red fox, the main target of predator control, and the grey wolf. All species and poisoned event distributions were modeled independently with a set of environmental variables applying a favourability function. Favourability models of the different predator species were overlaid with the poisoned event model, and potentially conflicting areas were extracted from that combination. In the literature, a conflict area is defined as the one with higher risk of population decline or extinction for a specific threat. Therefore, in our study they were considered to have a low favourability value for a predator species and high scores for the occurrence of poisoned events. The index could be useful as a prevention management tool because it focuses the attention on one the most vulnerable areas for the species.

150. PUTTING HYPOTHESIZED NATIVE-RANGE PHYLOGEOGRAPHIC PATTERNS OF *CACTOBLASTIS CACTORUM* TO THE TEST USING GENETIC, CLIMATIC, AND HOST SPECIES DATA

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Combining gene sequence data with present and historical environmental data is an approach that can be used to investigate hypothesized historical phylogeographic patterns. Such studies can be used to develop predictions of future distributions of invading species or distributional shifts in response to future environmental change. *Cactoblastis cactorum* is a cactophagous moth native to South America that now has known naturalized populations in Australia, South Africa, and North America. Previous research has shown that the non-native populations of this insect originated with exports from eastern Argentina. Genetic data from the native range demonstrated clear mitochondrial cytochrome oxidase I (COI) phylogroups in environmentally distinct geographic regions of northern Argentina. In the present research, we tested whether 1) nuclear and mitochondrial genomes provide a congruent history of phylogeography in the native range of Argentina, and 2) geography and demography of *C. cactorum* populations correlate with the distribution of available host species (*Opuntia* cacti), environment, or both. We tested these hypotheses using sequence data from one nuclear and two mitochondrial genes, current and historical environmental data modeled by WorldClim, and host plant information collected at each sample site.

151. CONCERTED VERSUS INDEPENDENT EVOLUTION AND THE SEARCH FOR MULTIPLE REFUGIA

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Phylogeographic structure and its underlying causes are not necessarily shared among community members, with important implications for using individual organisms as indicators for ecosystem evolution, such as the identification of forest refugia. We used over 1000 mitochondrial DNA (COI) sequences and newly developed coalescent phylogeography models to construct geo-spatial histories for five co-distributed New Zealand forest beetles. These methods identify patterns of historical dispersal and gene flow via ancestral state reconstruction. We also used ecological niche models to reconstruct the potential geographic distribution of each species during the Last Glacial Maximum (LGM). Results for all five species yielded a complex picture of temperate forest community evolution. Each shared some features of its LGM distribution or range expansion pathways with every other, but no general patterns were detected among all five. These results indicate that forest species retreated into and expanded out from the same refugia by a variety of routes, rather than travelling together as an intact forest community.

152. SPATIO-TEMPORAL PATTERNS IN DEMERSAL ELASMOBRANCHS FROM TRAWL SURVEYS IN THE EASTERN ENGLISH CHANNEL (1988–2008)

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Elasmobranchs have life-history characteristics that make them more vulnerable to fishing than many teleost fish. As commercial landings data are usually not sufficient for the monitoring and assessment of elasmobranchs, fisheries-independent data, geostatistics and Geographic Information Systems were used to investigate the spatio-temporal patterns of sharks (6 species), skates (9 species) and stingray in the eastern English Channel. Temporal trends in relative abundance and distributions of total-length frequencies were investigated using data collected over 21 yr from an annual survey using a Grande Ouverture Verticale (GOV) trawl. Temporal trends in relative abundance were examined qualitatively in relation to the reported conservation status for the various species. Most individuals captured for 7 of the species were immature. The GOV trawl was more efficient at sampling demersal sharks than batoids (skates and rays), especially small-sized batoids. Geostatistics were effectively used to explore, identify and quantify the spatial structure of the distributions of 13 species. The more abundant species displayed significantly larger patch diameters. Three shark species (*Scyliorhinus canicula*, *S. stellaris* and *Galeorhinus galeus*) were found to be spatially segregated by sex. The shark species tended to occur in the deeper waters of the area, while skates were found to be more coastal in their distribution.

153. TESTING OLD AND NEW METHODS IN HISTORICAL BIOGEOGRAPHY USING SIMULATION: THE ROLE OF EXTINCTION AND FOSSILS

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Historical biogeography has long been plagued by disputes over how best to estimate the geographical history of lineages. These disputes have sometimes been almost philosophical (e.g. the privileging of vicariance over dispersal), and despite the proliferation of new methods, virtually all methods ever proposed (ranging back to panbiogeography and before) are still current in that they are employed in recent literature. Despite the widespread use of simulations to test methods in phylogenetics, few attempts have been made to use simulations to test methods in historical biogeography. Here, a sophisticated simulation is developed that allows users to set many relevant parameters, including rates of range extension, range reduction, sympatric (within-region) and allopatric (between-region) speciation, and long-distance dispersal; additional parameters include regional carrying capacity (including whether or not approaching the carrying capacity decreases speciation, or increases extinction), maximum range size, and connectivity between regions. The simulated phylogeny, including all extinct lineages, can be sampled to discover “fossils”, either randomly, or biased by age and/or region. Given the same simulated datasets, the performance of various algorithms can be compared, including Fitch parsimony, DIVA, and Lagrange. In particular, the role of fossils is explored in simulations with realistic extinction rates (i.e., rates far above 0); results indicate that a substantial number of fossils must be included (5 or more) to significantly ameliorate the estimation problems caused by lineages not sampled in the Recent due to extinction. The difficulties involved with including fossils in phylogeny-based methods are discussed, as is the potential of a new historical biogeography method I have devised, named phylogenetic kriging, to deal with these problems.

154. GEOGRAPHIC VARIATIONS OF SUGAR MAPLE GERMINATION, MORTALITY, AND GROWTH

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If current temperature trends continue and increase as predicted by general circulation models, the persistence and migration of sugar maple (*Acer saccharum*) at its northern limit will become crucial to its continued existence in North America. Specifically, anthropogenic warming may affect germination success and growth of sugar maple. To evaluate this potential limitation, our study addressed whether sugar maple germination as well as subsequent growth and mortality rates showed evidence of geographic variation under current climatic conditions by means of a Common Garden experiment within the northern and central sugar maple range limit. We found that the germination of seeds from sugar maples' northern range limit were significantly reduced and their subsequent seedling mortality rates were significantly increased when grown at a more southerly latitude, within their central range limit. Local adaptation was also evident with respect to germination, survival, and growth. Ultimately, these results suggest that temperature may in fact be one of the environmental variables that limit the future establishment of sugar maple as climate changes, thereby expanding our understanding of how predicted anthropogenic climate change may affect the regeneration of sugar maple in the future.

155. RANGE-WIDE URBANIZATION EFFECTS ON CYPRESS (*TAXODIUM DISTICHUM*) WETLANDS

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The species range for cypress (*Taxodium distichum*) includes many of the United States' fastest growing cities. Urbanization fragments and disturbs natural ecosystems, including wetlands dominated by cypress ("cypress domes"). Using Orlando, Florida, USA as a case study, we evaluated the effects of urbanization on cypress dome number, size, and pattern across space and time. Cypress domes are distinguishable on color infrared photographs making landscape level analysis possible in Orlando from 1984 to 2004. Over 3,000 cypress domes were identified in 1984 and 895 were lost or degraded by 2004. Due to changed land use, many remaining cypress domes formerly surrounded by natural lands became urban, which caused urban cypress domes to become more spatially clustered. Cypress dome sizes became more homogeneous with the loss of small natural and agricultural domes and large urban domes. Urbanization, and alterations to the fire and hydrology regimes that accompany it, will likely cause reduced gene flow between cypress domes, decreased genetic diversity within cypress domes, lower recruitment of cypress, and reduced regional species diversity. Assuming range wide similarities, this study represents how urbanization could drive a common species to become rare.

156. CLIMATE SHAPES EPIPHYTIC BRYOPHYTE DIVERSITY IN THE EDGE OF THE MEDITERRANEAN

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Spatial variation in species richness is one of the most frequently studied patterns in macroecology. However, the relative importance of different factors affecting richness across scales and for some groups of small-sized organisms still remains unclear. We evaluated the relative importance of climate and the regional species pool in shaping epiphytic moss richness and abundance at the boundary between Atlantic and Mediterranean regions in the NW of Spain. Results show a strong correlation between climate and richness, a widely reported pattern, but also raise some interesting questions about changes in the significance of the variables influencing richness across scales, the effects of boundaries, the influence of competition and the relevance of the idiosyncratic characteristics of the group under study.

157. RANGE-WIDE LANDSCAPE GENETICS REVEAL HUMAN-AIDED INVASION PATTERNS

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Non-native species are often introduced into new regions by long-distance human-aided transport. Once established, an invasive species can rapidly spread by a combination of natural and human-aided dispersal to fill in their new range. We used a combined landscape- and traditional- population genetics approach to test predictions about dispersal patterns for the invasive disease vector, *Aedes albopictus* Skuse (Asian tiger mosquito) in the US. The Asian tiger mosquito was introduced from southeastern Asia to the US in 1985 and rapidly spread across 14° latitude to extend across most of the eastern US. Because of its rapid spread, many experts predicted it was travelling as dormant eggs and larvae in shipments of used tires and lucky bamboo. We evaluated this prediction by comparing the ability of least-cost highway distances (human-aided dispersal routes along high-volume highways) and straight-line distances (quasi-natural dispersal routes) to explain genetic distance among 26 US populations of *A. albopictus*. In the range core, highway distances explained significantly more genetic variation than straight-line distance alone. However, among range-edge populations and across all populations, isolation-by-distance was not detected using either distance measure. These results suggest that human-aided transport along highways is important to range-core populations, but other processes likely overwhelm isolation-by-distance patterns near the range edge.

158. THE EFFECTS OF LAND-USE CHANGE ON ARTHROPOD RICHNESS AND ABUNDANCE IN THE AZORES

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We study how endemic, native and introduced arthropod species richness, abundance, diversity and community composition vary between four different habitat types (native forest, exotic forest of *Cryptomeria japonica*, semi-natural pasture and intensive pasture) and how arthropod richness and abundance change with increasing distance from the native forest in adjacent habitat types in Santa Maria Island, the Azores. Arthropods were sampled in four 150 m long transects in each habitat type. Arthropods were identified to species level and classified as Azorean endemic, single-island endemic (SIE), native, or introduced. The native forest had the highest values for species richness of Azorean endemics, SIEs and natives; and also had highest values of Azorean endemic diversity (Fisher's alpha). In contrast, the intensive pasture had the lowest values for endemic and native species richness and diversity, but the highest values of total arthropod abundance and introduced species richness and diversity. Arthropod community composition was significantly different between the four habitat types. In the semi-natural pasture, the number of SIE species decreased with increasing distance from the native forest, and in the exotic forest the abundance of both Azorean endemics and SIEs decreased with increasing distance from the native forest. There is a gradient of decreasing arthropod richness and abundance from the native forest to the intensive pasture. Although this study demonstrates the important role of the native forest in arthropod conservation in the Azores, it also shows that unmanaged exotic forests have provided alternative habitat suitable for some native species of forest specialist arthropods, particularly saproxylic beetles.

159. THE ISLAND SYNDROME IN LIZARDS

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Insular vertebrates are often thought to evolve a predictable suit of characters that set them apart from mainland relatives (=“the island syndrome”). These include medium body size, few large offspring, a greater susceptibility for extinction and, in lizards, a more herbivorous diet. I used a dataset of all the world lizard species to determine whether insular endemics (n = 1694) and mainland species (n = 3872) differed systematically. Island endemic lizards are, indeed, herbivorous more often than their mainland counterparts; they lay smaller clutches and mature later (though the latter result is marginally non-significant). Their size, however, tends more towards the extremes than towards the medium. Furthermore, hatchling size and laying frequency of mainland and insular species (reproductive characteristics corrected for family and adult size) are similar. Thus productivity rates are lower on islands because of the differences in clutch size only. Body temperatures do not differ between island and mainland species, and the proportions of diurnal and nocturnal species are similar. A much greater proportion of the insular species that were evaluated by the IUCN are threatened with extinction than mainland species, but in terms of population trend estimates (declining, increasing or stable) island and mainland species do not differ. Island lizards thus show some, but not all, of the aspects of the island syndrome. The lack of avian and mammalian predation may be a crucial driving force promoting the observed differences.

160. WHY A HIGHLY FOREST-FIRE ADAPTED SPECIES HAS DISAPPEARED FROM AN ENVIRONMENT PRONE TO FOREST FIRES? THE CASE OF THE CANARY ISLANDS PINE

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The Canary Island pine (*Pinus canariensis*) is a paleoendemic species which is currently restricted to the Canary Islands but was distributed in the Mediterranean basin until at least 2 million years ago. After the closure of the Panama strait (2.5 My BP), which favored the emergence of the Mediterranean climate and an increased frequency of forest wildfires, the Canary Island pine disappeared from the Mediterranean and was replaced by several related pine species whose regeneration by seeds depend of forest fires, such as *P. pinaster* or *P. halepensis*. Although the Canary Island pine has characteristics that allow adults to survive a forest fire, recent studies show that its sexual regeneration is not especially adapted to fire, unlike the Mediterranean pine species mentioned. In addition, nowadays the species can grow in the climatic conditions of the Mediterranean basin. The question that arises is why the Canary Island pine disappeared from the Mediterranean? In addition to the changes that occurred after the Plio-Pleistocene climatic deterioration which displaced other Tertiary ecosystems, as the laurel forest, towards Macaronesia, the decline of this species may be related to a competitive disadvantage in the sexual regeneration compared to other Mediterranean pines.

161. PREDICTING BIRD-MEDIATED SPREAD OF INVASIVE PLANTS ACROSS NORTHEASTERN NORTH AMERICA

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As invasive plants continue to spread across the landscape, it's essential to develop general, mechanistic models that predict and explain their spread. Using a cellular automata framework, we develop general spread models incorporating three mechanisms – plant population growth, local bird dispersal and long distance dispersal – to predict broad scale spread patterns in heterogeneous landscapes. We apply the model to *Celastrus orbiculatus* (Oriental bittersweet), one of the most aggressive alien plant species spreading through eastern North America, with dispersal by *Sturnus vulgaris* (European starling). We find excellent quantitative agreement with independent, historical spread records over the last century that is critically linked to the geometry of heterogeneous landscapes and each of the explanatory mechanisms considered. Spread prior to 1960 was primarily driven by high growth rates in developed and agricultural landscapes while subsequent spread was mediated by expansion into deciduous and coniferous forest. Large, continuous patches of coniferous forests in the north appear to substantially impede invasion. The success of *C. orbiculatus* suggests troublesome predictions for the spread of many other invasive, fleshy-fruited plant species across northeastern North America. We conclude by discussing application of our modeling approach to the spread of other plant species with differing dispersal syndromes.

162. IN AND OUT OF THE SAHARA: A STUDY ON THE AGE AND BIOGEOGRAPHY OF THE SAHARA DESERT USING *STENODACTYLUS* (REPTILIA: GEKKOTA) AS A MODEL

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The Sahara, the main arid region in North Africa, is by far the biggest desert in the world, covering some nine million square kilometers. In spite of the harsh environment, it hosts rich endemic floras and faunas. This raises the question of how such biotas are gained and maintained, something that can be explored using reptiles, one of the commonest desert inhabitant. The geckos of the genus *Stenodactylus* Fitzinger, 1826, are one of the principal faunal components of the deserts of North Africa and Arabia. They are highly adapted to the arid conditions and, thus, constitute an excellent model for the study of the colonization and adaptation processes to this environment. In this study, a complete and calibrated molecular phylogeny of *Stenodactylus* is inferred for the first time, based on four molecular markers (2070bp). The analyses suggest that North Africa was invaded from Arabia during the Mid-Miocene, indicating a relatively old origin for the Sahara. Moreover, a back colonization from North Africa to Arabia is revealed by the data. Our results support the hypothesis that faunal exchange between Arabia and North Africa has played an important role in the biogeography of this area.

163. ASSOCIATIONS OF SHELL SCULPTURE, SIZE AND SHAPE WITH ENVIRONMENTAL GRADIENTS IN A ROCK-DWELLING LAND SNAIL

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Morphological adaptations in sculpture, size and shape are crucial for land snails that live in arid habitats. However, idiosyncratic and differential responses often result in obscure patterns. We examined, using geometric morphometrics and a phylogenetically controlled analysis, the hypotheses of association between: (i) shell traits (sculpture, size, and shape), and (ii) habitat characteristics (climate, geography, insularity), for 62 populations belonging to 26 species of the pulmonate genus *Albinaria*. Our results demonstrate a clear size and shape discrimination among the three sculpture morphotypes (smooth, semiribbed and ribbed), suggesting that morphological divergence is constrained by the association of shell properties concerning size, shape and ribbing. Ribbed shells tend to be lighter, taller, slimmer and with a smaller and narrower aperture than smooth ones. Phenotypic variability is also well associated with geographic and climatic gradients. Shells tend to be significantly smaller in northern latitudes and shells from islands are significantly larger than those from mainland. Shape variation is more complex and the role of climatic factors is more vague. This implies that a large part of the evolution of shell morphology in that genus can be attributed to selection by ecological and environmental factors, however differential adaptive responses to environmental pressures might result in inter-/intra-specific phenotypic shell variation, subject to further examination.

164. KEY PHYLOGEOGRAPHICAL INSIGHTS TO EXPLAIN THE DIVERSIFICATION OF THE MEDITERRANEAN FLORA

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The Mediterranean region is an outstanding biogeographical crossroad which results from a complex history and highly heterogeneous environmental factors. Within the Palearctic, the Mediterranean can be considered as a hotspot of plant evolutionary history where genetic lineages of different Tertiary origins were shaped by the Quaternary glacial and interglacial cycles. A review of the literature allows identification of congruent phylogeographical patterns for plants, focusing on the delimitation of centres of genetic diversity, migrations routes and genetic discontinuities. Furthermore, we discuss the key results of a recent meta-analysis of published population genetics papers, notably the congruent longitudinal phylogeographical patterns for plants, influenced by East-West recolonizations and clinal LGM climate. Life history traits, taxonomy and ecological requirements are sources of heterogeneity for this pattern. Then, we provide a particular focus on thermo-Mediterranean plants with our recent findings on the phylogeography of the genus *Myrtus*, one of the few cases of circum-Mediterranean plants to have been studied at the scale of its whole distribution. The Tertiary genus *Myrtus* bears witness to the evolutionary response of the flora to the Quaternary climatic oscillations. Our comprehensive sampling of the populations of *Myrtus communis* and the central-Saharan endemic *Myrtus nivellei* was analyzed using multimarker and genome-scan approaches to depict the counter-intuitive historical biogeography of this genus.

165. USING SPATIAL SIMULATION TO ANALYZE DYNAMIC INTERACTION BETWEEN BROWN HYENA PAIRS IN NORTHERN BOTSWANA

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Information on the frequency and duration of interactions among individuals in an animal population is vital to understanding mating and territorial behavior, resource use, as well as infectious disease epidemiology. Spatial interaction between individuals is typically estimated by calculating home range overlap ('static interaction' Doncaster 1990); however, this does not account for the possibility of temporal. 'Dynamic interaction' (Doncaster 1990) between two individuals provides information on possible attraction and repulsion of animals that are in the same area at the same time. Using modern equipment such as remote download GPS (global positioning systems) collars in concert with sophisticated spatial analysis techniques facilitated in a GIS, it is now possible to explore previously unknown aspects of the spatial ecology of many wildlife species. Dynamic interaction for an individual is defined as occurring when another individual is located within a defined distance, both spatio- (ex. 500 m.) and temporal (ex. 60 minutes). These interactions have been summarized using, for example, mean time between interactions and the interaction rates compared as a function of differences in sex, season, resource availability, and clan membership. However, none of these interaction metrics facilitates an understanding of whether these encounters occur more or less frequently than they would occur if the individuals were moving randomly across their range, suggesting evidence of attraction and avoidance respectively. This study examines the spatial and behavioral ecology of brown hyenas (*Hyaena brunnea*) in Northern Botswana using a novel technique based on spatial simulation (correlated random walks) and spatiotemporal analysis.

166. COMPARISON OF LATE HOLOCENE AND LAST INTERGLACIAL VEGETATION: IMPLICATIONS FOR IBERIAN BIOGEOGRAPHY

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The Iberian Peninsula contains a complex of bioclimatic divisions that serve as transitions between Mediterranean and Temperate Broadleaf biomes. The rough division between these biomes can be drawn at approximately 42°N spanning the peninsula's northern coast where key species of the Temperate Broadleaf Biome, such as beech (*Fagus sylvatica*), ash (*Fraxinus excelsior*), or oak (*Quercus petraea*) currently grow. Pollen evidence from a sediment core from Lagoa Clementina (39.61°N Lat; -9.02°W Long; 53 m Elev) provides evidence for a southerly distribution of *Fagus* into the middle-to-late Holocene, with a disappearance ca. 1900 cal yr BP. This region has experienced a long history of increasing anthropogenic activity, as well as a progressive climatic change towards drier and warmer conditions over the period of record. Understanding and identifying drivers of these changes is difficult because of the simultaneity of anthropogenic and climate changes. Here we compare the pollen sequence from Lagoa Clementina with a sequence from neighboring Praia Rei Cortico, which covers the later portion of the last interglacial (~105–125 ka BP), to partition out the various contributions and interactions between these drivers, and discuss the implications for present and future biogeography on the Atlantic coast.

167. DO THE OLDEST SUBFOSSIL INVERTEBRATES FROM SEDIMENTS COME FROM CAVES?

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Cave sediments preserve a broad range of proxies that can be used for past climate change reconstruction. Subfossil remains from cave sediments can give indications on sediments origin, conditions for deposition and paleoenvironment. Samples of suspended sediments from three caves were taken from Slovenian Dinaric karst. Few fragments of identifiable aquatic and terrestrial invertebrates were assigned to group or species level. Paleomagnetic properties of sediments, vertebrate fossils and invertebrate subfossils were used as proxies in an integrated study of cave sediments. The presence of the subfossils are explained in the frame of the paleoenvironmental and paleoclimatic context and are supporting the proposed hypotheses about time and condition for sediment deposition and paleogeographic evolution. The age of sediment deposition was established as Pliocene which makes these the oldest known subfossils in world's continental sediments.

168. HIGH LEVEL PHYLOGENETIC RELATIONSHIPS AND NET PRIMARY PRODUCTIVITY EXPLAIN MOST OF THE GLOBAL BIRD BODY SIZE GRADIENT

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The most common explanation for latitudinal gradients in the body size of endotherms has been Bergmann's rule, based on a heat conservation mechanism. However, phylogenetically conserved processes are known to affect traits, and body size in particular. We examine the extent to which the global bird body size gradient is influenced by higher level phylogenetic relationships using phylogenetic eigenvector regression (PVR), finding that about two thirds of the gradient can be explained by the phylogenetic structure at the family level. We also found that adaptive responses mixed with phylogenetic responses below the family level favor selection of larger sizes in less productive environments. Thus, across cold and warm environments, resistance to starvation probably plays an important role in bird body size gradients. However, there is also regional idiosyncrasy in the patterns, suggesting that there is no “one size fits all” explanation for globally extensive body size gradients.

169. TEMPORAL TURNOVER OF LOCAL BIOTAS: EFFECTS OF THE REGIONAL SPECIES POOL

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Although the spatial turnover of species (e.g., the species-area relationship) has been of longstanding interest, the temporal turnover of species has received little attention until recently. Spatial turnover in species composition tends to increase with regional richness, but the same may not be true for temporal turnover. In fact, several studies have found seemingly contradictory results that temporal turnover may increase or decrease with regional diversity and latitude. These observed contradictions, however, may be due to different interpretations of the theoretical underpinnings of temporal turnover. Two levels of turnover are generated from island biogeography: instantaneous and absolute turnover. If immigration rate is more affected by species pool size than the extinction rate, absolute turnover increases with species pool size. Instantaneous turnover, however, is a function of the difference between regional and local richness and can diverge from instantaneous turnover, even yielding opposite patterns. Recognizing these different types of turnover helps to reconcile previous results and emphasizes that the way in which turnover is measured can qualitatively affect one's conclusions.

170. THE PAST DISTRIBUTION OF *PINUS NIGRA* ARNOLD IN NORTHERN IBERIA. CONTRIBUTION FROM ITS MACROREMAINS

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The presence of *Pinus nigra* in central Spain, where its natural populations are very rare, has led to different interpretations of the current vegetation dynamics. Complementary to the available palynological evidence, macroremains provide local information of high taxonomic resolution that helps to reconstruct the palaeobiogeography of a given species. Here we present new macrofossil data from Tubilla del Lago, a small palaeolake located at the eastern part of the northern Iberian Meseta. We identified 17 wood samples and 71 cones on the basis of their wood anatomy and morphology, respectively. Some of the fossil samples were radiocarbon dated (~4.230-3210 years cal BP). The results demonstrate the Holocene presence of *P. nigra* in the study area, where it is currently extinct. This evidence, together with other published palaeobotanical studies, indicates that the forests dominated by *P. nigra* must have had a larger importance on the landscape prior to the anthropogenic influence on the northern Iberian Meseta.

171. HIGH-RESOLUTION HOLOCENE RECORDS OF VEGETATION CHANGE AND DISTURBANCE FROM HUMAN, WILDFIRE AND SPRUCE BEETLE ON THE SUBALPINE RANGES OF THE CENTRAL AND SOUTHERN UTAH, USA

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Wildfire and bark beetles (*Dendroctonus*) are important disturbance agents in conifer-dominated landscapes in western North America. This research provides new insights into the ecology and climate-forcing mechanisms of disturbances in subalpine spruce/fir forests of the Rocky Mountains and Great Basin. Holocene lake sediment records retrieved from 3000+ meters above sea level on the Wasatch, Markagunt and Aquarius Plateaus in Utah suggest that spruce beetle (*D. rufipennis*) outbreaks have pronounced impacts on vegetation communities as recorded by varying pollen accumulation rates and recur at multi-centennial timescales. The mean fire return interval for stand-replacing fire events are similarly long, ranging between 300-500 years. These data suggest that little interaction exists between bark beetle outbreaks and antecedent wildfire, supporting tree-ring studies conducted elsewhere in the region. Our records also demonstrate that forest composition is important in disturbance ecology, particularly when considered over longer timescales. As these ecosystems evolved from the relatively cool temperatures of the terminal Pleistocene / early Holocene to the relatively warm middle Holocene, a distinct transition occurred from spruce parkland to closed-canopy spruce/fir forests. In some locations, the middle Holocene is characterized by increased occurrence of fire and spruce beetle disturbance, probably in response to greater fuel continuity and suitable host availability. At the southerly location in the study area (Markagunt Plateau) stand density also increases, though fire activity is reduced, probably due to elevated summer precipitation from an invigorated North American Monsoon and ENSO. The 20th century portion of these records shows a general absence of fire and the most significant spruce beetle outbreaks observed over the Holocene. The intensity of these recent spruce beetle outbreaks are likely associated with anthropogenic modifications to the subalpine landscape during the historic period, including logging, ungulate grazing, and fire suppression.

172. PHYLOGENY AND BIOGEOGRAPHY OF RICINULEI

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Very little has been published about the interrelationships of the ca. 60 species of Ricinulei (Arachnida). Here we present a molecular data set based on multiple markers for the entire distribution range of the group to generate the first molecular phylogeny of Ricinulei in order to test the monophyly of the three genera within the family Ricinodidae, Ricinoides in West Africa, and *Cryptocellus* – *Pseudocellus* in the Neotropical region. We use this phylogeny to discuss biogeographic aspects of this group of arachnids with low vagility and compare it to other studies on groups that overlap with Ricinulei in their distribution range.

173. BIOGEOGRAPHY AND BIODIVERSITY OF CACTI

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The Cactaceae is the second largest family of succulent plants with 1,433 species and is a characteristic element of the dry vegetation of the New World (Hunt 2006). However, virtually the only hypotheses concerning the biogeography and evolutionary history of the family date back to the 1940s. Here, we present biogeographical and macroecological analyses of the diversity patterns of this plant family. The three main centres of species richness are north-eastern Mexico, the eastern Andes of Bolivia and Argentina and south-eastern Brazil – each with different taxonomic groups dominating. Centres of species-richness and genus-richness do not necessarily coincide. We analyse the diversity patterns of taxonomical vs. ecological subsets of species and the role of current environment and evolutionary history on diversity patterns in these centres. Current environmental conditions do not explain patterns such as the divergent diversity patterns of the two main groups of epiphytic cacti. Due to small distribution ranges many cactus species are not covered by existing protected areas. We present a gap analysis identifying the important priority sites for the conservation of cacti.

174. COMPARING BIOGEOGRAPHICAL, SPATIAL, AND ENVIRONMENTAL INFLUENCES ON PATTERNS OF β -DIVERSITY AMONG TEMPERATE AND TROPICAL FORESTS

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A fundamental question at the interface of ecology, evolution, and biogeography is whether the mechanisms of community assembly, and their relative importance, vary across temperate and tropical ecosystems. Observed variation in species composition among communities (β -diversity) is often higher at tropical relative to temperate latitudes. This pattern can reflect at least three non-mutually exclusive mechanisms. First, larger species pools (γ -diversity) in the tropics can increase β -diversity through sampling effects, where higher γ -diversity causes greater regional “spillover” of species among local communities. Second, in high-diversity regions with many rare species, dispersal limitation and priority effects can increase β -diversity. Third, higher β -diversity in the tropics may reflect deterministic processes such as niche partitioning along environmental gradients. Here, we evaluate these hypotheses by comparing spatial patterns of β -diversity between temperate and tropical forests that span a 10-fold difference in γ -diversity. We compare β -diversity of woody plant species between the Ozark Ecoregion of Missouri, USA (γ -diversity = 50 species) and Madidi National Park, Bolivia (γ -diversity = 600 species). In each region, we measured all stems >2.5-cm DBH in 40, 0.1-ha plots spanning similar elevational, geographic, and environmental gradients. Preliminary null-model analyses, based on random sampling from the species pool, suggest that sampling effects account for some, but not all, differences in β -diversity between regions. Using variance-partitioning methods, we extend this analysis to examine the extent to which spatial and environmental processes explain β -diversity. We conclude by highlighting how our comparative approach provides insights into ecological and evolutionary mechanisms influencing community assembly along biodiversity gradients.

175. SPATIAL AUTOCORRELATION IN PREDICTORS REDUCES THE IMPACT OF POSITIONAL UNCERTAINTY IN OCCURRENCE DATA ON SPECIES DISTRIBUTION MODELING

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In this study the impact of positional uncertainty in species occurrences on the prediction of seven commonly used species distribution models (SDMs), and its interaction with spatial autocorrelation in predictors has been investigated. A series of artificial datasets covering 155 scenarios including different combination of five positional uncertainty scenarios and 31 spatial autocorrelation scenarios were simulated. Each dataset included two environmental gradients (predictor variables) and one species occurrence sample point (response variable). Seven modelling algorithms were selected including Generalized Linear Model (GLM), Generalized Additive Models (GAM), Boosted Regression Trees (BRT), Multivariate Adaptive Regression Spline (MARS), Random Forest (RF), Genetic Algorithm for Rule-set Production (GARP), and Maximum Entropy (MaxEnt) to develop SDMs. A probabilistic approach was employed to model and simulate 5 levels of error in the species locations. To analyze the propagation of positional uncertainty, Monte Carlo (MC) simulation was applied to each scenario for each SDM. The models were evaluated for performance using simulated independent test data and two statistics of Cohen's Kappa and the area under the receiver operating characteristic curve (AUC). This was summarized in graphs and tables. All SDMs were influenced by positional uncertainty, with varying ranges of decreasing performance due to different degrees of spatial autocorrelation in predictors and the levels of error in sample locations. It was shown that, when the error in location was less than or equal to the range of spatial autocorrelation in the predictors, the models were less impacted by error and, consequently, had smaller decreases in their performance. Models where sample points had error in location larger than the range of spatial autocorrelation in predictors performed poorly in all scenarios. Our analyses suggest that the potential impact of positional uncertainty in species occurrences on predictions of SDMs can be understood by comparing it with the spatial autocorrelation range in predictor variables.

176. BIOGEOGRAPHIC FACTORS IN MONKEYPOX VIRUS DIFFERENTIATION

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Monkeypox is a zoonotic disease caused by a member of the *Orthopoxvirus* genus and its clinical manifestation in humans is very similar to that of smallpox. Although its natural reservoir host has not been identified, this virus can infect a wide variety of animal species. Based on epidemiological and genetic evidence, monkeypox is divided into West African and Central African clades. In this work, we use ecological niche models to reconstruct the geographic distribution of this virus in the past and identify possible factors contributing to its differentiation. Ecological niche models were based on the recorded cases of monkeypox in humans; these models were then projected into climatic conditions 21,000 years ago and compared to phylogenetic and geographic features to reconstruct the recent differentiation between these clades. Our results suggest that, during the Last Glacial Maximum, monkeypox had a restricted refugial distribution from which a possible expansion into its present-day geographic range occurred as climate became warmer. Sea level rise and the physical barrier represented by the Cameroon highlands are factors that could have contributed to the differentiation of the two monkeypox clades. Additional studies on suspected monkeypox reservoir host animals could provide insight about the species involved in maintaining the natural cycle of this virus.

177. COMPLEX RESPONSES TO CLIMATE AND LAND-USE CHANGES IN A COUPLED DEMOGRAPHIC AND BIOCLIMATIC ENVELOPE MODEL

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Recently correlative bioclimatic envelope models (BEM) have been linked to demographic models. The combination of two models leads to more detailed mechanistic models to disentangle the possible future responses to a changing environment. A model incorporating scenarios of climate and land-use change was created for Tropical Andes Hotspot tree *Polylepis pepeii* (Rosaceae, VU-IUCN). Current population size was estimated from detailed cover maps of single-species patches. Distribution and climate data were used to map future climatic suitability. Tree functional traits and dispersal patterns were used to create demographic models for the land-use change scenarios: fire, grazing and wood-cutting. Future population sizes were simulated by linking the BEM and demographic models. We obtained extinction probabilities under combinations of changes in climatic suitability and disturbances to population processes. Both climate and land-use changes were found to increase extinction probabilities, with complex interactions identified. By including the actual population size and effects of human impacts, additional realism was added to linked BEM-demographic models. The modelling method can be used to investigate other species threatened by multiple factors. Results are useful in the design of management plans to mitigate the effects of climate and land-use changes.

178. DOWNSCALING SPECIES ATLAS DATA USING EXPERT-SYSTEM

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A noticeable amount of knowledge, either in the form of literature or expert's opinion, is often available at local scales, whereas it has not been addressed adequately in species distribution modeling (SDM). In this presentation, incorporation of existing knowledge into SDMs is outlined by enhancing the sampling scheme from coarse resolution atlas to yield more accurate predication at a finer resolution. A coarse-resolution distribution map of *Aquila fasciata* (Short-toed Eagle) in southern Spain, was obtained from the Atlas of breeding birds. Bayesian Theorem was used to generate an "expert-enhanced" sampling scheme based on existing knowledge in the literature. The maximum entropy approach was employed to predict distribution maps using two treatments: control, where models were calibrated with conventional random sampling species data from the atlas, and expert, where species sampling data were enhanced by the expert system. Four categories of environmental explanatory variables, topographic, bioclimatic, biologic, and anthropogenic were served into Maxent. Independent breeding territories were used to evaluate the predictive performance of models. Serving the expert-enhanced sampling scheme into SDM, prediction accuracy improved significantly. Existing knowledge may prove useful to enhance classical random sampling into more reliable sampling scheme in downscaling from coarse resolution species distribution atlases to finer suitability prediction maps; however, the usefulness of this approach may be limited to well-known species.

179. RESILIENCE OF WESTERN GHATS FOREST TO 7000 YEARS OF ENVIRONMENTAL CHANGE

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There is increasing recognition of the need for conservation beyond formally protected areas. However, conservation management in these regions requires an understanding of long-term landscape dynamics. One key question that needs to be answered is how resilient are such landscapes to anthropogenic land use changes. Here we present 7000-year palaeoecological reconstruction of a mid-elevation Western Ghats landscape which is currently under coffee cultivation. We computed palynological richness, turnover and rate of change of pollen taxa over this time period. Our results indicate that the vegetation at this site has remained remarkably resilient throughout the last 7000 years despite changes in climate and land use. This suggests that despite these changes the landscape retained its semi-evergreen species composition and possibly retained open woodland with fern, grass and sedge understorey. Such semi-open landscape structure is similar to the present-day agroforestry systems in this region, where coffee is grown under shade of native trees. Based on the 7000-year reconstruction, we suggest that maintenance of native tree cover in this landscape is crucial to prevent future loss of forest biodiversity in the Western Ghats.

180. CLIMATE PREDICTORS OF LATE QUATERNARY EXTINCTIONS

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Between 50,000 and 3,000 years before present (BP) 65% of mammal genera weighing over 44 kg went extinct, together with a lower proportion of small mammals. Why species went extinct in such large numbers is hotly debated. One of the arguments proposes that climate changes underlie Late Quaternary extinctions, but global quantitative evidence for this hypothesis is still lacking. We test the potential role of global climate change on the extinction of mammals during the Late Quaternary. Our results suggest that continents with the highest climate footprint values, in other words, with climate changes of greater magnitudes during the Late Quaternary, witnessed more extinctions than continents with lower climate footprint values, with the exception of South America. Our results are consistent across species with different body masses, reinforcing the view that past climate changes contributed to global extinctions. Our model outputs, the climate change footprint dataset, provide a new research venue to test hypotheses about biodiversity dynamics during the Late Quaternary from the genetic to the species richness level.

181. LIMITED POSTGLACIAL MIGRATION SUPPLEMENTS CLIMATE IN DETERMINING EUROPEAN PLANT SPECIES RANGES

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The influence of dispersal limitation on geographic distributions within temperate/boreal regions remains controversial. Considering the dramatic impacts of the Ice Age in Europe, species might not have tracked climate changes through time and, as a consequence, have present-day ranges that are not in equilibrium with climate. For 1,016 European plant species, we assessed the relative importance of contemporary climate and limited postglacial migration in determining species ranges using regression modelling and explanatory variables representing climate and a novel species-specific hindcasting-based measure of accessibility to postglacial colonization. Climate was of primary importance in determining species ranges, but postglacial colonization also constrained the ranges of >50% of the species, particularly those with limited long-distance dispersal ability, seed plants compared to ferns, and small-range species in Southern Europe. Our results suggest that the many small-range species in Southern Europe are particularly unlikely to successfully track anticipated 21st century climate changes.

182. MULTISCALE ASSESSMENT OF BETA DIVERSITY OF MEXICAN TERRESTRIAL VERTEBRATES

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Beta-diversity has frequently been associated with environmental heterogeneity. Notwithstanding there is an increasing interest in searching the relationships of β -diversity with different aspects of heterogeneity such relationship remains unclear. Our objective is to evaluate the effect of different surrogates of environmental heterogeneity on β -diversity identifying the most important environmental heterogeneity variable at different scales. We measured β -diversity using the multiplicative formula proposed by Whittaker (1960) at five different scales. We calculated surrogates of heterogeneity with the ranges and coefficient of variation from temperature, precipitation, and elevation, as well as diversity of soils and vegetation. We performed GLMs to test the response of β -diversity to those heterogeneity surrogates at different scales. We used range distribution models of 2523 species of Mexican terrestrial vertebrates; each group was analysed separately. In the models significant variables differed across scale and taxa. A tendency of obtaining higher significant variables resulted at the finer resolution. At that scale precipitation and elevation were significant for beta diversity of all the taxonomic groups. Precipitation resulted significantly at all the scales in amphibians and mammal meanwhile elevation resulted significantly for reptiles. The comparisons of the heterogeneity surrogates at different scales represent an advance in the understanding of the processes behind the spatial patterns of beta diversity.

183. CLIMATIC NICHE CONSERVATISM AND THE MACROEVOLUTIONARY DYNAMICS IN SPECIES' RANGE BOUNDARIES: CONGRUENCE ACROSS MAMMALS AND AMPHIBIANS GLOBALLY

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Understanding the global distribution of biodiversity has long been a major challenge in biogeography. Phylogenetic niche conservatism, under which lineages retain their ancestral niches over long timescales, is emerging as a promising framework for explaining large-scale biogeographic patterns. Evidence has so far been mixed, depending on spatial and taxonomic scale. While numerous studies have investigated the expected macroevolutionary dynamics of geographic range sizes, few studies have focused explicitly on range boundaries. Here we quantify and compare phylogenetic conservatism and macroevolution in the climatic variables defining range boundaries in mammals and amphibians and investigate spatial aggregation of phylogenetically conserved assemblages versus those dominated by species demonstrating recent niche evolution. We quantify the phylogenetic signal of climatic tolerances in extant continental mammals and amphibians and then use ancestral trait reconstructions to estimate independent evolution in species' climatic requirements. We map assemblages dominated by species with large deviations from their ancestral niches and investigate whether escape from conservatism has affected diversification rates. Amphibians and mammals show congruent patterns of conservatism in cold tolerance, with escapee assemblages aggregated in the North Temperate Zone. Escapee clades are not more diverse than their stay-at-home relatives. Although the escapee clades identified may have no problem coping with increased temperatures, the vast majority of biodiversity remains restricted to the tropics. Thus, phylogenetic niche conservatism and rapid climate change provide the necessary ingredients for major biotic turnover in the coming century.

184. A NEW METADATABASE ON VEGETATION-PLOT DATA: THE GLOBAL INDEX OF VEGETATION-PLOT DATABASES (GIVD)

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Vegetation-plot records or relevés, broadly defined as records of plant taxon co-occurrence at particular sites, constitute the primary descriptive data on which much of vegetation science is based and serve as the single most important data resource available to vegetation scientists. However, how many vegetation-plot records (relevés) are available in electronic databases today, how they are distributed geographically, what their properties are and how might they be discovered and obtained for use in subsequent studies, are questions that have remained unanswered. To aid researchers in discovery of vegetation-plot records, we have created and invite data submissions to the Global Index of Vegetation-Plot Databases (GIVD; <http://www.givd.info>), an internet-based resource aimed at registration of metadata on existing vegetation databases. This poster presents the (I) current state of the Index in terms of numbers of registered databases and their distributions, (II) features an example fact-sheet that describes available information for each registered database, and (III) some strengths, shortcomings and potential applications of the database in macroecology and biodiversity research. Register your database now at <http://www.givd.info>.

185. ALIEN VISITORS OR LONG TIME RESIDENTS? POPULATION HISTORY AND PHYLOGEOGRAPHIC PATTERNS OF THE EUROPEAN FUNNEL-WEB SPIDERS (ARANEAE, HEXATHELIDAE)

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The growth of global commerce has enhanced the emergence of alien species. Funnel web spiders are mostly restricted to Australasia and South East Asia. However, two species are found in Europe: *Macrothele calpeiana*, from the southern Iberian Peninsula, and *Macrothele cretica*, endemic to Crete. The origins of the European funnel web spiders are uncertain. Some authors suggest that *Macrothele* colonized Europe from tropical Africa, while others support an Asian origin or even a recent introduction from China. The European species have received conservation attention. *M. calpeiana* is the only spider protected by European Union legislation, due to its putative role as quality bioindicator of the diminishing cork oak forests. However, increasing sampling effort has revealed that climatic variables and historical factors are better predictors of its presence. In recent years, new populations of *M. calpeiana* have been found in south-eastern Spain, and the species has been reported for the first time in southern Portugal and north-western Europe. These populations are frequently found at localities where climatic conditions are non-optimal, and they have been interpreted as the result of human-mediated dispersal associated to olive tree commerce. Here we investigate population history of *M. calpeiana* by analysing mtDNA sequence data of 280 specimens from 50 localities distributed across its known range. Our results identify some putative aliens among the newly found populations, but also provide evidence for a long evolutionary history of the populations inhabiting areas poorly predicted by potential niche modelling techniques, which suggests the existence of local, suitable microclimates

186. PALEOREFUGIA AND NEOREFUGIA IN RIVERS OF SOUTHERN SOUTH AMERICA: A RESULT OF DIFFERENTIAL PROCESS OF EXTINCTION AND COLONIZATION?

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The geographic distribution range of Patagonian species is related to deep environmental changes generated by Pleistocene glaciations. Diversity patterns of freshwater ichthyofauna are explained by river capture, lake distributions, position of the continental divide and glacial refuges. Nevertheless, these aspects are still unknown for fluvial macroinvertebrates. This study aimed to determine the possible geographic areas that performed as glacial refuges in LGM, analyzing spatial distribution of macroinvertebrates richness with high and low vagility. We sampled 300 Patagonian Rivers, including continental and insular hydrographic basins along 1440 km. The samples were obtained semi-quantitatively covering a surface of 200m². We found mainly Plecoptera (37 species), Ephemeroptera (27 species) and Decapoda (6 species). Plecoptera and Ephemeroptera richness was negatively correlated with latitude and longitude, decreasing in East-West direction, towards Patagonian archipelagos, and in North-South direction, to Tierra del Fuego. It was found a high proportion of flightless species on the islands of Chiloé, Guambin and Duque de York. Further, we found a significant nested pattern in the species composition, dominated by species whose adults are flying. We define that Patagonian islands with Pacific exposition could be localized glacial refuges for fluvial macroinvertebrates, areas for conservation of freshwater ecosystems.

187. MOLECULAR PHYLOGENY AND HISTORICAL BIOGEOGRAPHY OF SWIFTS (APODIDAE: APUS, TACHYMARPTIS)

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We present a near complete swift phylogeny for two closely related genera *Apus* and *Tachymarptis* based on mitochondrial and nuclear markers. Each of the two genera represents a monophyletic clade, i.e. neither of the two *Tachymarptis* species is nested in *Apus* as previously considered. Genus *Apus* comprises four major clades two of which comprise both Palearctic and Afrotropic species. One exclusively Asian clade represents a basal split from the *Apus* tree; its phylogeographic structure contradicts current systematics of Himalayan and Southeast Asian species. A large second clade comprises all European species together with those of the Macaronesian islands and four further Afrotropical species. Branch lengths are considerably short and two terminal taxa (*A. apus* and *A. pallidus*) cannot be reliably distinguished by any of the genetic markers used. Internal topology of the *Apus* tree suggests multiple events of faunal interchange between the Palearctic and the Afrotropics during a considerably short evolutionary time frame. Discussion of historical biogeography is based on ancestral range reconstructions and molecular dating.

188. ANT DIVERSITY: BIOGEOGRAPHICAL CONSERVATION IN ARID AND SEMI ARID ECOREGIONS OF IRAN

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In this study, we mainly investigated whether World Wildlife Fund's ecoregion units are the appropriate scale for conserving ant diversity in Iran. Ants were sampled from a nested sampling design including four spatial levels along 10 degrees latitudinal gradient across four main arid and semi arid ecoregions of Iran. We applied hierarchical partitioning of species richness and diversity to our data. Hierarchical cluster analysis was applied to evaluate similarity of ant species composition among ecoregions. Further, we applied canonical analysis to disentangle the relative importance of environmental and spatial processes. Partitioning of whole-region species richness showed that 85% of the species richness was generated by beta diversity among ecoregions and landscapes. Ecoregions showed different patterns of diversity partitioning. Four distinct ant species compositions were identified by cluster analysis; however, landscapes of one ecoregion were split into two distinct groups. Our environmental and spatial models explained 62% of the variation in the species composition of ants. Species composition was dominantly controlled by the spatial-dependent environment component (39%), including the variables annual rainfall, summer rainfall, and temperature range. Whole-region diversity partitioning indicates that ecoregions represent the appropriate scale for conserving ant diversity, and that each ecoregion has a distinctive ant fauna. However, different conservation strategies should be considered for different ecoregions due to the differing scales of variation within them. Boundaries of ecoregions remain a subject for further studies. The influence of climate change on ecoregional boundaries should be considered and should be predicted with respect to future conservation maps.

189. THE TRANSECT AS A TECHNIQUE TO STUDY THE SPATIAL VARIATIONS OF VEGETATION. APPLICATION TO THE CANARIAN LAUREL FOREST (TENERIFE, CANARY ISLANDS, SPAIN)

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The transect technique was used to describe and analyze spatial variation of species and vegetation on Anaga (Tenerife, Canary Islands, Spain). The vegetation consists of xeric and thermophile scrub on the lower slopes and dense laurel forests on the slopes above. We established 36 sections of 250 x 500 m along an N-S transect, from sea level to 761 meters at the highest point. A full inventory of vascular plants was made in every section, by recording the abundance value on an ordinal scale. We related these results to various environmental variables. We assess which taxa are significantly associated with the different environments, with individual species patterns being represented as chorological profiles. The main features that emerged were asymmetry of species distributions on the two slopes, variable relative abundance of some species, differences in richness and biological diversity among the sections, phenological changes, location of biotope refuges, regeneration factors related to use changes, and responses to exceptional natural phenomena.

190. FROM PLOTS TO ISLANDS: PLANT SPECIES DIVERSITY AT DIFFERENT SCALES

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The relationship between local and regional diversity is among the most pervasive issues in macroecology and island biogeography, and can be examined at a variety of scales and by using a variety of methods and sampling procedures. Here, we explore certain aspects of this relationships using data on plant species richness from a number of Aegean islands (Greece) that have been collected at two scales: in 100 × 100 m² plots within each island using a proportional sampling approach, and at the level of the whole island. We test for correlations among various measures of beta-diversity and total species richness, as well as the effect of island area on patterns of alpha- and beta-diversity within islands. We also apply several models of Species Accumulation Curves (SACs) to evaluate predictions of observed whole-island species richness from plot samples. Local species richness is not affected by island area or overall species richness, and the same is true for certain measures of beta-diversity that give emphasis to community dissimilarity. Nevertheless, indices of beta-diversity that measure species turnover are strongly correlated with overall species richness and negatively correlated with richness per unit area indicating that 'regional' species richness reflects heterogeneity of local communities. The semi-logarithmic model of SACs (Gleason's) provides a fairly good prediction of observed species richness, as has been repeatedly found for plot data on plants, but some other models (namely, the "Rational function" and "Monod") fare better.

191. ENDEMISM OF DEEP-SEA CORALS ON NW ATLANTIC AND SW PACIFIC SEAMOUNTS

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Seamounts are underwater mountains commonly characterized by accelerated currents and exposed hard-substrates, features that differentiate them from surrounding soft-sediment plains. Seamounts are therefore physically-isolated habitat patches, a condition that led authors to hypothesize that seamount fauna experience genetic isolation and high endemism levels. We have recently shown that octocorals show no evidence of endemism on seamount peaks and chains in the NW Atlantic, apparent geographic isolation being confounded by small sample sizes. Here we report data on the geographic isolation of octocorals from two SW Pacific seamount chains (Norfolk and Loyalty Ridges). 213 colonies of the octocoral genus *Chrysogorgia* were genotyped at the mitochondrial marker msh1. Preliminary morphological data suggest that molecular variation at msh1 is adequate to separate species. Additional specimens collected between New Zealand and the Solomon Islands, and Hawaii, were genotyped to establish faunal connectivity across a wider geographical range. Fifteen haplotypes were identified, six of which had a geographic range > 400 km. No haplotype was found on both chains, however most haplotypes were rare (73% represented by <12 colonies). As for previously investigated chains in the NW Atlantic, evidence for seamount-level coral endemism is weak at the time and spatial scales considered.

192. ISLAND BIOGEOGRAPHY OF SPECIES AND GENOTYPES IN THE CENTRAL AEGEAN ARCHIPELAGO

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Continental islands that have recently become isolated from the mainland provide a unique setting to test the parallel effects of ecological and genetic drift on community and population structure. The process of 'relaxation', i.e. the decrease in species number that follows island isolation, as predicted by the equilibrium theory of island biogeography, can now be revisited in the light of the Species - Genetic Diversity Correlation (SGDC; Vellend, 2003) and Hubbell's (2001) neutral theory of biodiversity: smaller and isolated islands lose species and genotypes due to drift and end up with reduced species richness and genetic diversity, while bigger islands or the ones close to the mainland retain higher diversity at both levels. We here tested this idea in the tenebrionid communities the central Aegean archipelago. Fifteen islands of different sizes, distances to the mainland and ages of isolation were sampled thoroughly and over a thousand individuals were sequenced for Cytochrome Oxidase I and Muscular protein 20. The results confirmed a positive SGDC at alpha- and beta-diversity level, driven primarily by island size and geographic distances. A strong relationship was found between total haplotype richness and island size, which resembled the species-area curve but had a steeper slope. A negative exponential function fitted the distance - decay of community similarity when calculated based on species, nuclear and mtDNA haplotypes, with the decay being faster for the latter. These results demonstrate the potential utility of genotype data for exploring biogeographic processes in poorly known biota and predicting macroecological patterns.

193. GENETIC DIVERSITY PATTERNS OF A WIDESPREAD COASTAL ISOPOD SPECIES REVEAL HIDDEN CLADE DIVERGENCE

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The family Sphaeromatidae (Flabellifera) includes species that exploit marine shorelines, as well as freshwater habitats, such as *Sphaeroma serratum* (Fabricius, 1787), a species with wide distribution in the shallows of the tidal zone. We studied the phylogeography of many Greek populations of *S. serratum*, in order to search for possible geographic structure in their genetic make-up. The material used was collected from both marine and brackish waters in western and central continental Greece, as well as from Aegean islands. We applied PCR amplification of two mitochondrial markers (16S rRNA & COI), and estimated haplotype phylogeny using Neighbor Joining, Maximum Parsimony and Bayesian Inference methods. All methods gave almost identical results, revealing a great divergence among *S. serratum* populations that does not show a clear geographic structure. Instead there is a clear-cut clade divergence related with salinity levels in the sampling sites, with all populations coming from brackish waters forming a separate clade. The marine populations exhibit some geographic structure, with Aegean populations forming a distinct clade. The large genetic distances between populations suggest that *S. serratum* might actually be a species complex. The global monophyly and differentiation of the brackish water clade is under ongoing research, in conjunction with similar patterns found in a parallel work on a fish species (*Atherina boyeri*).

194. ALTERED MICROCLIMATE AS A MECHANISM FOR AVIAN EXTIRPATION IN FRAGMENTED TROPICAL FORESTS

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A number of studies in Neotropical rainforests have documented non-random species loss in the wake of deforestation. Why some bird species or guilds should be more vulnerable and others more resistant to habitat loss remains an important question. There is some evidence that dispersal is limited in tropical forest birds, and it has been suggested that tropical birds have large home range requirements. Another key hypothesis, one largely untested despite being posited several decades ago, is that tropical forest birds are constrained physiologically to the relatively humid, cool, and dark of a forest's interior and therefore cannot tolerate the drier, warmer, and brighter conditions that inevitably develop with increasing edge exposure. We laid groundwork for testing this crucial hypothesis with surveys in southern Mexico and northern Belize. We established a series of transects perpendicular to forest edge. At 50-m intervals we censused birds within a fixed-radius and measured microclimate—wind speed and direction, relative humidity, ambient temperature, heat index, and light exposure from canopy cover—using a hand-held Kestrel 4500, a densiometer, and a light meter. Work is on-going, but preliminary data and analysis suggest, among certain forest birds, a distinct pattern of edge avoidance correlated with changes in microclimate.

195. MOLECULAR PHYLOGENY, HISTORICAL BIOGEOGRAPHY AND ORIGIN OF PARTHENOGENESIS IN *LEPOSOMA* (SQUAMATA: GYMNOPTHALMIDAE) FROM NEOTROPICAL FORESTS

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Lizards of the genus *Leposoma* are a conspicuous component of forest litter herpetofauna of South and Central American forests. The current 15 bisexual and one parthenogenetic species are allocated to the parietale and scincoides groups on the basis of external morphology. Analyses of combined mtDNA and nuclear sequences were performed in 62 specimens of five species from Amazonian and Panamanian forests (parietale group), and six from the Atlantic forest (scincoides group). Different phylogenetic methods were explored, and outgroup included *Anotosaura vanzolinia* and *Colobosauroides cearensis*. The monophyly of the both groups is strongly supported. Contrary to previous hypothesis suggesting a recent contact between the Atlantic and Amazon forests, our divergence time estimates indicate a split during the Miocene. The basal placement of *L. baturitensis* (scincoides group) associated with its relictual distribution in forested areas in the semiarid Caatingas of northeastern Brazil, suggests an ancient isolation with no indication of a secondary contact with forests of the eastern coast. Our data do not permit unambiguous assignment of parental ancestors of the unisexual *L. percarinatum*, but point to multiples and ancient events of hybridization. Occurrence of two highly divergent 2n and 3n lineages suggests that the unisexual represent a species complex.

196. SITE EFFECT ON SUCCESSION MECHANISMS AND PATHWAYS FROM PHRYGANIC TO FOREST ECOSYSTEMS, ON ABANDONED AGRICULTURAL LAND, IN THE WHITE MOUNTAINS OF WESTERN CRETE

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The present study synthesizes and evaluates research results, concerning the influence of site factors, and especially the role of phryganic vegetation, in the colonization of forest tree species on phrygana communities. Emphasis is given to the spatial variability of the establishment mechanisms and characteristics, as related to a range of ecological site units, which express a variety of ecological conditions. The results show that facilitation is the key mechanism, determining the establishment of *Cupressus sempervirens* var. *horizontalis* and *Pinus brutia* ssp. *brutia*, the main tree colonizers of abandoned agricultural land in the White Mountains. These species establish directly under the sparse cover of *Coridothymus capitatus* and *Sarcopoterium spinosum* phrygana species, in the harsher, southern aspects of the massif. The favorable microenvironment created under the cover of phryganic species, seems to be the main parameter facilitating the tree species establishment. However, tree species colonization becomes indifferent of phrygana cover in mesic sites. A complete inhibition of conifer establishment occurs on the terraces of the northern aspects, where *Cytisus creticus* and *Pteridium aquilinum*, dense phrygana-fern vegetation, dominates. At the same time, at these last sites, the broad-leaved forest tree species are easily established.

197. GENETIC VARIATION AND BIOGEOGRAPHY OF THE DISJUNCT *VITIS* SUBGENUS *VITIS* (VITACEAE)

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Vitis subg. *Vitis* provides an example of a plant disjunction occurring in the Northern Hemisphere. Based on a comprehensive sampling of taxa and polymorphism in both chloroplast and nuclear DNA, we assessed genetic variation within this subgenus. Our aims were to clarify the relationships among species and to examine their historical biogeography. Polymorphism in chloroplast DNA was assessed in trnL and trnH-psbA-trnK sequences and in 15 microsatellite loci. We also obtained nuclear data for size variation at 24 microsatellite loci. Chloroplast polymorphisms resolved subg. *Vitis* as a monophyletic group with limited genetic variation. The ancestral haplotypes were found in Eurasia. American taxa harboured derived haplotypes and formed a monophyletic group that did not include *V. californica*. The four main haplotypes in the European *V. vinifera* corresponded to two different origins. Nuclear microsatellites indicated that genetic variation was especially large in North America. Asian species exhibited a lower level of nuclear divergence and *V. vinifera* corresponded to a differentiated nuclear lineage. We therefore obtained some evidence that subg. *Vitis* has an Asian origin and then dispersed to Europe and North America. Geographic separation was followed by diversification, presumably during the Pleistocene, resulting in phylogeographic patterns similar to other biota. In contrast to chloroplast DNA, nuclear DNA shows a larger than expected genetic variation.

198. WHAT'S ON YOUR BOOTS? AN INVESTIGATION INTO THE ROLE HUMANS PLAY IN PROTISTIAN DISPERSAL

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The biogeography of protists is an emerging topic that has been strongly debated over the last decades. Dictyostelids, or cellular slime molds, are a ubiquitous group of protists that spend most of their life cycle as single-cell amoebae feeding on bacteria in the soil. When starved, the amoebae aggregate to form a multi-cellular fruiting body with spores in a mass at the terminus that are later dispersed through passive attachment to soil-arthropods, small vertebrates and birds. There is no evidence for wind dispersal in this group and little is known about the mechanisms that drive their worldwide distribution. Here we consider the potential role humans play in dictyostelid dispersal. To do this, soil samples were collected from the underside of boots from scientists after their summer field seasons in various localities around the world. Samples were analyzed using a soil dilution plating technique. The samples yielded dictyostelid spores and amoebae capable of producing viable fruiting bodies. This demonstrates that humans could potentially be responsible for dispersing protists over long distances, a finding that corroborates earlier studies performed on testate amoeba. These findings have implications regarding how naturally occurring protistan faunas are surveyed and understood. As such, these issues should be taken into account when considering the biogeography and natural distribution of protists.

199. THE INFLUENCE OF LANDSCAPE FEATURES ON THE DISEASE ECOLOGY OF SYLVATIC PLAGUE

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In the western Great Plains, the exotic disease sylvatic plague causes frequent local extinctions of black-tailed prairie dogs (*Cynomys ludovicianus*) and may threaten the long-term survival of regional metapopulations. As prairie dogs are considered a keystone species, plague could also have far-reaching effects on the prairie ecosystem. To better understand and manage this threat, we need more information concerning the factors affecting plague transmission among prairie dog colonies. In this study, we investigate how landscape features influence plague transmission rate. We monitored plague epizootics in prairie dogs within Cimarron and Comanche National Grasslands from 2004 through 2009. We noted which year each colony experienced a >90% decrease in area and attributed the loss to plague: the only known cause of such conspicuous, abrupt mortality in the absence of poisoning. We then employed ArcGIS and Circuitscape software to create isolation by resistance models, incorporating hypothesized effects of various landscape features on plague transmission between colonies. We used Mantel tests to determine which models best explained the time in years separating plague-induced mortality events. Preliminary results suggest that roads and drainage systems act as corridors for plague transmission. Identifying such corridors will improve our understanding of disease dynamics at landscape scales.

200. THE EVOLUTIONARY DYNAMICS OF GEOGRAPHIC RANGES AND SPECIES DIVERSITY

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The process of species diversification is an inherently spatial process. However, the role of species geographic ranges in the evolution of diversity remain poorly understood. Here, I examine how the size and shape of species geographic ranges influence rates of speciation and extinction across birds, mammals and amphibians. I then develop a spatially explicit model of cladogenesis, incorporating the interactions between geographic speciation and range dynamics, and explore the effects of this on present day species distributions and the shape of phylogenetic trees. The results highlight the importance of the geographical structure and dynamics of species distributions to the evolution of broad scale patterns of species diversity.

201. GENETIC VARIATION AND COMPARATIVE DEMOGRAPHY OF ISLAND BIRD POPULATIONS IN THE SOUTHERN LESSER ANTILLES

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We examined genetic diversity in populations of the bananaquit *Coereba flaveola*, the Lesser Antillean bullfinch *Loxigilla noctis*, and the black-faced grassquit *Tiaris bicolor* on Saint Vincent (344 km²) and Grenada (310 km²). The Lesser Antilles support discrete, often genetically differentiated, populations on multiple islands. Genetic variability within island populations permits inferences concerning population demography. We are sequencing three mitochondrial genes (ATP synthase, cytochrome b and NADH dehydrogenase 2) to calculate haplotype networks, population expansion indexes, genetic diversity indexes, analysis of molecular variance (AMOVA), quantification of gene flow, and correlation between genetic and geographical distances. Preliminary results suggest that the three species have similar levels of genetic variability and demographic history on each island, but that these differ between islands. In particular, populations on Saint Vincent are genetically more diverse and demographically more stable than populations of the same species on Grenada, where populations appear to have experienced recent bottlenecks followed by re-expansion.

202. HOW COMMON ARE SPECIES INTERACTIONS INFERRED FROM PRESENCE-ABSENCE MATRICES? A PAIR-WISE APPROACH TO SPECIES CO-OCCURRENCE PATTERNS

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Significant patterns of species co-occurrence are often studied using null models. In null-model approaches a metric is calculated from observed data (usually a presence-absence matrix) and is compared with the respective values derived from randomized matrices based on the observed and constructed according to pre-defined criteria. Deviations from random expectations can be evaluated either at the community level ('ensemble' metrics) or at species by species level (pair-wise comparisons etc). In this work we apply the pair-wise approach to a large number of artificial and real presence-absence data sets in order to evaluate the performance of different metrics and to detect the extent of significant patterns of species interactions, either negative ('segregation' or 'competition') or positive ('aggregation' or 'co-occurrence'). Matrices are randomized using the trial-swap algorithm and two pair-wise metrics, the C-score and the natural metric, are applied in order to identify deviating species pairs. The proneness of the metrics to Type I (false positives) and Type II (false rejections) errors are evaluated using artificial matrices with known attributes. Both metrics give almost identical results and a very good 'behavior' regarding errors. The application of the metrics on real data sets reveals that significant deviations from random species pairs' associations are restricted to a few cases, some of which were used as pivotal examples of biotic 'assembly rules' leading to a long and productive discussion that might have been missing if the authors had tested predictions against large numbers of data sets.

203. DATING THE ORIGIN AND EARLY DIVERSIFICATION OF APIACEAE (MAGNOLIOPHYTA)

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The family Apiaceae (euasterids II, Apiales) comprises four subfamilies of which Azorelloideae and Mackinlayoideae are mostly of South American and Australasian distribution. Subfamilies Apioideae and Saniculoideae, although occurring predominantly in the temperate regions of the northern hemisphere, are of southern African provenance based on the distributions of their early branching lineages. Such distribution patterns suggest a Gondwanan origin for the entire family and subsequent vicariance events after the break-up of this supercontinent. However, hitherto published calibrated molecular phylogenies do not support this hypothesis as they estimate the origin of the inclusive order Apiales at 63-95 MA, which is later than the separation of the major landmasses of Gondwana. These phylogenies comprised large-scale studies with a limited representation of Apiaceae and did not include any calibration points for this group. In this study, we estimate the divergence times for early lineages of Apiaceae using cpDNA rps16 intron sequence data for 97 representatives of the family. These analyses were performed with BEAST using fossil pollen data from the early Tertiary as calibration points. Our results suggest an early Cretaceous origin of the family at 94 MA (with 95% HPD 80-113 MA), with subsequent divergence events of its major lineages occurring between 87 and 77 MA, which is earlier than previous estimates. Nevertheless, these results allow for a rejection of the Gondwanan vicariance hypothesis.

204. NOT SO BANAL AFTER ALL; LATEST EVIDENCE ON LOXOSCELES DIVERSITY IN CANARY ISLANDS AND NORTHWESTERN AFRICA

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The venomous spider genus *Loxosceles* has a widespread distribution, and the vast majority of its species are concentrated in North and South America. The cosmopolitan *Loxosceles rufescens* (Dufour, 1820) has its original distribution range in the Mediterranean basin, and has been the only valid representative of the genus in this area until the recently discovered *Loxosceles mrazig* Ribera & Planas, 2009 from Tunisia. Recent collecting trips carried out in Morocco and Canaries provided us with abundant material of *Loxosceles*. In this contribution, we present the preliminary results on biogeography and taxonomy of this genus in the Mediterranean and Canary Islands, based on morphology and molecular data. Canary Islands harbor an endemic group of *Loxosceles* species. Until now we have identified 5 endemic species: 1 from Fuerteventura and Lanzarote, 2 from Tenerife and 2 from Gran Canaria. Our data suggest a single colonization event to the eastern Canary Islands (Fuerteventura and Lanzarote) and a posterior interinsular colonization to Gran Canaria and Tenerife. Within the *L. rufescens* lineage, preliminary results, including individuals from the type locality and a large number of specimens from the Mediterranean Basin, show several independent evolutionary lineages that could suggest a cryptic speciation.

205. MAPPING THE DISTRIBUTION OF A BIRD SPECIES OF EUROPEAN CONSERVATION CONCERN (THE WOODLARK *LULLULA ARBOREA*) IN CENTRAL GREECE

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We censused *Lullula arborea* during the 2008, 2009 and 2010 breeding seasons (late April to mid June) using the point count method of 50m radius. The survey was carried out on 627 plots by random sampling in a total area of 600 km². Different landscape scales were investigated including a local scale (within 125 meters of the point) and landscape scale (within a kilometer of the point). Landscape composition was estimated from the proportion of area occupied by agricultural land, grasslands and shrublands, and forests, quantified by Geographic Information System using land cover maps. Maps were based on ASTER and Landsat 5 TM satellite images of 2009, which were validated through systematic field checking of the sampling plots. Landscape configuration was estimated from the percentage of core forest area in the landscape, patch density, edge density and the area weighted mean shape index of forest and arable patches. Landscape metrics were analysed with FRAGSTATS software to obtain landscape configuration. This analysis demonstrated that the majority of plots were associated with two main habitat types; grasslands (59%) and sparse forest (24%). Species presence in sparse forest indicates this habitat is highly important for forest management. We discuss the best landscape configuration for the woodlark conservation.

206. VEGETATION RESPONSES TO CLIMATE CHANGE NEAR THE QUELCCAYA ICE CAP

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Global environmental change has transformed the tropical highlands. In the Andean tropics, effects of climate change are most apparent in the form of glacial retreat. The accelerated retreat of tropical glaciers since the 1970s has uncovered substrates on which ecological and successional processes are occurring, reinforcing the importance of analyzing vegetation shifts in high altitude landscapes. In addition, newly established vegetation is soon used by local people as pastures. Yet, research on the ecology of alpine plants is sparse in the Andes. Gathering data from 113 quadrats (1m²) in four glacier outlets of Quelccaya Ice Cap, I analyzed successional paths over an altitudinal range from 5100 to 4800 m.a.s.l.; assessed whether distance from the glacier or altitude is the most relevant factor for explaining species richness, diversity, and vegetation cover; and evaluated the spatial heterogeneity of species composition. The results show that species' upper limit is shifting upwards; that the best model to explain species richness and the Shannon diversity Index was vegetation cover, distance from glacier and the interaction between them. Further, there is a high spatial heterogeneity with a mean of dissimilarity for all the quadrat-to-quadrat comparisons of 0.8122. This is the first study in the Andes showing vegetation dynamics on recently ice-free soil, and it suggests that species' physiological limits due to altitude have been overcome by new environmental conditions enacted by climate change. Finally, changes in composition of high-elevation vegetation due to climate change, agriculture frontier expansion upwards and increased societal pressure on mountain ecosystems, hinder pastoralists' livelihoods and other ecosystem services; urging the need for policies of sustainable science and management aiming lessen resources exploitation and improved efficiency of livelihoods strategies.

207. A SYNTHESIS OF PLANT INVASION EFFECTS ON BIODIVERSITY ACROSS SPATIAL SCALES

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Invasive plant species are often thought to pose a large threat to biodiversity, and studies at local spatial scales often find dramatic declines in biodiversity in the presence of invasive plants. However, others have noted that invasive plants have rarely caused regional or global extinctions. We synthesize this seemingly conflicting literature by evaluating the effects of invasive plants across spatial scales. We first conducted a meta-analysis, and found a negative relationship between the effect size of invasive plants on species richness and the spatial extent at which a study was carried out. We also conducted three invasive plant surveys across the USA to evaluate scale-dependent effects of a single plant invasion across spatial scales (i.e., as manifested through changes in the slope of the logged Species-Area Relationship [SAR], z). These surveys revealed larger effects of invasions on species richness at small than broad scales, significantly increasing the slope (z) of the native species' SARs. Data on species-abundance distributions as well as simulation models suggest that this result will generally occur when plant invasions (1) cause large sampling effects (i.e., a loss of individuals), and (2) reduce the occupancy and/or abundance of common plant species to a greater degree than rare species. We suggest that future studies should consider abundance and occupancy-level changes in native species to inform general patterns of the influence of invasives across spatial scales. This approach will allow greater predictive ability for forecasting changes in biodiversity in the face of global invasions and inform invasive species management and restoration.

208. PLANT INVASIONS ON ITALIAN SMALL ISLANDS

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Within the national project "A survey of the Italian non-native flora" particular attention was paid to the presence, distribution and invasive status of alien plant species on 47 small Italian islands. We present preliminary results, focusing on 38 islands mainly distributed along the Tyrrhenian coast with a latitudinal variation from 44°02'30" (Palmaria, Liguria) to 35°29'24" (Lampedusa, Sicily). Our research aims are: (a) to provide a general overview of the composition and structure of the alien flora in these small islands; (b) to describe main distribution patterns and most successful species; (c) to relate island characteristics with the observed distribution pattern of alien species. The survey identified 190 taxa, including species and subspecies, of which 154 (81%) are neophytes. We also recorded a group of 21 species that had not been observed since 1950. According to their current invasion status, 67 non-native plants were classified as casuals while 123 were regarded as naturalised, i.e. able to establish self-sustaining populations. Within naturalised species, only 29 taxa were considered as invasive on at least one island, on the basis of an assessed high rate of spread. We noticed a high taxonomic richness both at family (57) and genus (129) levels.

209. MODELING HAWAIIAN PLANT COMMUNITIES RELATIVE TO GLOBAL CLIMATE CHANGE

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The diverse range of climates in the Hawaiian Islands underlies a complex geography of plant communities and species ranges. To assess potential changes under future climate projections for the period 2070 – 2100, we utilize statistical downsampling of five IPCC climate change scenarios for Hawai'i. We spatially analyze each scenario to produce projected future precipitation and temperature maps, then apply these to known parameters for existing plant communities, also considering land use and substrate type. Four of the models indicate a net drying, particularly in the presently driest areas. Models consistently suggest that high elevation rainfall and temperature patterns changing in different ways, leading to diminished high elevation wet and mesic communities. We assess how future conditions may affect plant species (particularly rare and endangered taxa) relative to present reserve areas, and also consider the complexities presented by invasive species response to these changes.

210. INCORPORATION OF GENETIC DIVERSITY IN THE SPECIES-AREA RELATIONSHIP: A FIRST APPROACH

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The number of species increases continuously as area increases. This rule of biodiversity is described by the Species-Area Relationship (SPAR) and is one of ecology's few laws. Here, we investigate the possibility of incorporating genetic diversity (GD) in the SPAR, using the land snails of the island group of Astypalea as a case study. The "true" number of species in classic species-area equations was replaced by the genetic diversity of the land snails of each island, which is estimated as the nucleotide diversity (π diversity) of the gene pool of each island using the 16S rRNA of mitochondrial genome as marker. The R^2 values were used to compare the fit of the equation with GD to the Arrhenius species-area model. Preliminary results showed that the proposed model, which uses the genetic diversity of the species and their ecomorphs on each island and the area, gave a better fit, with lower z value (slope), than the classic species-area model. These findings provide a new to the species area relationship. The incorporation of multiple components (such as genetic diversity, functional diversity, and environmental heterogeneity) will lead to the opening of new avenues in the research of island biogeography which should help us to understand the mechanisms that define biodiversity in space and time.

211. COMPARATIVE PHYLOGEOGRAPHY OF FOUR COLD-ADAPTED SISTER SPECIES OF LEAF BEETLES: INSIGHTS FROM MULTILOCUS ANALYSIS AND SDM APPROACH

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Our aim is to investigate the impact of Pleistocene climatic oscillations on today's geographic distribution of genetic variation in cold-adapted organisms, with a focus on four boreo-montane species of leaf beetles in Europe. Several DNA fragments were sequenced for individuals sampled from the entire geographic range of these species. A gene genealogy was inferred for each locus. The comparison of these genealogies revealed (1) complementary, (2) concordant and sometimes (3) conflicting phylogeographic patterns which reflects the importance of working with multiple independent loci. Combining (1) simulations of population evolution according to different coalescence models, with (2) models of the past geographic distribution of these species and their host plant, we compare alternative hypotheses over the historical events that have shaped the current distribution of genetic diversity in these species.

212. PHYLOGEOGRAPHIC PATTERNS IN MARINE AMPHIPODS: INSIGHTS FROM DNA BARCODING

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DNA barcoding was proposed as a standard tool for species identification and discovery (by flagging divergent intraspecific clusters), providing at the same time permanent species tags that are unchanged during taxonomic revisions. A molecular approach enables rapid and accurate identification of species life history stages, invasive species, parasites, disease vectors, illegally-traded endangered species or sources of processed food. Besides its increasing popularity and use in biodiversity studies, DNA barcoding with its large-scale approach (>1 million barcodes in the Barcode of Life Data Systems, October 2010) could provide an unprecedented boost in other research areas such as comparative phylogeography, molecular evolution and cryptic speciation. Here we present results on phylogeographic patterns inferred from DNA barcodes of marine amphipods from North Atlantic and Arctic waters. Major genetic breaks (3-18% intraspecific divergence), indicative of potential cryptic species, were found in *Platorchestia platensis* (170 sequences) between Gulf of St. Lawrence and Gulf of Mexico and in *Gammarus oceanicus* (270 sequences) between cold-temperate Atlantic Canada and Arctic. Species with amphioceanic distribution showed a range of patterns from little or no genetic variation at large spatial scales (*G. finmarchicus*, *G. obtusatus*, *G. wilkitzkii*) to deep divergence between intraspecific clusters (*G. setosus*, *G. tigrinus*, *G. duebeni*). This study highlights the importance of including geographic aspects during sampling for barcoding studies to uncover the extent of intraspecific variation.

213. INTERSPECIFIC ABUNDANCE-OCCUPANCY RELATIONSHIP REMAINING STABLE ACROSS ISLANDS FOR EPIGAEIC ARTHROPODS: IS THE COMMUNITY AT EQUILIBRIUM?

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The interspecific abundance-occupancy relationship (IAOR) is one of the most common patterns in ecology. In conservation, IAOR provides useful tools to identify species facing extinction risk and invaders that could increase their range. Here, IAOR characteristics of arthropods from native forest were investigated for six Azorean islands with different forest fragment sizes. First, IAOR were modelled and compared for the epigaeic arthropod communities of each island, to provide the best fit and define a consensual IAOR for all islands; model selection and model-averaging were applied to six main IAOR models extracted from the literature. The mean departure from the overall interspecific relationship for various grouping of species was measured according to colonization categories (endemic, native, exotic), taxonomic group (e.g., Araneae, Coleoptera) and trophic level (predator, herbivore, saprophagous). Finally, generalised linear mixed modelling was used to test for the differences in (i) occupancy, (ii) mean abundance and (iii) mean departure from the predicted IAOR between groups among and within islands. Results show no clear differences for these variables, suggesting that the remaining forest fragments display unsaturated communities with species randomly distributed along the overall IAOR, regardless of the size of the fragment and the fragmentation for each island. Therefore, across all islands there is evidence that exotic species with larger occupancy are more likely to attain higher local densities as they spread. In addition, endemic species of conservation concern may face extinction due to continuous fragmentation and land-use changes.

214. CLIMATE CHANGE, SUGAR MAPLE GROWTH AND MICROBIAL DIVERSITY: FEEDBACKS AND LINKAGES

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Sugar maple, an ecologically important species in the deciduous forests of North America, is likely to be affected by altered climates near its northern limit. These effects may include altered growth rates, changes in survivorship and changes in the plant/soil community dynamics including long term associations with soil microbial partners. This project evaluated the impact of anthropogenic climate change on soil microbial communities associated with sugar maple seedlings under an artificial temperature and precipitation manipulation experiment. Soil microbial communities play a key role in geochemical processes including nutrient mineralization and soil organic matter transformation, but feedbacks between soil microorganisms and plant community composition/diversity are largely unknown. Microbial diversity was evaluated in a three-fold manner: a) via polymerase chain reaction (PCR)-based product analysis, b) via cultivation of microbes, and c) via phospholipid fatty acid (PLFA) analysis. Research questions included, 1) how will climate change alter soil microbial diversity and soil microbe community structure and 2) what role does the soil microbe community play in the feedback between climate change and soil respiration at the boreal-deciduous forest boundary where sugar maple is dominant. Data indicated a decrease in soil microbial diversity during the study, a distinct shift in carbon utilization and PLFA biosignatures, and a positive correlation between sugar maple seedling growth and soil microbial diversity and activity. These data suggest that increased rates of seedling growth and increased levels of microbial diversity and metabolic activity may be causally linked.

215. ASSESSING THE ROLE OF QUATERNARY (2.6 MA) SEA LEVEL FLUCTUATIONS AND ISLAND GEOMETRY CHANGES ON THE BIODIVERSITY OF OCEANIC ISLANDS

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The abundance of species and endemics of vascular plants of the Mascarenes islands are anomalously high when compared to other volcanic archipelagos, such as the Hawaiian Islands. To evaluate why these island are so diverse we modify rules from island biogeography theory to include landscape heterogeneity and a dynamic description of island size. The current interglaciale sea level is anomalously high compared to the past 1 Myr when sea level was on average 30-40 m lower and during glacial maxima when sea levels were up to 120 m lower. With such water depth changes the currently submerged topography of the Mascarene ridge in the SW Ocean emerged. This led to the creation of additional islands with sizes totaling to at least a third of the UK mainland. We hypothesize that these land masses increased the connectivity between the Mascarene Islands, the Comoros and Madagascar and also provided more habitat space thus favoring higher species richness than currently observed. Sea level rise coinciding with loss of area and connectivity led to the current interglacial island configuration characterized by higher isolation and lower height / size indices. Shrinkage and connectivity loss may have led to increased species abundances and densities. The extinction debt resulting from the current reduced area and increased isolation may add negative pressures to the current stressed island ecosystems which have experienced 80% deforestation. We use spatial linear models with a simultaneous autoregressive model (SAR) to assess the influence of series of geographic factors that compare both past and present island configurations and size metrics on island diversity.

216. THE RESILIENCE OF ISLAND VERTEBRATES TO NATURAL EXTREMES VS. THEIR VULNERABILITY TO HUMAN IMPACT: EVIDENCE FROM THE OCEANIC ISLAND OF MAURITIUS

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Although it is debated whether human activities, rather than climatic extremes caused vertebrate extinctions on continental land masses, evidence for human induced extinctions of insular vertebrates on oceanic islands is comparatively clear cut. Multiple carbon isotope datings on dodo and giant tortoise bones that are part of a bone bed extending for 2 ha and comprising est. 0.5 M vertebrate individuals suggest that a natural mass mortality occurred on the volcanic island of Mauritius ca. 4.2 Myr ago. Independent palaeoclimatic and hydrological data suggest that prolonged droughts led to desiccation and water quality change of a fresh water lake, causing mass mortalities. The data suggest that although the impact to the vertebrate communities was severe, the fauna was able to persist. While on continents species can move with climate change, on small islands this is impossible. Selection on islands may therefore be strong on traits that deal with stresses induced by climatic extremes causing insular species to become generalists. Despite the past mass dieoffs, insular fauna were resilient to climatic extremes. These species only became extinct during human colonization in the 17th century, indicating that humans had the catastrophic effects on insular biota.

217. DEEP TIME (MYR-KYR) DYNAMICS OF VOLCANIC ISLAND CHAINS AND BIODIVERSITY IMPLICATIONS IN THE SOUTHWEST (SW) INDIAN OCEAN

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Based on a compilation of published geological and radiometric data in the SW Indian Ocean we present a model able to reconstruct the change of connectivity, sizes and rise and sinking of volcanic island chains. Our conceptual model provides spatiotemporal boundary conditions (island size changes and connectivity changes through time) that can be tested against DNA based phylogenies. Since Darwin's publication on the formation of coral islands and atolls in 1842 the perception of static volcanic island configurations has radically changed. In particular the advent of radiometric dating and geomagnetic based palimpsestic maps has led to detailed insights into the spatiotemporal dynamism of island configurations. The duration of emergence and rate of sinking as well the relationships between tectonic plate movement and composition can be used to reconstruct the position and size of islands through deep time (Myr-kyr). Changes in size and connectivity are induced tectonically and by sea level fluctuations. Combined with palaeoclimatic data and known rates of sub-areal erosion of volcanic landscapes a good indication of habitat diversity change through time can be reconstructed. We will assess these geological island parameters for the southwest Indian Oceanic islands since their formation 67 Myr ago and discuss them with respect to phylogenetic spatiotemporal trends of some key stone species.

218. THE ORIGIN AND EARLY DIVERSIFICATION OF GRAPHIDACEAE (ASCOMYCOTA: OSTROPALES): A WINDOW INTO THE EVOLUTION OF MODERN TROPICAL RAINFORESTS

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The first molecular dating analysis focusing on the origin and evolution of traits of the lichen family Graphidaceae is presented. We used a 6-gene phylogeny of 108 Ascomycota to date the origin of Graphidaceae and a 3-gene phylogeny of Graphidaceae to estimate diversification dates of its major lineages. Phylogenetic analyses using maximum likelihood and Bayesian approaches were performed and a relaxed molecular clock was employed. While the Ascomycota tree was calibrated using eleven selected fossils, the Graphidaceae tree was calibrated using the resulting basal node age estimation for Graphidaceae from the Ascomycota tree. Furthermore, an ancestral character state reconstruction analysis was performed where we scored the terminal units with the following ecological preferences: precipitation-temperature regime, substrate, and light exposure. The ancestral ecology for the family was reconstructed as essentially shady-wet-tropical. With the age of the Pezizomycotina stem node set to 400 ± 10 million years, the following ages were estimated: crown node ages of the major class-level lineages within Ascomycota: between 150 and 300 mya; crown node of Lecanoromycetes (core of lichenized Ascomycota): ~270 mya; and Graphidaceae: ~160 mya. Paleoclimatic studies show that wet tropical forests originated ~180 mya (early Jurassic), first composed of spermatophytes and gymnosperms, but ~120 mya gradually replaced by angiosperms (Cretaceous). The early diversification of Graphidaceae corresponds well to the evolution of modern tropical rainforest precursors, however, the diversification of all genus-level lineages within the family happened after the K/T-boundary, suggesting that there was some degree of species-level extinction ~65 mya, and species-level diversification again occurred thereafter.

219. MODELING RANGE BOUNDARIES TO ASSESS THE VALIDITY OF CLIMATE-CHANGE INDUCED RANGE SHIFTS

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One of the common consequences of recent climate changes are range shifts of animals and plants. Many works show poleward shifts of ranges as a consequence of global warming. However, many of these studies treat edges of distributions arbitrarily, assigning southernmost and northernmost observations as boundaries. This fails to account for the fact that real distributions of species are always unknown to us and our observations are merely a sample of their true distribution. In this work we aimed at formally modeling the edges of a spatial distribution along a north-south axis. We then developed a statistical test to examine if indeed a shift in the spatial distribution has occurred between two time frames. The model estimates a spatial distribution based on presence/absence grid-cell data. We used the bounded Beta distribution to estimate occupancy of cells along a north-south axis. The distribution's edge parameters were estimated using an optimization procedure. We used likelihood ratios to conduct a statistical test between the null (no shift in range) and alternative (possible shift in range) hypotheses. We first tested the model on simulated data and then applied it to data on British bird distributions between two time frames. Our analysis gave different indications of actual shifts in distribution when compared to previous works analyzing the same dataset without formal statistical modeling. All in all, this work emphasizes the importance of carefully formulated statistical models when estimating distributions of organisms in space, as for example, is needed in testing the effects of climate change.

220. EFFECTS OF CLIMATE CHANGE ON THE DISTRIBUTIONS OF THREATENED REPTILES IN MAINLAND SPAIN

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We made models to determine how changes in climate conditions may affect the distributions of threatened reptiles in mainland Spain, according to a set of environmental variables. Nine reptiles recorded as vulnerable, endangered or critically endangered (IUCN criterion adapted to Spain) were considered. Environmental variables were related to space, orography, human influence and climate. The climate variables used follow the Atmosphere-Ocean General Circulation Model ECHAM4 and two special reports on emission scenarios. We made a 'current' model (1961-1990), and later we obtained models for the future (2011-2040, 2041-2070 and 2071-2100). To obtain those models we performed a stepwise logistic regression of the species distributions on the climatic values for the period 1961-1990, and then a favourability function was applied to make predictions independent from the presence/absence initial rate. Current climatic values were later replaced in the favourability models with future values. By comparing current and future favourabilities, we observed a favourability increase in two species, a stable development in three, and a decrease in two. Climate variables were not chosen by two of the models. Climate was the most important factor for the species that looked favoured by the climate change, whereas this factor was less important than space and orography for the species whose distributions were forecast to decrease with climate change.

221. THE PLIO-PLEISTOCENE ENDEMIC BOVIDS FROM SARDINIA (ITALY)

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Bovids are unusual components of endemic insular faunas, recorded only in some Mediterranean and South East Asian islands. Plio-Pleistocene endemic bovids were infrequent in insular Mediterranean faunas, but included some enigmatic and highly peculiar taxa, such as *Myotragus* in the Balearic Islands and the Sardinian bovids. The latter have been reported from several Late Pliocene - Early Pleistocene sites on the island, such as Mandriola, Capo Mannu, Capo Figari, Monte Tuttavista and from an unknown site in the Campidano area. The analysis of the Monte Tuttavista (Orosei, central Western Sardinia) material suggested that more than one taxon occurred within the same fossiliferous deposit. The peculiarity of these taxa, similar in body size and showing a combination of “Caprinae” and “non-Caprinae” features, makes the attempt to clarify their taxonomic identity and phylogenetic relationships undoubtedly challenging. Four morphotypes were reported from this site on the basis of the shape and position of horn-cores and cranial and dental morphology: *Nesogoral* sp.1 aff. *N. melonii* (morphotype A), *Nesogoral* sp.2 (morphotype B), *Asoletragus gentryi* (morphotype C) and Caprinae gen. et sp. indet. The occurrences of different morphotypes were also noted for long bones and phalanges. Did these taxa result from adaptive radiation? Did they occupy different niches? Did environmental context in anyway affect their evolution? Discrete traits of selected bones (astragalus, phalanges, metapodials) of Sardinian bovids have been examined for testing the usefulness of morphometric methods in inferring palaeohabitats of insular bovids and discriminating between ecomorphological and taxonomic characters.

222. PALAEOBIOGEOGRAPHICAL PERSPECTIVES ON *PINUS PINEA*, A CONTROVERSIAL AND ENIGMATIC MEDITERRANEAN PINE

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The origins of some species of economic importance occurring over the Mediterranean Basin have been a traditional matter of debate that has important implications for land management. The case of *Pinus pinea* L. (Stone pine) is probably one of the most controversial, due to its documented long-term interaction with humans and its presence as a symbolic tree in certain areas of the Mediterranean (e.g., southwestern Iberia and Tuscany). Among the rest of the Mediterranean pines, several features make this pine unique (it has a characteristic crown shape, an edible kernel, cones that require three years to mature, and a very depauperate genetic diversity across its range). In addition, its palaeoecological information is rather limited, as the taxonomic precision attained by pollen analysts is insufficient for this tree and macroremains (such as kernels or anatomically well preserved wood) are needed to unequivocally detect the species in the fossil record. Recent findings of macrofossils of *Pinus pinea* in inland Iberia (Duero Basin) extend the late-Holocene range of the species, but the palaeobiogeographical information and the exhaustive genetic data available still suggest a very limited natural area (but still not sufficiently well defined) and a long and intense history of linkage to humans.

223. DOES FRAGMENTATION INCREASE EXTINCTION THRESHOLDS? A WESTERN EUROPEAN-WIDE TEST IN SEVEN FOREST BIRDS

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The extinction threshold hypothesis predicts the existence of a threshold along a continuum of habitat amount below which population extinction probability increases dramatically. Whereas theoretical results support this hypothesis, indicating that fragmentation *sensu strictu* aggravates the impacts of habitat loss on population persistence, empirical studies find that the effects of fragmentation are weaker than those of habitat amount. Here, we analyze seven forest bird species in relation with forest amount and fragmentation in Western Europe to determine whether fragmentation is related with their extinction thresholds. We used the percentage of forest amount and the proportion of this percentage occurring in the largest forest patch to distinguish between scenarios reflecting low and high fragmentation. We found that the extinction threshold hypothesis was supported for two species, the capercaillie and the hazel grouse, characterized by their highly specialized habitat requirements and reduced dispersion. One species, the black woodpecker, was favored by forest fragmentation whereas four other species were unaffected. We conclude that the extinction threshold hypothesis applies primarily to extreme forest specialists with limited dispersal abilities.

224. MODELING HABITAT SUITABILITY TO PREDICT THE POTENTIAL DISTRIBUTION OF TWO AMPHIBIAN SPECIES, THE COMMON SPADEFOOT (*PELOBATES FUSCUS*) AND THE SYRIAN SPADEFOOT (*PELOBATES SYRIACUS*) TOADS IN EUROPE

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The Common Spadefoot toad (*Pelobates fuscus*) is widely distributed on the main continental Europe and in the north of the Balkan region. The Syrian spadefoot toad (*Pelobates syriacus*) has a range covering parts of the Balkans, the Caucasus and the Middle East. Though IUCN classified both species as Least Concern, they are considered priority species for conservation within the EU since their populations are declining in many regions; therefore niche modeling may act as a powerful tool in assessing their current or future distributions. Maxent and openModeller were used to predict the habitat suitability of these two species based on presence-only occurrence data compiled from several thousand records of UTM or CGRS referenced data and quite a few GPS records for each species in combination with various bioclimatic, topographic and vegetation variables. The most important factors contributing to the spadefoot toads distribution were precipitation and temperature variables, altitude, insolation and NDVI. The area predicted as suitable encompassed the expected habitat range, but also a much broader habitat range.

225. USING MOLECULAR TECHNIQUES IN ECOLOGY AND ISLAND BIOGEOGRAPHY: COMPARING ISLAND AND MAINLAND PARASITOID COMMUNITIES OF MACARONESIA

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Individual organisms arriving on islands are likely to face ecological conditions that differ from those where their source populations evolved, and therefore must be able to use different resources to survive. One can thus assume that generalists should be more successful in colonizing islands. Parasitoid faunas are probably no exception to this, as preferred hosts of individuals arriving to islands may be absent; they must either attack less-preferred hosts, or fail to establish. However, studies on the biogeography of host-parasitoid interactions are scarce, mainly due to technical difficulties associated with rearing and species identification. We used a protocol based on host dissection and DNA barcoding to study the parasitoid communities associated with the moth *Acroclita subsequana* (Lepidoptera: Tortricidae) in the Macaronesian region, testing whether species richness differs between islands and mainland, and whether island parasitoid faunas are biased towards generalist species. Results show that species richness was lower on mainland, with most of the species being specialists. In contrast, island communities showed a greater proportion of generalist species. Overall parasitism rates were similar between islands and mainland, but islands had higher rates of parasitism by generalists, and mainland areas showed the highest parasitism rates by specialists. These results suggest that island parasitoid communities are dominated by generalists when compared with mainland communities.

226. PLANT SPECIES RICHNESS ON OCEANIC ISLANDS THROUGH GEOLOGIC TIME: TESTING THE GENERAL DYNAMIC MODEL WITH PROCESS-BASED MODEL

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Recently, Whittaker and colleagues proposed a General Dynamic Model (GDM) expanding island biogeography theory by including island geologic history. This made theory dynamic and produced several new predictions. We addressed core GDM predictions by simulating island biogeographic and demographic processes for insular plant species through time. Island size varied over time mimicking island emergence and expansion from volcanic activity and posterior erosion. We simulated dispersal, germination, growth, mortality, reproduction, speciation, local extinction. Species competed for space and varied in size and in demographic properties. Consistent with GDM predictions, species richness was a hump-shaped function of island age, being highest for less isolated islands. At advanced ages, richness tended towards a saturation level common to islands with different isolation degrees. Furthermore, speciation and endemic species richness were humped-shaped, with an increasing number of endemic lineages towards island maturity. In contrast to GDM, immigration and extinction curves were hump-shaped, with immigration being more important for younger islands and extinction for older islands. Less isolated islands had more diversifying lineages (species sharing the colonizing mother-species), but more isolated islands produced more species per lineage. Proportional endemism and species number per diversifying lineage increased with time. Results indicate the usefulness of process-based models for simulating species richness and enhancing biogeographical theory with mechanistic understanding.

227. REPEATED TRANSOCEANIC LONG-DISTANCE DISPERSAL IN THE HISTORY OF THE PANTROPICAL GENUS *PTEROCARPUS* (FABACEAE: DALBERGIEAE)

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Traditional views on Gondwanan plant distributions suggest historical vicariance. However, several studies have highlighted the role of long-distance dispersal posterior to the Gondwana break-up in such distributional patterns. *Pterocarpus* (Fabaceae) is a pantropical genus with its main centre of diversity in tropical Africa (14 taxa), followed by the Neotropics (8 taxa) and Indomalesia (6 taxa). Two species (*P. santalinoides* and *P. officinalis*) have amphiatlantic distributions between South and/or Central America and western Africa. Previous studies using a family-wide sampling and several fossil calibration points showed that the age of the genus is substantially younger than the Gondwanan split, refuting Gondwanan vicariance. We generated DNA sequence data from five plastid and nuclear DNA markers for all species of *Pterocarpus*, analysed them under maximum likelihood and Bayesian criteria and produced a robust ultrametric phylogenetic tree, calibrated using fossil and secondary data. Our results reveal at least four independent events of transoceanic long-distance dispersal in the history of *Pterocarpus*. It arose in the Neotropics in the Miocene, dispersed to tropical Africa and subsequently to Indomalesia. *Pterocarpus santalinoides* dispersed from South America to western Africa, while *P. officinalis* crossed the Atlantic in the opposite direction. Both these dispersal events took place in the Pliocene.

228. CLIMATE OF THE LATE QUATERNARY MAY EXPLAIN THE PRESENT GENETIC DIVERSITY OF THE ATLANTIC FOREST PITVIPER *BOTHROPS JARARACA*

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The Brazilian Atlantic forest harbors a surprisingly diverse biota, with a high proportion of endemics. The pitviper *Bothrops jararaca* is widespread and endemic to the Atlantic Forest. Recent analysis (cytochrome b and microsatellites) revealed two distinct population groups of *B. jararaca*: a highly structured northern group, and a less diverse southern group. The microsatellites diversity of the southernmost populations is similar to that found on islands, which indicates a severe demographic bottleneck in the recent past. We tested whether a higher degree of population fragmentation in the south is related to climate change. We compared the potential distribution of *B. jararaca* in the present with that of the last glacial maximum, in the late Quaternary (21,000 years bp), through ecological niche modelling. We used 323 records of *B. jararaca* and 10' layers of climatic variables from Worldclim, and CCSM and MIROC 21K scenarios, to generate predictive models in Maxent. Late Quaternary models indicate a more fragmented and less suitable potential distribution of *B. jararaca* in southern portions of the Atlantic forest. Thus, the present lower genetic diversity of southern populations of *Bothrops jararaca* may reflect changes in climate and possible forest fragmentation.

229. DO HISTORICAL OR CONTEMPORARY BIOGEOGRAPHICAL PROCESSES DRIVE POPULATION STRUCTURE IN THE GREATER PRAIRIE-CHICKEN (*TYMPANUCHUS CUPIDO*)?

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The distribution and population structure of species is the product of both historical and contemporary biogeographical processes. The Great Plains grassland ecosystem has been subject to massive changes in distribution and composition since the late Pleistocene. More recently, grasslands in the Great Plains are declining as a result of anthropogenic influence and climate change. We evaluated genetic diversity and structure in the Greater Prairie Chicken, a grassland obligate species, to determine whether historical or contemporary biogeographic processes have shaped the current distribution and structure of populations. Using 6 microsatellite markers on 1056 individuals from multiple populations across the Great Plains, we found the mean expected heterozygosity was 0.72. As a null hypothesis, we tested the expectation that no process except the Euclidian distances between two populations was responsible for genetic differences by assessing the relationship between genetic and geographic distance. Isolation by distance was not apparent ($r^2=0.097$, $p=0.202$) suggesting that these populations were not in drift-migration equilibrium. Because grassland habitat was distributed further east in the Prairie Peninsula during the late Pleistocene and Holocene, we tested the hypothesis of range expansion from east to west and regressed average allelic richness in each population to Euclidian distance from the eastern-most population; results were not significant ($r^2=-0.2578$, $p=0.6998$). To test the hypothesis that contemporary biogeography was driving genetic structure of Greater Prairie chicken populations, we used an isolation by resistance model of contemporary land cover and connectivity. We found that when habitat suitability was highest between populations, populations were more genetically similar ($r=0.457$, $p=0.017$). These results suggest that contemporary habitat features are driving the distribution of this species making populations vulnerable to isolation and extirpation.

230. THE SPIDER FAUNA OF THE ALADJAGIOLA WETLAND COMPLEX (NESTOS DELTA, NE GREECE) - A REFLECTION OF A UNIQUE ZOOGEOGRAPHICAL TRANSITION ZONE IN EUROPE

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In an aim to improve the arachnological knowledge for Greece, an investigation of the arachnofauna of the Aladjagiola wetland complex, part of the Nestos Delta, Northeast Greece, was conducted in spring 2008. Spiders were collected from 28 sites using pitfall traps. In total, 206 species from 31 families were identified, including Balkan endemics and new records for Europe, Greece and Macedonia. Apart from widespread elements which represented the largest share of the species inventory, chorological analysis indicated that the study area reflects the transition from the European towards the Mediterranean and Ponto-Anatolian fauna. Taken in combination, these three affect the local fauna. Balkan endemics further underline the unique identity of the area. Based on comparisons with data sets from the country's southernmost island, i.e. Crete, Greece can be regarded as a zoogeographical gradient: in the northern edge (e.g. Aladjagiola), European and Anatolian elements dominate the species inventory, while in the southern edge (e.g. Crete), endemic, Mediterranean and Eastern elements create a more local and insular zoogeographical character. In conclusion, Greece cannot be viewed as a uniform zoogeographical unit, but rather as a mosaic of various regional zoogeographical patterns.

231. CONFLICT BETWEEN HUMAN ACTIVITIES AND THE CONSERVATION OF ISLAND ENDEMIC IN A GLOBAL BIODIVERSITY HOTSPOT

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This work presents the main objectives of a recently started project on the conflicts between human activities and the conservation of endemic terrestrial arthropods in Madeira Island. Our aim is to provide information to support the identification of conservation priorities, at both taxonomic and spatial levels, and advice for the sustainable management of native habitats. The methodological plan of our project consists of intensive large-scale sampling using three standard methods (soil sample collection, pitfall trapping and standard net beating) along disturbance gradients and on different habitat-types (Laurisilva, forest monoculture, altitude vegetation subjected to different grazing regimes) and our targets are several species-rich groups of terrestrial arthropods (e.g. Araneae, Hemiptera, Coleoptera, Formicidae). Biogeographical principles and analyses will be applied to interpret the distribution patterns at multiple spatial scales and we are particularly interested in determining how elements of biodiversity (particularly, endemic and exotic species) respond to specific changes in habitat characteristics.

232. GEOGRAPHICAL PATTERN OF TREE SPECIES RICHNESS IN CHINESE FORESTS: DETERMINANTS AT REGIONAL AND LOCAL SCALES

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The geographical pattern of species richness has long been a focus in biogeography but still poorly understood. Empirical evidence with a broad extent and adequately fine grain size is especially in need. The present study was based on community-level data of 1494 plots covering 24 major mountain ranges in China. We applied principal component analysis and stepwise regression as variable filter, and used variation partitioning approach to disentangle the contribution of spatial and environmental factors to the geographic pattern of woody plant species richness in Chinese mountains. We showed, for the first time, that the national-level pattern of woody species richness is dominated by regional climate zones, i.e., warm-humid subtropic, cold temperate, and arid continental. Climatic indices acted as a second factor. Local habitat showed a significant while minor contribution to the pattern. For all species pooled, 70~75% of spatial variation in species richness was explained, but the proportions of variation explained by the same set of covariates to gymnosperm, deciduous and evergreen broad-leaved woody species were 35.3%, 45.6% and 85.3%, respectively. The reasons for this difference, the interaction among the explanatory factors, and the difference between regional versus historical factors are discussed. Our results point to the importance of scale in understanding the spatial pattern of biodiversity and for differentiating mechanisms in macroecology.

233. EFFECTS OF CLIMATE VARIABILITY ON SPRUCE BEETLE (*DENDROCTONUS RUFIPENNIS*) ACTIVITY IN SOUTH-CENTRAL ALASKA

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Understanding past and present disturbance-climate interactions provide a basis for identifying ecosystem resilience in context of climate change scenarios, and help to identify ecological thresholds that may shift ecosystems into new directions. We used tree-ring data that spanned the years AD 1601-2007 to examine the occurrence of and climatic influences on spruce beetle (*Dendroctonus rufipennis*) outbreaks across south-central Alaska. Using new approaches to examine temporal synchrony in spruce beetle activity, we found evidence of regional-scale outbreaks dating from the late 1700s. Over interannual time scales, El Niño years, combined with severe late-summer drought, appeared to contribute significantly to outbreaks, presumably by increasing the susceptibility of drought-stressed trees to beetle attack. Over multidecadal time scales (up to ca. 40 years), cool-phase Pacific Decadal Oscillation (PDO) conditions tended to precede beetle outbreaks, regardless of the phase of El Niño-Southern Oscillation (ENSO). Two lines of evidence thus point to climate (i.e., temperature, precipitation) as a primary driver of spruce beetle outbreaks in southern Alaska: (1) the highly synchronized timing of outbreaks at interannual to centennial time scales suggest the importance of broad-scale climate variability, and (2) associations between cool-phase PDO conditions and outbreaks suggest that extended periods of reduced winter precipitation, in particular, may predispose these stands to beetle attack.

234. BIOGEOGRAPHIC PATTERNS OF CENTIPEDES IN THE MEDITERRANEAN REGION

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The known centipede fauna in the Mediterranean area allowed us to explore certain biogeographic patterns of the taxon in the area. In total, 156 islands and islets from two distinct geographical regions of the Mediterranean area are included. We delineate the faunal similarity, we investigate patterns of centipede species-area relationships (SARs), and we evaluate the possible existence of Small-Island Effects (SIEs). All islands fall into two distinct faunal and geographical areas (a) eastern and (b) western Mediterranean islands. The slope of the power regression line is 0.121 in the eastern Mediterranean islands (Aegean archipelago) and 0.253 in the western Mediterranean islands (Italian islands). Although the comparison of slopes shows statistically indistinguishable z-values between the eastern and the western geographical compartments, the longer period of isolation could explain the relatively higher slope in the western Mediterranean islands. Regarding the phenomenon of the SIE, we believe that it should be treated with circumspection. Among those models that propose a breakpoint in centipede species-area relationship, the surface thresholds show significant differences between eastern and western Mediterranean groups of islands. In the Aegean archipelago, the threshold area calculated by the model of Lomolino & Weiser is 3.17 km², whereas in Italy, the threshold area is 0.01 km². We also note that the area threshold of the SIE in centipedes is relatively higher compared to small herbivores and saprophytic organisms such as land snails, woodlice, and beetles from the same geographical area.

235. INVESTIGATING BIODIVERSITY OF SUBLITTORAL SCIAPHILIC COMMUNITIES IN THE NE AEGEAN SEA, THROUGH THE USE OF A PHOTOGRAPHIC METHOD

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Biogeographical studies greatly depend on the existence of baseline information regarding the distribution and ecological characteristics of the species, communities or habitats under investigation. Existing knowledge regarding the distribution, community composition and structure of sublittoral sciaphilic assemblages (a habitat of high conservation value) is rather limited, especially in the Eastern Mediterranean, mainly due to the inherent difficulties of data collection by means of SCUBA diving. In the effort to enhance current understanding, a quantitative study of the megabenthic species composition of sciaphilic assemblages off Lesvos Island is realized by a non-destructive photographic method. Pictures of randomly placed quadrates (625 cm²) are taken by means of high resolution digital cameras. The photographs are then analyzed through the use of photoQuad®, a new standalone custom software developed in MatLab environment, which enables processing and management of the photographic material, provides tools for the identification of species, creation of species libraries, estimation of coverage and numerical abundances, and other morphometric measurements. The current work presents preliminary data on the abundance and distribution of the main megabenthic species comprising the sciaphilic communities of this N.E. Aegean area, and introduces an advanced methodological tool that may potentially facilitate future studies on the ecology and biogeography of this difficult to approach habitat.

236. GEOGRAPHIC RARITY AND EXTINCTION RISK: ARE RESTRICTED SPECIES DISPROPORTIONATELY EXTINCTION-PRONE?

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It is commonly accepted that locally restricted (e.g., endemic) species are at greater risk of extinction than are more regionally widespread species. This principle can be true owing to two distinct reasons. First, probabilistically, locally restricted species are more prone to extinction because of a lack of geographic redundancy. In the most extreme case, an endemic species will go extinct if it is extirpated from a single location, whereas more common species will still occur elsewhere if extirpated from a single location. Second, ecologically, locally restricted species may be more prone to extinction because they tend to occur in lower abundances and cannot benefit from rescue effects from other populations. The probabilistic explanation for extinction-proneness is self-evident based on chance, while the ecological explanation suggests that populations of geographically-rare species are disproportionately subject to local extirpation, which leads to disproportionately high extinction rates. It has previously been difficult to disentangle these two explanations. Here, I describe a simulation procedure that can disentangle the roles of probability versus ecology in the extinction of widespread versus restricted species and I apply this to a unique dataset of amphibian extirpations and extinctions. The results suggest that the extinction rates of geographically-restricted species is primarily driven by probability, thus endemic species were not disproportionately at risk of extirpation in this study. In contrast, more common species are driven extinct more frequently than probability would dictate.

237. FROM DUST BOWL TO BREAD BASKET: LAND USE CHANGES AND ODONATA DISTRIBUTION IN THE SOUTHERN GREAT PLAINS

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All species in the insect order Odonata, the damselflies and dragonflies, have an amphibious life history. Nymphs mature in freshwater habitats, either still or flowing, and adults typically stay at or near water through their lives. Burgeoning human populations have greatly altered availability of fresh water in virtually all terrestrial ecosystems. As a result, we ought to expect that the geographic distribution or phenology of aquatic organisms varies with the geographic extent of available water. In particular, reservoir construction is predicted to lead to range expansion of lentic species, whereas lotic species will not be affected as drastically, if at all. Conversely, lotic species are predicted to be affected chiefly by altered flow in rivers and streams, whereas lentic species will not be affected by such changes. We tested these predictions with historical and current data on the distribution of Odonata in Oklahoma, USA. We constructed ecological niche models using the Mahalanobis D2 method on the basis of occurrences in the 1920s and 1930s, before there were any lakes in the state. Numerous reservoirs were built across Oklahoma in the wake of the infamous dustbowl of the 1930s. Hence, Odonata habitat—in terms of water availability—differs vastly now. Our results will be useful to land-use planners and conservationists as we deal with changing climate that may lead to further dam construction across the globe.

238. EVOLUTION OF *DUGESIA* GENUS (PLATYHELMINTHES, TRICLADIDA, DUGESIIDAE) IN THE NORTHEASTERN MEDITERRANEAN REGION

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Dugesia is a free-living freshwater triclad genus that presents a wide distribution, inhabiting Europe, Africa, Asia and Australia. These animals have a limited dispersal capability, since they are prone to desiccation. Up to date over 70 *Dugesia* species have been described, around 20 in the Mediterranean region, and 9 of them are endemic to Greece. This is a well-suited area to perform biogeographical studies, due to its complex paleogeographical history, that includes tectonism, eustatism and vulcanism, and due to the high levels of biodiversity and endemism present in the islands. Major events of the geological processes that during the last 13 million years shaped this region are well known and dated, allowing the calibration of molecular clocks. We used molecular analysis tools in order to reveal how *Dugesia* species evolved in this area, obtain a proper phylogenetic tree for this group, and relate it with the geological history of Aegean area. Our results show that they speciated according to the paleogeographical history and new species has been suggested. Additionally, we obtained a molecular clock for this genus for which there is no fossil record.

239. PHYTOGEOGRAPHIC AFFINITIES OF CHIOS ISLAND (GREECE) AND ÇEŞME-KARABURUN PENINSULA (TURKEY): THE CASE OF THE LABIATAE FAMILY

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Chios Island (Greece) and Çeşme-Karaburun Peninsula (Turkey), two adjacent regions sharing common palaeogeographical history, are located at the edge of the Anatolian phytogeographical region, an important center of origin for Labiatae plants. With the Labiatae family as case-example, recent research has shown strong affinities of Chios and Çeşme-Karaburun based on species presence/absence and chorological data. The present study aims to explore affinities of Chios and Çeşme-Karaburun on the basis of habitat type preference of the Labiatae in the two regions. The European Union habitat types were used, areas defined by their geographic, biotic and abiotic features. Several visits to Chios and Çeşme-Karaburun were carried out. The habitat types where Labiatae plants occur were recorded in the field and identified using the Interpretation Manual of European Union Habitats and the Technical Guide for identification, description and mapping of habitat types of Greece. Hierarchical cluster analysis with various linkage methods was performed in order to explore possible common trends among species regarding habitat type preference in the two regions. Labiatae plants were recorded in overall eleven habitat types, most of which (eight) both in Chios and Çeşme-Karaburun. The species were joined in similar groups in the two regions according to habitat type preference.

240. PRELIMINARY STUDY ON GEOGRAPHIC VARIATION IN CRANIAL MORPHOMETRICS OF THE EUROPEAN WILD CAT (*FELIS SILVESTRIS*) IN GERMANY

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The European wild cat has been prosecuted heavily, particularly in the 19th century, but is now under special protection in Europe. We explored the craniometric variability within and geographic differences among populations of the wild cat in Germany and other regions samples from the Eifel, Rhineland, Hesse, Harz, Thuringia, Spain and Romania, as well as domestic cats from Germany. The samples from Spain and Romania are very few and these were only briefly considered. Only adult skulls were studied: 50 linear and derived variables were determined and some nonmetric variables were also recorded. Discriminant analyses with different sets of variables were used to assess if geographic groups could be separated by cranial morphometrics. The overall morphometric variability of wild cats was fairly large. Wild cat samples from Germany alone could not be separated according to geographic areas. Only when domestic cats were included, did western (Eifel, Rhineland, Hesse) and eastern (Harz, Thuringia) German wild cats show some, weak separation along a factor mainly representing coronoid height and width across the bullae. Correspondingly, molecular studies have indicated a western and eastern group of German wild cats.

241. DISTANCE-DECAY IN SIMILARITY OF SPECIES COMPOSITION DEPENDS ON STUDY EXTENT AND PLOT SIZE - BUT THERE ARE APPLICATIONS

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We shall I) demonstrate limitations of distance-decay studies and II) show a possible application. The relationship between geographic distance and similarity in species composition is regularly used as a measure of species turnover and beta diversity. Distance-decay analyses are applied, cited and compared over several spatial scales. In addition different sized plots (like islands or states) are regularly used within such analyses, implicitly assuming that the distance-decay relation is independent from plot size. We use an artificial one-dimensional "landscape" to show that the slope and goodness of fit measure R^2 of the distance-decay relationship is influenced by plot size and extent of the study. A comparison between different studies must thus be done with caution or be restricted to those cases where sampling scale and pattern is constant. We illustrate such an example by comparing the distance-decay relation of an area dominated by agriculture in southern Germany with a nearby semi-natural military training area that is not exposed to agricultural use. While distance decay is still present in the semi-natural area, no distance decay was found in the agricultural area in close proximity. It is likely that the human disturbance regimes in the agricultural landscape dominates over niche processes as a driver of beta-diversity.

242. EASTERN INVASIONS AND NORTHERN GLACIERS – IMPACTS ON THE BIOGEOGRAPHY OF EUROPEAN MAMMALS

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What determines species diversity patterns is a core issue in ecology and biogeography. We here investigate this issue for the European mammal fauna. There is little doubt that current climate affects the distribution of mammals. However, mammal distributions are also affected by other factors such as biotic interactions, and dispersal limitation. This raises the possibility that current mammal diversity patterns may not only reflect current climate, but also historical factors such as past climate change (such as Pleistocene glaciations) and biogeographic isolation effects (peninsular dynamics, as Europe can be considered a Eurasian peninsula, with invasions from Asian source areas and relict survival and evolutionary differentiation in isolated parts). We investigated the importance of these factors using spatial modelling of mammal species richness and compositional patterns across Europe. As expected, current climate emerged as an important driver of both species richness and composition. However, there was also a strong peninsula effect on widespread and endemic species richness, and a glacial effect on endemic species richness. Similarly, there were also patterns in compositional dissimilarity consistent with the effects of peninsular dynamics (increasing nestedness-driven dissimilarity with geographic distance in an east–west direction) and glacial refugia (strong longitudinal species turnover within the relatively stable southern Europe). In sum, while current climate is a major driver of mammal diversity patterns, Pleistocene glaciations and peninsular dynamics also play important roles. These findings suggest that a key challenge for climate-change predictive studies will be taking the influence of such historical factors into account.

243. VULNERABILITY OF OBLIGATE FIRE SEEDERS TO SIMULTANEOUS CHANGING FIRE REGIMES AND CLIMATE CHANGE

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Plants are threatened by range shifts under projected climatic changes. For plants in fire prone ecosystems, changing fire intervals are also a threat. Evaluating which threat is most influential on species vulnerability, and how species might respond to mitigate these threats is a goal of conservation biology. We evaluated the threats of habitat shift due to climate change and changing fire frequency for two fire obligate seeders: *Leucopogon setiger*, a shrub from the Australian heathland, and *Ceanothus greggii*, a shrub from the California chaparral. A spatially explicit stochastic matrix model, incorporating simulation of various fire return intervals, was linked with a dynamic bioclimate envelope model to evaluate relative vulnerability of each species to these dual threats. Both species were found to be sensitive to fire frequency, with shorter and longer intervals reducing expected minimum abundances (EMAs). Spatial decoupling of fires across the landscape mitigated vulnerability. Shifting habitat, while reducing EMAs, was less of a threat to the species. Incorporating life history traits into habitat suitability allows us to evaluate the impact of threatening processes on extinction risk, highlight the life history traits that make species vulnerable to extinction, and can help elucidate how particular bioecological factors can affect species experiencing global climate change.

244. EVOLUTIONARY DYNAMICS OF GLOBAL ENDEMISM: A FISH EYE'S VIEW

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The understanding of what determines the spatial variation in endemism is an essential question in evolutionary and conservation biology. While it is well accepted that endemism patterns ultimately arise through the processes of speciation, extinction and dispersal, few studies consider both evolutionary and biogeographic processes in explaining these patterns. Here, we used a uniquely comprehensive data set of riverine fish species distributions to map their global endemism patterns. We demonstrate that two distinct processes generate two specific forms of endemism characterized by different spatial distribution, related to habitat size and heterogeneity, isolation and glacial history. The former, positively related to drainage basin overall richness, is essentially linked to in-situ cladogenetic speciation (i.e. neo-endemic species). The latter, not directly contributing to drainage basin richness, is a pure process of extinction through range contraction, and/or isolation through time (i.e. paleo-endemic species). The proportions of these two types of endemic species also show specific trends between families, when considering their mean body size, median latitude of occurrence and origination time. The non-random spatial distribution of these two forms of endemism sharply reflect the role of evolutionary processes and provide a strategy to conserve areas of high present and potentially future diversification.

245. RECENT POPULATION EXPANSION AND CONNECTIVITY IN THE HYDROTHERMAL SHRIMP *RIMICARIS EXOCULATA* ALONG THE MID-ATLANTIC RIDGE

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Deep-sea hydrothermal vents are unstable habitats that are both spatially and temporally fragmented. In endemic vent species, a 'short-term insurance' hypothesis would lead us to expect mostly self recruitment, limiting the loss of larvae in the deep ocean or water column and increasing genetic differentiation over the time elapsed since colonization. Alternatively, a 'long-term insurance' hypothesis would support the prediction of selection for large scale dispersal, to ensure long-term persistence in these ephemeral habitats. The main goal of this study was to infer the spatial and temporal distribution of genetic diversity of the shrimp *Rimicaris exoculata*, on hydrothermal vents along the Mid-Atlantic ridge, using sequences of mitochondrial cytochrome c oxidase subunit I (COI, 710 bp). Our results revealed very high haplotype diversity across the entire region, indicating current large effective population size and low drift. The star-like shape of the network of haplotypes, the lack of spatial genetic structure and the significance of tests reflecting demographic effects, together with the fitting of a population expansion model, all support a recent population expansion of this species along the Mid-Atlantic Ridge.

246. HIERARCHICAL SPATIAL COUNT MODELS OF MAMMALIAN ABUNDANCE: INFLUENCE OF VARYING SPATIAL RESOLUTION

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Most species distribution models examining environmental effects at multiple spatial scales vary in spatial extent. Spatial scale, however, is the integration of extent and resolution, or grain. I developed models for 6 mammalian nest predators in the Prairie Pothole Region of the north-central United States, varying model response as a function of spatial resolution. The original counts of predators were systematically collected using track surveys on a 50,873 km² grid resolved to a resolution of 16 mi². I developed hierarchical spatial count models predicting mammalian abundance at this resolution and at resolutions of 4 mi² and 1 mi². The models I developed improved prediction of areas of absence as resolution became finer. However, models consistently under-predicted abundance at all scales, and as the resolution became finer, the ability to correctly predict counts declined relative to the models at coarser resolution. Thus, there was a tension between correct prediction of areas occupied at the finest scale and correct prediction of abundance at the coarsest scale. For the most abundant species (raccoon and coyote) we were able to develop scaling relations among model parameters to predict species occurrence and abundance at finer and coarser scales than we modeled. Our models and maps allow managers to focus their conservation resources to finer areas of the region, ostensibly improving the efficacy of conservation action.

247. THE ISLAND SPECIES-AREA RELATIONSHIP: BIOLOGY AND STATISTICS

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The species–area relationship has been studied for more than 150 years now and thousands of studies have reported the pattern for a wide variety of taxa and scales, recently for microorganisms too and types of ecosystems, qualified as one of ecology's few laws. Thirty-two years after Connor and McCoy's seminal review paper (1979) on the statistics and biology of the species–area relationship, and despite the conceptual advances and the accumulation of the available information, a general quantitative analysis of the island species–area relationship (ISAR), across island types, organisms and mathematical formulas is still lacking. Here we report the results of the most general analysis applied so far, using 601 data sets and applying all, but one, the mathematical formulas (20 in total) proposed so far for the description of the species–area relationship. Three fundamental questions of the ISAR research program are assessed: (1) Is there an overall best-fit model for the island species-area relationship? (2) Is there a best fit family of models of the ISAR? (3) Is there a best-fit shape of the ISAR and does it include an asymptote? The above questions are addressed using multivariate regressions and multivariate analyses.

248. ELEVATIONAL GRADIENT OF VASCULAR PLANT SPECIES RICHNESS AND ENDEMISM IN CRETE

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Although many studies on elevational gradient of vascular plant species richness and endemism for the main mountain massifs of the world have been published, the combined effect of mountain and island isolation mechanisms in shaping these patterns has not been studied in detail. In the present study extended field surveys, herbarium specimens and all the available published data were used to interpolate gamma diversity. In total, 1825 native vascular plant taxa (species and subspecies) of Crete were used in the analyses, 10.6 % of which are Cretan endemics. Their presence between the minimum and maximum recorded elevations gives estimates of vascular plant species richness and endemism patterns at each 100-m elevation interval. Total species richness monotonically decreases with elevation, while endemic species richness shows a hump-shaped pattern with a maximum between 1100 and 1800 m a.s.l. The proportion of endemics increases steadily from low to high elevations reaching more than 40% at the higher gradients. Species density also monotonically decreases with elevation, while endemic species density monotonically increases from sea level to 1800 m and then gently decreases to 2500 m a.s.l. Among the examined factors affecting elevational patterns of endemism, area is very powerful in explaining variation in endemic species richness.

249. DISTINCT GENETIC LINEAGES IN SOUTHERN EUROPEAN AND MEDITERRANEAN COAL TITS (*PERIPARUS ATER*)

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At the intraspecific differentiation level the coal tit (*Periparus ater*) comprises at least six distinct mitochondrial lineages and even more genetic variation is supposed to be found in the Mediterranean region. This is confirmed by mitochondrial (control region) and nuclear markers (microsatellites, ten loci) used in this study. Four distinct genetic units can be identified in a circum-Mediterranean breeding area of this species: North African ssp. *atlas*, S European ssp. *abietum* plus two distinct island populations (ssp. *cypriones* on Cyprus; ssp. *sardus* on Corsica and Sardinia). Within-group genetic variation was lowest in the latter two island subspecies. A zone of secondary contact between genetically distinct birds of the Northern European nominate *ater* group and birds of the Southern and Central European *abietum* group extends at least throughout whole Germany. Flanking bioacoustic analysis and playback experiments suggest subtle differentiation of territorial songs, too.

250. COMPARATIVE PHYLOGEOGRAPHY AND DNA BARCODING OF INDO-MALAY CARANGIDAE (TELEOSTEII: PERCIFORMES)

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South East Asia is one of the most diverse marine ecosystems on the planet. Tectonic evolution, Pleistocene glaciations and related sea level changes over the past few million years have had a dramatic influence on the geography of this region, resulting in a number of land-bridges and sea-barriers in recent past. Molecular analyses at two levels - the species- and the population-level - will investigate the biogeographic history and population genetic structure of the commercially-important teleost marine fish family Carangidae within this region. The species-level work will include phylogenetic analyses and DNA barcoding studies to identify species specific mitochondrial cytochrome c oxidase 1 (CO1) sequences in the Carangidae from this region, while analyses at the population-level will examine population structuring and comparative phylogeography utilising two other markers; the mtDNA control region (D-loop) and a nuclear gene (Rag 1). Documenting the levels and distribution of diversity at the population and species level will allow exploration of the impact of historical and contemporary processes driving diversification. Carangidae have been sampled within four regions; South China Sea, Straits of Malacca, Sulu Sea and Sulawesi Sea. Initial work examined a 450 bp region of the D-loop for 80 individuals of *Atule mate*. Results will not only be important for management and conservation of exploited taxa, but also reveal insights into the origins of biodiversity within this region from a comparative perspective.

251. UNDERSTANDING 65 YEARS OF CHANGE IN THE FORESTS OF GREAT SMOKY MOUNTAINS NATIONAL PARK, USA

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When Great Smoky Mountains National Park (GRSM) was placed under strict protection in 1934, about 20% of the landscape had never been directly disturbed by humans and about 80% was recovering from logging and settlement. Through the work of Whittaker (1956), the park's old-growth vegetation became an enduring textbook example of vegetation and species distributions, and we might expect that the GRSM landscape of today would comprise a mix of stable old-growth and successional forests. Despite protection, however, multiple indirect anthropogenic disturbances—including exotic pests, fire suppression, and atmospheric deposition—have continued to impact GRSM forests. For example, several important tree species (American chestnut, Fraser fir, and Eastern hemlock) have been decimated by a succession of exotic pests; hardwood species have invaded pine forests because of fire suppression; and atmospheric pollutants have reduced the vigor of many species. Here, we employ two vegetation surveys of GRSM, spanning the mid 1930s to the late 1990s, to 1) document changes in dominance of several important tree species across the park and 2) illustrate shifts in environmental niche for these species. We identify hot spots of forest change and reassess GRSM's forests with respect to the environmental gradients identified by Whittaker in 1956. This project is part of a larger effort to document vegetation dynamics in GRSM as a prerequisite to understanding the response of these forests to impending climate change.

252. PRE YOUNGER-DRYAS COLLAPSE OF MEGAFUANA IN CUATRO CIÉNEGAS, MEXICO, INFERRED FROM SPORES OF COPROPHILOUS FUNGI IN LATE-PLEISTOCENE POND SEDIMENTS

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Spores from coprophilous fungi preserved in Quaternary sediments have become a valuable proxy for evaluating hypotheses regarding the timing of the extinction of herbivorous megafauna on several continents. Analyses of fungal spores in late-glacial sediments from eastern North America support a substantial reduction in megaherbivore populations before the onset of the Younger Dryas and before a proposed yet disputed extraterrestrial impact. We recovered a 12.3 m sediment core from Poza Cortador in the Cuatro Ciénegas Valley in Mexico, an arid region where continuous sedimentary records spanning the late Pleistocene and Holocene are rare. AMS radiocarbon dates and counts of spores of the coprophilous fungi *Sporormiella* and *Sordaria* along with pollen show that coprophilous fungal palynomorphs reached >5% of the total pollen sum before 13,768 cal yr BP, declined to 1% by 13,398 cal yr BP, and were absent from pollen assemblages at 13,029 cal yr BP. The collapse in megafaunal populations at Cuatro Ciénegas thus preceeds both Younger Dryas cooling and the proposed impact event, indicating that neither phenomenon can explain local megafauna dynamics. The synchronicity in the decline of coprophilous fungi at our site in the Chihuahuan Desert and others in eastern North America lends support to continental scale extinction hypotheses, such as human hunting pressure or climate changes associated with the Allerød warm interval.

253. CAN WE USE SPECIES DISTRIBUTION MODELLING TO STUDY THE PAST DISTRIBUTIONS OF SPECIES?

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Palaeobiogeography is facing a new period, where the narrative biogeographic descriptions of species distributions across time provided by fossil data are now complemented with species distribution models (SDMs). This allows adopting a quantitative approach to some fundamental questions such as: what are the biogeographic consequences of an extreme climatic event; where were the species refuges located in those periods; or how important is the location of these refuges for explaining current biogeographic patterns. The results of this research will constitute a major advance in our understanding of the temporal dynamics of species distributions. However, a sound use of SDM for these purposes relies on establishing a strong theoretical and methodological framework. We review the main issues that need to be taken into account when using SDMs to predict the past distribution of species. Here, the main sources of uncertainty in SDM predictions are: i) the biases and incompleteness of the data on the presence and absence of species (which is particularly important in the case of the fossil record); ii) the difficulty of selecting the appropriate variables for constructing the models; and iii) the modelling methodology itself. We examine all these questions with the aim of stimulating the debate on how to develop SDMs that are robust enough to be projected into past climatic scenarios with reliability.

254. RICHNESS RESPONDED PREDICTABLY TO THE GLOBAL WARMING FOLLOWING THE LAST GLACIATION

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Projections of the effects of future climate change on diversity have provoked concern about potential massive species losses. Moreover, Blois et al. (2010) recently suggested that future global warming will lead to significant loss of richness, based on the observation that small mammal diversity declined in Northern California during the global warming at the Pleistocene-Holocene transition. Richness-climate models, however, predict for most taxa that regional richness should increase with temperature in all but the warmest and driest areas. To test this prediction, we used woody-plant family richness and the climatic fluctuations since the end of the last glacial period (last ~14,000) in North America. We found that woody plant family richness responded in the way predicted by current richness-climate models based on temperature and precipitation. In the northern and eastern North America, richness tended to increase with temperature. In contrast, in the southwestern US richness of woody plants families tended to decrease. Our study indicates that diversity is likely to respond similarly to future human-induced climate change: richness is likely to increase in most parts of North America, except in the warmest and driest areas.

255. NORTH ATLANTIC ISLANDS WITH NATIVE AND ALIEN TREES: ARE THERE DIFFERENCES IN DIVERSITY AND SPECIES-AREA-RELATIONSHIPS?

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The spread of alien conifers is likely to have negative impacts on biodiversity and landscape diversity, especially on small species-poor islands with a limited species pool. This prediction was tested on species-poor North Atlantic islets of western Norway forested with native Scots pine (*Pinus sylvestris*) or introduced Mountain/Dwarf pine (*Pinus mugo coll.*) and Sitka spruce (*Picea sitchensis*). The species-area-relationships and the effect of local species pool on plot richness were compared between islands with native (25) and introduced (28) forest. The prediction that *P. mugo coll.* have a negative impact on plant richness was rejected, but plot richness is low under canopies of *Picea sitchensis*. Ordination showed that beta diversity was highest on islands with forest of the introduced *P. mugo*. There were no statistical significant relationships between species richness and area on islands with native old growth forest, but an expected relationship was found on islands with introduced coniferous trees ($z=0.22$). There was a positive correlation between plot richness and the number of species on the islands (local species pool). Restoration of deforested islands with *P. mugo coll.* (Mountain and Dwarf pine) may be an ecological sound approach since islands with old-growth forest with native Scots pine have lower species richness and more uniform species than on islands reforested with the introduced Mountain and Dwarf pine.

256. ARE HIGHLY MOBILE MARINE SPECIES SENSITIVE TO BIOGEOGRAPHIC BREAKS? THE CASE OF THE ATLANTIC SPOTTED DOLPHIN

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Despite the apparent homogeneity and continuity of the marine environment, biogeographic barriers are known to structure coastal and oceanic communities. In the northwestern Atlantic (NWA) and northern Gulf of Mexico (GMx), four biogeographic breaks have been identified based on genetic differentiation and/or discontinuities in invertebrate and fish species distributions: Cape Hatteras (North Carolina), Cape Canaveral (Florida), the southern tip of Florida and a vicariant zone either at the Mississippi River Delta or Mobile Bay (Alabama). However, the influence these biogeographic breaks may have on highly mobile marine taxa is still poorly understood. We investigated population differentiation in the Atlantic spotted dolphin (*Stenella frontalis*) within this region using mitochondrial DNA control region sequences and 15 microsatellites. We found genetic discontinuities concordant with two of these biogeographic breaks: 1) the Florida peninsula appears to limit dispersal between the NWA and the GMx and 2) the Mississippi River Delta appears to act as a partial barrier differentiating western and eastern GMx populations. In addition, water depth seems to be an important factor in the NWA as one population is mostly restricted to depths < 200 meters. Due to the uneven distribution of threats (interaction with fisheries, oil exploration and exploitation) these populations face, recognizing them as different stocks is important for the conservation of this protected species.

257. GENETIC VARIATION AND BIOGEOGRAPHY OF THE CORFU TOOTHCARP *VALENCIA LETOURNEUXI* SAUVAGE, 1880 (PISCES, VALENCIIDAE) BASED ON MICROSATELLITE MARKERS AND MTDNA

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The Greek Valencia toothcarp, *Valencia letourneuxi*, is a small freshwater fish species, endemic to western Greece, Peloponnese and southern Albania. It is considered an endangered species characterised by low population densities. Studying its genetic variation is necessary to define the risk level and the appropriate protection strategies to follow. We used information coming from both nuclear (14 microsatellites) and mitochondrial (partial D-loop, cytochrome b and 12S-16S rRNA gene sequences) markers to assess population genetics parameters and study the genetic diversity as well as the phylogeographic relationships of seven Greek populations of the species. The analyses showed evidence of reduced genetic variation and heterozygosity and the phylogenetic relationships among populations seem to follow their geographic origin and therefore depict past gene flow and fragmentation due to geologic events.

258. PHYLOGEOGRAPHY OF THE STRIPED RED MULLET (*MULLUS SURMULETUS* L.) INFERRED FROM MICROSATELLITE MARKERS AND MTDNA

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The red striped mullet (*Mullus surmuletus*) is a highly-appreciated fish species with a considerable economic importance in fisheries. It is naturally distributed from the north-west coasts of Africa and the Atlantic Ocean to the Black Sea and the Mediterranean. We used 12 microsatellite loci and D-loop gene sequences to study the phylogeographic relationships of 24 *M. surmuletus* populations sampled from the Atlantic North Sea to the Mediterranean Syrian coasts. Analyses strongly suggest the quasi-absence of genetic structure among the populations of *M. surmuletus* from the Atlantic Ocean and the Mediterranean Sea. The discrimination of *M. surmuletus* individuals into three statistically differentiated genotype clusters ($p < 0.05$) was also revealed. Moreover, evidence of further population structure into these clusters was detected as well. Extensive gene flow and/or a recent population expansion could explain the observed population patterns.

259. PHYLOGEOGRAPHIC PATTERNS OF DIVERSITY WITHIN ALBULIDAE, A COSMOPOLITAN FAMILY OF MARINE FISHES

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Global levels of diversity within the family Albulidae remain an area of active research and debate. Currently 13 taxa are known to exist globally in tropical marine waters. Of these, six are morphologically cryptic species and three have yet to be formally described. These cryptic species occur in the Caribbean and Eastern Pacific, while albulids in other regions purportedly exhibit morphological differentiation and lower levels of species diversity. The reduced diversity occurs even in regions generally known as biodiversity hotspots for other marine taxa, such as Southeast Asia. However, studies combining molecular and morphological analyses are lacking for many regions. This study aims to identify global biogeographic patterns of these fishes using phylogenetic techniques. Deep divergences among clades and geographically distant sister taxa have been identified from mitochondrial sequence data. Within the Eastern Pacific and Caribbean clades, evidence for sister taxa across the Isthmus of Panama has been found from cytochrome b sequence data. Further, evidence of population structure has been found in only one of four Caribbean taxa. Through multi-loci phylogenetic analysis, this study will clarify the evolutionary relationships among members of Albulidae. These data will be used to further assess global patterns of diversification within this family.

260. PREDICTING HISTORICAL AND CONTEMPORARY DISTRIBUTIONS OF SIX NORTH ATLANTIC INTERTIDAL INVERTEBRATES USING MARINE AND TERRESTRIAL ECOLOGICAL NICHE MODELS

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The rocky intertidal community of the north Atlantic consists of disjunct populations or sister species codistributed on European and northeastern North American coastlines. This disjointed community occupies distinctly different climactic regions, and this divergence was likely more extreme during the last glacial maximum (LGM). Research suggests loss of western Atlantic rocky intertidal habitat resulted in local extinction, but there is also evidence that intertidal organisms were able to locally survive during glacial maxima. To examine whether western Atlantic intertidal invertebrates survived in local refugia or recently colonized from the eastern Atlantic, a recent study (Ilves et al. 2010) examined multiple taxa using approximate Bayesian computation (ABC) methods, concluding that most taxa were extirpated from the northwestern Atlantic. However these results were based on one mitochondrial locus and thus this inference could be due to selection. To independently investigate climatic processes underlying contemporary and Pleistocene distributions of north Atlantic intertidal invertebrates, we employ a novel application of ecological niche models (ENMs) for six amphi-Atlantic intertidal invertebrate taxa. We combine 19 terrestrial and 14 marine environmental variables to estimate present distributions for 6 intertidal taxa, and project these ENMs to the LGM. After selecting appropriate models and examining niche divergence between eastern and western populations, we compare results among the taxa, and to the independent phylogeographic predictions of Ilves et al. (2010).

261. TESTING MULTIPLE ASSEMBLY RULE MODELS IN AVIAN COMMUNITIES ON ISLANDS OF AN INUNDATED LAKE

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A fundamental question in ecology is whether general assembly rules determine the structure of natural communities. However, although many types of assembly rules have been proposed, including Diamond's Assembly Rules, Constant Body-size Ratios, Favored States and Nestedness, few studies have tested multiple assembly rule models simultaneously. In this study, we tested the above four assembly rule models and examined the causal basis for the observed patterns using bird data collected on 42 islands of the Thousand Island Lake, China. To ensure the results were not biased by the inclusion of species with extremely different ecologies, we conducted separate analyses for the entire assemblage and for various subset matrices classified according to foraging guilds. The bird assemblages in our system were significantly nested and were mainly shaped by extinction processes mediated through area effects and habitat nestedness. In contrast, bird assemblages did not support predictions by competitively structured assembly rule models, including Diamond's Assembly Rules, Constant Body-size Ratios, and Favored States. These results were very consistent regardless of whether the entire assemblage or the subset matrices were analyzed. From a conservation viewpoint, our results indicate that we should protect both the largest islands with most species-rich communities and habitat-rich islands to maximize the number of species preserved.

262. TOWARDS A UNIFIED MEASURE OF ISLAND ISOLATION

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Isolation is a core driver of species richness on islands. So far its effect has mostly been measured as the ordinary distance to the nearest continent hypothesizing that mainlands are the most important sources for colonization. We compared the explanatory power of eight fundamentally different isolation metrics in almost 100 variations on vascular plant species richness of 453 islands at global scale. We considered the distance to the nearest mainland, distance to other islands, stepping stones, the proportion and distance of neighboring landmass, prevailing wind and sea current directions as well as climatic similarity between source and target areas. In a multi-predictor model accounting for area, climate, topography, and island geology, stepping stone distances to source landmass of at least 100,000 km² as well as the proportion of neighboring landmass gained strongest support. Including both metrics significantly improved model fits compared to a model including the ordinary distance to the mainland. The model explained 82 % of the variation. Our results show that different colonization mechanisms influence plant species richness on islands. Such divergent mechanisms can even be found at macro-scales. However, due to multicollinearity among the isolation metrics it is difficult to disentangle their relative importance. We conclude that the ordinary distance between an island and the nearest mainland serves as an adequate and simple-to-calculate measure of island isolation even at global scale.

263. CLIMATIC NICHE SIMILARITY AND GEOGRAPHIC RANGE LIMITS IN ECOLOGICALLY SIMILAR CO-EXISTING DAMSELFLIES

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Identifying the causal factors that determine species' range limits is a topic of much interest. We investigated how abiotic factors and biotic interactions affect range limits and co-existence of two closely related damselfly species, *Calopteryx splendens* and *C. virgo*. Using spatial modelling, we identified (i) environmental habitat characteristics, amount of niche overlap and degree of specialisation, (ii) combined and interactive effects of environment and predators and (iii) ecological differences between allopatric and sympatric populations. Our models identified temperature and precipitation as key environmental factors limiting the range, and showed that the overall niche overlap was wide, with *C. virgo* being more generalised, although some interspecific differences were identified. At a local level, avian predator abundance and abiotic factors exhibited stronger effects on *C. splendens*, and sympatric and allopatric populations largely overlapped. Together it appears that climate is a key factor limiting the overall geographic distribution of this species pair, and the relatively large niche overlap indicates that ecological divergence in other variables is low. This is consistent with the general suggestion that speciation in odonates is predominantly driven by sexual selection, while ecological divergence occurs secondarily. Our study highlights and corroborates previous findings that ectotherms are highly sensitive to ongoing environmental change.

264. BIOGEOGRAPHY OF NON-MARINE OSTRACODES FROM A LATE-GLACIAL BERINGIAN LACUSTRINE RECORD

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New analysis of core 70-92 taken in the Chukchi Sea at 69°57.2', 165°21.6' during a previous investigation by the USGS indicates an ostracode record of terrestrial freshwater environments dated from ca 13,000 – 11,000 14C years BP. This record is composed of four ostracode zones beginning at 12,640 + 45 14C years BP with fresh to slightly oligohaline fauna (Zone 1), including Holarctic species *Pteroloxa cumuloidea* and *Candona rectangulata*. This system gives way to a freshwater habitat (< 1000 mg/l) ranging from ephemeral (Zone 2) to permanent (Zone 3) systems, ca 12,470 + 45 14C years BP. Zone 2 includes *Fabaeformiscandona rawsoni* and *Limnocythere inopinata*. Zone 3 is dominated by *Cytherissa lacustris* and *Candona candida*. This freshwater basin is subsequently infilled and replaced by wetland peats, containing species of *Cyclocypris* and *Cypria*. The final zone culminates in a marine transgression. Only Zone 1 contains species which are exclusively found in the high arctic today. Subsequent zones are characterized by freshwater species that occupy temperatures commonly present in modern mid-latitude North America and Eurasia. Biogeography of these species drawn from modern ostracode distributions highlights the absence of high arctic and polar fauna in Zones 2-4, suggesting that following Zone 1, temperatures were similar to modern sub-arctic mid-latitude ranges. This conclusion is consistent with results from other workers on pollen and plant macrofossil records for the region, and help to narrow the time window in which fauna and humans would have been most likely to cross the Bering land bridge.

265. THE RELATION OF ECOLOGY TO MORPHOLOGICAL VARIATION OF MOLARS IN TWO WOODRAT SPECIES: *NEOTOMA CINEREA* AND *N. LEPIDA*

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Mammals show a dizzying variety of tooth morphology. Tooth morphology is related to taxonomic history and diet, and is often used to identify species in the fossil record. But what factors contribute to dental variation within species, when taxonomic history and diet are probably similar? In this study, we examine the variation within two species of *Neotoma*: *N. cinerea*, the bushy-tailed woodrat, and *N. lepida*, the desert woodrat. We collected images of the occlusal surface of molars of 116 *N. cinerea* individuals and 83 *N. lepida* individuals from the collections in the Division of Mammals, NMNH. We quantified shape variation using landmark geometric morphometrics techniques. In previous research with this dataset we have established that these two species can easily be differentiated using their molar morphology, but that there is substantial intraspecies variation as well. We compared the shape variables of each species to geographic location as well as temperature and precipitation for their locality, and to body size of each individual. We will use the results of this study to understand the ecology of extinct species, which often survive in the fossil record only as molars, as well as little-studied extant species and populations of *Neotoma*.

266. POSTGLACIAL COLONIZATION AND THE COALESCENT PROCESS

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There is a growing consensus that much of the contemporary phylogeography of northern hemisphere coastal taxa reflects the impact of Pleistocene glaciation, when glaciers covered much of the coastline at higher latitudes and sea levels dropped by as much as 150 m. While the genetic signature of post-glacial recolonization has been detected in many marine species, the effects of coastal glaciation are not ubiquitous, leading to suggestions that species may intrinsically differ in their ability to respond to the environmental change associated with glacial cycles. Such variation may indeed have a biological basis, but apparent differences in population structure among taxa may also stem from our heavy reliance on mitochondrial loci, which are strongly influenced by stochasticity during coalescence. We investigated the contemporary population genetics of *Syngnathus typhle*, one of the most widespread European coastal fish species, using a multilocus dataset to investigate the influence of Pleistocene glaciation and reduced sea levels on its phylogeography. A strong signal of post-glacial recolonization was detected at both the northern and eastern edges of the species' distribution, while southern populations appear to have been relatively unaffected by the last glacial cycle. Patterns of population variation and differentiation at nuclear and mitochondrial loci differ significantly, but simulations indicate that these differences reflect the stochastic nature of the coalescent process. These results demonstrate the strength of a multilocus approach to phylogeography, and suggest that an overemphasized focus on mitochondrial loci may provide a misleading picture of aquatic biodiversity.

267. DEFORESTATION CHANGES THE DISTRIBUTION OF RESERVOIR HOSTS AND INCREASES THE RISK OF EXPOSURE TO ZONOTIC DISEASE IN PARAGUAY

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Deforestation is occurring at an alarming rate of 800 ha/day in the Chaco region of Paraguay. Worldwide, habitat destruction and degradation are linked to the emergence of zoonotic disease. We used a biogeographic approach to investigate the potential of deforestation to increase zoonotic disease exposure for humans and livestock in the Chaco region. We first forecasted how land cover change would impact the distribution of 4 species of native rodents in the region. We estimated the ecological niche of each species given past (70 ya prior to disturbance) and current land cover. We validated the estimated change in distribution for one species, capybara (*Hydrochoerus hydrochaeris*), by conducting a population genetic study. We then examined the risk of exposure of livestock to *Trypanosoma evansii*, an emerging disease in South America, and the risk of exposure to Hanta Virus in humans. We estimated risk of exposure using cumulative and differential models of risk given the change in distribution of reservoir hosts, humans, vector and livestock (for *T. evansii* only). We then validated our model using case data for each disease. Results of our validation suggest that our approach is a robust method for anticipating disease emergence and may be best used to guide the deployment of on the ground surveillance.

268. PHYTOGEOGRAPHY AND ENDEMISM OF AN ISOLATED MOUNTAIN RANGE (HEZAR-LALEHZAR) IN SOUTHERN IRAN

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Hezar-Lalehzar Mts., two jointed mountains, are located in southern Iran and completely surrounded by deserts. These mountains are biogeographically situated at the border between two important vegetation units: Irano-Turanian semi-desert *Artemisia* steppes and the northern Saharo-Arabian regions. The flora of the area is not well known and new expeditions resulted in the description of several new species. Vegetation from the lowlands to the peak of Hezar (4465m) is dominantly covered with *Artemisia* steppes. The dominant species in the alpine and the subnival zones is *Artemisia persica*. The lowland flora of the region is influenced by Saharo-Arabian elements. In spite of this, high altitude flora, especially that of the alpine and subnival zones, consists completely of Irano-Turanian elements. Despite the large geographical distance of these mountains from Hindu Kush and Central Asia Mts., with no high elevation between them, their floristic relationships are remarkable (ca. 30% for both). In the alpine and the subnival zones of these mountains some species are Central Asian and Hindu Kush elements with disjunct distribution in Iran, and their westernmost range reaches the Hezar-Lahlezar Mts. One of the important phytogeographic aspects of these mountains is the high level of endemism, which raises them to a local centre of endemism.

269. GEOGRAPHICAL DISCORDANCE BETWEEN THE DISTRIBUTION OF CYTOPLASMIC AND NUCLEAR GENETIC VARIATION IN A SECONDARY CONTACT ZONE OF THE MEXICAN BLACK IGUANA (*CTENOSAURA PECTINATA*)

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Evolutionary and demographic histories can only be elucidated by the study of the distribution of cytoplasmic and nuclear genetic variation. *Ctenosaura pectinata*, an iguana endemic to Mexico, has been revealed to be composed of several highly divergent mtDNA lineages. However, detailed information regarding the distribution of nuclear DNA variation is lacking. Here the hypothesis of concordance between the distribution of mtDNA and nuclear markers is tested and the existence of contact zones between mtDNA lineages assessed using cytoplasmic and nuclear data. A transect in the central region of the Pacific coast of Mexico was sampled, within the range of three previously described mtDNA clades. Microsatellite and mtDNA data do not follow concordant patterns of geographical distribution within this geographic region. A new mtDNA clade was found, closely related to northern mtDNA lineages, bringing the total to four geographically structured mtDNA clades distributed within the sampled area. In contrast to this only two nuclear gene pools were detected. The discordance can be explained in part by past introgressive hybridization together with ongoing nuclear gene flow via male-biased dispersal. These results highlight the importance of including cytoplasmic and nuclear markers for the inference of phylogeographic histories and have implications in the taxonomy and conservation planning of this threatened species.

270. WHAT DO SNAILS AND IGUANAS HAVE IN COMMON? COMPARING PHYLOGEOGRAPHIC PATTERNS IN THE NORTHERN NEOTROPICAL LOWLANDS

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The western lowlands of Mexico, at the northern limit of the Neotropics, are mostly covered by tropical deciduous forest. Past climate changes probably affected the distribution of this forest and the associated fauna. It is likely that the biota of this region has experienced periods of range fragmentation, contractions and expansion. This could result in substantial biodiversity within species in the form of geographic structuring of genetic variation. Here we present a comparison between the phylogeographic patterns of two taxa inhabiting the western coast of Mexico: snails of the genus *Orthalicus* and the black spiny tailed iguana *Ctenosaura pectinata*. Both taxa occur in the area and show deep genetic differentiation among sampled localities. There is certain geographical concordance in the distribution of the mitochondrial groups of both taxa. Neighbour-joining and haplotype network analyses cluster together haplotype groups that are geographically close. These results suggest that haplotype groups have been isolated for a long time allowing for genetic differentiation. Estimated times for lineage diversification within *C. pectinata* suggest an influence of Pleistocene climate changes. Whereas contact zones between mtDNA lineages of *C. pectinata* have been detected, mtDNA lineages of *Orthalicus* do not overlap. Our first approach reveals the existence of a high genetic diversity within these widespread taxa.

271. ADDITIONS AND AMENDMENTS TO THE MARINE ALIEN BIOTA OF GREEK WATERS (2010 UPDATE)

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An update of the inventory of alien marine species from the coastal and offshore waters of Greece is presented. Records were compiled based on the existing scientific and grey literature, including the HCMR database of Greek alien species (ELNAIS), technical reports, scientific congresses, academic dissertations, websites, and unpublished/personal observations. Forty-two species were added to the inventory, including 31 invertebrates, 1 vertebrate (fish), 3 plants, 7 protozoa, and 1 cyanobacterium. With the new records, the inventory of alien marine species of Greece now includes a total of 234 species, of which 34 macrophytes, 126 invertebrates, 44 vertebrates, 2 bacteria and 28 protozoans. Among these, the presence of the gastropod *Hypselodoris infucata*, the bivalves *Dendrostrea frons* and *Septifer forskali* and the chondrichthyan *Rhizoprionodon acutus* is reported here for the first time. The establishment success of earlier records was revised in the light of new data, and thus the fish *Enchelycore anatina*, *Seriola fasciata* and *Tylerius spinosissimus*, the red algae *Hypnea cornuta* and *Sarconema scinaoides*, the scyphomedusa *Cassiopeia andromeda*, the cephalopod *Sepioteuthis lessoniana*, the nudibranch *Chromodoris annulata* and the bivalves *Gastrochaena cymbium* and *Pseudochama corbieri* were upgraded from casual records to established populations. The increased rate of introductions of warm water species confirms previous findings, which link the rate of introduction in the eastern Mediterranean to climate change.

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