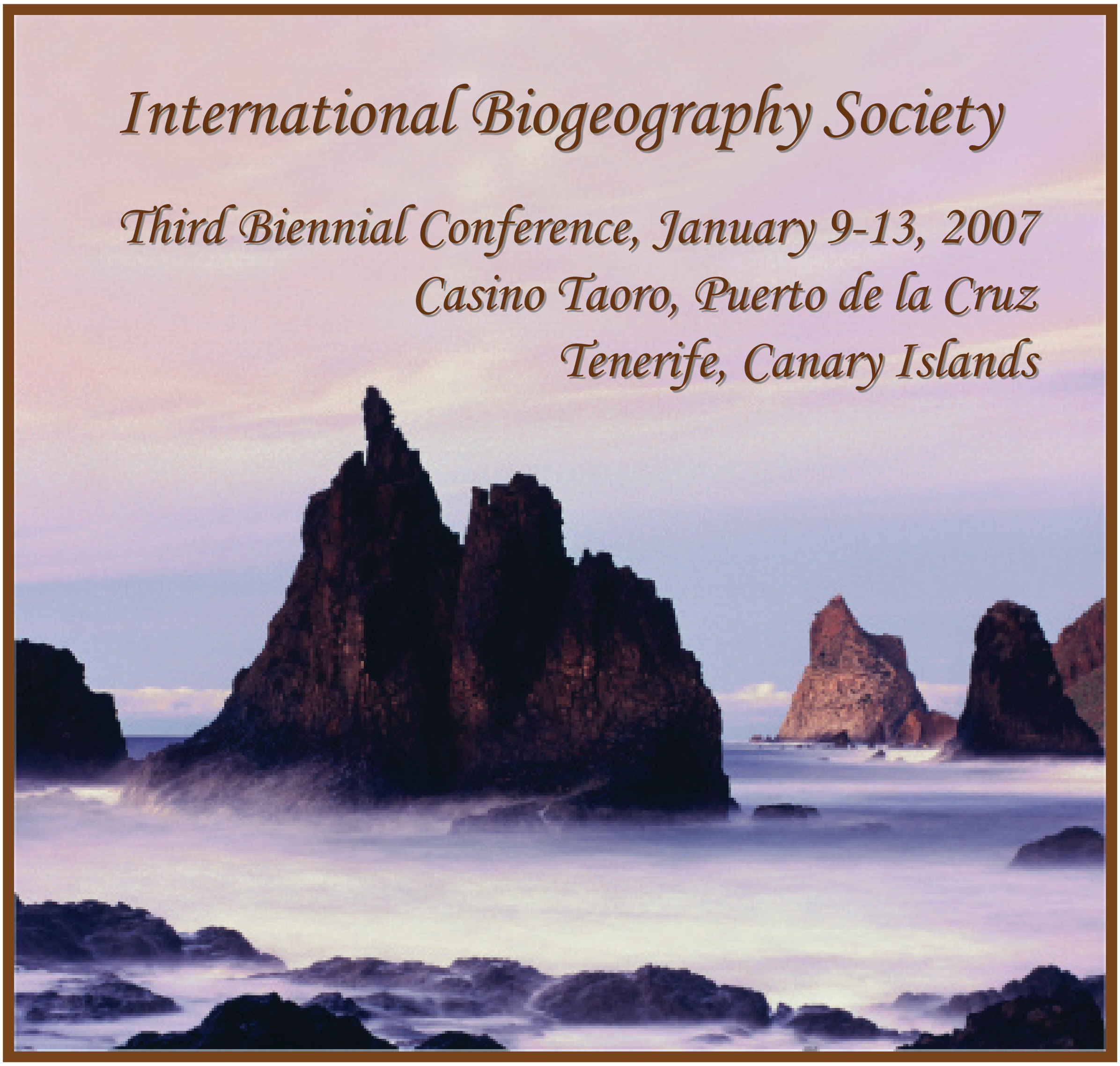
IBS



# International Biogeography Society

## Third Biennial Conference, January 9-13, 2007
Casino Taoro, Puerto de la Cruz
Tenerife, Canary Islands

Cabildo de Tenerife

Ministerio de Educación y Ciencia

CajaCanarias
Obra Social y Cultural

ULL Universidad de La Laguna

Excmo. Ayto. de
Puerto de la Cruz

**Third biennial conference of**

# THE INTERNATIONAL BIOGEOGRAPHY SOCIETY

**an international and interdisciplinary society contributing to the advancement of all studies of the geography of nature**

Casino Taoro, Puerto de la Cruz
January 9-13, 2007
Tenerife, Canary Islands

## Local Committee Members

José María Fernández-Palacios,
Rüdiger Otto, Juan Domingo Delgado, Óscar Socas,
Tamar de la Concepción, Silvia Fernández Lugo

*Cover photograph by Rüdiger Otto*

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*IBS website – www.biogeography.org*

# IBS Mission Statement

Biogeography, the study of 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 individulas 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.

# CONFERENCE PROGRAMME

## **Tuesday 9 January 2007 -** Conference registration, workshops and pre-conference field excursion

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|---|---|
| 8.15 am - 5.30 pm | Pre-conference field excursion to Anaga Rural Park |
| 8.30 am - 12.30 pm | Spatial Analysis in Macroecology workshop 1 |
| 1.30 pm - 5.30 pm | Spatial Analysis in Macroecology workshop 2 |
| 1.30 pm - 5.30 pm | Popular Science Writing workshop |

NOTE: *participation in the above excursion and workshops requires pre-booking.*

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| **6.00 pm - 7.00 pm** | **Post-Grad Mixer** |

## **Wednesday 10 January -** Symposia & poster sessions

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| **8.15 am - 8.40 am** | **Opening Ceremony** |
| **8.40 am - 12.00 pm** | **Symposium 1 - An integrative view of ecogeographic 'rules'** |

Organizers: Mark Lomolino & Dov Sax

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|---|---|---|
| 8.40 am | Kevin Gaston | Macroecological perspectives and geographic range structure |
| 9.10 am | Brian McNab | A physiological perspective on ecogeographic rules |
| 9.40 am | Maria Rita Palombo | How could endemic proboscideans help us in understanding the 'island rule'? |
| 10.10 am | *discussion* | |
| **10.20 am** | **tea / coffee break** | |
| 10.50 am | Robert McDowall | Jordan's rule and vertebral counts in fishes |
| 11.20 am | Dawn Kaufman | Geographic gradients in space and time: latitude, plants, and the late Pleistocene-Holocene of eastern North America |
| 11.50 am | *closing discussion* | |

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| **12.00 pm - 2.00 pm** | **lunch and posters** |
| **2.00 pm - 5.20 pm** | **Symposium 2 - Quaternary impacts on Holarctic biogeography** |

Organizers: Mike Douglas & Marlis Douglas

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|---|---|---|
| 2.00 pm | Johannes Vogel | Biogeography of Palearctic vegetation viewed with a Pleistocene lens |
| 2.30 pm | Pierre Taberlet | The Pleistocene and its effects on species and genes distributions: the case of alpine plants |
| 3.00 pm | Michael Douglas | Nearctic pitvipers and Pleistocene glaciations |
| 3.30 pm | *discussion* | |
| **3.40 pm** | **tea / coffee break** | |
| 4.10 pm | Donatella Magri | Quaternary refugia as a factor in the Holocene distribution of European beech |
| 4.40 pm | Godfrey Hewitt | Holarctic phylogeography and Quaternary biogeography: a synthesis |
| 5.10 pm | *closing discussion* | |

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| **5.30 pm - 7.00 pm** | **posters with cash bar** |
| **6.20 pm - 7.00 pm** | **Journal of Biogeography 'meet the editors' forum** |

## **Thursday 11 January -** Symposia & poster sessions

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| **8.15 am - 8.40 am** | **Presentation on the GBIF programme** |
| **8.40 am - 12.00 pm** | **Symposium 3 - Island biogeography** |

Organizers: José María Fernández-Palacios & Robert Whittaker

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|---|---|---|
| 8.40 am | Vicki Funk | Biogeographic patterns of evolution in the Pacific |
| 9.10 am | Robert Ricklefs | Geography, evolution, and ecology: insights from birds of the West Indies |
| 9.40 am | Isabel Sanmartin | A new Bayesian approach to island biogeography, with special reference to the Canary Islands |
| 10.10 am | *discussion* | |
| **10.20 am** | **tea / coffee break** | |
| 10.50 am | Brent Emerson | Insights into community assembly from evolutionary studies of island ecosystems |
| 11.20 am | Jacques Blondel | On humans and wildlife in Mediterranean islands across time and space |
| 11.50 am | *closing discussion* | |

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| **12.00 pm - 2.00 pm** | **lunch and posters** |
| **2.00 pm - 5.20 pm** | **Symposium 4 - Maritime connectivity** |

Organizers: Michael N. Dawson, John P. Wares & Anuschka Faucci

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|---|---|---|
| 2.00 pm | Michael Dawson | Maritime connectivity |
| 2.20 pm | Kate Darling | Global biogeographical patterns and inter-hemisphere evolutionary relationships in high latitude pelagic planktonic protists |
| 2.50 pm | Chris Meyer | Testing for simultaneous vicariance across time and space in the Indo-West Pacific |
| 3.20 pm | Jonathan Waters | Driven by the west wind drift? A review of southern temperate marine biogeography, with new directions for dispersalism |
| 3.50 pm | *discussion* | |
| **4.00 pm** | **tea / coffee break** | |
| 4.30 pm | Christine Maggs | The relative roles of dispersal and vicariance in biogeography of marine macroalgae |
| 5.00 pm | David Bellwood | Dispersal and vicariance in Indo-Pacific coral reef fishes |
| 5.30 pm | *closing discussion* | |

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| **5.40 pm - 7.00 pm** | **posters with cash bar** |

## **Friday 12 January** - Key note, Symposia, & poster sessions

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| **8.15 am - 9.00 am** | **Key Note - Steve Gaines - The geography of dispersal in the sea: implications for reserve design** |
| **9.00 am - 12.00 pm** | **Symposium 5 - Separating historical from environmental effects on species distributions** |

Organizers: Walter Jetz & Carsten Rahbek

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|---|---|---|
| 9.00 am | Jens-Christian Svenning | Historical controls of plant diversity patterns |
| 9.30 am | Miguel Araújo, Carsten Rahbek | Historical determinants of current patterns of species richness |
| 10.00 am | Walter Jetz | Environmental and historical effects on broad-scale gradients of diversity |
| 10.30 am | *discussion* | |
| **10.40 am** | **tea / coffee break** | |
| 11.10 am | Catherine Graham | History and rain forest biodiversity |
| 11.40 am | Mike Donoghue | Historical biogeography and rates of diversification as factors in explaining geographic patterns in species diversity |
| 12.10 am | *closing discussion* | |

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| **12.30 pm - 1.30 pm** | **lunch and posters** |
| **1.50 pm - 3.00 pm** | **Business Meeting** |
| **3.00 pm - 4.00 pm** | **Panel discussion: Biogeography in the public eye** |

Organizers: Robert Whittaker & George Stevens

A panel discussion of the hows and whys of the public's perception of biogeography. Panelists will be asked to explain the causes for the current level of biogeographical literacy among those who consider themselves reasonably well-educated and suggest ways to improve the public's understanding of science and the need for continued support for biogeographical research.

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|---|---|
| Dr Andrew Sugden | International Managing Editor of Science Magazine |
| Dr Richard Ladle | Oxford University Centre for the Environment |
| Dr. Vicki Funk | Smithsonian Institution |

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|---|---|
| **4.00 pm** | **tea / coffee break** |
| **4.30 pm - 5.40 pm** | **Awards ceremony and closing ceremony** |
| **8.30 pm** | **Conference dinner - courtesy of Ayuntamiento del Puerto de la Cruz** |

## **Saturday 13 January** - End of conference field excursions

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|---|---|
| 8.30 am - 7.00 pm | Teide National Park |
| 8.30 am - 6.00 pm | Teno Peninsula |

## SPATIAL ANALYSIS IN MACROECOLOGY WORKSHOP

Organizers: Richard Field & Lindsay Banin
Led by: José Alexandre Felizola Diniz-Filho & Thiago Fernando L.V.B. Rangel
Place: Hotel Atalaya

NOTE: *please bring your own laptop computer if you have one.*

**Introduction** (30 Minutes)

History of spatial analysis in biogeography, ecology and macroecology.
Why we need to do spatial analysis? The limitations of classical statistical techniques when used on spatial data.
What can (& cannot) be achieved with spatial analysis: exploratory & confirmatory spatial analyses.
Alternatives for modelling spatial data: when to use each type of spatial analysis, and why.

**Practical Sessions** (Total 3 hours excluding break periods)

1. *Introduction to the SAM (Spatial Analysis in Macroecology) computer package* (1 hour)
Distribution of CD-ROM with material (see below). Brief guided 'tour' through SAM modules, including details of data format and handling, mapping and basic statistical description, exploratory spatial analysis and spatial regression techniques, based on a small didactic example. To cater for varying abilities and levels of prior knowledge, more advanced users can start working on exercises (see #2 below) if this part of the workshop is too basic for them.

2. *Doing spatial analysis* (2 hours)
In this part of the workshop, people have a choice, to suit their needs best. One option is to work through exercises that involve some of the more common analyses, with help on hand from Alexandre Diniz-Filho & Thiago Rangel (more experts will be drafted in if numbers of participants require this). Different datasets will be available, differing in terms of the modules within SAM required, the nature of the problems being addressed, difficulty, etc. Alternatively, workshop participants are welcome to bring their own spatial data/problems to the session, to work through (with help on hand) instead of or in addition to the pre-prepared exercises.

**Debrief** (1 hour)

Take-home messages and any issues that arise during the practical session.
Discussions around different techniques and applications developed during the workshop.
Suggestions for further information and follow-up.
Any planned developments of / upgrades to SAM.

**CD-ROM**

The CD-ROM to be distributed will contain all material relating to the workshop, including lecture slides (plus notes giving further explanation), the exercises with explanatory comments, a tutorial for using SAM, literature relevant to the topics, relevant URLs, etc.

## POPULAR SCIENCE WRITING FOR SCIENTISTS WORKSHOP

Organizers: Richard Ladle & George Stevens
Place: Hotel Miramar

How does popular science writing differ from academic writing? How can I get my research into the news? How do I get a book deal? Can I be a popular science writer and maintain my scientific credibility? Can I make lots of money?

These questions and others will be answered during this half-day interactive workshop on popular science writing. Participants will be introduced to the tools required for successfully translating the (often) dry and depersonalized language of academia into the more dynamic and colorful text of press-releases, magazines, newspapers, weblogs and popular science books.

Participants will also be given useful tips and practical advice for floating ideas past editors, writing submission letters and contacting potential sources for publication.

Topics to be covered include the stylistic and technical differences between preparing pieces for scholarly journals and preparing materials for a more general audience, identifying likely sources for publication, editing and preparation of manuscripts, tax consequences and likely income from publication, negotiating book contracts, and how to develop successful themes and outlines.

Participants will be broken into small groups to work closely with successful authors from a variety of backgrounds.

## FIELD EXCURSION TO ANAGA RURAL PARK

**Route:** Puerto de la Cruz – La Laguna – Pico del Inglés – El Bailadero – Taganana – San Andrés – Santa Cruz – Puerto de la Cruz.

As many members will be recovering from their flights to the Canaries, this pre-conference excursion is being provided as a general introduction to the landscapes of Tenerife, and an alternative to the workshops, which run the same day.

The Anaga massif is the northeast corner of the island, comprising some 130 km$^2$ and today constituting a Rural Park, where outstanding nature coexists with a stable population of about 3,000 humans. It is slightly younger than Teno (7-8 Myr), and reaches 1,024 m elevation at its highest point, close to Pico del Inglés. Anaga harbours three altitudinal ecosystems, the subdesert coastal scrub, the thermophilous woodland, today very scarce, and good reserves of laurel forest.

We will depart early from **Puerto de la Cruz** and head in the direction of La Laguna, a UNESCO world heritage city and centre of the La Laguna University, an institution founded over two centuries ago. Our first stop will be the Jardina (c. 750 m elevation) viewpoint, located on the Anaga massif, where an impressive view of the city, the **La Laguna** Basin, and the central summit of the island is possible. From here we will go to the **Pico del Inglés** viewpoint (c. 1,000 m elevation), where we will explore the Monte de Aguirre laurel forest and get a nice view of the eastern part of the massif. Here we will have the opportunity to observe several laurel forest and thermophilous woodland species. Our next stop will be in **El Bailadero** (c. 800 m elevation), which has wonderful view of both the windward and leeward slopes of the Anaga massif, and where toilet facilities are available.

From El Bailadero we will descend to the spectacular coast of **Taganana**, where the windward sea waves erode the soft basaltic materials constructing the pretty, but dangerous, black-sand beaches; we also will be able to see impressive cliffs, such as the Roques the Anaga, a Natural Reserve. Here, while having lunch, we can discuss the processes involved in building and destroying volcanic islands, and their implication for their biogeography and ecology.

On our way home we will go through the **San Andrés** Valley, a huge erosional valley where the transition among the different zonal ecosystems of Anaga can be appreciated. Once in San Andrés, and after visiting its beach (Las Teresitas), we will drive through **Santa Cruz de Tenerife**, the capital of the island and together with Las Palmas de Gran Canaria, of the whole archipelago. Traveling from Santa Cruz to el **Puerto de la Cruz** will take approximately 45 minutes using the northern highway, which will allow us to arrive back in Puerto by 6:00 pm.

## FIELD EXCURSION TO TEIDE NATIONAL PARK

**Route:** Puerto de la Cruz – La Orotava – Aguamansa – El Portillo – Roques de García –Chinyero –
– Icod – Puerto de la Cruz.

This field excursion makes a transect from the lower forest limit upwards to the Teide caldera and then circles back to Puerto. It affords an opportunity to examine the variation in major ecosystem types afforded on Tenerife; a tour of some fantastic volcanic landscapes, and to consider how the dynamism of these volcanic islands can be incorporated into an understanding of evolution on these islands; the trip also will provide insights into the conservation problems and mitigation measures in use within Teide National Park.

We will depart early from **Puerto de la Cruz** taking the road that climbs through the Orotava valley, an intensively cutlivated and urbanized zone of Tenerife, leaving behind the lowland banana-cultivation zone near the coast. We will cross the city of **La Orotava**, which has a typical example of colonial style architecture used in the Canaries and later repeated in the Americas. Above La Orotava we will pass through a more mesic and varied agricultural zone with vineyards, potatoes, maize, wheat, and several types of fruit trees, all of which supply the local markets.

Our first stop will be at the village of **Aguamansa** (ca. 1,150 m elevation), where we will examine a stand of mixed Canarian pine (*Pinus canariensis*) with a laurel forest understory, principally made up of early successional species such as *Myrica faya* and *Erica arborea* (Tree Heather). This is a good site for spotting a few native forest bird species. Prior to the second stop we will cross a belt of Pinus radiata plantations, dating from the period after the Spanish Civil War, when the Franco regime was internationally isolated and timber was essential. Here we will notice the higher densities used in the plantations, as well as the lack of regeneration and understory.

The second stop will be in the Pine Forest zone, just above the cloud layer inversion, at a viewpoint known as **Rosa de Piedra** (ca. 1,500 m elevation), a curious basaltic defoliation form. This viewpoint affords excellent views across the giant collapse feature of the Orotava valley. The La Orotava valley slide is estimated to have been up to 1,000 m in thickness; it created an amphitheatre as much as 10 km wide, and 14 km long, with an offshore prolongation of several km in length. Large-scale collapse features are an important part of the geological evolution of the Canary Islands.

The third stop will be above treeline (ca. 2,000 m elevation), in an area degraded in the past by goat grazing (no longer practiced) and still of limited vegetative cover, where the legume *Chamaecytisus proliferus* dominates the landscape.

The fourth stop will be at the **Teide National Park Visitor Centre**. Here there is a small botanic garden featuring native and endemic species of the high altitude zone and a conservation programme involving propagation of some of the most endangered species of this zone. The bookshop sells a variety of natural history books, maps, and photos about the Teide National Park and Canarian nature. The tour will continue by road through the vast caldera, stopping at the far side, at the spectacular Natural Monument of Los Roques de García, where there will be an opportunity to explore some of the caldera by foot (providing there is not an unusual amount of snow cover). The Parador de Turismo (Hotel) provides a refreshment point.

The return trip will cross the historical lava flow of **Narices del Teide** (Teide Nose; AD 1798), where we will have the opportunity to appreciate the slow pace of primary succession as a result of the hydric and thermic stresses.

The next stop will be in the **Volcán del Chinyero** (ca. 1,600 m elevation), the last volcanic eruption on Tenerife (AD 1909), where a very species-poor pine forest is developing. Finally, we will come back to Puerto de la Cruz through the **Icod** valley, where we will have our last stop in order to appreciate the famous Icod de Los Vinos giant dragon tree (*Dracaena draco*), the symbol of the island. We will aim to return to Puerto de la Cruz by about 7:00 pm.

NOTE: *this field excursion will* ***not*** *involve the cable car ascent to the summit of Teide (over a thousand metres higher than the floor of the caldera) for reasons of time and cost.*

**Additional information:**

Declared a national park in 1954, the Parque Nacional de las Cañadas del Teide includes an enormous volcanic crater 16 km wide, out of which rises Mount Teide (pronounced the same as Lady) at a staggering 3,718 metres, making it the highest mountain in the whole of Spain.
The countryside on the slopes of the Teide mass is purely volcanic. During the winter months the peak of El Teide is covered with snow, which sometimes reaches down to the slope of the mountainside. During the summer months this arid landscape can reach temperatures above 40ºC.

A cable car carries visitors to the summit, but many prefer to hike the route to experience the flora and fauna.

Unique flora in the park include a number of rare species and there are a wealth of plants which have adapted perfectly to the elevation, the low temperatures, and dry conditions. Among the endemic plants to be found in Teide National Park are the Teide Violet (*Viola cheiranthifolia*), Teide bugloss (*Echium wildpretii*), Dwarf bugloss (*Echium auberianium*), Teide cat mint (*Nepeta teydea*), Teide Edelweiss (*Gnaphalium teydeum*), Cardo de plata (*Stemmacantha cynaroides*). On the cliffs grow the Canary cedars which are some of the only trees in the park. The most common plant is the Teide broom, which has a huge number of pinkish white flowers in spring.

The are three endemic lizards in the park: Canary Island Lizard (*Gallotia galloti galloti*), Canary Island wall gecko (*Tarentola delalandii*), Canary Island skink (*Chalcides viridanus viridanus*). The wild canary (*Serinus canaria*), blue chaffinch (*Fringilla teydea teydea*), are endemic birds found in the Canary Islands. The five species of bats are the only native mammals of the Park. The Canary Island long eared bat (*Plecotus teneriffae*) is endemic to the Canary Island, while the Madeira Pipistrelle (*Pipistrellus maderensis*) is endemic to Madeira and Canaries. Leisler´s bat (*Nyctalus leisleri*) is the most frequent species. All other species of mammals have been introduced to the Canary Islands.

In contrast to the poor vertebrate biodiversity, there is an enormous wealth of invertebrate species, in particular insect species, with over 700 species; most of which are endemic and of great scientific interest. The groups with the most species are spiders, beetles, dipterans, hemipterans and himenopterae. In all these groups, there is a large percentage of endemic species, giving an overall rate of endemic species of over 40%, including 70 species that are found only in the National Park.

From the peak, on a clear day, you have breathtaking views of Gran Canaria, La Palma, La Gomera, and El Hierro. This is the Canary Islands most visited tourist attraction and must not be missed.

## FIELD EXCURSION TO TENO PENINSULA

**Route:** Puerto de la Cruz – Garachico – Teno Bajo – Valle del Palmar – Teno Alto – Icod – Puerto de la Cruz.

The Teno massif is one of the three oldest parts of the island of Tenerife, dating back to the late Tertiary period (c. 9 Myr). It forms an impressive series of dissected landscapes, featuring two principal natural vegetation types, first, an open semi-arid succulent scrub vegetation dominated by several endemic *Euphorbia* species together with a rich set of native and endemic species, and second, laurel forest, which is dominated by a small number of palaeo-endemic evergreen tree species. Teno is characterized by its fertile valleys, like El Palmar, and its deep ravines, which, like the Masca Ravine, usually run down to the coast, ending in small coves or beaches. The Rural Park has an area of 8,000 ha, with a population of about 1,400. It was designated a Natural Park in 1987 and a Rural park in 1994. The rural park designation is designed to encourage sustainable development, maintenance of cultural landscapes, management of the tourist burden, and conservation goals. The area has a high biodiversity value and is one of the most scenically attractive parts of the island.

We will leave **Puerto de la Cruz** early in the morning. We will head in the direction of **Garachico**, a little village at the coast, where we will make our first stop; here we will be able to see the lava flow that destroyed this sites famous harbour in AD 1704 and see its famous Roque. From here we will continue to the Teno massif through the so called Isla Baja, a coastal platform formed by recent volcanoes. Along the way we will see the villages of **Los Silos** and **Buenavista**. Once in Buenavista, we will have entered the area designated Rural Park, allowing us to visit the Teno Bajo peninsula. Here we will make our second stop at the **Acantilados de El Fraile**, a huge sea cliff, c. 400 m hight, which has an exceptional view of the Isla Baja and Punta de Teno. Not far away from this point we will visit a mature community of the sub-desert coastal-scrub, dominated by succulent endemic *Euphorbia* bushes. Our third stop will be in **Punta de Teno**, the NW corner of Tenerife, just 85 km away from La Palma and 30 km from La Gomera. Here we will have the opportunity to contemplate the huge Los Gigantes cliffs, the western border of the Teno massif, with cliffs that tower 700 m above the sea. It was in this area that the recently discovered giant Teno lizard was first found.

Our next stop will be in the **Teno Rural Park headquarters**, where we will be introduced by the Rural Park staff to their day to day work in the Park, and where we will receive maps and information about the Park. Later we will go to the **Bolicos hostage**, where we will have lunch and take a short walk through the laurel forest of Monte del Agua, the best remnant of this forest in Tenerife. During the walk, details of the laurel forest dynamics will be explained, and we will learn to recognize the different tree and shrub species that compose this forest. During the afternoon, we will try to gain an understanding of the objectives, methods and issues involved in managing an impressive 'natural' area that has people living and working within its boundaries. We also will discuss the role of different protected area models in the Canarian context, and of issues focused around conservation of the cultivated zone in Tenerife. We will return to Puerto de la Cruz, by approximately 6:00 pm.

### Additional information:

An area of cliffs and black sand seashore but also very rich in endemic plant species. Plants such as the 'Cardon' (*Euphorbia canariensis*) grow on the peninsula. The precarious coast road goes past plantations and greenhouses then up through cliffs containing huge (1.5 m) *Sonchus acaulis* and on past steep gullies with banks of mixed Euphorbias (*Euphorbia atropurpurea*) and eventually reaches the black sands where several halophyte (salt tolerant) species such as *Mesembryanthemum* grow.

## *Symposium 1*

# An integrative view of ecogeographic ‘rules’

## A PHYSIOLOGICAL PERSPECTIVE ON ECOGEOGRAPHIC 'RULES'

McNab, B.K.

*Department of Zoology, University of Florida, Gainesville, FL 32611, USA. Email: bkm@zoo.ufl.edu*

Various ecogeographic rules are examined from a physiological perspective, and an attempt will be made to come to a consensus evaluation of the significance of these rules, as well as some other ecogeographic patterns. Although Bergmann's, Allen's, and Gloger's rules have often had a physiological explanation suggested, the most likely explanations are complex with a minor contribution made by physiological considerations. Thus, the claim that the increase in body mass at high latitudes (Bergmann's Rule) conserves body heat is erroneous, and the suggestion that the large appendages in mammals living in hot climates (Allen's Rule) permit the dumping of heat from the body to the environment works only under narrow circumstances, and preferentially in species of an intermediate mass. Other 'rules', including Rapoport's (larger geographic ranges at high latitudes) and Cope's (vertebrate mass increases with time) either appear not to have a physiological basis or can be questioned as to their validity. Some other geographical patterns that are not normally recognized as 'rules', such as the correlation of species diversity with latitude, the correlation of reproductive output with latitude, the island rule (large species get smaller and small species get larger on islands), and what might be called a 'continental' rule (continental endotherms, subject to resource limitations, maximize reproductive output to withstand intense levels of competition and predation) appear to be influenced, if not determined, by physiological factors.

## HOW COULD ENDEMIC PROBOSCIDEANS HELP US IN UNDERSTANDING THE 'ISLAND RULE'?

Palombo, M.R.

*Dipartimento di Scienze della Terra, Università degli Studi di Roma 'La Sapienza', CNR Istituto di Geologia Ambientale e Geoingegneria, Piazzale Aldo Moro, 5, 00185 Rome, Italy. Email: mariarita.palombo@uniroma1.it*

Several hypotheses have been advanced to explain size-change processes in terrestrial vertebrates on islands and in island-like ecosystems, emphasizing or rejecting the Foster's 'Island Rule' as a general pattern at least for mammals. Actually, body-size trends of insular mammals result from a combination of selective forces whose importance seems to fluctuate along a gradient from small to large species; moreover underlying mechanisms might differ in different lineages and at different trophic levels. Therefore, it is not easy to pinpoint which among several factors induced mammals to fitting to a niche where a smaller/larger size would be required. Extinct endemic insular proboscideans are especially appropriate subjects for investigating this issue, given the frequency with which proboscideans colonised islands, and the multiple patterns in size reduction experienced by endemic taxa on different islands, as well as on a single one. Their evolutionary patterns suggest that, in isolated environments, the body-size of small and large non carnivorous mammals depends on parsimonious optimisation of life-history traits, such as metabolic rate, age at maturation and gestation time, trophic level, home range, and population density. Accordingly, it is rational to hypothesise that insular large herbivores and small mammals change their body-size, perhaps developing novel ecological strategies, in accordance with the size of vacant competitor species and the most appropriate 'empty' niche available on islands.

## JORDAN'S RULE AND VERTEBRAL COUNTS IN FISHES

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Vertebral number is a fundamental meristic character used in descriptions of fish species. The count is fixed by the time an egg hatches and remains invariant through an individual's life. The count is strongly heritable, being fixed, or varying within limits, within a species. However, count is also influenced by environmental conditions during early ontogeny. Jordan's Rule suggests that the number of vertebrae in a species rises with latitude, usually attributed to differences in the temperatures during development. Larger species from a clade typically have more vertebrae than smaller congenerics (pleomerism). There is a phyletic tendency for vertebral counts to be lower in advanced fishes (Williston's Rule). Variation among individuals of a species is lower when the count is lower. Species with low counts often exhibit little response to environmental influences. Slender species may have more vertebrae than stockier species. Changes in body shape during ontogeny relate to changing swimming mode, with more slender species. Low vertebral counts provide a stiffer body and are adaptive for thunniform swimming in which thrust is generated by the tail. Vertebral counts are also influenced by the biome in which individuals live; counts in individuals/populations that spend their entire lives in fresh water are lower than diadromous conspecifics.

## GEOGRAPHIC GRADIENTS IN SPACE AND TIME: LATITUDE, PLANTS, AND THE LATE PLEISTOCENE-HOLOCENE OF EASTERN NORTH AMERICA

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The latitudinal gradient of diversity (LGD) - decreasing richness from the tropics toward either pole - is one of the oldest and most pervasive ecological patterns; yet, it also is one of the least understood. Many mechanisms have been proposed, but discriminating among hypotheses is challenging because of the strong correlations between and among latitude and environmental or historical variables. Abiotic factors (e.g. temperature) certainly are important and likely influence ecogeographic rules as well (e.g. Bergmann's rule [increased body size with increased latitude], Allen's rule [decreased appendage length]). However, biotic factors may be important as well, and potential gradients in predation or competition and concomitant defenses, or life history traits, also would influence the 'evolution' of LGDs. Although LGDs are known for numerous contemporary taxa, relatively little is known about the history of the LGD. Using fossil pollen and contemporary distributional data from the last 16,000 years (16 ky), we reconstructed past and present latitudinal patterns for plants in eastern North America (ENA). A significant LGD appeared in ENA in the late Pleistocene (~13 kya), with the gradient becoming steeper throughout that period (~6 ky) until the beginning of the Holocene (~10 kya). At that time, the steepness of the LGD appeared to stabilize and has been maintained through contemporary time. Understanding the manner in which plants interact with the environment through time should shed light on mechanisms underlying LGDs (and ecogeographic rules); further, changes through time have the unique potential to enable the decoupling of factors correlated in space.

## THE ROADSIDE *MODUS OPERANDI*. EASY WAY FOR EXOTIC PLANTS ON OCEANIC ISLANDS?

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Roads can facilitate invasion and pervasiveness of exotic plants on islands and change native assemblages. We studied floristic and vegetation structure along roadsides across an altitudinal gradient encompassing two contrasting aspects and from coastal scrub to laurel forest in the Anaga massif, NE Tenerife. Samples were taken every 50 m elevation along the road in rectangular plots of 50 $m^2$ at both sides, on leeward and windward slopes. We analysed variation in species richness and floristic composition (endemic, native non-endemic and alien plants) with environmental and human factors. We also studied the distribution of exotic species in relation with their region of origin. In general, exotic species comprised ca. 32% of the road side community. High richness of endemic species was related to rockiness, steep embankments and altitude, while exotic plant richness could be best explained by disturbance factors such as distance to urban nuclei and road side management, but also by the width of the road edge or the amount of soil at surface. The most important floristic gradient was related to altitude for both slopes and for all species groups, being the windward slope floristically more homogeneous along the elevation range, probably due to the influence of prevailing trade winds. Composition of alien species was strongly related to disturbance and soil variables.

## SPATIAL AND TEMPORAL PATTERNS OF BODY SIZE CHANGE IN CALIFORNIA GROUND SQUIRRELS (*SPERMOPHILUS BEECHEYI*)

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Body size change is a common response to habitat variability in small mammals and can indicate both ecological and evolutionary responses to environmental fluctuations. Mammals generally react to temperature directly or indirectly through response to vegetation change, and body size tracks these forces in different ways. Using Bergmann's Rule as a theoretical framework, body size should decrease with increasing temperature if mammals respond directly to climatic warming. However, we expect a more individualistic response based on the natural history of the organism if mammals respond to vegetation changes. One dramatic period of environmental change to affect extant animals was the Pleistocene-Holocene transition. We investigated how the California ground squirrel, *Spermophilus beecheyi*, responds to climate by quantifying diastemal length on two temporal groups of specimens: fossil specimens dated to the Last Glacial Maximum and modern museum specimens from throughout the range of this species. We found that ground squirrels conform to Bergmann's Rule across modern populations, but the temporal pattern of body size change was opposite that predicted by temperature change. We then investigated the influence of several other factors to better understand how body size is controlled in this species. Our data better inform us about the response of these mammalian survivors of the Pleistocene extinction event to future global warming.

## THE IMPORTANCE OF BIOREGIONAL IDENTITY AND SPECIES CHARACTERISTICS TO CONTINENTAL DIVERSITY PATTERNS

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While sampling efforts and improvements in remote sensing technology have advanced our ability to describe broad scale patterns of diversity, the processes generating these patterns remain poorly understood. Our study aims to determine the manner in which species characteristics and biome properties affect continental diversity patterns in North American mammals. We analyze geographic range data to determine levels of biome affinity, or overlap, between geographic ranges and biome extent. We find greater levels of biome affinity than predicted by a random null model of species ranges. The distribution of range size versus body size in those mammals with affinity compared to all mammals is not significantly different. We demonstrate how species with biome affinity contribute to continental diversity patterns in distinct ways, emphasizing the cryptic role that regional variation plays in continental patterns. Our novel methodology emphasizes the interplay of ecological and evolutionary species characteristics with regional variation on often-described continental patterns. Our results highlight the need for a macroecological research agenda that moves beyond simple correlation of continental patterns to one which advances our understanding of the unique role of species and their perception of the environment. We provide new insight into the non-uniform nature of regional source pools for diversity and we discuss the implications of these results for community assembly theory. Our analyses highlight the formerly unrecognized value in biome contributions to diversity that needs to be considered in conservation priority setting.

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## CULTURAL ECOGEOGRAPHY: MODELING INDIGENOUS CULTURAL DIVERSITY PATTERNS

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Indigenous human cultures display consistent ecogeographic patterns of ethnic and linguistic diversity and group and territory size. As with biological species, cultural groups are more concentrated in the tropics, especially in areas of high topographic relief. Although researchers have proposed hypotheses for these correlations, there is currently no rigorous mechanistic framework for explaining and predicting geographic patterns of human cultures. We hypothesize that these patterns are caused by the relative strength of ecologically-based cohesive and divisive forces (operating) within and among groups. Using a global dataset of the distribution of hunter-gatherer populations, we developed a mixed linear model to investigate mechanisms affecting the territory and population sizes of different cultural groups. Net primary production, topographical heterogeneity, standing biomass, and plant species richness constrain group territory size, allowing more groups to be packed into smaller areas and thereby increasing cultural diversity. Using a different worldwide dataset, our model accurately predicts global patterns of indigenous cultural diversity. This study adds to a small but growing body of work on human biogeography and strengthens the inference that environmental factors are the main forces structuring patterns of human cultural diversity.

## NEUTRAL SAMPLING, ABUNDANCE-EXTINCTION DYNAMICS AND NICHE-IMMIGRATION CONSTRAINTS EXPLAIN THE GENERATION OF SPECIES RICHNESS GRADIENTS

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The paradigm that species' patterns of distribution, abundance and coexistence are the result of adaptations of the species to their niches has recently been debated with evidence that similar patterns may be generated by simple neutral processes. We argue here that a better understanding of macroecological patterns requires an integration of both ecological and neutral approaches. We demonstrate the utility of such an integrative approach by testing the power of ecological and neutral processes to explain a species-energy relationship in forest bird species from a particularly well-surveyed Mediterranean region. Using a neutral model based on four conceptually different sampling procedures, we show that neutral processes predict a substantial part (40%) of the observed variation in species richness, but leave considerable variation unexplained. This remaining variation in species richness is better understood as result of non-neutral ecological processes. First, the power of the neutral model to explain observed species richness increases when the probability that a species colonises a new locality is assumed to increase with its niche width, suggesting that ecological differences between species matter when it comes to explain macroecological patterns. Second, extinction risk is significantly lower for species inhabiting high-energy regions, suggesting that abundance-extinction processes play a significant role in shaping species richness patterns. Thus, species-energy relationships may not simply be understood as a result of either ecological or neutral processes, but more likely as a combination of both.

## LINKING BIOGEOGRAPHIC AND LANDSCAPE SCALES THROUGH LANDSCAPE SELF-SIMILARITY: IMPLICATIONS FOR BIRD DISTRIBUTIONS

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Processes acting at local scales, such as site selection by birds, influence the biogeographic distribution of species. Using bird count data from North Dakota, USA, This paper examines the distribution of passerine birds in response to habitat availability at landscape and proximate scales. While site selection occurred simultaneously at both proximate and landscape scales, interactions among scales also helped explain patterns of bird distributions. Further, distributions at proximate and landscape scales helped explain the regional (biogeographic) distribution of species. The link between landscape scales and biogeographic scales was the self-similarity of landscapes across scales: that is, large fragments of a habitat type tended to occur near concentrations of similar habitat. Thus patches of trees tended to occur in regions of abundant tree cover. Versions of this phenomenon have been described in terms of fractal dimension and spatial autocorrelation. Self-similarity in landscapes points to a fundamental problem in island biogeography as it is applied to fragmentation studies: that island size and proximity often covary and are thus confounded. This paper examines self-similarity in the North Dakota study area, as well as other landscapes, and demonstrates that this phenomenon helps explain regional-scale distributions of species, especially birds, as a result of proximate-scale landscape composition.

## GIGANTISM IN MASKED SHREWS (*SOREX CINEREUS*) ON NEARSHORE ISLANDS

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The island rule for mammals has been defined as a graded trend in body size from gigantism in smaller species to dwarfism is larger species. While this pattern is well established within some mammalian taxonomic groups, the pattern is equivocal for Soricids. Here, I explore patterns of morphological variation in cranial, dental, and external characters in populations of masked shrews (*Sorex cinereus*) on small, nearshore islands of a freshwater lake. Surveys of small mammals distributed among fifteen islands and nearby mainland of Greenwood Lake, Cook Co., Minnesota, USA, were initially conducted to investigate island biogeographic relationships and assembly rules for species present on islands. Subsequent univariate and multivariate morphometric analyses distinguished populations of *Sorex cinereus* on three islands from mainland populations. These island populations were characterized by significantly larger body and skull size. Body and skull size did not vary significantly among mainland populations. Inclusion of museum voucher specimens collected in Cook County since 1929 strengthened the morphometric analyses. Inferences are drawn for the roles of density compensation, ecological character release, immigration ability, and resource requirements as selective forces. The island rule is supported for this study.

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## FACTORS DRIVING SPATIAL VARIATION IN FISH SPECIES COMPOSITION WITHIN THE IBERIAN PENINSULA

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The existence of barriers to dispersal among river basins is often considered to be the main factor constraining patterns of spatial variation in fish species composition. Here we test the proposition that dispersal limitation among basins is the most important factor driving current patterns of fish species composition. Occurrences of fish species and environmental variables were gathered from several published and unpublished sources. The number of environmental variables was reduced to two sets (topography, and climate) using cluster analysis, being the number of clusters constrained to be the same as the number of river basins ($c = 35$) to allow comparability between environmental clusters and river basins. Analysis of Similarity (ANOSIM) was used to test the degree of association between fish assemblages and the sets of variables used. We found that fish species composition was significantly different among basins, topographies, and climate ($P < 0.1\%$ for all comparisons), being basins the factor better segregating the species composition (*Global* R = 0.768). Our results support the view that dispersal limitation between isolated basins is the major factor determining species composition among fish assemblages in the Iberian Peninsula.

## IDENTIFICATION OF AREAS OF ENDEMISM FROM CO-OCCURRENCE PATTERNS

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Areas of endemism are considered the basic units in historical biogeography. However, there is no consensus on their definition and on the analytical methods for their delineation. Moreover, it has been argued that areas of endemism are not the proper units for biogeographical analyses, and it has been suggested that biotic elements, which are a group of taxa whose ranges are significantly more similar to each other than to the ranges of other taxa, are more appropriate. We combine the notions of biotic elements and of areas of endemism by developing and implementing a two-stage procedure. Fist, we use a null model approach to determine which pairs of areas (grids) and species have a significant degree of co-occurrence. Subsequently, we construct similarity matrices (using all grids, or alternatively only those where significant co-occurring species pairs exist), as input to a clustering algorithm, using binary coding for significant co-occurrence and its absence. To examine the utility of our method we analyze the well-known data set on *Sciobius* in southern Africa, as well as data on endemic invertebrate taxa in southern Greece. Our results are similar, but not identical, to those of previous analyses, and produce meaningful delineation of areas of endemism in southern Greece. We discuss our results in conjunction with other current approaches.

## ANOTHER FACE OF PLANT BIODIVERSITY AND RARENESS: THE CONTRIBUTION OF COMMON PLANTS AND DISTURBED HABITATS

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Plant conservation has been mainly focussed on endemic and very rare plants, often restricted to very well preserved habitats such as alpine grasslands, woodlands, etc. The abandoning of traditional economies, together with intensive agricultural practices, however, are changing the abundance of different habitats, and thus some groups of common or even invasives species are becoming scarce in the last years. The Aragon county, located in the NE of Spain, hosts 3,400 vascular plants, nearly 25% of the European flora in barely 50,000 km$^2$. Such biodiversity results from strong ecological gradients (altitude, climate, geology) and intensive traditional land use. We have analysed the spatial plant distribution regarding the main habitats where those plants usually occur and their degree of naturalness, in order to review criteria for conservation policies. Supraforestal pastures and rocky habitats (cliffs, screes, etc) host the highest number of species (778 and 368 respectively), while near 800 grow in agricultural lands and other areas of traditional uses. By classifying habitats into 4 categories of 'naturalness' (from highly anthropic to pristine), we found that 48% of the total flora occur in habitats considered of low or medium naturalness, and therefore are associated to an intensive human use. Nevertheless, different patterns can be observed when analysing parts of the territory with different topographic characteristics (mountains and valleys) or when considering only rare species. Overall, our results suggest that an important decrease in plant biodiversity is expected in mountain areas where traditional economies are being substituted during the last decades.

## IS BIGGER REALLY BETTER? ANALYSING GEOGRAPHIC VARIATION OF AVIAN BODY SIZES IN SOUTH AFRICA

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Bergmann's rule, which states that body size increases with latitude, is one of the oldest and most tested ecogeographic rules. Debate exists about the validity of the rule and about the mechanisms responsible for the generation of this pattern. We investigated spatial variation in median body size of South African avian assemblages. In addition to testing for associations of size with environmental variables that could be invoked to explain observed patterns of variation, the effect of sampling from the regional body size frequency distribution on size variation was investigated. South African birds do not exhibit a latitudinal body size cline. Seasonal variability in NDVI was the best predictor of median body size, suggesting that large body size may be advantageous in more seasonal environments by allowing birds to survive periods of low resource availability. However, random draw models were also good predictors of variability in body size. This illustrates the importance of considering the regional body size frequency distribution when assessing geographic body size variation, and indicates that the mechanisms generating regional body size frequency distributions may be affecting body sizes at local scales too.

## PHYLOGENETIC DISPERSION OF VASCULAR PLANT COMMUNITIES DIFFERS ALONG ELEVATION AND WITH SCALE

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Phylogenetic dispersion of species in a community may give valuable information about how communities assemble. The assemblage of species may be governed by different processes along an environmental gradient and with scale. We examine the ratio of mean number of species in a family for different communities to study the phylogenetic dispersion of vascular plant species at three different scales along 12 elevational gradients in Norway. The number of species per family is in all cases compared to an expectation from null models based on number of species in the sample and a defined species pool. The results are both scale dependent and vary with elevation. Generally more species per family are observed than expected in the communities, i.e. phylogenetic clustering. Phylogenetic clustering is strongest when the species pool is defined as all the species found on the mountain. Defining a more local species pool results in a weak, not statistically significant, trend of phylogenetic clustering. Trend in the species-to-family ratio with elevation shows that there are more species per family at higher altitudes than at low altitudes at the broadest sampling scale. The opposite pattern is observed for the smallest sampling scale, i.e. it is observed relatively higher number of species per family at low altitudes compared to high altitudes.

## THE SCALE-DEPENDENCE OF RANGE MAPS FOR CHARACTERIZING SPECIES DISTRIBUTIONS AND RICHNESS PATTERNS

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Range map data form the basis for many macroecological studies on the distribution of species and community level patterns. However, species distributions are typically much patchier than suggested by even the most detailed range maps and the spatial scale at which range maps accurately characterize those distributions is unclear. We used fine-scale bird atlas data from two regions of the globe, Australia and southern Africa, to explore the scale-dependence of range maps for representing species distributions and patterns of species richness. We found that at the finest resolution (one quarter degree), species typically only occurred over 45-55% of the grid cells at which they were expected to occur based on range maps. Range maps also vastly overestimate the number of species that coexist at finer spatial resolutions. At coarser scales, range map data become better approximations of atlas-based distributional patterns, and range occupancy values increase asymptotically towards unity. At two degrees resolution, the vast majority (>75%) of species are observed on at least 80% of the grid cells predicted by range maps. This is also the spatial resolution at which atlas- and range map-based measures of species richness appear to converge. Range map data is only relevant for testing macroecological hypotheses that invoke processes occurring at relatively coarse spatial scales.

## DOES SIZE MATTER FOR DISPERSAL DISTANCE?

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Does maximum dispersal distance vary with propagule size? And does the observed pattern differ for passive and active dispersers? Students in a Biogeography course collected 795 data values from the peer-reviewed literature for direct observations of maximal dispersal distance and mass of the dispersing organisms. Collected dispersal distance and mass data spanned 9 and 21 orders of magnitude, respectively, and were analyzed for macroecology patterns using EcoSim software and least-square regressions. Active dispersers moved significantly farther ($p < 0.001$) and were significantly greater in mass ($p < 0.001$) than passive dispersers. Actively-dispersing taxa differed widely in the clarity, significance, and slope of the distance-mass relationship, but overall, size matters: larger active dispersers attained greater maximum observed dispersal distances than smaller active dispersers. In contrast, passive disperser distances were random with respect to propagule mass, but not uniformly random, in part due to sparse data available for tiny propagules. Taxonomic variance in distance-mass relationships likely reflects life history differences and indicates that allometric scaling 'rules' for dispersal distance will not be universal. Claims that microbes disperse widely cannot be tested by current data based on direct observations of dispersal: indirect approaches will need to be applied. Distance-mass relationships should help resolve neutral- and niche-based metacommunity theories by helping scale expectations for dispersal limitation. Also, distance-mass relationships should inform analyses of latitudinal species richness and conservation biology topics such as fragmentation, umbrella species, and taxonomic homogenization.

## VEGETATION MAPPING OF NORTH-WESTERN FENNOSCANDIA USING LANDSAT TM/ETM+ DATA

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North-western Fennoscandia comprises the northern parts of Norway, Sweden, and Finland. The area represents a transition between humid, oceanic areas in the west and drier, more flat, continental parts towards the east. It also includes a transition from boreal forest in the south to treeless Arctic tundra in the north. Due to the gradients running in different directions the vegetation composition is varied and though difficult to portray consistently in vegetation maps. The overall aim of the performed mapping has been to generate a generalized, consistent, and seamless vegetation map for the selected area. Several Landsat TM/ETM+ images have been processed through six operational stages: (1) spectral classification, (2) spectral similarity analysis, (3) generation of classified image mosaics, (4) ancillary data analysis, (5) contextual correction, and (6) standardization of the final map products. Analysis performed on the spectral-only data is often denoted the pre-classification process, whereas the post-classification process involves an integration of ancillary data. The final vegetation map portrays the area with a ground resolution of 100 meter. The map produced has shown to be important in a wide range of studies, involving reindeer range studies, climate impact studies, land degradation and pollution impact studies.

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## LANDSCAPE POPULATION DYNAMICS FOR A RAIN FOREST CANOPY TREE: INTEGRATING BIOGEOGRAPHIC PERSPECTIVES WITH COMMUNITY ECOLOGY USING SATELLITE REMOTE SENSING.

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Testing biogeographic theory in community ecology requires integrating information across spatial scales and levels of ecological organization. In tropical rain forests, logistical constraints on sampling adult trees adequately have prevented a comprehensive marriage of these disciplines: densities for most tropical tree species are <1 individual · $ha^{-1}$, so that impractically large areas must be searched just to obtain modest samples High-spatial resolution satellite remote sensing technology (with pixels <1 $m^2$) can provide precise information on the distribution, abundance, and dynamics of individual trees, while retaining the essential capacity to deal with large landscapes. We used time series image data from the QuickBird satellite (0.6 $m^2$), and capture-mark-recapture modelling, to quantify landscape variation in survival, recruitment, and realized population growth for adult *Tabebuia guayacan*, a rain forest canopy tree on 16 $km^2$ Barro Colorado Island, Panama. Compensating effects of survival and recruitment generated variation in population growth. Adult abundance increased within 1,276 ha (81%) of the island, particularly in edge habitat and second-growth forest, but was not different from replacement levels deep within the forest interior. Our results demonstrate that satellite remote inventory is feasible for at least some tropical tree species, providing large samples, over geographic areas where field work is impractical.

## SPECIES RICHNESS OF BIRDS AND WOODY PLANTS: TESTING FUNCTIONAL RELATIONSHIPS

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The species richness of different taxa might be correlated due to (i) random coincidence, (ii) interactions between taxa, or (iii) similar response to environmental factors. Here we examine the spatial covariance in bird and woody plant species richness in Kenya by compiling a geographic database at a spatial scale of 0.5° latitude-longitude cells, summarizing all birds, native woody plants, and seven environmental variables (temperature, precipitation, topographic relief, productivity, habitat diversity, land cover diversity, percent woody cover). To test for functional relationships in cross-taxon congruence patterns, we classify bird species into four frugivore groups (obligate frugivores, partial frugivores, opportunistic fruit eaters, all other species), and woody plant species into three resource groups (*Ficus* species - a potential keystone plant resource for frugivores in the tropics, other fleshy-fruited plant species, and all other species). We test whether species richness of avian frugivores is largely determined by food-plant diversity, and whether climate, topography and habitat structure influence species richness patterns directly or indirectly. Our analyses address the question of whether species richness of some taxa can be used to predict species richness of other groups when functional relationships are taken into account.

## YEAST BIOGEOGRAPHY AND THE UBIQUITY DEBATE

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One currently advocated interpretation of Beijerinck's principle, "everything is everywhere", is that the microbial world consists of a relatively small number of very widely distributed species and consequently that the study of microbial biogeography is a vain pursuit (e.g. Fenchel & Finlay 2004 Bioscience 54:777-784). Here, I explore the question of ubiquity in two groups of related yeasts that were sampled extensively across the globe. Recent advances in sequence-based yeast identification methods have caused an explosion in the number of yeast species descriptions and have allowed biogeographic hypotheses to be tested. Yeasts assigned to the plant decay-associated *Sporopachydermia* clade belong to 21 phylotypes, 17 of which probably represent separate species. A single species, *S. lactativora* might be construed as cosmopolitan; in all other cases, the phylotypes have distributions that can be attributed to vicariance or dispersal, and many appear to be endemic. Likewise, a large collection of *Metschnikowia* and related species isolated from ephemeral flowers and their nitidulid beetles or other insects can be assigned clearly to 22 biological species whose distributions follow patterns that are consistent with biogeographic history. Endemism predominates, although some cosmopolitain species also exit. Of special interest is the recent discovery that endemic beetles that live on endemic plants of Hawai'i harbour at least six endemic sister species of *Metschnikowia*. In addition, yeast species found in ephemeral flowers and associated insects exhibit a latitudinal species richness gradient. Taken together, these results provide strong support to the view that in effect, many microorganisms are subject to the rules of historical biogeography.

## ASSESSING THE RELEVANCE OF UNAVOIDABLY COLONIZATION ROUTES IN CURRENT BIODIVERSITY PATTERNS

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The geomorphological and topographic characteristics of a territory should impose limitations to the connectivity of localities as well as to the dispersal of organisms under climate change scenarios. Building a friction surface considering both altitude and the distance-to-rivers the cost of dispersion from northern and western Europe source localities to the Iberian Peninsula has been calculated and subsequently related with the species richness of those endemic species that inhabit Iberian mountains, highlighting the importance of the spatial configuration of the territory to explain current distribution of southern Mediterranean endemics.

## ENVIRONMENTAL FACTORS INFLUENCING THE DISTRIBUTION OF THE FORESTS OF THE NORTHERN PARAGUAYAN CHACO

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The Chaco is one of the most interesting and original eco-regions in South-America. Its range, approximately 1 million square kilometers, covers a large part of the centre of the continent and includes a great diversity of ecological systems with different kinds of forests and dry, deciduous shrublands. This case study was carried out on the northern Paraguayan Chaco, with parallel 21º 30' as the southern limit in an extension of about 4,700,000 hectares. It includes 7 Protected Wild Areas. The temperature varies between 25 and 26.5 ºC according to the areas while the rainfall ranges between 300 in the west and 1,200 mm in the east. This work identifies both, soil and climatic factors characterizing the structure and composition of the 26 forests previously identified in the area.

## GEOGRAPHIC RANGE SIZE HERITABILITY: WHAT DO NEUTRAL MODELS WITH DIFFERENT MODES OF SPECIATION PREDICT?

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Phylogenetic conservatism or heritability of the geographic range sizes of species (i.e. the tendency for closely related species to share similar range sizes) has been predicted to occur because of the strong phylogenetic conservatism of niche traits. However, the extent of such heritability in range size is disputed and the role of biology in shaping this attribute remains unclear. Here, we investigate the level of heritability of geographic range sizes that is generated from neutral models assuming no biological differences between species. We used three different neutral models, which differ in their speciation mode, to simulate the life-history of 250,000 individuals in a square lattice of 50 x 50 cells according to stochastic events. The heritability of geographic range size was assessed using an asymmetry coefficient between range sizes of sister species and using the coefficient of correlation between the range sizes of ancestors and their descendants. Our results demonstrated the ability of neutral models to mimic some important observed patterns in the heritability of geographic range size. Consistently, sister species exhibited higher asymmetry in range sizes than expected by chance, and correlations between the range sizes of ancestor-descendant species pairs, although often weak, were almost invariably positive. Our findings suggest that, even without any biological trait differences, statistically significant heritability in the geographic range sizes of species can be found. This heritability is weaker than that observed in some empirical studies, but suggests that even here a substantial component of heritability may not necessarily be associated with niche conservatism.

## THE INFLUENCE OF BODY SIZE ON NORTH AMERICAN LAND SNAIL DISTANCE DECAY RATES

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Limited theory and empirical investigation suggests that the species richness Body Size Distribution (BSD) may simply reflect a rarefaction of the individual abundance BSD. The distribution of North American land snail abundances along the body size spectrum exhibits a strong right-skew from site to regional scales for both northeastern bedrock outcrops (146,750 individuals, 144 taxa, 320 sites) and southwestern montane forests (36,402 individuals, 86 taxa, 90 sites). While the distribution of species richness mimics this pattern at site scales, large taxa are strongly overrepresented at regional scales. To better understand the mechanisms underlying this decoupling, compostional similarity (based on Jaccard's Index) was compared to geographic distance between all pairwise combinations of sites. Distance decay rates were calculated separately for small (maximum shell dimension < 5 mm), medium (5-10 mm), and large (> 10 mm) taxa by determining best fit negative exponential functions. These analyses demonstrate that large taxa experience 2-14 times greater distance decay rates as compared to medium and small taxa. In the southwest, where this discrepancy is most pronounced, most large taxa represent endemics limited to single mountain ranges while smaller taxa tend to occur on multiple ranges. This suggests that large taxa experience lower rates of long-distance passive dispersal, allowing for heightened rates of allopatric speciation and greater rates of geographic turnover.

## IMPORTANCE OF DISPERSAL, LOCAL DOMINANCE, NICHE BREADTH AND NICHE POSITION FOR THE RANGE SIZE OF EUROPEAN PLANT SPECIES

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Why are some species more widespread than others? Several hypotheses try to answer this fundamental ecological question. Here, we test four of these on ~400 European plant species, i.e. the extent to which high dispersal ability, high local dominance, low niche position (i.e. common environment), or a broad niche confers relatively large range sizes. With respect to dispersal ability, we furthermore examine the relative importance of human-mediated contra natural dispersal vectors as range size controls. Range size was derived from Atlas Florae Europaeae. Dispersal ability was estimated as the number of dispersal vectors cited for each species. Local dominance was an estimate of the degree of dominance exhibited at occupied local sites. Niche position and niche breadth were expressed in terms of the commonness and range of environmental conditions preferred or experienced by a species at purely local, local and regional, or European scales. Range size was related in the hypothesized manner to all four species traits. Together these traits accounted for 18-62% of variation in range size among species. The observed patterns remained significant when tested using phylogenetically independent contrasts, and when accounting for a possible purely statistical relationship between range size and the number of dispersal vectors cited per species. The importance of dispersal ability was mainly due to dispersal by humans, but natural dispersal mechanisms, especially endozoochory and epizoochory, also contributed. In conclusion, European plant species range sizes appear to be about equally controlled by dispersal ability, local dominance, niche breadth and niche position.

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## A TEST OF RAPOPORT'S RULE COMPARING THE MIGRATORY AND SEDENTARY PASSERINE BIRDS OF THE WESTERN PALEARCTIC

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That organisms residing on high latitudes generally endure a wider range of climatic conditions over the seasons than low-latitude organisms is a popular yet controversial explanation for 'Rapoport's rule', the tendency of species range sizes to grow with increasing latitude. This explanation relies on a prediction that species like migratory birds, which escape the most of the local seasonality in climate, should be exceptions to Rapoport's rule. It has also been proposed to link latitudinally increasing range sizes to why species richness usually declines with latitude. We analyzed the ranges of 257 passerine bird species and their subspecies, breeding in the Western Palearctic between 20° and 72°30' N, and found patterns conforming to Rapoport's rule on both taxonomic levels, but in migratory rather than resident species. Species range distributions were bimodal rather than gradient, with small ranges in the south and large ranges in the north. A concomitant latitudinal decrease in species richness appeared to be a statistical artifact without biological significance. These relationships challenge the seasonal climatic variability hypothesis as well as its proposed role as a link between Rapoport's rule and latitudinal gradients in species richness.

## THE GEOGRAPHY OF AMPHIBIAN BODY SIZE IN THE HOLARCTIC

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We describe the broad-scale patterns of mean body size of the European and North American amphibian faunas. We also explore relationships between body size and environmental predictors to test six hypotheses: heat balance, size dependence, migration ability, primary productivity, seasonality, and water availability. We use OLS multiple regression and AIC-based model selection techniques to evaluate the relative support for each hypothesis. We found consistent body size gradients and similar dependencies on environmental variables within each amphibian group in Europe and North America. Annual potential evapotranspiration, a measure of environmental energy, was the strongest predictor of mean body size in both regions. However, the contrasting responses to ambient energy in each amphibian group resulted in opposite body size trends, i.e. anurans increased in size from high to low energy areas in both continents, whilst urodeles showed the opposite pattern. Our results support the heat balance hypothesis, suggesting that the thermoregulatory abilities of anurans would allow them to reach larger sizes in colder climates by optimizing the trade-off between heating and cooling rates, whereas a lack of such strategies among urodele faunas would explain why these organisms tend to be smaller in cooler areas. These findings may also have implications for the role of climate warming on global amphibian declines.

## SCALE AND BETA DIVERSITY OF VERTEBRATES IN MEXICO

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Mexico is a megadiverse country, ranking as one of the richest in terrestrial vertebrate species. Surprisingly, no multi-taxa analyses have been done for understanding the factors explaining this extraordinary diversity. The aim of this study is to analyze the scaling of beta diversity of the Mexican terrestrial vertebrates in five contrasting regions. Distributional data for species of different terrestrial vertebrate groups were generated by an ecological niche modelling approach. We then created log species-scale plots, which allowed us to depict alpha, beta and gamma diversity simultaneously. Analyses were performed for eight scales, ranging from 1/32º (~12 km$^2$) to 4º (~190,000 km$^2$) Squares. Results showed contrasting patterns of diversity between the different taxonomic groups. Beta diversity was higher at the three larger scales in all vertebrates, particularly at Central and Southern latitudes of Mexico. However, strong differences were found between the regions and between taxa. While beta diversity of reptiles and amphibians was high almost along all scales, mammals were more sensitive to larger scales. Conversely, birds were the least sensitive group, showing lower beta diversity countrywide. Results confirmed the important role of beta diversity in the conformation of biogeographic patterns of Mexico's megadiversity.

## DOES THE LIFE HISTORY OF *MUSCARDINUS AVELLANARIUS* (MAMMALIA) FOLLOW AN ECOGEOGRAPHIC GRADIENT?

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Hibernation is a significant feature of Glirids' life history, as it influences survival and reproduction. Field studies on *Muscardinus avellanarius* evidenced the lack of hibernation in some Mediterranean ecosystems. Therefore, I reviewed the literature to find out other discontinuities in its hibernation, from Lithuania to Sicily. Initially, I employed a General Linear Model design to extract the significant predictors of hibernation. Next, I searched for an altitudinal/latitudinal pattern in the hibernation presence/absence, by the macroecology module of ECOSIM. These analyses evidenced the determinant role of altitude/latitude, suggesting that the hibernation zone of *M. avellanarius* moves down to lower altitudes as the latitude increases; as consequence such a zone would approach to 0 m asl at around 45° N (Turin latitude). Lastly, I used the life history parameters (n and mean size of litters, mean weight of reproductive female, mean survival of population, etc) from a long-term study (1995-2005, 16,636 checks of 100-150 artificial nest-boxes, 1,086 handled individuals) and arranged them according to the vegetation belts (Mediterranean, Colchic, Subatlantic) of Northern Sicily. The species' life history among the three belts is different, as in the Subatlantic (>1,300 m asl) dormice show the customary North-European strategy (i.e. winter hibernation and summer reproduction) whereas, hibernation is absent in the Mediterranean or much reduced in the Colchic. Accordingly, dormice lack autumnal fattening, aestivate in the hottest months and reproduce all the year round.

## GLOBAL DISTRIBUTIONAL PATTERNS OF TERRESTRIAL ISOPODS

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Terrestrial isopods (Isopoda, Onsicidea) are adapted almost to the whole range of terrestrial habitats, have a worldwide distribution and relatively high species diversity. A recent global inventory reported more than 3,500 species. All terrestrial isopod records till 2005 were analyzed in an attempt to explore global distributional patterns of general biogeographic interest. Emphasis was given in three aspects of global patterns: (a) 'hotspot' analysis was performed using various criteria and taxonomic ranks. Circum-Mediterranean regions exhibit the highest diversity, together with some tropical insular areas (e.g. Seychelles) and some other regions with Mediterranean-Type Ecosystems (e.g. South Africa). (b) latitudinal gradients were explored at different geographical scales, taking into account variation in sampling effort and effects of land cover within each band. There are suggestive trends of decreasing diversity with latitude at local scale, although globally diversity peaks at medium latitudes. (c) Rapoport's rule was also investigated at different scales, revealing a pattern in conformity with the rule's principles, but not necessarily with its expression as a latitudinal trend. Distributional ranges seem to decline in relation to species richness, which for Oniscidea peaks at northern temperate and southern tropical insular regions. A hypothesis for the establishment of terrestrial isopod diversity, taking into account the ecological characteristics of the group, is given.

## A TALE OF TWO SPECIES: EXTIRPATION, RANGE EXPANSION AND EVOLUTION IN AN EXTREME ENVIRONMENT DURING THE LATE QUATERNARY

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Death Valley, California is today the hottest and driest area in the western Hemisphere, with temperatures of 134ºF (57ºC) recorded. During the late Quaternary, pluvial lake Manly covered much of the Valley floor and contributed to a much more moderate climate. The abrupt draining of Lake Manly in the mid-Holocene led to dramatic shifts in temperature and aridity and exerted substantial selection pressure on organisms living in this area. Our research investigates the adaptive response of *Neotoma* (woodrats) to temperature change over the late Quaternary along a steep elevational and environmental gradient (-84 to >3,400 m). By combining field-work, examination of museum specimens, and collection of paleomiddens, our project reconstructs the divergent evolutionary histories of animals from the Valley floor and nearby mountain gradients. We report on recent paleomidden work investigating the transition zone along the Grapevine Mountains for two species of woodrats differing significantly in size and habitat preferences (*N. lepida*, desert woodrat and *N. cinerea*, bushy-tailed woodrat). Here, at the limits of animal's thermal and ecological thresholds, we demonstrate dramatic fluctuations in the range boundaries between these species over the Holocene as climate shifted. Moreover, we find fundamental differences in the adaptive response of these two species related to the elevation of the site and local microclimate. Results indicate that although *N. cinerea* are currently extirpated in this area, they were ubiquitous throughout the late Pleistocene and were found as low as 400 m elevation.

## QUANTITATIVE TESTING OF LATITUDINAL BIODIVERSITY GRADIENTS USING BENTHIC FORAMINIFERA IN THE DEEP ATLANTIC OCEAN

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The pattern of increasing diversity toward low latitudes has been demonstrated in many terrestrial and pelagic groups, as well as some benthic groups. A variety of hypotheses have been proposed to explain patterns of diversity with latitude, including species-area, mid-domain, competition-predation, and environmental stability/predictability. Many of these hypotheses invoke such diversity determinants as temperature or light to explain observed patterns. Deep sea benthic foraminiferal diversity is ideal as a test of several proposed latitudinal biodiversity hypotheses because the deep sea has virtually no latitudinal temperature gradient. The very different environmental conditions of the deep sea compared to the surface ocean imply that the same hypotheses will predict very different patterns in diversity. Here we determine the pattern of species richness in deep sea benthic foraminifera in the Atlantic Ocean, and use this pattern to quantitatively test several diversity hypotheses. The data suggests that the deep sea diversity of benthic foraminifera is low compared to shallower groups, with only a slight increase in species richness toward the equator. This relatively flat distribution of benthos compared to the peaked distribution of surface water biodiversity suggests that energy, rather than area or biological factors, may be an important determinant for latitudinal diversity patterns in the ocean.

## DOES THE GENOME SIZE INFLUENCE RARITY OF PLANTS AND VERTEBRATES?

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Accumulation of selfish DNA in cells has fundamental consequences for organism metabolism. Detrimental effects of large genome size have been demonstrated in several aspects of performance of plant and animal species. Here we check if large genome affects rarity among plants and vertebrates. We show that that genome size is universally correlated with rarity of Polish plants and birds, as well as European mammals, reptiles and amphibians. While phylogeny is included into the model correlation weakens. Detection of this pattern provides clue to important idea that large scale patterns stem from differences observed at cellular level.

## *Symposium 2*

# Quaternary impacts on Holarctic biogeography

## U-SHAPED EVOLUTION OF THE BLUE TIT COMPLEX AROUND THE MEDITERRANEAN SEA

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The blue tit complex is comprised of three recognized species, the Blue tit (*Parus caeruleus*), the Ultramarine tit (*Parus teneriffae*) and the Azure tit (*Parus cyanus*). The mitochondrial phylogeny of these three species has been previously studied and it was found that the Azure tit is phylogenetically nested within the Blue tit clade, whereas the Ultramarine tit forms a separate monophyletic clade. We have sequenced a part of the mitochondrial control region from populations belonging to the blue tit complex originating from all over the distribution range of the three species, Europe, Northern Africa, the Canary Islands, Near-East and Asia. Phylogenetic analyses showed that several subspecies of these three species are congruent with the 'traditional' morphological classification, but some not. Phylogeographical analyses show, that the complex has evolved around the Mediterranean Sea, forming a U-shaped pattern, where the phylogenetically most distant ends do not come into contact. Populations close to the Mediterranean are genetically more diverse than populations further north or east. The origin and evolutionary history of the species complex is discussed in the light of these findings.

## RELATING GEOGRAPHICAL VARIATION IN POLLINATION TYPES TO ENVIRONMENTAL AND SPATIAL FACTORS

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The relative frequencies of functional traits of plant species show notable spatial variation, which is often related to environmental factors. Pollination type (insect-, wind- or self-pollination) is a critical trait for plant reproduction and provision of ecosystem services. We mapped the distribution of pollination types across Germany by combining databases on plant distribution and plant pollination types. Applying a new method, we modelled the composition of pollination types using a set of 12 environmental variables as predictors within a Bayesian framework which allows for the analysis of compositional data in the presence of spatial autocorrelation. A clear biogeographical pattern in the distribution of pollination types was revealed which was adequately captured by our model. The most striking relationship was a relative increase of insect-pollination, and corresponding decrease of selfing, with increasing altitude. Further important factors were wind speed, geology and land use. We present a powerful tool to analyse the distribution patterns of plant functional types such as pollination types and their relationship with environmental parameters in a spatially explicit framework.

## BIOGEOGRAPHY OF PALEARCTIC VEGETATION VIEWED WITH A PLEISTOCENE LENS

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In this talk we will summarize current ideas on Palearctic biogeography and contrast these findings, which are mainly based on flowering plants, with examples from spore bearing plants. Cryptogamic plants differ in particular in their diversity of reproductive biology, wind-born spores, up to three distinct breeding systems and sexual vs clonal reproduction. Exploring discontinuities within taxa in (1) distribution patterns, (2) ploidy levels, (3) breeding systems and (4) genetic diversity we gain new and interesting insights in discovering phylogeographic patterns, evolutionary processes during the Pleistocene and delimiting long-term glacial refugia, thus potentially aiding conservation priority setting.

## NEARCTIC PITVIPERS AND PLEISTOCENE GLACIATIONS

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Although Pleistocene effects were discussed both by Darwin and Wallace, the manner in which they have shaped Holarctic biodiversity remains nebulous. The passive vicariance of ice sheets impacted species and distributions, yet their active role in driving and/or amplifying global climate variability is less appreciated. Thus, while scale and timing of Pleistocene climatic change is known at a fine-grained level (i.e. Greenland Ice Core Project), effects on speciation and biotic diversification are equivocal. However, molecular genetic techniques now allow the last 2 million years of evolution to be confidently interpreted, to include an understanding of how Holarctic biodiversity has been fragmented, isolated, expanded and coalesced through time and space. Here, we utilize nuclear and mitochondrial (mt) DNA data to investigate the Quaternary biogeography of four eastern North American pitvipers [Massasauga (*Sistrurus catenatus*), Timber Rattlesnake (*Crotalus horridus*), and Copperhead (*Agkistrodon contortrix*), Watermoccasin (*A. piscivorus*)]. We were interested in the manner by which past climate had impacted the migrations, retreats, refugial stases and eventual post-glacial expansions of these ectothermic animals. We sought answers using parsimony and maximum likelihood analyses, tested intraspecific clades for population expansions, applied an isolation-with-migration model to determine bi-directional migration rates (*m*) among regions, and inferred divergence times for species and clades by applying a semi-parametric penalized likelihood approach to our mtDNA data. All taxa were significantly (and differentially) affected by the Laurentide glacier with each showing evidence of glacial refugia within their distributions and subsequent expansions from these as climate improved.

## QUATERNARY REFUGIA AS A FACTOR IN THE HOLOCENE DISTRIBUTION OF EUROPEAN BEECH

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The European beech (*Fagus sylvatica* L.) is a widely distributed European tree that has been the subject of countless scientific investigations. A wealth of fossil data document its past distribution and many genetic surveys with different markers and statistical approaches have been carried out to describe its modern genetic structure. The present paper combines fossil and genetic data to outline the Holocene history of the European beech, with reference to the duration, location, number and extent of its glacial refugia and modes of its postglacial expansion. The main results can be summarized as follows: (1) the modern genetic diversity was shaped over multiple glacial-interglacial cycles, (2) beech started the Holocene spread from multiple refuge areas, (3) the central European refugia were separated from the Mediterranean ones, (4) the Mediterranean refugia did not contribute to the colonization of central and northern Europe, (5) some populations considerably expanded during the postglacial, while others experienced only a limited expansion, (6) the overall postglacial increase of beech forest cover was exponential, (7) the last glacial refugia for beech were hundred times smaller than its modern potential cover.

## HOLARCTIC PHYLOGEOGRAPHY AND QUATERNARY BIOGEOGRAPHY: A SYNTHESIS

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Phylogeography is young, and its exponential growth is due to advances in Paleoclimatology and Genetics. This ability to see genes in space and time is having an impact on our understanding of historical biogeography and evolution. The extent of our knowledge of the Holarctic is considerable for Europe and North America, but Asia is little studied, and so too the Deserts, Tropics and Oceans. What does Paleoclimatic, fossil and genetic data, and their combination tell us? The ice ages have repeatedly modified species ranges, and produced genetic divergence among populations across the range, which can be used to deduce evolutionary history, postglacial colonization routes and glacial refugia. A few examples will be dealt with in detail to illustrate the major points. Since species differ in niche, geographic range and genetic history, we need to study many species to see general trends and principles. Comparisons will be made among different continents and regions using pertinent examples from the Arctic, Temperate plains and mountains, and plants and animals, leading to current debates and future prospects.

## *ARABIDOPSIS LYRATA* SSP. *PETRAEA*: NON-MODEL PATTERNS OF GLACIAL HISTORY IN A MODEL PLANT

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*Arabidopsis lyrata*, a close relative to *A. thaliana*, is an emerging model organism for evolutionary and ecological genetics of plants. Climate oscillations during Quaternary have caused dramatic geographic structuring of variation in this plant due to range fragmentation, genetic drift and recolonisation. With no fossil remains and no extant populations in putative southern European glacial refugia, the lack of a phylogeographic hypothesis is hindering the study of selection and adaptation in natural populations. Populations from its entire and disjunct European range were studied for nuclear and cpDNA diversity. All populations were highly genetically variable, but geographic location and genetic diversity did not correlate. Population differentiation between central and northern Europe areas was significant, but differentiation is only moderate within regions. Chloroplast DNA confirmed the existence of two gene pools and identified population admixture around the southern edges of northern distribution ranges. Thus, during the last glaciation the small perennial plant survived in two refugia between the Nordic and Alpine glaciers, one cryptic, one in central Europe. Postglacial recolonisation may have occurred in two waves with entire populations undergoing range expansion at the margin of receding glaciers, preserving genetic diversity and subsequently forming widespread admixture zones.

## BIOGEOGRAPHY OF ITALIAN MOUNTAIN RANGES: EVIDENCE FROM *ARABIS ALPINA* (BRASSICACEAEA)

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*Arabis alpina* is a widespread plant in European arctic and alpine environments, including all major mountain ranges in Italy. We sampled populations from Sicily in the south to Lake Garda in the north, studying nuclear and cpDNA diversity. Populations in the Alps had significantly lower levels of nuclear genetic variation (*P*, *Ae*, *Ho*, and gene diversity) compared to the Italian peninsular populations. Both the Western and Eastern Alps had significant departures from Hardy-Weinberg Equilibrium expectations ($F_{IS}$=0.368 and 0.598), suggesting a breakdown in self-incompatibility (possibly coinciding with leading-edge colonisation), while the Italian peninsular populations were all outbreeding ($F_{IS}$=0.076). Genetic variation was strongly partitioned between the Alps and the Italian peninsular ($F_{ST}$=0.430) and local differentiation was detected at all geographic scales. We conclude that *Arabis alpina* initially colonised the Italian peninsular during the early Quaternary, and remnants of that original colonisation are still found in Sicily. Climate oscillation, range fragmentation and genetic drift resulted in the formation of multiple refugia along the Italian peninsular. The western Alps were probably re-colonised from a northern Italian gene pool, but the eastern Alps population probably originate from a very recent postglacial expansion from outside the Italian refugia.

## SPECIES SURVIVAL IN NORTHERLY GLACIAL REFUGIA OF EUROPE: CHANCE OR CHOICE?

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The Iberian, Italian and Balkan peninsulas are considered to have been refugia for many temperate species during the last glaciation. It is believed that these were source areas for species that migrated northwards following the glacial retreat. However, recent fossil evidence suggests that many species also survived in cryptic northern refugia and rapidly colonized northern Europe following the glacial retreat. So the question is: which species survived in the three Mediterranean peninsulas and which survived elsewhere? The cryptic northern refugia were presumably small patches of suitable habitat in inhospitable landscapes – somewhat similar to forest patches in fragmented landscapes. Work on presently fragmented landscapes and the ecological traits of species in them, has demonstrated that these species possess a number of key characteristics pertinent to their survival. We obtained fossil and genetic evidence of species survival in Pleistocene glacial refugia through a literature search and scored each species thus surveyed for a number of distribution, habitat and life-history traits. Here we explore these traits in relation to the fossil and genetic evidence for over hundred species that survived in Pleistocene glacial refugia of Europe and ask whether northerly survival was a matter of chance or choice.

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## VEGETATION DURING THE LATE-HOLOCENE IN TENERIFE (CANARY ISLANDS) AND CHANGES RELATED TO HUMANS AND CLIMATE

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Preliminary results obtained from the first fossil pollen analysis carried out for the Canary Islands are presented. Reaching almost the boundary of Mid-Holocene period ca. 4300 cal. years BP, a sedimentary sequence from a former lake in the city of La Laguna, provides a first approach to the vegetation and environmental variability prior to and following human colonization in the island of Tenerife.

A key finding in the fossil record is the existence of two taxa, *Carpinus* and *Quercus*, today absent from the native flora. These trees were abundant elements of the forest in the region suggesting the possibility of a lost forest type. Pollen percentages also indicate the dominance of laurel forest taxa over the pine forest or thermophilous woodland species. Although laurel forest was present in the basin of La Laguna until the arrival of Spanish colonists to the island, some variation is detected 2000 cal. years BP coinciding with the presence of first prehistoric settlements in Tenerife. The decline of *Carpinus* and *Quercus*, as well as a fall of hygrophytes and the increase of taxa related with anthropogenic activities and the raise in the fire intensity suggests that prehistoric human activity may have had an intense impact on the nature of the archipelago than previously thought.

## ABRUPT END OF EASTERN MEDITERRANEAN LITTORAL VEGETATION REFUGIA BETWEEN -18 KYR AND -5KYR BEFORE PRESENT

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From paleobotanical data, we present new information and hypothesis about the importance of the littoral and sub littoral eastern mediterranean basin, as a reservoir of vegetal biodiversity through the last glacial-interglacial time. Our evidences are provided mostly by anthracological data from archaeological sites in southern Italy. These data are compared with pollen published evidences provided by several continental, marine and littoral sites located around and within the eastern Mediterranean basin. A particular attention is given to *Pistacia*, which is proposed to be used as a bio marker of the destroyed littoral refugia controlled by rapid changes of the eustatic level during the so called 'Termination I' (transitional time between the last Glacial period and our Interglacial time).

## PHYLOGEOGRAPHY OF THE SUB-MEDITERRANEAN BRYOPHYTE *PLEUROCHAETE SQUARROSA*

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The dioecious moss *Pleurochaete squarrosa* is a widespread and common bryophyte in the Mediterranean Basin, whereas it is restricted to south-facing, open habitats in Central and Northwest Europe. This plant can reproduce sexually via spores or asexually via fragments. Populations were studied from across its European and North African range for a range of nuclear and plastidic markers. In the Mediterranean a significant decline in genetic variation within populations was observed along a west – east gradient. High values for coefficients of gene diversity ($G_{ST}$) provided evidence of geographic isolation and limited gene flow among populations (1) within islands, (2) within mainland areas, and (3) between islands and mainland, but no difference in gene diversity and $G_{ST}$ between islands and mainland areas was observed. While sexually reproducing populations were found all over the Mediterranean Basin, high levels of multilocus linkage disequilibrium provide evidence of mainly vegetative reproduction elsewhere. Central European populations showed contrasting patterns of genetic diversity. In all but one area populations were entirely clonal, representing at least ten postglacial colonisations from the Mediterranean Basin northwards. Distribution patterns of allozyme multilocus genotypes and DNA haplotypes provide evidence for effective local dispersal (< 50 km) that followed the historic or recent long-distance dispersal from the south.

## LATITUDINAL PATTERNS IN SPECIES RICHNESS OF EUROPEAN FRESHWATER ANIMALS ARE NOT CONCORDANT ACROSS HABITAT TYPES

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To explain the latitudinal gradient of species richness, area, energy availability and historical influences are proposed to be the most important factors. However, relevance and scope of these explanations are still a matter of debate. Here we show that species richness of European freshwater animals (>14,000 species) peaks in central Europe and is not correlated to area. Furthermore, the relationship between species richness and latitude is not concordant across habitats: Groundwater and lotic habitats show a monotonous decrease of species richness with increasing latitude, whereas for lentic habitats and generalists the relationship is hump-shaped. This difference calls for an explanation considering habitat conditions as well as traits of species adapted to these habitats. Lentic habitats are less persistent than lotic or groundwater habitats, and species occurring in lentic environments evolved more efficient strategies for dispersal than lotic or groundwater species. Therefore, after the last glaciation lentic species recolonised central and northern European regions faster than lotic species. Additionally, the increasing aridity of Mediterranean regions during the Holocene decreased the availability and predictability of lentic habitats, which led to extinctions of lentic species within Mediterranean regions. Our data demonstrate that historical influences account for a large part of the variation of species richness in freshwater animals across Europe.

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## BIOGEOGRAPHY OF THE LATE PLEISTOCENE-HOLOCENE FAUNAL TRANSITION IN CENTRAL EUROPE AND THE EASTERN MEDITERRANEAN

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Regional differences in the Late Pleistocene-Holocene rearrangements of mammalian communities were analyzed based on a rich fossil record obtained from continuous sedimentary sequences in Czech Republic and Slovakia (800 community samples, 29,000 MNI) and neighbouring countries of Central Europe. Despite common general trends (substantial rearrangements of community structure), with aid of multiple records we demonstrated stricking local and regional specificities. Among other they include (a) continuous survival of several woodland elements *(Clethrionomys glareolus, Sorex araneus, Micotus subterraneus, Microtus agrestis)* throughout Weichselian (including LGM) in the Carpathians, (b) prolonged survival of the glacial elements *Ochotona pusilla* and *Microtus gregalis* in Pannonian basin and (c) *Dicrostonyx gulielmi* in the Carpathian foredeep, contrasting to (d) the early disappearance of them in S-Germany and Bohemia, and (e) similar difference were found also in other cenologic traits. While the glacial communities were nearly homogenous in their structure throughout whole the region, the Holocene development produced a considerable faunal provincialism, which was the most pronounced during Boreal. In contrast to central Europe, the available sequences from the SE-Europe and Asia Minor show only minute faunal changes during the Vistulian and Holocene, no essential rearrangements in community structure were observed (at least as the core species are concerned) and except for *Lagurus* no glacial immigrant did invade the region. At the same time a degree of local provincialism was continuously high and, in a regional scale, it continously exceeded that of the Boreal central Europe.

## PONDEROSA PINE IN TIME AND SPACE: INTEGRATED DEMOGRAPHIC AND GENETIC STUDIES OF DISJUNCT POPULATIONS IN THE BIGHORN BASIN, WYOMING

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Understanding the mechanisms underlying tree species migration and colonization is essential to predict tree species response to changing environmental conditions. Ponderosa pine (*Pinus ponderosa*) offers a unique opportunity in western North America to study such processes. Paleoecological records from packrat middens show that ponderosa pine did not colonize the western Bighorn Mountains of Wyoming until ca. 1,500 years BP. Three disjunct stands occur in the Bighorn Basin, some 80 km west of the Bighorn Mountains. These stands represent a unique opportunity to study patterns and processes of tree species migration. The largest stand (Cottonwood Creek) has been mapped and aged using tree-ring analysis. Ponderosa pine first established in the 17th Century, but did not expand until the late 18th Century. This expansion appears to have been triggered by a multidecadal wet period, but the population did not expand during earlier wet intervals. Initial low genetic diversity may have inhibited reproduction. This hypothesis is being tested by studies of molecular markers in tandem with the demographic data. Additional genetic and demographic studies at Cottonwood Creek, the other disjunct stands, and presumed source populations should reveal detailed patterns of colonization and the relative roles of climate, disturbance, and dispersal in the migration of a tree species.

## HEMLOCK DECLINES AND THE PREDICTIVE POWER OF PALEO-ECOLOGICAL RECORDS

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Predicting the response of native communities to exotic species is at the forefront of conservation biology. In this study, we aim to forecast potential shifts in vegetation in response to an exotic insect introduced to the eastern United States. Since its arrival in the mid 1960s, the invasive hemlock woolly adelgid (*Adelges tsugae*) (HWA) has caused drastic declines in eastern hemlock (*Tsuga canadensis*) populations. This impact has alarmed scientists and management officials and has initiated a surge of research into the effects of this herbivorous parasite on forest structure. Though previous studies have explored impacts on hemlocks themselves, there has been little work done on forecasting shifts in vegetation following potential declines in hemlocks. Here we examined historical declines in *Tsuga canadensis* using 76 paleo-ecological pollen cores from across North America and compared these to 10 sites in the northeastern US currently impacted by the HWA. Our results showed that both historical pollen data and contemporary sites of impact showed similar increases in several species, most notably birches, maples, and oaks. These results indicate that analysis of historical declines can aid in forecasting future vegetative shifts and have the potential to be applied to other threatened areas.

## THE MULTIGLACIAL ORIGIN OF ARCTIC-ALPINE DISTRIBUTIONS

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Many species of the cold-adapted fauna show a discontinuous distribution in the European high mountains and in Scandinavia – the arctic-alpine disjunction. Until recently, this pattern has been explained by postglacial fragmentation of a contiguous area which was assumed during the last glaciation in the tundras of periglacial Europe. A rangewide phylogeographic study of wolf spiders of the *Pardosa saltuaria* group revealed that at least two vicariance events are involved in the formation of the present distribution. We provide two lines of evidence. First, the mean Kimura 2 parameter distance between populations from the Pyrenees, Balkans and a 'northern clade' (Alps, Scandinavia, Carpathians, Sudetians) is 3.6-4%, whereas within clade divergence is substantially lower (< 1%). Calibaration with the standard insect mitochondrial clock results in ancient separation of these three clades some 1.5 Mya. Application of the isolation with migration coalescent method corroborates the deduction of vicariance events at different temporal scales. The *t*-estimates for population comparisons between major clades (Pyrenees, Balkans, northern clade) are at least 5 times higher (highest probability density of $t$>15) than between the populations of the northern clade (1.8-3.4). IM analysis also suggests asynchronous separation of the northern clade, with the most recent connection between Scandinavia and the Carpathians. There was even a strong signal for ongoing gene flow between these remote areas.

## PALAEOVEGETATION PATTERNS IN A MOUNTAIN-BASIN-OASIS SYSTEM, TIANSHAN MOUNTAINS, NORTHWESTERN CHINA

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The Tianshan Mountains in the middle of Xinjiang Uygur Autonomous Region, northwestern China, face in the north the Gurbantunggut Desert in the Junggar Basin and in the south the Taklimakan Desert in the Tarim Basin. Eight pollen profiles at six sites were selected along the northern slope, and in total 411 pollen samples were investigated. 96 surface pollen samples along a mountain transect from elevations 3500 m to 500 m and 134 surface pollen samples along two basin transects in the Junggar Basin were collected, in order to study the relationships between modern vegetation and pollen. Pollen-based palaeovegetation reconstruction and the analyses of grain size, susceptibility and loss-on-ignition (LOI) reveal the changes of palaeoenvironment in this region during the Holocene. The palaeoclimate had the fluctuations of cooling and warming, but the dry condition didn't significantly change in the north of central Tianshan Mountains. The general patterns of forests in the mountainous area, steppe and desert steppe on the lowland, and desert and steppe desert on the plain had no obvious changes during the Holocene compared to modern vegetation distribution. However, the positions of the upper and lower tree-lines, the growth of the forests in some valleys and the area of some lowland meadows have been changed following the fluctuations of climate. The upper limit of the montane *Picea schrenkiana* forest shifted upward and its lower limit shifted downward when climate got warmer and wetter. The lowland lakes were strongly influenced by the environmental changes, especially since the late Holocene. The lake levels changed frequently, for example the high lake levels occurred under the warmer and wetter climate conditions, and verse versa under the cooler and drier conditions. The large impacts of human activities on natural environments (mainly the water system and natural oasis) in this region occurred only in recent hundred years.

## HISTORICAL BIOGEOGRAPHY OF COASTAL DUNES OF CATALONIA (SPAIN) IN THE LAST 150 YEARS

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Changes in coastal landscapes that occurred in the last century under the pressure of urbanisation processes, and were driven in most places by tourism activities, have profoundly transformed the ancient coastal dune landscapes of Catalonia. To evaluate the degree of transformation and to know the current state of dune landscapes, we developed a methodology that combines historical research to obtain information about the dynamics of change in the near past, with chorological mapping using a grid of squares with 500 meters of side, to check the geographical distribution of a selected group of sand dune species. The results show that changes in the Catalan dune landscapes began to occur at the end of the XIX century when the dune fields were fixed and forested with native tree species such as Mediterranean pines (*Pinus pinea*, *Pinus halepensis*). In the second half of the XX$^{th}$ century tourism development brought new buildings, campsites, roads and boulevards that destroyed dunes or transformed them into new recreational use areas. As a result, the species composition of the plant communities in the dune landscapes has become impoverished. The species most affected are those related with stable dune environments such as those belonging to *Crucianellion* phytosociological taxon.

## BIOGEOGRAPHICAL BOUNDARIES AND MONMONIER'S ALGORITHM: A CASE STUDY FROM THE NORTHERN NEOTROPICS

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Inferring the boundaries between faunal realms provides insight into geologic and evolutionary history and into current community structure. But how boundaries are determined can be contentious and subjective. A repeatable and objective way to establish the location of faunal boundaries is through use of Monmonier's algorithm for detecting maximum-difference barriers. This technique can not only elucidate locations of realm boundaries, but the 'strength' of a boundary can be tested for statistical significance. We used such an implementation of Monmonier's algorithm to establish the locations of boundaries among avifauna of the northern Neotropical region. Our data set consisted of species occurrences of breeding birds at some thirty sites from the Sierra de los Tuxtlas of Mexico south to the Magdalena Valley of Colombia and included at least one site from each major geopolitical area in that span. Locations of boundaries among realms coincided with both current ecological biomes and historical geography, suggesting a combination of these factors shaped the distributions of avifauna in this region.

## PATTERNS OF THE IBEROMAGHREBIAN FLORA - RELATIONSHIP BETWEEN CENTRES OF ENDEMICITY OF SOUTH-WESTERN MEDITERRANEAN BASIN

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The SW Mediterranean Basin is a territory with a widely recognised floristic richness. In order to elucidate the patterns of the shared elements of the flora of Iberian Peninsula and North-western Maghreb, a database of the chorology of the common flora elements of Andalusia, Morocco and NW Algeria was developed. Classification analysis (RA) and parsimony analysis of endemicity (PAE) were applied to the database. Results depict a close relationship between the Rif Mountains and the Baetic Ranges, especially with the set Ronda-Grazalema. The other large cluster contains the arid regions of the SE Iberian Peninsula and Moroccan NE and Tell and Oran regions (Algeria). As can be expected due to its high altitude and aridity, High and Middle Atlas are intermediate between the previous groups. These territories are drawn according to a rain precipitation gradient (from Spanish Atlantic Coast to Sahara) and according to latitude (from Sierra Nevada to Sahara). In this complex scenario various geological events have influenced the interchange of plant species between both continents: the closure of the Guadalhorce Corridor and the Messinian Salinity Crisis when the Mediterranean dried up.

## ROLE OF GLACIATION CENTRES IN THE BIOGEOGRAPHY RICHNESS OF BALKAN PENINSULA (SE EUROPE)

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All high mountains of Balkan Peninsula were during glaciation time covered with snow and ice. At that point, broad-leafed forests of oak and thermophilous beech that used to be widely distributed up to then have vanished suddenly. Last Ice Age has without doubt left clear marks on current image of the world. There have been created special forms of flora and vegetation that even today give a specific and unique imprinting to the phytogeographic picture of high mountainous Balkan area. It is right to glacier activities that at present-days exist centers of glacial flora and vegetation whose contribution to the biodiversity richness is at regional scale recognized to be very significant. From the point of view of phytogeography, the area that was affected by glaciation process is abstracted to Alpine-high Nordic region, with dominance of high Dinaric province. Thanks to the occurrence of many glacial relicts, this area, in terms of phytogeography, is being divided into several sectors: High Velebit, High Vranica, High Maglic, High Durmitor, High Sara Mts. On the base of these investigations there have been identified following phytogeographic units with glacial-relict character: Class *Salicetea herbaceae*, Order *Salicetalia herbaceae*, Alliance *Ranunculion crenati* and associations: *Gnaphalio supinae-Ranunculetum crenati, Nardo-Plantaginetum gentianoides*, *Geo montani-Poetum cenisiae, Poetum cenisiae bosniacum*; Order *Salicetalia retusae-serpyllifoliae*, Alliance *Salicion retusae* and associations: S*oldanelo-Salicetum retusae*, *Polygono vivipari- Salicetum retusae*, *Violo zoysii-Salicetum retusae* and *Ranunculo-Plantaginetum atratae.*

## LONG TERM STABILITY AND MULTIPLE ALTERNATIVE STABLE STAGES IN PLEISTOCENE MAMMAL ASSEMBLAGES

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Paleoecologists usually base their inferences in the assumption that functional group composition of mammal assemblages is determined by the environment. However, remarkable constancy in functional group composition is observed in mammalian assemblages from the Atapuerca sites (Burgos, Spain) over a 600 Kyr sequence, despite concurrent changes in species composition. This stability, termed Structural Continuity, contrasts with the existence of various climatic cycles that induced changes in the vegetation throughout this period. Structural continuity has also been observed in middle Pleistocene assemblages from other sites of the Iberian Peninsula and in the Italian Peninsula, but not at higher latitudes. On the contrary, the pattern observed in northern European assemblages supports the existence of Multiple Alternative Stable States for glacial and interglacial assemblages. The different behavior of Northern and Southern European mammal assemblages is explained by the moderate intensity of the environmental disturbance in the Mediterranean area during the middle Pleistocene, that was not disrupting. In Central and Northern Europe disturbance was considerably more disruptive, the regional species pool changed, and the assemblages were disrupted and disengaged after each climatic cycle. The glacial or interglacial assemblages reassembled roughly every 100,000 years, giving rise to more heterogeneous community structures, representing different Alternative Stable States.

## PHYLOGEOGRAPHY OF ALPINE PLANTS IN THE CARPATHIANS (CENTRAL EUROPE): LOOKING FOR GENETIC BREAKS AND PATTERNS OF DIFFERENTIATION

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Carpathians constitute one of major elements of European mountain system. They form a 1,300 km-long arch, with part of massifs reaching altitudes above 2,000 m a.s.l. and harbouring discontinuous alpine belt areas. The EU project IntraBioDiv brought first comprehensive genetic data (ca. 25 species sampled across all high massifs) concerning differentiation and phylogeography of high-mountain flora of Carpathians, in relation to European Alps – encompassing major mountain ranges of Central Europe. Most intraspecific datasets unraveled significant phylogeographic structures. Presence of different patterns showed, that contemporary distribution of Carpathian high-mountain flora was shaped by various species histories. Repeated tendencies could, however, be identified, as strong genetic breaks between Alps and Carpathians, relationships between the Carpathian and Eastern- or Southern-Alpine populations, or clear subordering of one range. Overall, a relatively ancient break and not recent recolonizations in many taxa can be supposed. Within Carpathians, only few species did not reveal any genetic spatial structure. Main genetic break, supported by most taxa, separated Western and South-Eastern Carpathians (in line with floristic observations), suggesting independent alpine plant histories of these areas at least during and after last glacial period. Observation of several further breaks suggests presence of several refugial areas in many species rather than glacial or postglacial range expansion in the late Quaternary.

## ALPINE BIOGEOGRAPHY RECONSIDERED: COMPARING PHYLOGEOGRAPHIC AND BIOGEOGRAPHIC LINES IN THE EUROPEAN ALPS

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There is a long history of studying the flora in the European Alps and its biogeography. Since the early 19th century, scientists have attempted to localize floristically similar regions and its delimitations and to explain these with geological or climatic factors. A most widely discussed biogeographic line is the one between the eastern and western Alps. However, this hypothesized line between the two flora regions has never been statistically tested. Here, we propose a new approach to geographically identify biogeographic lines. We use an exhaustive dataset of the distribution of alpine plant species, compiled in the frame of the project IntraBioDiv. Data on species occurrences refer to a regular spatial grid laid over the whole range of the European Alps. On the same grid, we assessed the genetic structure of several widely distributed alpine plant species to identify common phylogeographic lines in the Alps. We expect that biogeographic and phylogeographic lines are largely congruent in the Alps due to historical processes acting at both the genetic and the species level in the same direction. Such processes, e.g. isolation, regional extinction or range-expansion are related to Quaternary ice ages, which had a substantial influence on present alpine biota.

## PHYLOGEOGRAPHY OF A FISH PARASITE: SOME HISTORY OF THE FRESHWATER BASINS IN CENTRAL MEXICO

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Geological history suggests that extant freshwater basins of the west-central region of Mexico are the outcome of different vicariant events that resulted in the fragmentation of watercourses and lakes within those basins. Freshwater fauna seems to have speciated as an outcome of those events. Our aim was to infer the biogeographical history of fragmentation and recent evolution of the Mesa Central drainages with a nematode parasite specific to endemic Goodeids, *Rhabdochona lichtenfelsi.* We evaluated the genetic variation and phylogeographic structure of 10 populations sampled from the species complete range, using sequences of the cytochrome *c* oxidase subunit I. Results showed high overall haplotype diversity in the populations (basins) sampled, unique haplotypes, and significant population structure. The distribution of *R. lichtenfelsi* haplotypes does not correspond to the present distribution of basins inhabited by its hosts, but reflects the distribution of those basins during a recent geological period (Pleistocene). While our understanding about the evolution and geographical relationships of the Mesa Central basins comes from freshwater fish studies, revealing a more ancient history, our results suggest that during the last million years, old basins and connections existed where today stand isolated freshwater bodies, unravelling a novel biogeographical history for the Mesa Central of Mexico.

## PHYLOGEOGRAPHY OF THE LOW ALPINE *EPHEDRA DISTACHYA* (EPHEDRACEAE) IN THE EUROPEAN ALPS

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One of the great amount of connecting floristic elements in the inner alpine dry valleys between the Durance valley in France and the Vinschgau in South Tyrol, which fascinate botanists with their unique sub Mediterranean steppe vegetation fascinate botanist since the first explorations of the alpine flora is *Ephedra distachya* subsp. *helvetica* Meyer. It is a perennial dioecious evergreen small shrub with straight or prostrate stems, which bear small scale leafs. The endangered plant is restricted to extreme dry rocky locations at hot and scarped southward slopes in an altitude range from 360 m to 1,360 m. The few populations outside the Wallis are small, sometimes minute and comprise sometimes only a few individuals. The poster presents first results of a molecular study of the of *Ephedra distachya* subsp. populations in comparison to populations of *Ephedra distachya* from the Mediterranean coast and Eastern Europe. PsbA and ITS sequences as well as AFLP markers suggest that the populations from the Alps are very closely related. The results point to a unique immigration of *Ephedra distachya* into the Alps from the Mediterranean coast in the Pleistocene with a subsequent separating of the few remained populations.

## *Symposium 3*

# Island biogeography

## BIOGEOGRAPHIC PATTERNS OF EVOLUTION IN THE PACIFIC

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The study of evolution on islands continues to bring new discoveries to our understanding of the history of life on earth. Progress has accelerated since molecular phylogenetics has been added to systematics. Research is particularly active in the Pacific islands with Hawaii as a central focus. Recent studies reveal several trends. First, islands are appearing in phylogenies as the source of radiations to other islands/mainland as is exemplified by groups such as sandalwood, monarch flycatchers, and the cosmopolitan genus *Scaptomyza* (sister clade to Hawaiian Drosophila). Second, although the old world and Pacific areas are still important, North America is increasingly seen as a source of dispersal events to the Pacific islands with examples including Hawaiian mints, honeyeaters, and long legged flies. Third, while biologists continue to work on taxa that have the pattern of dispersal followed by radiation, other taxa with fewer species that have not radiated much are yielding insights into how organisms evolve including studies on *Metrosideros*, Hawaiian geese, craneflies and blow flies. Fourth, many groups now have enough data that we can investigate questions concerning community associations, patterns of speciation, species-area relationships, hybridization, etc. as exemplified by projects on the plants of the Hawaiian Islands, spiders, and snail eating moths. Finally, new fossil data are giving a better understanding of the importance of extinction in our understanding of evolution, e.g. Honeycreepers. The story of the evolution of the biota of the Pacific islands has become more complicated and more interesting.

## GEOGRAPHY, EVOLUTION, AND ECOLOGY: INSIGHTS FROM BIRDS OF THE WEST INDIES

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The species composition of island biotas reflects colonization, extinction, and diversification within islands and within archipelagoes. Phylogeographic studies of a large proportion of the bird species of the West Indies, in collaboration with Eldredge Bermingham, have provided an historical context for examining the dynamics of the modern avifauna. Colonization is selective, with many groups of forest birds with weak flight not reaching the islands. Colonization also appears to be episodic, in which individual species have phases of heightened movement through the archipelago. Extinction is infrequent, judging from the occurrence of gaps in distributions, with the average residence time of populations on the larger Lesser Antillean islands approaching two million years. There is little evidence of archipelago-wide extinction, and the avifauna clearly is not in colonization-extinction equilibrium. Lineages of birds have not diversified within the West Indies, as they have in more remote archipelagoes. Although the reason for this is not clear, it might be related to apparent incompatibilities that prevent secondary sympatry of long-separated sister populations. Populations of West Indian birds undergo characteristic shifts in ecological distribution on the islands, from lowland, relatively open habitats, to mountain forests, apparently initially reflecting ecological release and then in response competition from new colonists. These shifts are reversible in some cases, leading to secondary phases of expansion, occasionally extending to continental landmasses. Evolutionary and geographic dynamics of species in the West Indies also anticipate the vulnerability of island populations to habitat alteration and other human-caused threats.

## A NEW BAYESIAN APPROACH TO ISLAND BIOGEOGRAPHY, WITH SPECIAL REFERENCE TO THE CANARY ISLANDS

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Oceanic islands represent a special challenge to biogeographers. Island-to-island distances and isolation from mainland make dispersal the dominant biogeographic process, a scenario difficult to analyze with current vicariance-based biogeographic methods. Here, we describe a new Bayesian approach to island biogeography that models dispersal as discrete-state continuous-time Markov models similar to those used in molecular evolution. Island relationships are assumed to be constant through time and dispersal between islands is modeled as a matrix specifying the instantaneous rate of dispersal from one island to another. Bayesian MCMC methods are used to estimate the posterior distribution of the model parameters, the island 'carrying capacities' (i.e. stationary frequencies) and the dispersal rates, by assuming different dispersal models (e.g. unconstrained vs. stepping-stone dispersal). We test these models on a data set of published phylogenies of Canary Island organisms to examine overall dispersal rates and correlation of rates with explanatory factors such as geographic proximity and area size. This is the first time stochastic dispersal models are applied simultaneously to many groups evolving on different phylogenies. Bayesian inference has the advantage over parsimony and likelihood approaches that it can account for phylogenetic uncertainty – inferences on parameters such as dispersal rates are independent from the underlying phylogeny.

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## INSIGHTS INTO COMMUNITY ASSEMBLY FROM EVOLUTIONARY STUDIES OF ISLAND ECOSYSTEMS

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Oceanic island ecosystems have for a long time been recognised as natural laboratories for studying evolution owing to their discrete geographical nature and diversity of species and habitats. The origin and maintenance of species diversity within an archipelago and on individual islands are of great interest to biologists, and the development of molecular genetic methods for phylogenetic reconstruction provides a useful tool to address these issues. In this talk I will focus particular attention on the roles of speciation and extinction in community assembly on island ecosystems. While the evidence for speciation on island archipelagos is clear, evidence for extinction is less obvious. However, absence of evidence does not mean absence of process, and failure to account for this will lead to false conclusions such as greater rates of speciation on younger islands followed by increasing evolutionary stasis as islands mature. An appreciation of the mutual importance of both extinction and speciation provides a more satisfying dynamic of community assembly.

## ON HUMANS AND WILDLIFE IN MEDITERRANEAN ISLANDS ACROSS TIME AND SPACE

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This presentation will focus on two long term consequences of environmental changes on birds in Mediterranean islands. First, at the scale of habitat gradients and long time scales, recent studies suggest that the extent of species ranges along altitudinal gradients – the niche-breadth – depends on the age of taxa and the history they experienced during the Pleistocene with well-differentiated subspecies-level endemics being more likely to expand their ranges than recent colonisers. In the framework of the taxon cycle, the rationale is that long lasting endemic forms experienced several glacial-interglacial cycles with repeated up and down shifts of their distribution that favoured their persistence at mi-altitudes and the evolution of a larger niche. In contrast, recent colonisers, especially those that benefited from human action through habitat changes, tend to have narrower niches than their mainland counterparts. Second, at the scale of landscapes, human-induced changes in land use patterns resulted in habitat mosaics which include several types of habitat patches which much differ in the phenology and abundance of resources. One example will be provided from long term studies of blue tits which exhibit a large amount of phenotypic variation in relation to habitat heterogeneity. Depending on habitats and the geographic configuration of landscapes, I will show that this variation results either from phenotypic plasticity or from local specialization, and leads to a higher population differentiation on islands. An increase in intraspecific diversity compensates to some extent the decrease in interspecific diversity which is one of the main features of insular biotas.

## (WHY) ARE ISLAND ENDEMICS INTERESTING?

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Oceanic islands are well known for their high proportion of endemic species, and it is often stated that island endemics represent odd life forms (Mauritius dodos), extreme radiation (Galapagos finches) or queer ecologies (Christmas Island crabs). But are these features anecdotes or patterns? To answer this, the following question is relevant: Are island endemics more odd, extreme or queer than their native co-islanders? This can be approached by using the native contingency of island floras/faunas as 'outgroups' for the endemic contingency, with respect to the attributes in questions. The following examples are presented: (1) endemic Galápagos plants show higher tendency to produce cyanogenic compounds than, (2) endemic Galápagos plants are more vulnerable to influence by alien plants and animals than, (3) endemic Galápagos plants have other species-area relationship than, (4) endemic Galápagos land birds have higher species/genus ratio than, endemic Mascarene plants have as high medical potential as --their native co-islanders. This biogeographical approach can be used to study other island biology questions.

## SYSTEMATICS AND BIOGEOGRAPHY OF THE PANTROPICAL GENUS *MANILKARA* (SAPOTACEAE)

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The pantropical genus *Manilkara* comprises 82 species worldwide. The 30 Neotropical and 37 African species have recently been revised. However, the 15 Asian and Pacific Island species are in need of review. This project will complete the monograph and add to a preliminary DNA sequence data set, giving a better understanding of the historical biogeography of the genus. Internal transcribed spacers of ribosomal DNA in combination with chloroplast spacers have been used to reconstruct a phylogeny of 13 *Manilkara* species and putative relatives (Clayton unpubl. M.Sc. thesis). Four main clades were recognised: a neotropical clade, an African clade, an Asian clade and a clade comprising the genus *Faucherea*. The relationships between these clades suggest a pattern of deep history with little subsequent intercontinental dispersal. However age estimates based on ITS substitution rates from other taxa with similar generation times discount a Gondwanan origin for *Manilkara*. A Tertiary African origin is instead supported. Asian and Pacific Island species groups may have had two independent origins and neotropical species are believed to have migrated from their African ancestors across the Tertiary land bridge and then south though the Americas. Future research will focus on testing the timing of evolutionary events with broader sampling and alternative dating approaches using fossil and geological calibration points.

## MEDITERRANEAN BIOGEOGRAPHY AND ISLAND EVOLUTION, AS EXEMPLIFIED BY THE SPIDER FAMILY DYSDERIDAE

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The spider family Dysderidae is a group of medium size spiders that includes about 500 species classified in 24 genera. Dysderidae spiders are extremely conservative in terms of morphology and ecology, most species are nocturnal wandering hunters in warm and wet ground habitats, and also frequent in caves. The family is mostly circum-Mediterranean. The Macaronesian archipelagos constitute the westernmost limit of their distributional range. The woodlouse-hunter spider *Dysdera* is the family's most species rich genus (250 species) and the only one that has colonized these archipelagos, in some of which has undergone local diversification. For the last eight years our research group has been using the spider family Dysderidae as a model for the study of island evolution, and for the comparative analyses of the tempo and mode of diversification between islands and continents. We present some examples of our ongoing research. A particularly interesting aspect of the family is the restricted distribution of most genera in areas of endemism, which coupled with the well-dated geochronology of the Mediterranean, allow biogeographic calibrations of molecular trees and hence provide a time framework for the evolutionary history of these spiders.

## BIOGEOGRAPHY OF HAWAIIAN LEAFHOPPERS (CICADELLIDAE: *NESOPHROSYNE)*

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The Hawaiian island system and its native biota is a hotspot for extraordinary native biodiversity. This extensive array of native fauna is driven by individual islands' extreme climatic and topographic diversity, and unrivaled isolation from other landmasses. The known dates of island formation provide a stable basis for dating colonization and speciation events. This project will examine the diverse Hawaiian leafhoppers (Cicadellidae: *Nesophrosyne*) as a model for investigating patterns of evolution and biodiversity. The genus *Nesophrosyne* is in the subfamily Deltocephalinae, with 62 documented species on all islands in the archipelago. The specific objectives are to (1) circumscribe the distribution of and ecological association of Hawaiian leafhoppers and improve taxonomic knowledge and identification tools; (2) conduct a phylogenetic analysis to examine the rates, patterns, and geographic history of speciation in an effort to understand the generation and maintenance of biodiversity on the Hawaiian Islands. Three previous collection trips have provided enough material to document the species and ecology of *Nesophrosyne* on the island of Hawaii. A thorough phylogenetic study utilizing maximum parsimony, maximum likelihood and Bayesian methods will allow for the investigation of the evolutionary hypotheses and history of the *Nesophrosyne* lineage.

## FACTORS DRIVING ARTHROPOD SPECIATION AT THE AZOREAN ARCHIPELAGO

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This work explores the role of diversity and island characteristics in arthropod diversification in an oceanic archipelago. Speciation patterns were explored using data from the Azorean islands regarding to all the arthropods and three specific groups (beetles, butterflies and moths, and spiders), in order to account for the differences provided by their different life-stories and dispersal ability. We investigated the effects of four factors that have been claimed to promote speciation on islands: habitat heterogeneity, island age, isolation, and indigenous species richness, using a new Speciation Index ($SI_{BH}$) based in species checklists (due to the absence of molecular data). We also compared such index to the index proposed by Emerson & Kolm (2005a); $SI_{BH}$ is statistically independent of species diversity and measures patterns of diversification only in the speciose genera. The explanatory capacity of the studied factors was assessed through General Linear Models and partial regressions. Habitat diversity was the most important effect of overall arthropod speciation. In addition, the new speciation index was able to disentangle important differences in the diversification patterns of beetles, spiders, and moths and butterflies; geological age and isolation explain most of beetle speciation, whereas isolation and habitat heterogeneity explain Lepidoptera and spider speciation. In sum, island area, habitat diversity, isolation and island age had an important role on the speciation of Azorean arthropods. Interestingly, some independent influence of indigenous species richness was also found.

## ASSEMBLY OF ISLAND COMMUNITIES: BODY SIZE, MORPHOLOGY, AND COEXISTENCE IN PREHISTORIC AVIAN GUILDS

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In 1975, Diamond put forth assembly rules to explain the modern distribution of landbirds on certain Pacific islands. These rules are fueled by interspecific competition, in the absence of which any combinations of species, related or unrelated, should be able to coexist. However, recent fossil discoveries have shown that coexisting congeneric species pairs and triplets were much more common on Pacific islands before human colonization and the subsequent anthropogenic extinction event. These previously unknown combinations call into question many widely held beliefs about the importance of competition in structuring communities. Here I examine body size and morphology in prehistorically coexisting congeneric species pairs and triplets in the islands of Tonga for evidence of character displacement and differential extinction rates. I find very little evidence of character dispacement among coexisting Rallids, Megapodes and fruit doves, however, these groups do show a tendency for increased extinction rates among coexisting congeners.

## AREAS OF ENDEMISM IN CLADISTIC BIOGEOGRAPHY: A CASE STUDY FROM THE CANARY ISLANDS

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Areas of Endemism (AoE) are the fundamental units of cladistic biogeography. However, whilst rigorous and explicit techniques for determining relationships between AoE have been established, the way in which these fundamental units themselves should be delimited remains contentious. In addition to ad hoc approaches adopted by many authors, several explicit analytic techniques for the delimitation of AoE have been proposed. These include Parsimony Analysis of Endemicity (PAE), NDM and phenetic clustering and ordination methods together with methods for examining spatial distribution patterns (e.g. WORLDMAP). The Canary Islands vascular plant flora comprises over 750 endemic taxa. The geological history of the archipelago has been well-documented and, in contrast to endemic-rich areas in many parts of the world, species distributions are relatively well known. The Canary Islands flora therefore provides a suitable model system with which to examine the performance of competing methods for deteriming AoE. In this study, we have assembled a dataset of endemic vascular plant taxa (species and subspecies) for over 90% of the archipelagos endemic flora on a 10 x 10 km grid. The data have been analysed using WORLDMAP, PAE, NDM and phenetic clustering and ordination methods. The results of these analyses are presented and the relative performance of these difference approaches for the delimitation of AoE considered.

## DO TROPICAL BIVALVES HAVE NARROWER REALISED NICHES THAN TEMPERATE BIVALVES?

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Although species richness along the latitudinal gradient is well-documented in ecology, little is known about how species richness relates to other environmental variables. Thus, studies examining how species are distributed along various environmental gradients within their local habitats will provide a greater understanding of species diversity. Using gradient analysis we examined the realised niches of bivalves at a species-rich tropical (Roebuck Bay, north western Australia) and species-poor temperate tidal flat (Wadden Sea, The Netherlands), with the expectation that the tropical bivalves will show specialised distributions. Bivalve distributions were described at each location with repeated grid mapping over three different years. These were examined in relation to the environmental gradients of sediment and submergence time, as these are known to relate to feeding and physiological stress in bivalves. Roebuck Bay offered wider environmental gradients compared to the Wadden Sea, but in the Wadden Sea bivalves occurred at higher densities. At each location Gaussian logit models were used to examine the realised niches of bivalves. Bivalves at Roebuck Bay did not have especially narrower niches than the Wadden Sea. Instead, bivalves at both locations displayed a range of niche widths in relation to sediment and tide. Some species at both locations also displayed a distinct preference for different sediments and tides. The differences between the realised niche widths of the species from Roebuck Bay and the Wadden Sea cannot be interpreted in relation to species diversity gradients at this point; to do this we are currently compiling data sets from another temperate and tropical site with matched environmental gradients.

## PATTERNS OF DIVERSIFICATION OF *SELENOPS* SPIDERS IN THE CARIBBEAN

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The interplay between vicariance, dispersal, and *in situ* evolution in shaping island biota has long been a subject of debate. This is particularly true of the Caribbean region, where biodiversity has been shaped by both the fragmentation of islands from continental landmasses and from other islands, as well as the formation of new land in the form of volcanic islands. The current study uses molecular and morphological data from spiders of the genus *Selenops* to examine whether observed patterns of evolution mirror those of geology. The data allow the examination of the frequency and relative timing of dispersal, vicariance and *in situ* evolution and their importance in dictating current patterns of diversity in the Caribbean. Results thus far indicate both similarities and differences with other taxa. Larger islands tend to be more diverse in terms of species numbers, a pattern seen in other groups. All Jamaican species (3) are endemic and appear to be the result of one radiation, while Hispaniolan species (>10) appear to have arisen from multiple dispersal or vicariant events. Finally, species in the southern Lesser Antilles are distantly related to species in the northern Lesser Antilles, a pattern also seen in *Anolis* lizards. In general, colonization is limited and subsequent diversification is dictated by island age, size and isolation.

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## PLANT ENDEMICITY IN THE FLORA OF PUERTO RICO: AN ASSESSMENT OF THE INTRA-ISLAND DISTRIBUTIONAL PATTERNS

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Although the flora of Puerto Rico has been a subject of considerable floristic investigation during the past 125 years, studies focusing on the phytogephraphical patterns of the island's endemic elements (which represents almost 10% of the flora) are limited to few specific plant groups, and is almost non-existent for the flora as a whole. Here we present a profile of the inter-island endemicity patterns based on a nested areas of endemism analysis. The study identifies major local centers of endemicity and their hierarchical importance in terms of number of endemic elements. Presence and importance of endemicity is assessed based on several factors, including altitude, substrate, and rainfall regime. We also discuss aspects of the methodology applied. This study has also the conservation (i.e. applied) objective of identifying areas of considerable endemicity within Puerto Rico are at still devoid of any protection.

# VEGETATION DISTRIBUTION ALONG AN ELEVATION GRADIENT IN TENERIFE (CANARY ISLANDS)

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Tenerife is an island particularly known for its large variety of habitats, being elevation the most responsible factor for the existence of up to five distinct ecosystems. However, little is known about how vegetation specifically varies within each ecosystem. This work is centered on the low vegetation belt known as coastal scrub, which grows from to cost up to 300 m a.s.l. on the windward slope and 600 m a.s.l. on the leeward slope. We analysed the variation from its lower border with the halophyte community to the maximum elevation we could reach (c. 200 m). We established 24 squared plots (100 m$^2$) along a transect on a relatively preserved area of Teno Rural Park, at the western part of the island, and measured the cover of the different vascular plants. With the help of multivariate analysis technics and generalised additive models we show that, despite of the studied gradient being very short, elevation has a great importance on the species distribution, richness and turn-over.

# HONEY BEES AND POLLEN AS INDICATORS OF EXOTIC PLANT SPECIES ALONG AN ELEVATION GRADIENT ON AN OCEANIC ISLAND (CANARIAN ARCHIPELAGO)

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The honeybee (*Apis mellifera* L., and its subspecies) is acknowledged as one of the most relevant invaders interfering with native systems on islands and fragmented ecosystems by competing with native pollinators for floral resources and interrupting native pollination mutualisms. High population sizes of introduced bees may also affect the establishment and spread of introduced plant species. Many examples exist of introduced bees visiting mainly introduced plants. However, few studies deal with this topic on oceanic islands, which often suffer from heavy invasions by both weeds and exotic pollinators. The use of pollen sources by honeybees may provide useful information on the presence of exotic species. Based on published information on pollen contents of honeys from beehives in La Palma (Canary Islands), we made an indirect evaluation of the relative use of exotic vs. native flowering plants by introduced honeybees along an elevation gradient of bee foraging areas. Exotic species comprised an average of 44% of plants visited by honeybees, but this portion as well as the total richness of visited introduced species was negatively correlated with altitude and distance to nearest urban nuclei. Results suggest that introduced honeybees forage preferently on introduced plants which grow at low altitudes near urbanizations. Pollen abundance of most exotics was also negatively related to altitude probably reflecting the actual distribution pattern of these species.

## CALLOSCIURINE TREE SQUIRRELS AND THE PLEISTOCENE HISTORY OF THE SUNDA SHELF, SOUTH-EAST ASIA

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The rainforests of the Sunda Shelf of South-east Asia (the Malay Peninsula, Sumatra, Java and Borneo) and the adjoining islands of the Philippines and Sulawesi are extremely species rich and diverse, with high levels of endemism. Many of these ecosystems are also highly threatened. The current pattern in richness is thought to have arisen due to the complex geological and climatic history of the area. Especially climatic changes during the Pleistocene epoch that started about 2 million years ago and ended only about 10,000 years ago, which created on and off landbridges among the different islands on the Sunda Shelf and produced shifts in vegetational belts. To better understand how and when this extraordinary rainforest diversity arose, or more precisely, if the Pleistocene ice ages and associated sea-level changes had a profound effect on the current distribution patterns and species richness, we examined the genetic diversity in the group of the rather non-descript callosciurine tree squirrels of the genus *Sundasciurus*. This genus is endemic to the Sunda Shelf and reaches the Philippine islands of Palawan group and southern islands of Mindanao, Leyte, Bohol and Samar and smaller adjoining islands.

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## COLONIZATION OF LARGE MEDITERRANEAN ISLANDS BY SHREWS (MAMMALIA, SORICIDAE) FROM PLIOCENE TO HOLOCENE INFERRED FROM MOLECULAR PHYLOGENETICS

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The Pleistocene fauna of large Mediterranean islands is known for its low mammalian diversity and extremely endemic fauna characterized by dwarf forms of large herbivores as well as giant forms of small mammals. These islands have been isolated from the African and European continents since the Messinian salinity crisis that occurred at the Miocene–Pliocene transition (about 5.3 Myr ago). This event marked the beginning of a prolonged period of evolution of insular mammals in isolation from the continental ones. In the present study, we sequenced the mitochondrial cytochrome-*b* of European and North African species of shrews (Soricidae), including species of large Island, in order to reconstruct their island colonization history. From our results, the Sicilian shrew colonized the Siculo-Maltese archipelago at the Miocene–Pliocene transition from a northern African ancestor, and the Cyprian lesser white-toothed shrew colonized Cyprus Island by rafting in the Lower Pleistocene. In contrast, the North African white-toothed shrew from Sardinia and Pantelleria and the lesser white-toothed shrew from Crete, Corsica, and Minorca were introduced respectively from North Africa and from the Near East through the Holocene by humans. In conclusion, all traceable living insular species of shrews are originating from a North African or Near East ancestor.

## THE BIOGEOGRAPHICAL HISTORY OF NEW CALEDONIAN TRICHOPTERA

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This study focuses on the use of molecular based phylogenetic analyses and molecular dating to elucidate the processes that shaped the evolution of the very rich fauna of New Caledonia. Trichoptera (caddisflies) will serve as a model organism for the study. Ultramafic substrate covers substantial areas on the southern half of New Caledonia and a goal of the project is to examine the significance of ultrabasic substrate on diversification processes. Other environmental factors such as the major climate changes during the Tertiary and Quaternary will also be investigated. The project will be the first to overtly test longstanding assertions about New Caledonian biogeography in particular, and Trichoptera biogeography in general.

## THE BIOGEOGRAPHICAL HISTORY OF NEW CALEDONIAN TRICHOPTERA - THE NEW CALEDONIAN ENDEMIC GENUS *XANTHOCHOREMA* (TRICHOPTERA, HYDROBIOSIDAE)

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The New Caledonian endemic genus *Xanthochorema* (Hydrobiosidae) is used as an example for the study of the biogeographical history of New Caledonian Trichoptera. A phylogenetic analysis shows that the 12 species of the genus form a monophyletic group, and thus the species radiation has occurred on New Caledonia. The vicariance-dispersal (DIVA) analysis demonstrates independent, early and repeated dispersals of ancestral *Xanthochorema* species from non-ultrabasic into ultrabasic substrate. These dispersals were followed by subsequent speciations, except in two cases. In early lineages only on non-ultrabasic substrate, no speciation has occurred, indicating that presence of ultramafic substrate might have contributed to the diversification of *Xanthochorema* on New Caledonia.

## HULLED WHEATS IN ISOLATED AREAS OF SOUTHERN ITALY: PALAEO-ETHNOBOTANICAL AND AGRONOMICAL PERSPECTIVES

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The three old species of hulled wheats known in Italy as 'farro' are still cultivated in few limited areas around the mediterranean. These eco-geographical islands are the last refuge areas for these plant genetic resources. The same areas were scientifically investigated both by Paleo-Archeobotany and Agrobiodiversity point of view. The combination of results shows the evolution of these old crops according anthropisation in the region, starting from the Neolithic age until today. It is still possible to find some old landraces of *Triticum dicoccon* Schrank, *T. monococcum* L. and *T. spelta* L. that are cultivated and used in traditional farms as fodder and food.

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## ISLAND BIOGEOGRAPHY OF BATS IN BAJA CALIFORNIA, MEXICO: PATTERNS OF BAT SPECIES RICHNESS IN A NEAR-SHORE DESERT ARCHIPELAGO

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MacArthur and Wilson's (1963, 1967) influential equilibrium theory of island biogeography has inspired four decades of research on species richness patterns of various taxa in different archipelago settings. However, biogeography research on insular bat faunas remains scant, particularly in near-shore archipelagos. We investigated the influence of island size and isolation on bat species richness patterns in a near-shore archipelago in Baja California, Mexico to evaluate forces important in determining bat community structure in isolated habitats. Presence/absence surveys for bat species were conducted on 34 islands in the Sea of Cortés. Using an information-theoretic approach, we developed and compared *a priori* candidate models to estimate the effects of area, isolation, and island group on bat richness. Area had a positive effect on bat richness and isolation significantly decreased bat species richness. Southern islands, which are associated with denser vegetation structure from receiving summer monsoon rains, supported more bat species than northern islands. Our results demonstrate that even highly vagile organisms like bats can be affected by moderate isolation distances in some landscape contexts. Furthermore, regional differences in habitat structure may also have an important influence on bat richness.

## I USED TO THINK THAT SINKHOLES ARE ISLANDS, BUT I GREW OUT OF IT: DRAGONFLIES EXPERIENCE AN ONTOGENETIC SHIFT IN LANDSCAPE FUNCTION

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Island biogeography theory attempts to explain how habitat patch size can affect species diversity, with larger patches often supporting higher numbers of species. Although they could offer additional insight into the general applicability of this theory, studies that explicitly compare patterns exhibited by multiple life stages (e.g. adults and larvae) of a single taxonomic group are uncommon. Dragonflies may represent an ideal group for this application because these insects experience dramatic changes in environmental requirements and dispersal abilities during the maturation process from aquatic larva to terrestrial adult. I examined the effects of water quality and physical habitat parameters on adult and larval dragonfly species diversity in a desert sinkhole complex over the course of three years. As predicted by island biogeography theory, the species diversity of both life stages increased with increasing sinkhole surface area, but the slopes of the respective species-area curves suggest that the sinkhole complex functions as a mainland landscape for volant adult dragonflies and as an island system for larval dragonflies. Sinkhole water salinity had more influence on species diversity than did surface area for each life stage, perhaps because salinity strongly affects other site selection cues used by adult dragonflies and the ability of larvae to survive until emergence.

## THE BRYOPHYTE FLORA OF SÃO TOMÉ ISLAND PROJECT. COMMUNITIES' CHARACTERIZATION AND INDICATORS SELECTION

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The abundance and luxuriance vegetation of São Tomé Island have attracted many investigators since the 19th century. However, the bryoflora is still incompletely known, as in many African countries. Several naturalists passing through, or purposefully visiting the Islands have made biological collections, some listed in scientific papers, which contain important information. The bryophyte collections are mainly due to the scientific expeditions during 19th century by Welwitsh (1853, 1860), Quintas (1885), Newton (1887) and Moller, (1888), as well as casual collections made by different botanists. With the knowledge of species richness and composition of particular areas in different times (from 19th century to nowadays) it will be possible to infer about alterations in the land use and biodiversity composition. A post-doctoral program and a national project were implemented in Portugal aiming to develop a new study concerning the main bryoflora communities of this region. The main goals are: Task 1 - To get knowledge about the biological resources. Taxonomic revision of all herbarium samples from the region, including material not studied, according recent taxonomic criteria. Task 2 - New scientific fieldwork will be planed according the information about former expeditions. Task 3 - Characterization of principal communities and indicators selection (management, climatic, altitudinal, among others) with special emphasis to the epiphytic vegetation in primary and secondary forests. Task 4 - Identification of relevant areas for conservation based on floristic research and the selection of areas with high incidence of endemic or rare species. Task 5 - Biogeographic relationships between the São Tomé bryoflora and selected taxa occurring in other Atlantic Island as well as continental areas. The first results of this study mainly the Task 1 will be presented in the present work.

## INTERPLAY BETWEEN SEQUENTIAL COLONIZATION OF CANARY ISLANDS AND POPULATION DIVERGENCE IN *OLEA EUROPAEA* SUBSP *GUANCHICA* P.VARGAS ET AL.

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The major drawback to evolutionary studies is the fact that we cannot experiment with evolution. In spite of this, oceanic islands are an ideal scenario to infer both patterns of colonization and the evolutionary process. Among oceanic archipelagos, the Canary Islands have been a useful framework for such studies, due to geological complexity, high habitat diversity, seven major islands -that enhances population isolation- and a sequential age increase of the islands from east (20.6 million years) to west (700,000 years). It has been suggested that inter-island colonization between similar ecological zones was responsible primarily for speciation of the Canarian flora. However, few and scattered data have been published *at the species level*. In the present study the taxon subject to study is *Olea europaea* subsp. *guanchica* (Canarian wild olive tree), which is endemic to the Canary Islands. Using the AFLP technique on 20 populations, we addressed a two-fold analysis of (1) genetic divergence of populations occurring on the same islands but in contrasted environments (xeric vs. mesic) and (2) genetic divergence of populations occurring on different islands but sharing similar environments. Patterns of colonization of the *Olea europaea* complex to Macaronesian archipelagoes are also discussed.

## EVOLUTION OF SPIDERS IN THE REMOTE ISLANDS OF OCEANIA: COMMUNITIES AND CONNECTIONS

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In recent years studies have started to incorporate phylogenetic history into the investigation of community assembly. While most of these studies argue for the non-random nature of community composition, they have demonstrated opposing forces in shaping communities -- habitat filtering, in which only taxa with certain traits colonize a community, can lead to phylogenetic clustering, while competitive exclusion, in which taxa that exploit similar resources will complete and exclude each other, can lead to phylogenetic overdispersion. Oceanic islands have played a key role in the integration of phylogenetics and evolutionary biology into studies of community composition. Using the fact that a given island system often includes multiple representatives of the same lineage it is possible to infer how characters have changed to allow multiple species to co-occur within a given community. In general, such studies within archipelagoes have highlighted the role of convergent evolution, and suggest that community formation is somewhat deterministic. Here, I will present recent research on the phenomenon across different remote and far-flung archipelagoes in the Pacific, focusing on the Hawaiian Islands, French Polynesia, and eastern Micronesia. Using spiders in high and middle elevation habitats, I will examine the extent of phylogenetic relatedness of species across climatically similar communities, and assess ecological equivalence and hence levels of convergence.

## PATTERNS OF BODY SIZE CHANGES IN THE PLEISTOCENE ENDEMIC DEER FROM MEDITERRANEAN ISLANDS

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During the Pleistocene, endemic cervids were among the most common species in more or less unbalanced faunas of the Eastern (such as Crete, Kassos, Karpathos, Amorgos,Tilos) and Western Mediterranean islands (Sardinia and Corse, Capri, Sicily and Malta, Favignana). They belong to different mainland ancestors, but their phylogenetic relationships are sometimes not clear (especially as regards to Crete's deer), and different hypotheses have been postulated concerning origin, time of migration, and evolutionary processes. No form with an entirely comparable way of life existed on different islands and it is difficult to single out a dominant factor in their evolution. For instance, sympatric speciation and radiation, leading both to 'dwarfism' and 'gigantism' processes, should be suggested for Crete's deer, whereas in Sardinia and Sicily endemic deer undergone respectively a progressive decrease or not important variation in size. The body-mass (considered as the best proxy of body–size) trends in endemic species on different islands show that when more then one deer is present, radiation process led to species scaling in body size and the largest taxa appeared in more diversified faunas. On the other hand, similar size reductions occurred on islands that differ in area, physiography and primary productivity.

## THE CHATHAM ISLANDS: ANCIENT ROCKS – NEW BIOTA

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The Chatham Islands, comprising five small islands and several islets, are located on the Pacific Plate approximately 850 km east of New Zealand. A popular assumption is that the Chatham Islands have supported an ancient terrestrial biota since the break up of Gondwana (80-70 Ma), but new geological evidence suggests that the islands may have drowned several times with the last re-emergence less than 3.8 Ma ago. Biologists have also questioned the old age of the islands as the extant Chathams' biota does not show the high proportion of deep taxonomic endemism expected on ancient islands. Genetic data across a broad sample of taxa, primarily invertebrates and plants, is used to identify the genetic distance between the Chatham Islands taxa and their closest relatives in New Zealand. So far, no evidence of high genetic distances between New Zealand and Chatham's taxon representatives has been found, indicating that all the investigated species on the islands have indeed a recent over sea dispersal origin. Nevertheless, some taxon groups do include one or more morphologically distinguishable Chatham endemics. For example the cave cricket genus *Talitropsis* comprises a widespread New Zealand species and two allopatric Chatham species distributed across an archipelago that would have been continuous land during most of the Pleistocene.

## HABITAT SIMILARITY IS THE MAIN ENVIRONMENTAL FACTOR INVOLVED IN THE CURRENT DISTRIBUTION PATTERN OF BUTTERFLIES IN THE CANARY ISLANDS

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We analyzed the possible roles of inter-island proximity, habitat similarity, climatic similarity, and similarity in human activity, on the inter-insular colonization processes that yielded the current distribution pattern of butterflies in the Canary Islands. We studied the two families of the order Lepidoptera with best-known distribution in the Canaries, namely Geometridae and Noctuidae, separately, analyzing for each family the endemic and non-endemic species together and separately. We tested 11 hypotheses about factors that might have affected the inter-insular colonization processes, four related to inter-island proximity, four related to habitat similarity, one related to climatic similarity, and two related to similarity in human activity. We used a parsimonious analysis of distributions after building up cladograms of expected relationships among isles according to each explanatory hypothesis, which were later compared with the distribution pattern of Geometridae and Noctuidae species in the islands to select the most parsimonious hypothesis. Habitat similarity, considering phytoclimatic subregions, was the main environmental factor involved in the inter-insular colonization of the Canary Islands by butterflies for all the groups of species analyzed. Inter-island proximity was equally important only for endemic Geometridae species, and was a secondary factor for the rest of groups but non-endemic Noctuidae.

## MOLECULAR SYSTEMATICS AND PHYTOGEOGRAPHY OF THE MOSS GENUS *LEUCODON* IN EUROPE

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The pleurocarpous moss genus *Leucodon* (c. 40 species) is widely distributed in Eurasia, Africa, the Americas and Oceania. In Europe, five species occur, the widespread *L. sciuroides* and four species that are either endemic to the Macaronesian Archipelagos (*L. treleasei*, *L. canariensis*) or range from the eastern Mediterranean to the Caspian Sea (*L. flagellaris, L. immersus*). It can be supposed that the more narrowly distributed species may be derived from the widespread *L. sciuroides*, but evolutionary relationships of the European *Leucodon* species have not yet been investigated in detail. Besides, especially the distinction of the two Macaronesian endemics, which occur predominantly in the laurel forest (Laurisilva), and *L. sciuroides* is problematic based on morphological characters. In the present study we investigate molecular relationships of 10 Eurasian and American *Leucodon* species, focusing on samples from the Canary Islands, Madeira, Cape Verde and Azores. Phylogenetic analyses of *Leucodon* as well as other genera of Leucodontaceae and further pleurocarpous moss families were performed based on nuclear ribosomal ITS and chloroplast *atpB-rbcL* spacer sequences. In addition, AFLP (amplified fragment length polymorphism) fingerprinting analyses of *Leucodon* samples mainly from the Macaronesian Islands were conducted. With these analyses we aim (i) to test the monophyly of *Leucodon*, (ii) to clarify systematic relationships and phytogeographic affinities of European *Leucodon* species, (iii) provide molecular data for identification of the Macaronesian species, and (iv) reveal intraspecific variation of *Leucodon* in the Macaronesian Islands.

## FLYING FOXES OF THE MEDITERRANEAN REGION

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The distribution range of flying foxes (Chiroptera: Pteropodidae) is restricted to Palaeotropic and Australian regions. The extralimital range extension in the Mediterranean is a bit curious and calls for explanation. We reexamined all records of the Mediterranean flying fox, *Rousettus aegyptiacus*, supplemented them with a number of new records from Cyprus, Turkey, Syria, Lebanon, Egypt, Yemen and Iran, and collected samples for DNA analyses. The present contribution surveys some results with particular respect to history of its range in the region. Despite the Neogene records in the Western Mediterranean, the current range is restricted onto the eastern-most part of the region and the zone of thermo-Mediterranean (of Blondel & Aronson 2005). The species absents in all islands except for Cyprus. Genetic distances between local populations throughout the region (including Cyprus) are suprisingly low. In explaining it, we stress a close dependence of *Rousettus* on its ultimate winter diet - carob, *Ceratonia siliqua*, and dependence of its spread on the dispersal history of the latter. Since also the curious fructification strategy of carob (cf. cauliflory, long fructification period timed to winter, olfactoric instead of optic signs of fructification etc.) exhibits a strong adaptation to chiropterochory, we hypothesize that the Mediterranean ranges of both taxa evolved as a synchorological unit since onset of pronounced seasonality in the Late Caenozoic. The antropogenic spread of carob in the historical time effected essentially also the current range dynamics of the Mediterranean *Rousettus,* though, for more reasons, it responded it in the regional extent only.

## THE UNIQUE ABILITY OF AN ISLAND ENDEMIC PINE SPECIES TO RESPROUT AFTER FIRE THEREBY DRAINING FRESHWATER FROM TRADE WINDS

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Mono-dominant, natural pine forests composed of the endemic *Pinus canariensis* occur on the Canary Islands between 900 – 1,500 m a.s.l. These pine forests form the upper treeline, locally substituted by laurel forests. Here, trade winds carry clouds through the stands all year round, which are drained by long needles of the trees. Thus, *Pinus canariensis* is believed to play a crucial role in balancing the water household of the islands. However, the pine forests of the Canary Islands are prone to frequent fire. Over the last 30 years, fire frequency has increased by one power of magnitude. In response to fire, *Pinus canariensis* has developed a unique feature among all 112 pine species known: it is capable of resprouting extraordinary long needles from adventive buds in stems and branches, thus performing effective photosynthesis and fog drainage again soon after fire. We propose, that *Pinus canariensis* is an 'ecosystem engineer' shaping ecosystem functioning in the trade wind zone in terms of vegetation dynamics, hydrological cycling and fire regime. Here we report on results from analysing (1) the fire regime of the Canary Islands (using remote sensing techniques, and (2) the resprouting ability of *Pinus canariensis* after fire (using a fire history gradient).

## AFLP DIVERSITY ON ISLANDS – A COMPARISON OF *BARLIA METLESICSIANA* ENDEMIC TO TENERIFE (CANARY ISLANDS) WITH ITS MORE WIDESPREAD CONGENER, *BARLIA ROBERTIANA*

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The orchid *Barlia metlesicsiana* W.Teschner is endemic to Tenerife (Canary Islands), while its sister species *Barlia robertiana* (Loisel.) Greuter is widespread in the Mediterranean region including other islands (e.g. Cyprus, Sicily). Therefore, these closely related species allow comparing intraspecific genetic diversity patterns on oceanic and continental islands. With respect to Tenerife, when assuming recent colonisation the genetic diversity of *B. metlesicsiana* should be depauperate; however, given enough time *in-situ* diversification might lead to unique diversity. The analysis (n = 220) of Amplified Fragment Length Polymorphisms (AFLPs) mainly based on *Barlia* samples from Tenerife, Sicily, and Cyprus indicated the deepest split between the two species. Within *B. robertiana*, samples from Sicily and Cyprus were also well-separated, while samples from Sicily and the Italian mainland were intermingled. Based on the three islands solely (n = 186), hierarchical AMOVA revealed a larger portion of the variation among the three islands (32.11%) than among the two species (26.27%), thus indicating independent evolution on each island. As general tendency, unique genetic diversity was negatively correlated with island area. Given the highest amount of 'polymorphic private' AFLP fragments on Tenerife, recent colonisation of this oceanic island is rather unlikely.

## AGROBIODIVERSITY IN THE SMALL MEDITERRANEAN ISLANDS

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In industrialised countries only rarely it is possible to find some refuge areas for plant genetic resources. Geographical islands, for their isolation, are often richer in phytogenetic resources than continental areas with similar size. This circumstance is emphasized on small islands far from the coast, which are often less influenced by anthropisation. In these particular habitats it is still possible to find landraces and wild endemism, along with new ethno-botanical information. For this reason a joint project with a multidisciplinar approach was started among the Istituto di Genetica Vegetale of the National Research Council (Bari, Italy), the Laboratorio di Archeobotanica (University of Lecce - Italy) and the Institute of Crop Science, University of Kassel (Germany). The aim of the project is (a) to analyse the effects of isolation on landraces richness in Mediterranean islands with a prevalent agricultural economy; (b) to find out possible correlation with agricultural, climatic, eco-geographical and social features; (c) to use a paleoethnobotanical approach to analyse the results of the collecting activity. Preliminary results show that small islands are not only refuges for minor crop plants, but also serve as important reserves of plant genetic resources and model platforms for crop plant research. These results also indicate that islands represent: (1) Preservation centres for rare species, in some cases thought to be extinct (e.g. *Vicia articulata*); (2) Places of ongoing evolution/domestication (e.g. *Cucurbita moschata*); (3) Places of new introduction (e.g. *Solanum muricatum*); (4) Places of primary domestication (e.g. *Lavatera arborea*); (5) Areas with new species for crop plant research (e.g. *Diplotaxis muralis*); (6) Areas with new information for crop plant research (e.g. *Capsicum chinense*).

## THE LAST MARITIME PINES FROM THE BALEARIC ISLANDS

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Maritime pine (*Pinus pinaster* Aiton) is a forest species distributed throughout the Western Mediterranean Basin, including Western Mediterranean islands (Corsica, Sardinia, Pantelleria and Balearic Islands). At the Balearic Islands, the species is restricted to three small isolates, one in Ibiza (Ca n'Esteva, three trees) and two in Minorca (Es Milocar, two trees; Rafal Rubí, four trees), highly threatened by forest fires and competition with other Mediterranean pines (namely, *P. halepensis* Mill.). Despite historical and palaeobotanical records supporting the spontaneity of maritime pine in the Balearic Islands, current populations are commonly thought to be the remains of ancient plantations. Relic maritime pine occurrences in the islands were screened using molecular markers with contrasting inheritance modes (mitochondrial, chloroplast and nuclear DNA) and compared to populations from surrounding areas in the Iberian Peninsula, southeastern France, northern Africa and Corsica. Mitochondrial and nuclear DNA showed a Tyrrhenian origin of trees at Es Milocar, while Ca n'Esteva and Rafal Rubí had an Iberian filiation. On the other hand, chloroplast DNA showed similar patterns at all three locations, suggesting, along with palaeobotanical records, more continuous populations in the past and extensive pollen gene flow. Fragility of autochthonous maritime pine Balearic relics against perturbations makes necessary the urgent development of sound conservation strategies.

## GENETIC ARCHITECTURE OF THE MINORCAN CORK OAK POPULATION

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Cork oak (*Quercus suber* L.) is a forest tree whose distribution is restricted to acidic soil areas in the Western Mediterranean. The Minorcan population is composed of no more than 70 trees scattered in nine small isolates of less than 20 individuals each. Chloroplast and nuclear DNA were analysed in order to assess the genetic architecture of the fragmented Minorcan cork oak population in comparison with other stands from surrounding continental (Catalonia, eastern, south and central Spain) and insular (Sicily) regions. Chloroplast DNA showed a mixture of lineages of Tyrrhenian and Iberian origin, being the former present in eastern Minorcan locations and the latter in the central region. A molecular analysis of variance (AMOVA) with nine nuclear microsatellites did not show significant differentiation levels between pairs of Minorcan stands, suggesting that current gene flow among populations is likely to occur. In comparison to stands from surrounding regions, the Minorcan cork oak population showed the highest effective number of alleles and percentage of private alleles, along with Sicilian populations, where cork oak is more widespread. The genetic architecture of cork oak stands in Minorca supports the spontaneity of the species.

## ISLAND-RAFTED CORK OAKS IN THE MEDITERRANEAN: DNA MATCHES TERTIARY TECTONIC EVOLUTION

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Cork oak (*Quercus suber* L.) is an emblematic Mediterranean sclerophyllous tree, with a modern discontinuous distribution extending from the Atlantic coasts of North Africa and Iberian Peninsula to the southeastern regions of Italy, and including the main west-Mediterranean islands as well as the coastal belts of Maghreb. We have analysed 110 populations throughout the distribution range using cpDNA markers (microsatellites). We have identified five different haplotypes with a strong geographic structure that cannot be easily explained by isolation due to human activity and climatic oscillations. We found that the distribution of modern cork oak haplotypes is closely related to the Neogene tectonic evolution and palaeogeography of the Mediterranean domain, suggesting that a number of continental microterranes (Calabria, Sardinia, Corsica, Kabylies, Balearic Islands and the Rif-Betic range), rifted off the European-Iberian continental margin and drifted to their current locations, were vectors for cork oak populations. This implies that cpDNA divergence of cork oak populations occurred at a time of intense tectonic activity and microplate spreading (25-15 Myr) and was followed by a long period of stability of isolated populations, lasting over 15 Myr in spite of insularity conditions and Quaternary climate oscillations.

## EVIDENCE FOR MULTIPLE INVASIONS OF SEVERAL GENERA OF ARACEAE ON WESTERN MEDITERRANEAN ISLANDS

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Despite the remarkable species-richness of the Mediterranean flora, relatively few studies have investigated the temporal and spatial origins of this extraordinary diversity. The present study aims at elucidating the time frame and sequential events associated with the diversification of seven genera of Araceae in the Mediterranean Basin, with a particular focus on four species (*Ambrosina bassii*, *Arum pictum*, *Biarum dispar, Helicodiceros muscivorus*) (sub-) endemic to Corsica, Sardinia, and the Balearic Archipelago. These islands, which are the remnants of an old Hercynian block that detached from the Iberian plate in the late Oligocene, are ideal laboratories to test the relative contribution of vicariance, geodispersal, and over-water dispersal in shaping the present plant distribution in the Mediterranean. Our results support two main introductions of the Araceae in the region, with an *Arisarum* – *Ambrosina* clade diverging from the Peltandreae in the late Cretaceous (82.7 ± 6.8 Ma), and five genera of the Areae forming a clade originating in the late Eocene (37.8 ± 7.2 Ma). Based on these results, four different evolutionary histories are proposed for the respective Hercynian (sub-) endemics, further highlighting the tectonic and climatic complexity of the Western Mediterranean, and providing us with a window on the biogeography of the entire Basin.

## PHYLOGENETIC RELATIONSHIP AMONG PIGEON SPECIES FROM PALEARCTIC REGION AND MACARONESIAN ISLANDS

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The evolutionary relationships among Columbidae species from the Palearctic Region and Macaronesian archipelagos was examined using mitochondrial control region sequences. Morphological and behavioural studies have indicated the close relationships between the Wood Pigeon (*Columba palumbus*) from European mainland and the insular endemic pigeons, Madeira Laurel Pigeon (*C. trocaz*) from Madeira and Bolle's Laurel Pigeon (*C. bollii*) and White-tailed Laurel Pigeon (*C. junoniae*) from the Canary Islands. In the present molecular study, we also included the Stock Pigeon *(C. oenas*), the Rock Pigeon (*C. livia*) and the Azorean endemic subspecies of Wood Pigeon *C. palumbus azorica*, in the phylogenetic analysis. Preliminary results suggest that White-tailed Laurel Pigeon is basal, showing mitochondrial sequences divergent to the rest of pigeons studied. Madeira Laurel Pigeon and Bolle's Laurel Pigeon cluster with widely distributed Palearctic species. This work constitutes a genetic approach to the origin of threatened endemic pigeons that inhabit in the relic laurel forests of these Atlantic islands.

## THE ISLAND RULE AND THE EVOLUTION OF BODY SIZE IN THE DEEP SEA

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When isolated on islands, small-bodied species exhibit gigantism and large-bodied species become dwarfed. Here we test the island rule of body size, in a non-insular but analogous system; shallow and deep-water gastropods from the western Atlantic Ocean. Many species are hypothesized to have colonized the deep sea relatively recently from shallow water following an extinction event in the Cenozoic and undergone substantial body size changes from their hypothesized ancestors. Our results indicate that, consistent with the island rule, gastropod genera with small-bodied shallow-water species have significantly larger deep-sea representatives, while the opposite is true for genera that are large-bodied in shallow water. Bathymetric body size clines within the deep sea are also consistent with predictions based on the island rule. Like islands, the deep sea is characterized by low absolute food availability, leading us to hypothesize that the island rule is a result of selection in a resource poor environment.

## PREDICTIVE MODELLING FOR CONSERVATION PRIORITIZATION OF *ANDROCYMBIUM HIERRENSE*, AN ENDANGERED SPECIES ON A BIOSPHERE RESERVE (LA PALMA, CANARY ISLANDS)

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*Androcymbium hierrense* is an endemic and endangered species of the Canarian Archipelago, distributed on La Palma, La Gomera and El Hierro. The species presents a cumpled distribution on La Palma Island and it is threatened by the destruction of its habitat. For this reason, the aim of this contribution is to present the preliminary results of the study carried out in 2005 to know the current status and distribution of species, and to propose an application of a predictive modelling for establish a conservation program. Distribution was studied searching new localities near to the known populations within a similar habitat. Censuses was performed following located transects of contiguous quadrats. For the predictive modelling, we choose two analytical methods: a Geographic Information System (GIS) analytical method, to diagnose the ecological requirements of species; and a Genetic Algorithm for Rule-set Prediction (GARP), to provide an accurate assessment of the spatial distribution. The objective was to evaluate the accuracy of a GARP model to predict the spatial distribution of *A. hierrense*. Both models was based on the same environmental parameters. Five new localities of *A. hierrense* were found, being an increase in occupancy area for species of 200%, approximately. Species present a mean density of 0.22 ± 0.02 (n = 1,555) given a 95% confidence intervals of 7,603-357,126 mature plants for the entire population. From our model it was possible to locate an appropriate zone on the island to introduce a new population when a natural one was destroyed by a human action.

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## PHYTOGEOGRAPHIC ANALYSIS OF AN EDAPHIC ARCHIPELAGO - THE DOLMITOPHILOUS FLORA OF THE BAETIC MOUNTAINS (SOUTH SPAIN)

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The dolomitic outcrops of the Baetic Mountains (West Mediterranean Basin) have been widely reported by botanists. These substrates are real edaphic islands and harbour an extremely peculiar vegetation and flora with high levels of endemic species. This work is focused on the phytogeographic relationships between the floras of the different outcrops. The presence/absecence data of the dolomitophilous plant species were recorded on a 10 × 10 km UTM grid. These cells were used as Operational Geographic Units (OGUs). Subsequently, the most interesting phytogeographic patterns and centres of endemism were determined by applying a cluster analysis with the software PC-ORD and the parsimony analysis of endemicity (PAE) with the software PAUP 4.0. The results point out the floristic differences between the three main centres of dolomitophilous flora identified: Sub-baetic sierras, Sierra Nevada and the SW Baetic sierras. The latter centre was physically separated from the Iberian Peninsula by the Guadalhorce Corridor during the Messinian period and connected to North Africa. The groups derived from the analyses are compared with diverse classifications of the territories of the Baetic phytogeographic Province. Acknowledgments: This study was funded by the project 77/2002 of the Organismo Autónomo de Parques Nacionales (Spain).

## GUILD COMPOSITION AND MUSTELID MORPHOLOGY – CHARACTER DISPLACEMENT BUT NO CHARACTER RELEASE

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Competition is hypothesized to lead to evolution to reduce morphological overlap between competitors. Within guilds this is believed to lead to equal size ratios of teeth and skulls of adjacent-sized species. In allopatry conditions are believed to favor character release. We examined whether character displacement is prevalent in mainland musteline guilds and sought evidence for character release in adjacent island guilds. We find equal ratios between skull lengths but not canine diameters in all mainland guilds. Few insular guilds show equal ratios for either trait. There is scant evidence for character release: insular mustelines do not evolve towards the size of a missing guild member. We propose that different guild compositions in different localities produce different evolutionary trajectories. Similar sizes on islands and mainlands can be explained by similar prey sizes in both settings. Competition is probably not a ubiquitous force in the assembly and evolution of musteline guilds.

## STATE OF CONSERVATION OF *ATRACTYLIS PREAUXIANA* AN ENDEMIC ENDANGERED SPECIES IN TENERIFE (CANARY ISLANDS)

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The Canary Islands is a high biodiverse region with an approximate number of 18,000 species including native and introduced species, within this total, the 28.21% are endemic terrestrial species. Extinction of local endemisms implies an irreversible lost of biodiversity at a global scale, hence the fact that conservation of endemic species becomes of such an interest. The principal aim of this work has been to study the present state of populations of *Atractylis preauxiana*, a very rare plant known locally as 'piña de mar', scarcely studied, threatened and catalogued as an endangered species. Populations in the island were located, and its present state, size, structure and possible future tendencies have been studied, as well as threats that currently affect them. In this research a total of 2,716 individuals have been recorded, more than in previous census, and also new populations were found, but no one higher than 50 individuals. Trends of populations in relation to their phenological structure and size classes could not be clearly established thus a longer monitoring would be necessary. Although three populations are included in Natural Protected Areas, the rest (six) are threatened by herbivores and mostly by human pressure over the territory.

## FIRST STAGES OF RECOVERING OF THE LITTER ARTHROPODS COMMUNITY AFTER A FIRE EVENT IN THE PINE FOREST OF LA PALMA (CANARY ISLANDS)

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The pine forests of La Palma have been the most affected by fire events in the last decades. Last fire occurred in September 2005 burning around 2,000 hectares. Our aim in this research is to study how invertebrates, that live in the litter of these perturbed areas, evolve in composition, richness and diversity during the first stages of recovering. Litter from three affected plots was taken and also from a control plot placed adjacent to the burnt area. Litter was sieved and invertebrates were identified at the species and morphosepecies level. Results obtained provide new information about the initial recolonization process of the soil after fire, which is unknown for arthropods in the Canary Islands. This information becomes also relevant for a proper forest management as the invertebrates are an essential part for the optimal trophic functioning of the ecosystem.

## POPULATION STRUCTURE OF A RELICT POPULATION OF THE ENDEMIC PALM *PHOENIX CANARIENSIS*, LOCATED IN BARRANCO DEL CERCADO, TENERIFE

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The palm grove of Abicor (Barranco del Cercado, Tenerife) is mainly constituted by young individuals (<30 years) of pure *Phoenix canariensis,* with a few individuals which are hybrids with *P.dactylifera*. The potential vegetation of the area is a Canarian Termophilous Scrub with palms, but the whole valley was intensely cultivated with crops until a few decades ago and very little of the original vegetation was left. By studying old aerial photographs, we concluded that most of living palms grew after the abandonment of agriculture, which gave an opportunity to the few old palms surviving in the area to reproduce and create a larger population. Here we present a distribution map with a census of sex, trunk height and taxonomical status.

## INVASIVE PLANTS DISTRIBUTION USING REMOTE SENSING AND GIS: *PENNISETUM SETACEUM* IN GRAN CANARIA (CANARY ISLANDS). PRELIMINARY RESULTS

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*Pennisetum setaceum* ('rabo de gato', 'plumero', 'cola de caballo') is one of the most invasive plant species in the Canary Islands. In the island of Gran Canaria its documented presence dates back to the 1940's. *Pennisetum setaceum* is currently occupying a large area surrounding the insular perimeter and it is found at elevations of up to 600 meters and it is affecting several Protected Natural Areas. The objectives of our study were as follows: (a) to map the distribution of *Pennisetum setaceum* in the Eastern Protected Natural Areas of Gran Canaria island, (b) to make an inventory of *Pennisetum setaceum* in these Protected Areas, including population location and density and measurements of the impact to natural and agricultural areas, (c) to build a database connected with the GIS mapping as a control management tool, (d) to analyze the diachronic evolution of the populations and their distributions using data from 1994 as a baseline, and (e) to measure the spectral signature of the different populations of *Pennisetum setaceum* and to evaluate the potential for monitoring using remote sensing technology.

## PALM TREE COMMUNITY DISTRIBUTION IN GRAN CANARIA (CANARY ISLANDS). DEVELOPMENT BY GEOGRAPHICAL INFORMATION SYSTEM (GIS)

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A detailed analysis of the distribution of the palm populations from the Gran Canaria Island was carried out by GIS (Geographic Information System). A whole of 250 palm populations were recorded and analysed. In its development an exhaustive field inventory was made, extracting and quantifying more significant ecological traits of these vegetal formations, and designing a georeference data base. All the information was implemented and used in a GIS with multiples possible analysis, developments and updates.

## ENVIRONMENTAL, HISTORIC AND GEOGRAPHIC FACTORS PREDICTING NATIVE AND ALIEN SPECIES RICHNESS IN THE NATURALIZED FLORA OF EL HIERRO (CANARY ISLANDS)

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A complete floristic database on UTM-quadrates (1 km x 1 km) has been established for the Canary island of El Hierro. The combined evaluation of both environmental and chorological data using GIS allows to explore intra-island patterns of phytodiversity. We used regression analysis for revealing the relations of environmental, historic and geographic factors with the distribution of endemic, native and naturalized alien vascular plant species. To separate the spatial component of explanatory variables we applied partial regression including a cubic trend surface of coordinates. We also analized climate matching of alien species with respect to their biogeographic origin. High richness of endemic species was strongly related to steep slopes and intermediate altitudes, while diversity of local endemics was highest on geologically old surfaces and steep cliffs. Richness of native non-endemic species showed a strong unimodal relationship with altitude and mean annual precipitation. In contrast, alien species richness was best explained by historic factors such as disturbance intensity and distance to nearest urban nuclei, but was also related to precipitation and altitude. En general, most of the climatic and historic variables showed a strong spatial component, nevertheless, most relationships were still highly significant when controlling for coordinates. Furthermore, alien species showed differences in their distribution along the altitudinal gradient according to their biogeographical affinities and climatic tolerances. Propagule pressure and abiotic stress are proposed as main factors controlling alien species distribution on the island.

## ACCELERATED MITOCHONDRIAL SUBSTITUTION RATES IN ISLAND POPULATIONS – A CASE STUDY ON GOLDCRESTS (*REGULUS REGULUS*) AND ULTRAMARINE TITS (*PARUS TENERIFFAE*)

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In avian molecular systematics the 2% rule of thumb is still a frequently adopted paradigm, though the concept of a mitochondrial clock has recently been severely challenged. According to former studies, cytochrome *b* lineages of birds are thought to evolve at a rate of 2% base substitutions per million years. Based on mitochondrial sequence data of four subgenera of tits (*Parus*, *Cyanistes*, *Periparus*, *Poecile*) and of crests and kinglets (*Regulus*) several limitations of the 2% rule could be confirmed. Estimates of substitution rates differ between mitochondrial genes, cyt*b* and control region, and for each of these between taxonomic levels investigated and between different clades of the molecular trees. Island populations such as Ultramarine Tits and Goldcrests from the Canary Islands and the Azores tend to faster substitution rates than widespread continental populations. In *Parus teneriffae*, a 12 bp indel in domain II of the control region shared by the entire Canarian population except the one from La Palma is obviously the cause for the highest local rate estimate among parid data sets (about five to ten times higher than local rates in the European Blue Tit clade, *P. caeruleus*).

## CRYPTIC SPECIATION IN CANARY ISLAND SONGBIRDS – NEWLY DESCRIBED TAXA IN GOLDCRESTS (*REGULUS REGULUS*), ROBINS (*ERITHACUS RUBECULA*) AND ULTRAMARINE TITS (*PARUS TENERIFFAE*)

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Several Canary Island songbird populations underwent significant differentiation from their close continental relatives due to long-lasting geographic isolation. Based on molecular markers and diagnostic morphological and bioacoustic characters these endemics were consequently treated as species of their own by some authors. With respect to molecular, morphological and partly bioacoustic differentiation among the Canary Island populations the following taxa were recently newly described: in European Robins: *Erithacus rubecula marionae* Dietzen et al. 2003 from Gran Canaria; in Goldcrests: *Regulus regulus ellenthalerae* Päckert et al 2006 from La Palma and El Hierro. Both taxa represent distinct mitochondrial lineages (cytochrome *b* and control region) and genetic distances to their closest relatives on Tenerife (Robins), e.g. Tenerife and La Gomera (Goldcrests) range between 3.1 and 3.9% (cyt*b* distance). Contrasting the molecular results, morphological differentiation is subtle and differences in territorial song are measurable only in case of the Goldcrests. Recent molecular studies on Ultramarine Tits indicate a substructuring in nominate *Parus teneriffae teneriffae*, since the populations from Tenerife and La Gomera on the on hand and from Gran Canaria on the other hand belong to separate mitochondrial lineages.

## COMMUNITY CHANGE THROUGH TIME: SMALL ISLET PLANT COMMUNITIES AFTER TWO DECADES

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Plant communities of 32 small islets in the Aegean Sea had been thoroughly investigated in 1974 by Runemark, and again by one of the authors (MP) in the 90's. Sampling was performed on the whole surface of these islets during both sampling periods. This dataset provides an excellent chance to explore change of community properties in a time period large enough to allow species turnover affect community structure. Species richness on small islets is supposed to fluctuate due to stochastic factors, leading to increased turnover rates. Evidence for such processes is inferred from the presence of the well-known Small Island Effect. Nevertheless, the chances to actually document extensive change of insular community components are rare. According to standard equilibrium theory, the combined effect of immigration and extinction should lead to more or less steady species richness, regardless of species identity. Our dataset is comprised of islets around larger islands within a 'continental' archipelago. Thus, immigration should not be limited by isolation, especially for plants that have relatively good dispersal abilities. We explore species richness, species-area relationships, community nestedness, and the floral composition of eminent and variable components. We also explore the possible effects of grazing and sea-gull colonies on the patterns of community change through time.

## A TALE OF TWO ARCHIPELAGOES: COMPARING DIVERSIFICATION IN THE FLORAS OF THE CANARY AND HAWAIIAN ISLANDS

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The Canary and Hawaiian Islands have natural conditions which are exceptional for studying the interface between physical and biotic systems, exhibiting remarkable similarity in their geologic and climatic settings. Moreover, they exhibit comparable patterns of species richness and endemism in their floras. Both floras have been subjected to numerous phylogenetic studies of the evolutionary relationships of species. Here we use phylogenetic groupings within both archipelagoes to explore how evolutionary diversification contributes to island- and archipelago-scale species diversity. We analyze species-area relationships for islands, considering the physical and climatic attributes relating to species diversity and endemism. We then draw upon a wealth of phylogenetic studies to compare the role of evolutionary diversification in determining patterns of species richness and endemism in the two archipelagoes. In both archipelagoes, diverse lineages contain disproportionate numbers of species and single-island endemic species. However the number of diverse lineages and their individual species richness are less in the Canary Islands than in Hawaii. We propose that this is due both to differences in the range of environments available and to the availability of niche space, where a higher number of founder events from outside results in less niche space available for local adaptation in the Canary islands.

## THE ASSEMBLAGE AND EVOLUTION OF ISLAND FAUNAS – THERE IS MORE TO IT THAN ENDEMICS

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Despite the unquestioned role of the study of island faunas in the development of evolutionary biology and biogeography, there are still many questions which have been rarely addressed and for which we do not have adequate answers. The analyses of the origin of the island faunas is usually centred on the endemic species, but, specially in non-oceanic islands relatively close to the coast, most of the fauna is not endemic. By analysing molecular phylogenies/phylogeographies of whole lineages from the islands and surrounding continental areas it is possible to address many of these unanswered questions. In this poster, we use more than 1,500 sequenced specimens (including most of the island endemics) of multiple populations of species of water beetles of families Hydraenidae and Dytiscidae from Corsica, Sardinia, Mallorca, the Canaries and Madeira to try to answer three questions: (1) is there a continuum in the degree of genetic isolation of the island fauna, from phylogenetically isolated 'paleoendemics' to populations with regular gene flow with the continent, or are there clusters of relative genetic divergence corresponding to geological or historical events?; (2) is it possible to find correlates of the genetic divergence of the island species/populations? (e.g. population size, body size, ecology, phylogenetic background…); and (3) is there any recognisable difference in these global patterns between volcanic and continental islands?

## DISPERSAL BIOGEOGRAPHY: COLONIZATION AND DIVERSIFICATION OF REPTILES IN INDIAN OCEAN ISLANDS

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Molecular phylogenetic studies in island settings provide insights into the processes shaping biodiversity in these regions. Using mtDNA sequence data we are studying the origins, colonization routes and diversification patterns of several reptile taxa from Western Indian Ocean islands, comprising Madagascar and the archipelagos of Comoros, Aldabra and the Seychelles and also East African coastal islands like Zanzibar and Pemba. The Seychelles harbour mostly 'old' endemic species (interestingly a few clades of two species), of African, Malagasy or yet unknown origin. However, the reptile fauna of the Comoros, a volcanic archipelago situated between Madagascar and the East African coast, results both from natural ancient colonisations, recent natural colonisations and recent, probably human-aided, dispersals. Species genealogies reveal that multiple natural colonisations are common in the majority of the groups and that oceanic dispersal, more than archipelago radiations or within-island divergence lead to species diversification in the region and explains current species distribution patterns. For the Comoros, a common biogeographic pattern is emerging where most endemic forms, have their closest relatives in Madagascar, and not in East Africa. A few species, especially geckos have widespread distributions that probably result from anthropogenic introductions, and may represent important threats for endemic insular species.

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## POLLINATION BY GENERALIST VERTEBRATES IN ISLAND ECOSYSTEMS: PASSERINE BIRDS AND LIZARDS VISITING *ISOPLEXIS CANARIENSIS* (SCROPHULARIACEAE) IN THE CANARY ISLANDS

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Generalist vertebrates as mutualistic agents have been proposed as an insular phenomenon according to evidences about the frequency of island insectivorous lizards and birds visiting flowers for nectar/pollen and consuming fleshy fruits to compare with mainland relatives. This pattern have been explained as a result of particular ecological conditions operating on islands, i.e. low interspecific competition and predation risk. In consequence, vertebrates reach very high densities and amplify their dietary niche and become as potential mutualistic agents of insular flora. However, there is an incomplete knowledge of their pollination effectiveness, a conspicuous situation in the Macaronesian islands, where only qualitative information about flower-bird/lizard interactions have been reported. Eleven endemic macaronesian plant species have been reported as ornithophylous elements, but any specialist nectar feeding birds occurred (neither in the past). In the present communication we reported the relative contribution of lizards and passerine birds as true in one of the prominent element of the Canarian ornithophylous flora: *Isoplexis canariensis* (Scrophulariaceae). Molecular phylogenies suggest that the woody *Isoplexis* belongs to a clade which is derived from the continental herbaceous *Digitalis*, an insect-pollinated genus. The present data represents the first time that vertebrate pollination has been empirically demostrated in Macaronesian region. The breeding system of the plant was also examined through hand-pollination experiments to evaluate how important are such pollinators for plant reproduction.

## THE IMPORTANCE OF CAVES FOR BAT ASSEMBLAGES IN THE WEST INDIES

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I examine the patterns of bat faunas, long-term impact of hurricanes, and the role of cave roosting in the formation of bat assemblages in the West Indies. Twenty-eight, of the 56 extant species of West Indian bats, are endemic. The core community of these islands consists of one species of *Monophyllus*, one species of *Brachyphylla*, *Artibeus jamaicensis*, *Noctilio leporinus*, *Tadarida brasiliensis*, and *Molossus molossus*. On the Greater Antilles, four cave-dwelling species are added to this core community. These bat faunas are characterized by the reduction in tree-roosting species, compared to the tropical mainland, and with the exception of *M. molossus*, all members of this core community are exclusive or predominantly cave-dwellers. Over 40% of the bat fauna on most of the West Indies (80% in Puerto Rico) are cave-dwelling species. Many of these cave-dwelling species roost in hot-caves, where they form non-random assemblages and may function as physical ecosystem engineers. Endemic mormoopids, and phyllostomids like *Monophyllus* and *Erophylla*, show reduced metabolic rates and renal adaptations to life in hot-caves. Other species of phyllostomids and natalids endemic to the West Indies also seem especially adapted to roosting in hot caves. The impact of hurricanes on the structure of a bat assemblage is discussed, based on data obtained through a long term survey of a cave in Puerto Rico.

## SYSTEMATICS AND BIOGEOGRAPHY OF THE DIPLOMMATINID LAND SNAILS OF PALAU

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Palau (Belau) is a group of over 500 islands in the western Pacific (Micronesia). The majority of Palau's land snail species are endemic to Palau, and most of these species have restricted ranges. Sixty-five Palau land snail species are described, and approximately 200 species have been collected. The tiny (< 5 mm) leaf litter- and rock-dwelling diplommatinid land snails comprise a large proportion of this diversity. Shell morphologies correlate with habitat type. Twenty-five of the 65 described land snail species are diplommatinids; however, 92 diplommatinid land snails have been collected. Given the presence of diplommatinid species on most Palau islands and the relative low vagility of land snails, the Palau diplommatinids are an interesting system for exploring biogeographic questions. In this study I use DNA sequencing (COI and 16S mtDNA) to elucidate relationships among Palau diplommatinid land snail species. I also explore relationships between Palau species and relatives from other western Pacific islands (e.g. Yap, Guam, Pohnpei, Kosrae, Philippines and New Guinea). Phylogenetic reconstructions indicate that the Palau diplommatinids are the result of more than a single colonization event. Individual Palau islands do not contain monophyletic groups of diplommatinid species, and in some cases, sister taxa are from distant islands.

## PHYLOGENY OF *RUTA* (RUTACEAE): IMPLICATIONS FOR BIOGEOGRAPHIC PATTERNS IN THE MEDITERRANEAN BASIN

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In its current circumscription *Ruta* includes 8 species of perennial shrubs: four species have a peri-Mediterranean distribution (*R.chalepensis*, *R.graveolens*, *R.angustifolia*, and *R.montana*), and four species are island endemics (*R.corsica* is endemic to the Corso-Sardinian microplate; and *R.pinnata*, *R.oreojasme*, and *R.microcarpa* are endemic to the Canary Islands). The Mediterranean basin, with its complex but well-known history of microplate movements and climatic oscillations, provides the geological backdrop for the diversification of *Ruta*. Phylogenetic analyses of three chloroplast DNA regions (*mat*K, *rpl*16, and *trn*LF) support the monophyly of *Ruta*. Within *Ruta*, the monophyly of the species endemic to the Canary Islands indicates a single origin of the lineage, followed by diversification within the archipelago. Furthermore, the relative temporal order of splitting within this clade is congruent with the order of island formation in the Canarian archipelago.Within *R.corsica,* the populations from Corsica and Sardinia, respectively, form two well-supported clades. This result confirms recent morphological and karyological work that identified the populations of the two islands as two species, and suggests that the Strait of Bonifacio, separating the two islands, acted as a barrier to gene flow.

## BIOGEOGRAPHY OF SEED-PLANT GENERA ENDEMIC TO THE CARIBBEAN ISLAND BIODIVERSITY HOTSPOT

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With approximately 1,000 islands and islets the Caribbean Island biodiversity hotspot is composed by the Bahamas, the Greater Antilles, the Lesser Antilles and some of the islands offshore the Venezuelan coast. This region represents the most important insular system of the New World and has biogeographical links both with Laurasia and Gondwana. We summarize updated data on seed-plant genera endemic to these islands, as part of our ongoing research projects on the biogeography of endemic lineages of the region. A total of 178 seed plant genera are endemic. Only one genus is endemic to the Lesser Antilles (*Charianthus*), and none reaches the islands north of Venezuela. There is a direct relationship between island area and number of genera, with Cuba harboring the highest number of endemic genera. The serpentinitic areas of Cuba and Hispaniola hold a considerable amount of this endemicity. The few available molecular phylogenies reveal a complex biogeographical pattern which seems to mirror the complex history of these archipelagos.

## ECOLOGICAL SATURATION ON OCEANIC ISLANDS: RECONCILING CONFLICTING EVIDENCE FROM PLANT AND BIRD INVASIONS

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Here we evaluate evidence for species saturation on islands by examining patterns of species addition (through exotic species introduction and establishment) and species loss (through native species extinction). We find that patterns of introduction of exotics and extinction of natives are not congruent among different taxonomic groups. For land bird species, the total number of species has remained largely unchanged over the past few centuries. This has occurred because species extinctions have been largely matched by species naturalizations, with nearly 80 percent of the variance in the number of naturalized species explained by the number of native extinctions. In contrast, for vascular plants, the number of species present on islands has dramatically increased over the past few centuries, as few species have gone extinct and many have become naturalized. Further, the rate of plant species addition has generally remained more or less linear over time across a number of oceanic islands. At first glance, these data suggest that bird richness on islands is saturated, while plant richness is not. We examine the robustness of this characterization by considering the interaction between propagule pressure of species introductions and rates of species establishment. Finally, we discuss the implications of these findings for the future of biodiversity on oceanic islands.

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## SPECIES DIVERSITY, ENDEMISM AND BIOGEOGRAPHY OF THE BEETLES OF THE MADEIRAN ISLANDS

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This work presents the main objectives of a project on the biodiversity, endemism and biogeography of the beetles (Coleoptera) of the Madeiran islands. During the last few years, the knowledge on the invertebrate fauna of Azores, Canaries and Cape Verde was updated and considerably improved due to the combined efforts addressed by researchers, policy makers and non-govermental agencies. In Madeira, however, there is still lacking a reference work on the terrestrial invertebrate fauna, where updated and concise information could be presented following a thorough analysis of the scientific data reported in the multiple contributions made during the last decades. The main objectives of our research project are: (a) update the knowledge on the beetle specific richness and endemism of the five islands of the Madeira Archipelago; (b) identify hotspots of biodiversity and endemicity in the Archipelago of Madeira and establish priorities for conservation within the beetle endemic fauna; (c) identify the ecological and the historical factors responsible for the observed spatial patterns of biodiversity and endemicity; (d) look for scale variation of species richness (alpha, beta and gamma) evaluating the relative importance of beta diversity measured at different scales (plot, fragment, reserve) using additive partitioning of species richness; and (e) evaluate if the beetles follow a nested distribution pattern and discuss the applicability of the nested subset analysis for the conservation planning of the Madeiran native forest fragments.

## PATCHES AS ISLANDS: WHICH SYSTEMS ARE EQUIVALENT AND WHICH ARE NOT?

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Ever since the publication of the MacArthur Wilson Theory of Island Biogeography patchy systems of all types have been defined as islands. From cushion plants and thistles to vernal pools and conservation refuges, island theory has been invoked to predict species diversity patterns. However, these systems differ from one another and from oceanic islands in both spatial and temporal relations and we argue that as a result, different predictions are expected for different systems. Using data from a study of microbiotic crusts in arid systems we demonstrate the importance of defining patches according to several traits: permeability of the surrounding matrix, time between disturbances and patch formation relative to the surrounding matrix. Of these three traits, only the last is actually a trait of the patch itself. The other two factors can only be determined based on the organisms associated with the patches.

## BRYOPHYTES FROM MADEIRA ISLAND: AN OVERVIEW ON CONSERVATIONAL STATUS AND PHYTOGEOGRAPHICAL AFFINITIES

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Due to its particular geographic, climatic and insular characteristics, Madeira Archipelago comprises an important floristic diversity. Its main forest formation, the Laurisilva is considered to be a relict of the forests of the Tertiary period that dominated southern Europe and northern Africa millions of years ago. About 540 bryophyte taxa are considered to be present in Madeira Archipelago. Of these, 70% correspond to mosses and 30% to liverworts and hornworts. Approximately 31 taxa are endemic to Macaronesia, including 15 taxa exclusive to Madeira. In the past 5 years, extensive research projects, involving various national and foreign institutions and researchers, have been contributing to a deeper understanding of the relationships between the bryophyte flora communities in the Madeira Island. These involve distinct habitats, namely the slopes along 'levadas', the ripicolous and the epiphytic ones. Together the three habitats comprise a total of 255 taxa, 23 Macaronesian endemics and 5 Madeira endemics. So far, the higher diversity was found on the slopes (186 taxa), comparing with the ripicolous (127 taxa) and epiphytic (80 taxa) communities. The slopes are also richer in Macaronesia endemic and threatened taxa (21 and 9 taxa, respectively). New data on community composition and phytogeographic affinities of selected bryophyte taxa will be presented and discussed. The biodiversity studies developed are also a good support to update the threatened status of some red-listed species. These understandings can lead to the development of effective management measures of the natural resources, allowing their sustainable use and protection.

## GENETIC CHARACTERISATION OF *SAMBUCUS PALMENSIS* IN THE CANARY ISLANDS

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*Sambucus palmensis* is an endangered plant species, endemic to the Canary Islands, that inhabits the laurisilva forest. It has been described in four islands (La Palma, Tenerife, Gomera and Gran Canaria). Its natural populations are very scarce, and consist of small numbers of very isolated individuals. Their number has increased in the last few years as a consequence of several conservation programmes carried out, above all, in Gomera. However, their numbers total less than 400 individuals in the whole of the Canarian archipelago. The genetic diversity of 165 individuals (both natural and reintroduced) has been studied through the analysis of five microsatellite loci, and significant levels of inter-insular genetic differentiation have been detected. In La Palma most individuals screened were clonal contrasting with Tenerife where most of the plants were genetically distinct. At an island level, 18 out of 34 alleles detected were exclusive to one island (Tenerife). In addition, all the individuals were clustered into 59 different multiloci genotypes, of which 36 were singular and unique. The results obtained suggest the need to carry out a conservation programme for each island, in particular, amongst other actions, addressing the movement and positioning of the genetically different specimens, with the aim of avoiding an increase in levels of inbreeding.

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## NESTEDNESS OF REMNANT SONORAN DESERT PLANT COMMUNITIES IN METROPOLITAN PHOENIX, ARIZONA

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Urbanization can have profound effects on the plant communities persisting in remnant habitats. That process can be explored by examining patterns of nestedness. Species composition for a set of communities exhibits a nested pattern if species composing progressively richer assemblages form a series of subsets. Nestedness can form as a result of the dynamic processes of extinction or colonization; it can also reflect a nested distribution of habitats among the sites or the differential abundance properties of species through passive sampling. This study investigates whether Sonoran Desert vegetation in remnant habitat islands within metropolitan Phoenix is nested, and explores which mechanisms are responsible for the pattern. Both the woody and herbaceous communities were significantly nested. Analysis of woody species abundance characteristics suggest that individual taxa respond to divergent ecological mechanisms. Thus, nestedness in woody vegetation arises as a consequence of an aggregate response of constituent species to multiple mechanisms, and is manifest at the island and habitat-levels. Nestedness in herbaceous communities arises from an area effect, involving either extinction or passive sampling, and is reinforced by colonization of exotic species. Hence, nestedness in plant communities can result from a complex set of contributors and may not be attributable to a single factor.

## RATES OF BODY SIZE EVOLUTION IN *ANOLIS* LIZARDS

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Is morphological evolution more rapid on islands than on the mainland? As predicted by the species area relationship islands are generally more species poor than mainland areas. This means for populations colonizing islands new niches may be available, prompting rapid evolutionary change. Consequently, we might expect that rates of morphological character divergence will be higher among island endemics than among mainland species. We use a recent phylogenetic comparative approach to test for different rates of divergence in body size between species inhabiting small islands, large islands or the mainland among *Anolis* lizards. We find that the rate of divergence of female body size (measured as maximum snout-vent length) is lower among small island species than among large island or mainland species. Conversely, male body size shows a general trend towards more rapid divergence among small island species. Furthermore, sexual size dimorphism shows more rapid evolution in small island species when compared to large island or mainland species. Taken together, our results show that male and female body size evolved at different evolutionary rates on small islands implying that selection pressures on males differs from selection pressures on females following colonization.

## EVOLUTIONARY SPECIES-AREA CURVES AS REVEALED BY SINGLE-ISLAND ENDEMICS. INSIGHTS FOR THE INTERPROVINCIAL SPECIES-AREA RELATIONSHIP

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The species-area relationship between different biological provinces is one of the most interesting but less studied aspects of the species-area pattern (SAR). Following that a biological province is a region whose species have for the most part evolved within it, rather than immigrating from somewhere else, we propose that the use of single island endemics, for which islands can be considered as biological provinces, can offer great insights for the processes and their interactions establishing biodiversity in large scales of time and space. We analyzed 14 different data sets for the construction of single island endemics-area relationships (SERs). All the SERs were statistically significant and the variance of single island endemics explained by area was quite high, ranging from 0.53 to 0.96. The z-values of the statistically significant SERs ranged from 0.47 to 1.23, with a mean value of 0.79 (±0.31). The SERs' slope are similar with those calculated for inter-provincial SARs, indicating that, regardless of spatial scale, when speciation becomes the dominant process establishing species richness high z-values of SARs should be anticipated. These results suggest a general use of an evolutionary theory for diversity whose further exploration should prove fruitful. Additionally, SERs exhibiting great similarity with inter-provincial SARs can offer significant insights for the processes involved in the establishment of biodiversity in large scales of time and space.

## DIVERSIFICATION IN PHILIPPINE *RHINOLOPHUS* BATS: CRYPTIC VARIATION IN AN OCEANIC ARCHIPELAGO

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Diversity in the Philippine archipelago has been strongly influenced by both colonization of islands and *in situ* speciation. In contrast to much of the mammalian fauna, relatively little is known about the processes of colonization and diversification for most bats of the Philippines. Recent collections include two forms of the arcuate horseshoe bat, *Rhinolophus arcuatus*, which are broadly sympatric throughout the archipelago. Cryptic diversity within islands is confounded by variation across islands and has made conclusions hard to reach. DNA sequences from the mitochondrial genome show two genetically divergent lineages that correspond to “wide” and “narrow” morphotypes based on characters of the noseleaf. Phylogeographic patterns vary between these lineages and are discussed with regard to two competing hypotheses. Geographic isolation and allopatry explain much of the data in the “narrow” lineage, however, a very close relationship with *R. inops* also is indicated. An alternative hypothesis of ecological divergence is discussed for these data and Southeast Asian horseshoe bats more generally.

## DISPERSAL AS A KEY ELEMENT OF COMMUNITY STRUCTURE: THE CASE OF GROUND BEETLES ON LAKE ISLANDS

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In order to study the influence of dispersal ability on community structure of ground beetles, 15 lake islands and 2 mainland sites of the lake Mamry archipelago, northern Poland, were sampled by using pitfall traps. Of the 71 ground beetle species detected, 47 were macropterous, 16 wing-dimorphic and 8 brachypterous. Macropterous species had lower site abundances and occupied fewer sites than dimorphic and brachypterous species. There were trends from macropterous to brachypterous species towards a nested distribution across the sites and towards over-dispersed (aggregated) species co-occurrences. Canonical correspondence analysis pointed to site isolation and area as main factors influencing site abundance and spatial distribution. Our results imply that further studies on species cooccurrences and community assembly have to consider dispersal ability as a key element influencing ecological distributions at the regional scale.

## NONMARINE OSTRACODA OF THE CANARY ISLANDS: NEW DATA ON SPECIES DISTRIBUTION IN TENERIFE AND LA PALMA AND ANALYSIS OF SPECIES-ENVIRONMENT RELATIONSHIPS

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Despite previous studies on the ostracod fauna of the Canary Islands, this crustacean group is still poorly known in the archipelago. In the present study, we present new data on limnetic ostracods collected in January 2006 from 25 sites of the islands of Tenerife and La Palma. These ostracod communities are poor in species (an average of 3.2 species per site), the most frequent species being the widely distributed species *Heterocypris incongruens* (Ramdohr, 1808), found in 15 stations. Regional species richness accounts for 27 species cited to date in the Canary Islands, a relatively high figure if we take into account the low number of studies carried out to date in the archipelago. *Candonopsis scourfieldi* Brady, 1910, *Eucypris virens* (Jurine, 1820), *Fabaeformiscandona* sp. Krstić, 1972, *Potamocypris unicaudata* Schaäfer, 1943 and *P. producta* (Sars, 1924) are new to the Canary Islands. Most of the species found, so as the dominant *H. incongruens*, are typical inhabitants of temporary environments. Based on multivariate ordination techniques, we can see that the ostracod community structure seems mainly determined by water chemistry environmental gradients (pH, oxygen, ionic composition).

## THE NONMARINE OSTRACOD (CRUSTACEA: OSTRACODA) FAUNA OF THE BALEARIC ISLANDS: SPECIES RICHNESS AND ASSEMBLY ORDINATION

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The present survey examines the ostracod composition of more than 300 samples from diverse water bodies of the Balearic Islands collected between 1988 and 2003. Environmental data (conductivity, alkalinity and chloride concentration) were analysed for more than 100 of these samples. Species richness per island and for the whole archipelago is high compared to other islands, and the influence on this of sampling effort and island size is discussed in comparison to other datasets from Mediterranean or Atlantic islands and continental European areas. In total, 55 taxa have been found, 36 of which are new for the archipelago. Pioneer, widely distributed species tolerant to desiccation, such as *Sarscypridopsis aculeata* (Costa, 1847) and *Eucypris virens* (Jurine, 1820) are the most frequent on the islands, together with circum-Mediterranean species. No ostracod endemics are known to date for the Balearic islands, although our data include rare cave dwelling taxa with unknown specific affiliation that could be new species to science. Multivariate ordination analyses show that water ionic composition and concentration, together with seasonality of the aquatic habitat are essential factors affecting ostracod assembly ordination, and these factors are in turn related to geographical (geology, hydrology, climate) traits of the islands.

## *Symposium 4*

# Maritime connectivity

## MARITIME CONNECTIVITY

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The concept of 'connectivity' – "the demographic connection maintained between neighboring populations of a species due to the migration of individuals (particularly dispersing larvae) between them" [Mora & Sale 2002] – has risen to prominence in marine science since the turn of the century. Often considered in terms of networks of marine protected areas, 'connectivity' has also become an umbrella term under which diverse issues previously discussed in disciplines such as physical oceanography, population genetics, and ecology are being integrated. Discussions of connectivity usually highlight the importance of dispersal ("one of the most important life-history traits involved in species evolution and persistence" [Mora & Sale 2002]) and so should also consider vicariance and other historical processes that have influenced modern-day patterns of marine diversity at infra- and super-specific levels. Here, as an introduction to the symposium, we illustrate some of the processes thought to affect connectivity using population genetic data and computer simulations, clarify terms, and highlight some topics that have received a lot of attention and some that appear to be relevant but largely unexplored.

## GLOBAL BIOGEOGRAPHICAL PATTERNS AND INTER-HEMISPHERE EVOLUTIONARY RELATIONSHIPS IN HIGH LATITUDE PELAGIC PLANKTONIC PROTISTS

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The marine pelagic environment appears to have few barriers to dispersal, yet diversity clearly prevails in many groups of marine taxa. The planktonic foraminifera are proving a particularly useful model protist with which to investigate the drivers of diversity in this open ocean environment on a global scale. They are carried over enormous distances which often results in cosmopolitanism but they also meet ecological and geographical barriers which can lead to biogeographic structure. A molecular phylogeographic study of the high-latitude planktonic foraminiferan *Neogloboquadrina pachyderma* reveals a stepwise progression of diversification starting with the allopatric isolation of Atlantic Arctic and Antarctic populations following the onset of the Northern Hemisphere glaciation. Further diversification occurred later in the Southern Hemisphere and in the North Pacific linked to glacial-interglacial climate dynamics. However, Arctic circumpolar isolation in this protist has prevailed through time.

## TESTING FOR SIMULTANEOUS VICARIANCE ACROSS TIME AND SPACE IN THE INDO-WEST PACIFIC

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The Indo-west Pacific (IWP) is the most diverse marine region, but our understanding of diversification processes is hampered by species' ranges that are often wide and sympatric. Based on a comprehensive phylogeny of a diverse (>250), reef-associated group of mollusks – cowries – spatio-temporal patterns of diversification within the region can be deconstructed. Contrary to expectations, most (>95%) younger (≤10 Ma) sister taxa are geographically structured, implying that sympatric speciation is rare, and allopatry persists for millions of years. Geographic boundaries (phylogeographic breaks) between sisters cluster in seven areas and support all three current models of IWP diversification (Centers of Origin, Accumulation, and Overlap) and also suggest a significant role for ecology in driving diversification. I compare both nonparametric and approximate Bayesian computation (ABC) methods for tests of simultaneous vicariance at these congruent breaks. Results indicate that while geographic boundaries are shared by many species pairs, they are spread out in time, indicating either recurrent vicariance or a larger role for stochastic dispersal events.

## DRIVEN BY THE WEST WIND DRIFT? A REVIEW OF SOUTHERN TEMPERATE MARINE BIOGEOGRAPHY, WITH NEW DIRECTIONS FOR DISPERSALISM

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20th century biogeographers developed intriguing hypotheses involving West Wind Drift dispersal of Southern Hemisphere biota, but such models were largely abandoned in favour of vicariance following the development of plate tectonic theory. Recent molecular studies, however, have provided strong evidence for dispersal, and relatively little evidence for the biogeographic role of plate tectonics in distributing southern marine taxa. Despite confident panbiogeographic claims to the contrary, molecular and ecological studies of buoyant macroalgae such as *Macrocystis*, for example, indicate that dispersal predominates. While vicariance theory certainly facilitates the development of testable hypotheses, it does not necessarily follow that vicariance explains much of contemporary southern biogeography. Ironically, some of the better-supported evidence for marine vicariance in southern waters has little or nothing to do with plate tectonics. Rather, it involves far more localised and recent vicariant models, such as the isolating effect of the Bassian Isthmus during Pleistocene low sea-level stands (*Nerita*). Recent phylogeographic studies of southern taxa (e.g. *Diloma*, *Parvulastra*) imply that passive rafting cannot be ignored as an important mechanism of long-distance dispersal. We suggest that studies of rafting should maximise the chance of success by focusing on taxa that have an ecological propensity for rafting. We therefore outline a new direction for dispersalism, involving genetic analysis of bull-kelp (*Durvillaea*) and its associated holdfast invertebrate communities.

## THE RELATIVE ROLES OF DISPERSAL AND VICARIANCE IN BIOGEOGRAPHY OF MARINE MACROALGAE

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The relative contributions of vicariance and dispersal in determining the distributions of marine taxa are still controversial. For seaweeds, two disjunct distributions patterns are particularly pertinent: (1) Pairs of species/sibling species in the North Pacific and North Atlantic Oceans, dating from the opening of the Bering Strait 5.5-3.5 Ma. (2) Bipolar or antitropical disjunctions. Both patterns are exhibited by the red seaweed *Rhodochorton purpureum,* which is circumpolar in both hemispheres. We chose this species because its exceptionally wide environmental tolerances might have permitted it to survive glaciations and hence reveal evidence of old vicariant events. Cultured isolates and field collections from throughout the range of *R. purpureum* were sequenced for a nuclear marker (ribosomal ITS2) and a plastid marker (*tuf*A-*rps*7-*rps*12-*rpl*31). Pronounced geographic structure revealed a complex biogeographic history. Three cryptic species in the North Pacific there are interpreted as the imprints of vicariant diversification, probably in the Miocene. Multiple crossings of different lineages through the Bering Strait at various times, possibly by ice rafting through the Arctic, are indicated. High genetic diversity in the North Atlantic shows that *R. purpureum* survived Pleistocene glaciations, and hybridization between different lineages was detected. The shallow divergence between Arctic and Antarctic isolates indicates recent transequatorial passage. Phylogeographic analysis of *R. purpureum* thus reveal the importance of both vicariance and dispersal in its evolutionary history.

## DISPERSAL AND VICARIANCE IN INDO-PACIFIC CORAL REEF FISHES

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Studies of coral reef biogeography have presented strongly contrasting views on the role and relative importance of vicariance and dispersal. This often reflects differing methods and spatial scales. Vicariance is frequently emphasized in large scale evolutionary studies, while dispersal is strongly associated with smaller scale ecological research. Any resolution to these alternate views has been stymied by confusion over the origins vs. maintenance of patterns and the constraints imposed by the available evidence. Historical information, in particular, is scarce. However, recent molecular evidence has triggered a re-evaluation of the relative roles of vicariance and dispersal in reef fish biogeography. These findings suggest that reef fish species are characterized by considerable antiquity, complex histories and dynamic geographic ranges. At the same time, the emphasis on dispersal in reef fish ecology is waning with increasing evidence of closed rather than open populations. Finally, we are beginning to find a common ground with paleontology, molecular phylogenetics and phylogeography, and ecological evidence providing a rare and welcome concensus.

## GENETIC DIFFERENTIATION IN THE SEAGRASS *CYMODOCEA NODOSA* ACROSS THE MEDITERRANEAN-ATLANTIC TRANSITION REGION

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A central question in evolutionary ecology is the nature of environmental barriers susceptible to limit gene flow and to induce population genetic divergence, a first step toward speciation. Here we study the geographical barrier formed by the transition zone between the Atlantic Ocean and the Mediterranean Sea, using as model *Cymodocea nodosa,* a seagrass distributed throughout the Mediterranean and in the Atlantic, from central Portugal to Banc d'Arguin in Mauritania. We used eight microsatellite markers to compare 18 meadows in the Atlantic and 27 meadows in the Mediterranean, focusing on the transition between both these basins. Populations from these two regions form coherent groups containing several unique high frequency alleles for the Atlantic and for the Mediterranean, with some admixture on the Atlantic side and west of the Almeria-Oran Front, a pattern typical of a secondary contact zone. This coincides with populations where only one or a few genotypes were found, for all but Cadiz (Portugal, SW Spain and Morocco), but remarkably still show the footprint of a contact zone. The most significantly divergent groups are the two groups at the range limits: particularly the southernmost Atlantic populations (Mauritania, Madeira and Canary Islands), probably due to founder effects and geographic isolation, but also the easternmost Mediterranean, also a potential footprint of vicariance. Significantly higher allelic richness ($\hat{A}$) was found in the Mediterranean than in the Atlantic; this and the extremely high value found for Cyprus, the easternmost sample, suggest that colonization proceeded from the Mediterranean to the Atlantic.

## ARE $F_{ST}$ VALUES COMPARABLE? STANDARDIZING $F_{ST}$

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$F_{ST}$ is the most commonly utilized statistical index of genetic differentiation in studies attempting to infer larval dispersal and population connectivity. $F_{ST}$ should range from zero to one, along a continuum from complete connectivity to complete isolation, respectively. However, AMOVA's rarely yield an $F_{ST}$ of one, even when there are no shared haplotypes between populations, and $F_{ST}$ is often less than zero when samples from the same effective population are compared. Consequently, the comparison of $F_{ST}$ values is often misleading. Here we use mock data sets to assess the effects of unequal sample sizes, number of alleles, allele frequency distribution, genetic diversity, and number of populations on the minimum and maximum $F_{ST}$ values calculated with AMOVA. All of these predictive factors affect the realized range of $F_{ST}$. The maximum possible $F_{ST}$ can range from zero to one, thus even a very small $F_{ST}$ may indicate complete isolation. Using multiple linear regression, we derive equations that successfully predict the maximum and minimum possible $F_{ST}$ values, given the characteristics of the populations being compared. A standardized $F_{ST}$ statistic is calculated by dividing the difference between $F_{ST}$ and $F_{ST\mathrm{min}}$ by the difference between $F_{ST\mathrm{max}}$ and $F_{ST\mathrm{min}}$. In a real data set of Hawaiian limpets, we show that standardizing the $F_{ST}$ fundamentally changes erroneous conclusions based on unstandardized $F_{ST}$'s.

## INSIGHTS GAINED FROM A WEB-BASED ATLAS OF HALOCYPRID OSTRACODS OF THE SOUTHERN OCEAN

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Planktonic are an important but poorly studied component of oceanic plankton communities at all depths, playing a significant role in detrital cycles. A web-based atlas (http://ocean.iopan.gda.pl/ostracoda) of the distribution of Southern Ocean planktonic ostracods has been developed using all extractable published data together with a considerable amount of unpublished data based on samples collected during *Discovery Investigations* (1929-1952). The northern boundary of the Southern Ocean was taken as 52°S. The site includes distributional maps, taxonomic drawings (mostly original), size data, and systematic notes on 47 species. All the data are freely downloadable as PDF files and is thus available to anyone, anywhere, with access to the web. The data are subject to a number of errors emanating from systematic confusions and some identification errors, some clear patterns emerge, notably the circumpolar distributions of the truly polar species. Little evidence emerges for the main oceanographic frontal systems delimiting the species' distribution. Nor was the spatial coverage sufficient to demonstrate convincingly that the species can be used as indicators of the spread of the water masses, although in several cases there were indications. The data can be re-processed in the future to seek changes in ranges resulting from shifts in climate.

## BIOGEOGRAPHIC PATTERNS OF ROCKY INTERTIDAL COMMUNITY STRUCTURE ALONG THE WEST COAST OF NORTH AMERICA

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Recent studies suggest that nearshore oceanographic conditions can have important effects on the structure of benthic communities. To evaluate latitudinal variation in community structure in relation to previously described biogeographic provinces and prevailing oceanographic current patterns, we conducted surveys of benthic rocky intertidal communities at 67 sites along the Pacific Coast of North America from Baja California Sur, Mexico (26.7°N latitude) to southern Alaska, USA (58.3°N latitude), spanning a coastal distance of approximately 5,500 km. We found a high degree of spatial structure in the similarity of intertidal communities along the coast. Community structure differed significantly among 6 major biogeographic regions. Breaks between regions generally corresponded well with coastal features correlated with oceanographic transition zones and biogeographic boundaries previously described for mollusks and marine algae. We identified 13 major community structure 'groups' using cluster analysis, which corresponded well with major biogeographic regions. Similarity in community structure at the large scale was highly correlated with distance among sites and with long-term mean sea surface temperature. We suggest that oceanographic patterns may largely determine patterns of intertidal community structure along the Pacific coast of North America, and we identify important biogeographic breaks delimiting regions of community similarity.

## GENETIC ISOLATION-BY-DISTANCE AMONG *NASSARIUS RETICULAUS* L. POPULATIONS ALONG THE EUROPEAN ATLANTIC COASTLINE

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Genetic diversity within and between populations serves as an indirect measure of gene flow and population connectivity, and can illuminate historical demographic events. Here, we explored the gastropod *Nassarius reticulatus* as a model species to investigate the dispersal and historical demography of marine organisms along European Atlantic coastlines. Partial cytochrome c oxidase subunit I (COI) sequences were obtained from 156 individuals collected within six populations across 1,700 km. Across all populations, there was a weak, nonsignificant population level of genetic differentiation ($F_{ST} < 0.001$). Despite this weak population structure, we detected a shallow but statistically significant increase in genetic isolation with geographic distance (IBD), suggesting that *N. reticulatus* populations are not panmictic. Assuming a stable, stepping stone model of gene flow, the IBD slope is consistent with an average larval dispersal distance of ~75 km per generation. These results are in broad agreement with the life history (pelagic larval duration = 30-60 days) and ecology (euryoecious) of the species. A mismatch analysis indicated that a demographic expansion begun 64,000 – 162,000 years ago, a date far older than the most recent glacial maxima. Further, a significant parabolic relationship between genetic diversity and latitude is interpreted as the signature of historic populations within the centrally-located Bay of Biscay that subsequently that expanded northward and southward.

## CONCORDANT PHYLOGENIES AND DISCORDANT PHYLOGEOGRAPHIC PATTERNS IN TWO SYMPATRIC GASTROPODS WITH LONG-LIVED LARVAE

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We compare phylogeographic patterns in two species of highly dispersive Neritid gastropod: *Nerita albicilla* and *Nerita plicata*. These species have nearly sympatric ranges that span the Indo-Pacific, and extensive sampling of more than 1,000 individuals from 97 sites mirrors their distributions well. Both species exhibited two divergent clades for mitochondrial COI, which result from vicariance in response to a periodic barrier at the Indonesian-Australian Archipelago (IAA) that is driven by Pleistocene sea-level change. *Nerita albicilla* has retained reciprocal monophyly following the disappearance of the barrier, and shows a phylogenetic break along the coastline of the Malay Peninsula, despite modern oceanographic conditions that should promote mixing between the Pacific and Indian Oceans. High gene flow estimates between demes within the Pacific Ocean suggest that this break is maintained by post-dispersal processes rather than limited dispersal. In contrast, *N. plicata* displays a genetic cline in the Central Pacific, not the IAA. However, the similar phylogenetic topology and shortage of genetic structure suggest that divergence occurred in the IAA. An explanation for discordant phylogeographic patterns may be found in relatively minor differences in larval period or microhabitat association. Phlyogeography at the IAA may be more similar to temperate systems than previously considered.

## PHYLOGEOGRAPHY AND CONSERVATION OF A WIDE SPREAD CORAL REEF FISH, *HALICHOERES HORTULANUS*

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Understanding larval connectivity in marine taxa is an important component to elucidating their evolutionary history, ecological connections and in developing effective management strategies. Here we investigate the phylogeography of a common widespread reef fish, *Halichoeres hortulanus*. Using information from the mitochondrial and nuclear genomes we demonstrate that there are clear differences between Pacific Ocean and Indian Ocean fish. These differences appear to be centered around the Flores sea. We show that this biogeographic boundary appears to act as a near complete one-way filter with haplotypes moving from the Pacific to the Indian, but not in the other direction. Similarly we demonstrate a signal of rapid population expansion in the Indian Ocean samples suggesting that there has been a recent invasion from East to West. Our results indicate that while the fish has the potential for long distance dispersal, several factors, including paleohistory and modern day ocean currents serve to restrict this dispersal capability. This study implies that despite the broad geographic range of this species, effective management must incorporate biogeographic data, and that stocks in Indonesia represent two separate evolutionary lineages.

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## MARINE BIOGEOGRAPHY IN SOUTHEAST ALASKA: INFLUENCES OF LARVAL DISPERSAL AND RECENT DEGLACIATION

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Southeast Alaska, located in the North Pacific, approximately 1,800 km from Seattle and roughly the same size as the state of Florida, is an intricate network of islands where the marine habitat is fragmented and water exchange with the open ocean is limited. The marine ecosystem in Southeast Alaska is unique because of its tidewater and coastal glaciers, large inputs of freshwater from precipitation, strong influence of coasts and islands, and rich marine resources. Marine population and community dynamics are strongly influenced by the history of deglaciation, strong gradients in abiotic conditions, and larval supply. Glacier Bay is an example of a deglaciated fjord in Southeast Alaska in which marine intertidal species richness declines along a gradient from the mouth to the head. Glacier Bay lacks refuges from glaciation because this fjord was deglaciated in the last several hundred years, however genetic evidence suggests that lower intertidal species may have had refuges from glaciation in other locations in the region. Teasing apart the role of larval supply, abiotic conditions, and deglaciation as causes for species diversity patterns is a challenge. This poster examines biodiversity patterns in Glacier Bay as a function of tidal height, larval dispersal potential, and abiotic factors as a first step to elucidate mechanisms for species diversity patterns.

## PHYLOGEOGRAPHY AND POPULATION CONNECTIVITY OF VERMETID GASTROPODS IN THE HAWAIIAN ISLANDS

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The knowledge of dispersal and connectivity of populations is critical in designing marine protected areas and assessing the feasibility of such refuges to the conservation of organisms and their habitats. It has been shown that re-colonization, recovery, and persistence of populations in an isolated reserve are dependent on the distance between reserves in relation to larval dispersal distance. Population genetic data can be used as an indirect measure of realized larval dispersal. Vermetids or wormsnails are sessile, suspension-feeding gastropods found in shallow marine waters. They show a wide range of dispersal potential from pelagic larvae, which reside in the plankton for several weeks, to species with direct developing benthic juveniles, which lack a planktonic phase. The Vermetidae in Hawaii comprise nine species. Most species are locally abundant and distributed throughout the Hawaiian Archipelago. A 569 base pair region of the mitochondrial gene cytochrome oxidase I (COI) was sequenced for the nine species from most Hawaiian Islands, including the Northwestern Hawaiian Islands. Species with limited larval dispersal potential show structured populations throughout the Hawaiian Archipelago, suggesting no or very limited connectivity among islands. Furthermore, results concerning historical colonization patterns, source areas of biodiversity, and dispersal routes among and within Hawaiian Islands are addressed.

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## THE CENOZOIC MARINE FOSSIL RECORD OF THE BAJA CALIFORNIA PENINSULA AND ITS IMPLICATION ON GLOBAL AND REGIONAL SEAWAYS

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The Cenozoic marine fossil record of the Baja California Peninsula begins with the Middle Paleocene to Late Eocene marine faunas from the Tepetate, Bateque and Tetas de Cabra formations. Those represent an influence of the Tethys realm, reflecting the Middle America Seaway. The Middle Late Oligocene record of the San Gregorio and El Cien Formations, denotes a faunal change possibly related to the Eocene-Oligocene Transition recorded world wide. Could be possible a closing of the seaway around the late Oligocene, because of the temporal land bridge between Venezuela, The Caribbean Islands and the Florida Peninsula. The Miocene formations records the transformation from an active to passive continental margin on the Pacific of the California Terrane, including the formation of the Gulf of California. A Late Miocene seaway was developed between the proto-Gulf and the Pacific Ocean, in the area between San Ignacio Lagoon and Santa Rosalia Basin. The Pliocene records along the Pacific and Gulf margins document the development of the Gulf and the process of terrestrial and marine speciations in the peninsula, and at the same time the permanent closing of the Panama seaway between the Pacific and Atlantic oceans. There is no fossil record supporting a Pleistocene-Holocene seaway in the Middle of the Baja Peninsula.

## SPATIAL PATTERNS OF THE INVASIVE *GAMMARUS TIGRINUS* SEXTON (CRUSTACEA, AMPHIPODA) IN RELATION TO ENVIRONMENTAL CONDITIONS AND NATIVE GAMMARIDS IN THE NORTHERN BALTIC SEA

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The invasive North American amphipod *Gammarus tigrinus* Sexton was found for the first time in the Northern Baltic Sea in 2003. During two years the species became established and even dominant gammarid in many locations throughout the northern Gulf of Riga. Following the establishment *G. tigrinus* and native gammarid species seldom existed in the same site indicating spatial separation between native and invasive species. The invasive species was more successful in shallow and sheltered soft bottom areas than in deeper and exposed stony areas. The abundance structure of *G. tigrinus* was mostly related to the biomass of green algae, charophytes and higher plants. The densities of native gammarids were best explained by the biomass of brown and red algae. Concurrent with the invasion the density of native gammarids declined manifold whereas the overall density of gammarids did not change. This indicates that space and/or food is limiting the population growth of gammarids and competition causes spatial separation between native gammarids and *G. tigrinus.*

## DISCORDANT GENETIC BREAKS ALONG THE NORTHEASTERN PACIFIC COAST FOR SYMPATRIC SISTER SPECIES OF ROCKFISH

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Several locations along the Northeastern Pacific coast are hypothesized to act as barriers to dispersal for marine taxa having a pelagic larval phase. I examined the population genetics of black (*Sebastes melanops*) and yellowtail (*Sebastes flavidus*) rockfish to test whether a difference in adult depth preference was correlated with genetic structure. Depth preference is hypothesized to restrict gene-flow in shallower-dwelling species compared to deeper-dwelling due to greater larval retention in the former and the isolating effect of island-like spacing of suitable shallow habitat. Contrary to predictions, deeper yellowtail shows a higher level of differentiation at mtDNA locus cytochrome b and six microsatellite markers. A significant genetic break ($F_{ST}$=0.021, 95% C.I. 0.016-0.026) was found in Northern California which is concordant with breaks found in studies of blue rockfish and acorn barnacles. The shallower dwelling black rockfish did not show genetic breaks within the continental coast populations; instead, I detected a genetic break occurring between a group of Alaskan populations and the group of continental coast populations ($F_{ST}$=0.021, 95% C.I. 0.011-0.030). Analysis of the mtDNA data suggest that discordance in location of genetic breaks for black and yellowtail may be due to dissimilar histories of these species (differences in post-glacial range expansion) rather than presence/absence of a barrier to dispersal.

## GLOBAL SURFACE OCEAN HABITATS AND COMMUNITY STRUCTURE OF PELAGIC FORAMINIFERA

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For over 100 years biogeographic provinces have been used to identify different habitat types in the pelagic realm; however, the discovery of remarkable levels of cryptic diversity calls this method into question. As the absence of a global comparison of oceanic habitats obfuscates the study of pelagic macroecology, we have used multivariate analysis of physical oceanographic data to provide the first quantitative analysis of global surface ocean habitat types. We have quantified disturbance frequency and amplitude among oceanic regions through multivariate analysis of the coefficient of variation of monthly, seasonal and annual data in addition to the mean values. Parameters used to identify oceanic habitats include both physical (temperature, salinity, buoyancy frequency, and mixed layer depth) and chemical (dissolved oxygen, percent oxygen saturation, nitrate, phosphate, and silicate) data from the World Ocean Atlas and the mixed layer database of de Boyer Montégut *et al.* We proceed to use these new habitat delineations to examine the variation in community structure of pelagic foraminifera. Namely, we derive the first species volume curves and determine the effect of habitat variability on planktonic foraminifera species richness and evenness, length frequency distributions, and the ratio of photosymbiotic to asymbiotic species. This work provides a basic characterization and comparison of ocean habitats and their effect on community structure.

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## CENOZOIC HOLARCTIC BIOGEOGRAPHY OF THE NORTHERN HEMISPHERE SMELT FAMILY OSMERIDAE (PISCES)

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Examining patterns of evolution across the Holarctic has long been a topic of interest to biogeographers. To help understand the roles of northern hemisphere ocean basins as evolutionary centres of diversification, we present a molecular investigation of the phylogenetic and biogeographic relationships among the 15 species of the Holarctic smelt family Osmeridae. Phylogenetic analyses of sequence data from two mitochondrial (cyt*b* and 16S) and three nuclear (ITS2, S71, and RAG1) loci yielded relationships within this family that are discordant from previously published morphological phylogenies. Based on the molecular phylogeny, area cladogram and maximum likelihood (ML) methods were used to reconstruct the biogeographic history of the family through the Cenozoic. The area cladogram method suggested a western Pacific origin for the family, contrary to historical hypotheses that put the origin of the family in the more speciose eastern Pacific, while the ML method supported a more widespread ancestor. Despite the apparent conflict regarding the ancestral area of origin, phylogenetic and biogeographic analyses point to the importance of both the eastern and western Pacific basins in the evolution of these fishes and reveal patterns of parallel evolution, as well as trans-Pacific distributions that are observed across many other groups of similarly distributed taxa.

## IDENTIFICATION OF SPATIAL SCALES IN WHICH ENVIRONMENTAL VARIABILITY PREDICTS THE PATTERN OF BENTHIC INVERTEBRATE COMMUNITIES IN THE GULF OF RIGA, BALTIC SEA

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Benthic habitats have high structural variability at multitude of scales and this variability is closely linked with physical setting. Identification of the relevant spatial scales in which environmental variability predicts the patterns in benthic communities helps us to unveil factors and processes generating these patterns. Large-scale processes e.g. storm events result in spatially correlated communities whereas small scale disturbances e.g. biological interactions result in spatially independent communities. In the presence of both type of disturbances the pattern of community has scale invariance, i.e. strong content of variability through all spatial scales. If large scale variability is predominant then there is strong connectivity between invertebrate communities, especially those species with pelagic larval stage. In prevalence of small scale variability the active mobility of invertebrates determines connectivity and distribution pattern of communities.

## PHYLOGEOGRAPHY AND POPULATION GENETICS OF BIVALVES AT EUROPEAN COASTS

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In coastal sediments, bivalves dominate biomass and as effective filter feeders are crucial to ecosystem functioning. Although local population extinctions are common, little is known on connectivity between coastal bivalve populations within and across regions. Phylogeographic and population genetic analyses started at the Wadden Sea Station Sylt with studies on *Mya arenaria*. This clam is widely distributed across the Northern Hemisphere. It went extinct in Europe during glaciation but became spread again by human transports in historic times. Cytb and ITS sequence data suggest a 'recent' recolonisation of Europe by clams from the North American East Coast. Identical sequence types and very low sequence diversity of European compared to American populations were ascertained. An ongoing study on the abundant cockle *Cerastoderma edule* by AFLP markers and COI sequences revealed only slight geographic separation of populations from Norway to Morocco. We assume that extended larval drift with longshore currents connects populations across regions. RAPD analysis of the fragmented and apparently isolated populations of the sister species *C. glaucum* in the southern North Sea revealed surprisingly high genetic homogeneity. This may be explained either by a rather recent separation or by migrant birds. The three examples suggest a high level of European marine bivalve integration.

## BIODIVERSITY AND BIOGEOGRAPHY OF ANTARCTIC AND SUB-ANTARCTIC MOLLUSCA

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For many decades molluscan data have been critical to the establishment of the global-scale increase in species richness from the poles to the equator. Low polar diversity is key to this latitudinal cline in diversity. Here we investigate richness patterns in the two largest classes of molluscs at both local and regional scales throughout the Southern Ocean. We show that biodiversity is very patchy in the Southern Ocean (at the thousand km scale) and test the validity of historical biogeographic sub-regions and provinces. We used multivariate analysis of biodiversity patterns at species, genus and family levels to define richness hotspots within the Southern Ocean and transition areas. This process identified the following distinct sub-regions in the Southern Ocean: Antarctic Peninsula, Weddell Sea, East Antarctic - Dronning Maud Land, East Antarctic - Enderby Land, East Antarctic - Wilkes Land, Ross Sea, and the independent Scotia arc and sub Antarctic islands. Patterns of endemism were very different between the bivalves and gastropods. On the basis of distributional ranges and radiation centres of evolutionarily successful families and genera we define three biogeographic provinces in the Southern Ocean: (1) the continental high Antarctic province excluding the Antarctic Peninsula, (2) the Scotia Sea province including the Antarctic Peninsula and (3) the sub Antarctic province comprising the islands in the vicinity of the Antarctic Circumpolar Current.

## SPATIAL SCALES OF MARINE CONNECTIVITY AT THE CANARY ISLANDS: THE CASE OF THE SUBTIDAL CLONAL ANGIOSPERM *CYMODOCEA NODOSA*

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The clonal marine angiosperm *Cymodocea nodosa* forms a unique community in the Canary Islands. The species here is close to its Western distributional range on isolated island habitats. The archipelago itself constitutes an East to West gradient of separation from mainland providing an excellent model to study marine colonization and connectivity. A recent microsatellite study of *C. nodosa* genetic differentiation within and among the Canary islands did not allow the detection of any relationship between genetic and geographic distances. Is possible that the minimum separation between populations used in the later study exceeded the spatial scale where gene flow balances the effect of genetic drift as the dispersal potential of the species is very restricted. Here we used an extensive sampling of the species throughout the archipelago (40 sites on 6 islands) and a hierarchical sampling design (8 sites on each of 2 islands) to address the spatial scales of genetic connectivity and genotypic richness. A total of 1,570 samples were analyzed with 8 microsatellite loci. We completed a gene-flow analysis with the help of assignment tests and isolation by distance approaches and a hierarchical analysis of spatial genetic variation. A bayesian method implemented by 2MOD software was used to reassess the previous advanced hypothesis, of an isolated system dominated by the diversifying effects of genetic drift and less by the homogenizing effects of gene flow. Hot-spots of genetic diversity (both allelic richness and genotypic diversity) are revealed by this characterization of *C. nodosa* genetic diversity throughout the archipelago.

## CREST NETS IN THE CARIBBEAN: THE SUPPLY OF REEF FISH LARVAE TO TURNEFFE ATOLL, BELIZE

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Identifying the spatial and temporal patterns of larval fish supply and settlement is a key step in understanding population connectivity. Crest nets have been widely used in the Pacific to quantify larval abundance of coral reef fish immediately prior to settlement. However, there have been no reports of this technique being implemented in the Caribbean. This poster presents the results of daily crest net sampling over 8 months divided among three periods in 2005/6 at Turneffe Atoll, Belize, Central America. The catch was compared with that of the more widely used channel nets, which were deployed simultaneously. The influence of abiotic factors, such as wind, lunar phase and water temperature, were investigated. The crest nets were found to capture a higher abundance and diversity of larvae than channel nets. Despite crest nets being more labour intensive, this study shows that this efficient sampling method is easily transferable to Caribbean habitats.

## DEEP DIVERGENCE SUPPORTS ANCIENT ORIGINS OF ENDEMIC CORALS OF BRAZIL

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The corals of Brazil comprise a low diversity fauna of 18 species, many of which are endemic to Brazilian waters. Morphological affinities to Tethyan corals and a fossil occurrence in the Caribbean (Florida) indicate that the most abundant reef builders in Brazil, members of the endemic genus, *Mussismilia*, may be relicts of a previously more widespread population, possibly ancient in its origins. Recent genetic work on various coral genera has shown that convergent morphologies can be misleading for resolving phylogenetic relationships in corals, complicating our understanding of evolutionary patterns in this group. Here we show DNA sequence data from 2 loci, one nuclear and one mitochondrial, confirming an ancient split between the *Mussismilia* and extant Caribbean mussids. In addition, the data show that the Brazilian endemic *Favia leptophylla* is much more closely related to the *Mussismilia* than other species of *Favia*, and has most likely been incorrectly placed in this genus. In comparison, the other endemic *Favia* species found in Brazil, *F. gravida*, has strong affinities to its Caribbean congener, *F. fragum*. Our results support the hypothesis that *Mussismilia* represents an ancient coral clade, emphasizing the importance of preserving this fauna not only for its uniqueness but also for its value as a living representative of what past reefs may have looked like.

## SCALE DEPENDENT RELATIONSHIPS BETWEEN ALGAL COMMUNITIES AND DIFFERENT FEEDING GUILDS OF MACROZOOBENTHOS IN THE GULF OF RIGA, BALTIC SEA

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In many systems complex interactions occur between processes operating at different scales suggesting that spatial and temporal variability is information rather than random noise. The Gulf of Riga is characterized by extensive reaches of boulders with lush benthic vegetation. We studied the ecological significance of the structure of plant communities on the functional diversity of macrozoobenthos in those shallow water areas. Using the data on within and between site spatial heterogeneity we sought which algal species were important at different spatial scales and over which scales the interactions were strongest. In general the structure of algal communities at local and landscape scales had stronger linkage to the abundance and biomass of macrozoobenthos compared to regional scale. The importance of scale depended on algal life expectancy, invertebrate feeding mode and mobility.

## FRESHWATER SHRIMP AS A MODEL FOR BIOGEOGRAPHY AT MULTIPLE SCALES

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Freshwater shrimp from the family Atyidae are widespread throughout the globe. The combination of a wide distribution and the dispersal limitations of a small freshwater obligate animal make it an excellent taxon with which to infer evolutionary and biogeographic histories. We have focused on the main genera of atyids found in Australia, namely *Caridina* and *Paratya*, at a series of geographic scales, using molecular phylogenetic techniques. We wanted to understand Australia's place in the evolution of freshwater taxa within the Indo-Pacific and to see whether Gondwanan vicariance or more recent dispersal best explains the current patterns. We found that dispersal is the best explanation for both genera at this scale, but *Paratya* appears to have colonised the continent only once, whereas *Caridina* has colonised independently many times. We also investigated species boundaries and phylogeography within a cryptic complex of *Caridina* species in eastern Australia. We found that, surprisingly, cryptic species had very different histories from each other, probably linked to differing dispersal abilities linked to differences in egg sizes. Vicariance due to Miocene/Pliocene climate change probably led to the divergence of these cryptic species. At the smallest geographic and temporal scales, vicariance due to Pleistocene sea-level changes likely structured a cryptic taxon found on the sand barrier islands to the east of Brisbane.

## CONCORDANCE OF BIOGEOGRAPHIC AND PHYLOGEOGRAPHIC BREAKS IN COASTAL MARINE SPECIES

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Biogeographic boundaries in the ocean may arise from steep temperature gradients, flow-mediated dispersal boundaries, historical separations, and major gaps in habitat availability. Recently, researchers have investigated whether these mechanisms also lead to concordance in genetic discontinuities within species. This question has generated debate in the literature, in part because studies do not generally distinguish predictions based on the various processes that lead to species boundaries and genetic discontinuities. However, flow-mediated dispersal barriers, sharp gradients in physical factors, and gaps in habitat availability each would be expected to generate different patterns of range boundaries and phylogeographic breaks. In this project, we generate predictions for whether biogeographic breaks are expected to be concordant with phylogeographic breaks and concordant across species with differing ranges and life histories, based on the distinct mechanisms creating the boundaries. Then we review data from phylogeographic studies from the east and west coasts of the United States to determine whether existing data are consistent with these predictions. Finally, we introduce a quantitative method for analyzing the concordance of breaks, which can be applied to either biogeographic or phylogeographic data.

## DISPERSAL ECOLOGY OF SCYPHOMEDUSAE *PELAGIA NOCTILUCA* AND *RHIZOSTOMA PULMO* IN THE EUROPEAN SOUTHERN SEAS

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Scyphomedusae have life history traits that favour their capability for high dispersal rates. Regional studies of biogeography of bloom forming *Pelagia noctiluca* and *Rhizostoma pulmo* based on species morphology indicated their widespread distribution in the European Southern Seas (ESS). The aim of the present study was to investigate genetic diversity and geographic distribution of mitochondrial DNA haplotypes based on COI gene sequences in order to identify gene flow among distant sampling sites in the ESS. Phylogenetic analyses showed different haplotypes of *R. pulmo* collected in the northern Adriatic (Mediterranean Sea) compared to specimen collected in the northeastern part of Black sea (Blue Bay). In contrast, several haplotypes detected in *P. noctiluca* from the Adriatic and Eastern Mediterranean (Ionian Sea and South Aegean Sea) but some of the haplotypes were common to both locations. Analysis of genetic structure was based on 450bp alignment of COI gene sequences in *R. pulmo* and 560bp in *P. noctiluca,* respectively. Genetic distance calculated for the sampling site of *P. noctiluca* span from 0.010 to 0.029 and in Rhizostoma pulmo 0.261. Based on the preliminary data we assume that the Eastern Mediterranean share common pool of *P. noctiluca.* The role of the margin marine environment such is the Northern Adriatic and its possible influence on the genetic structure should be considered in more details.

## DISPERSAL PATTERNS OF THE LIMPET *PATELLA DEPRESSA* EXAMINED WITH A SIMULATION MODEL AND COMPARISON WITH OBSERVED LEVELS OF GENETIC POPULATION STRUCTURE USING MICROSATELLITES

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Many sedentary marine species depend on a planktonic larval stage for dispersal. In general, species with longer larval phases are thought to disperse longer distances and have lower levels of genetic differentiation among populations. However, numerous exceptions to this rule have been reported, suggesting the existence of oceanographic barriers to dispersal and also that local retention may be more common that previously thought. Here we address dispersal and connectivity in a marine gastropod species with a planktonic stage, *Patella depressa*, following a dual approach. A stochastic simulation model of dispersal was developed for most of the species range, incorporating larval pre-competency and competency periods assessed by laboratory rearing experiments, as well as coastal oceanographic flow field data. Several modeling scenarios were considered to evaluate spatial and temporal variability in dispersal. These results were compared with observed patterns of genetic population structure using microsatellites.

## GLOBAL BIOGEOGRAPHIC PATTERNS OF MARINE MACROALGAE

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The study of large-scale diversity patterns has received a revived interest among phycologists. Depending on study area, taxonomic detail, and data sources, different hypotheses have been proposed to describe general patterns in marine phytogeography. In order to analyze these findings on a global scale, we have compiled a dataset of benthic marine macroalgae based on online resources, scientific papers, and gray literature. The complete distributional database consists of 131,300 records, further reduced to a basic dataset of 52,680 species-locality records by applying geographic and taxonomic filters. Patterns in macroalgal richness and endemism deviate markedly from other well-studied marine organisms like corals and fishes. In this presentation, we identify various patterns of taxonomic richness, taxonomic composition, and distributional spread for different algal groups and thermogeographic scales. These findings suggest that evolutionary processes can differ between species and genera in relation to temperature.

## MAPPING MARINE HABITATS OF THE NORTH SEA BY MEANS OF GEOSTATISTICS AND CARTOGRAPHY IN A GIS ENVIRONMENT

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The presentation is on a biogeographic approach to integrate research data into a Marine Geo-Information-System (Mar_GIS) and to identify distinct ecological provinces at the seafloor of the North Sea. As known from terrestrial ecology and environmental planning for many years, such ecoregions are a prerequisite for planning and management needs, such as the installation of offshore wind power plants or the declaration of protection zones in marine ecosystems (Hughes 1997; Moog et al. 2004; Reiniger 1997). As recommended by Wiens (2002), the approach is adopted form landscape ecology and consists of two main working steps: (1) by applying geostatistical methods such as variogram analysis and kriging, grid maps are calculated from sample point measurement data on sediments, temperature, salinity, nutrients, dissolved oxygen, and on benthic communities; and (2) Classification and Regression Trees (CART) and GIS-techniques are then used to calculate ecological sea floor provinces from the kriging grid maps. The results of this CARTography-approach are exemplified by the German Exclusive Economic Zone (EEZ) of the North Sea. The investigation was conducted together with the Alfred Wegener-Institute for Polar and Marine Research and financed by the German Research Ministry and the German Research Foundation.

## FORESEEING A MUTLISCALE STATISTICAL APPROACH OF THE GENETICAL HETEROGENITY OF THE MACROALGAE *CODIUM ELISABETHAE* AND *CODIUM BURSA* WITHIN WESTERN MEDITERRANNEAN AND MACARONESIA: FROM BENTHIC HABITAT CONNECTIVITY TO ISLAND ISOLATION

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*Codium elisabethae* and *Codium bursa* are very similar macroalgae with interesting ecological particularities. *Codium bursa* extention ranges from the western Mediterranean, the european Atlantic coast, till several of the Canarian islands. *Codium elisabethae* is found in the Azores and Madeira, but extend at least to the most northerly and easterly of the Canarian Islands, as Chacana (2002) repertoriated in Lanzarotte the only range overlap of both species. Following Duarte (1999), these long living organisms could provide an insight into the ecosystem responses to changes if they could be appropriately interrogated. Population age structure and dynamics where extensively studied for both species (Cala da Jonca, Spain, Vidondo, 1998) as in the Atlantic (Faial island, Azores, Sirjacobs, unpublished). Investigating the link between environmental changes and modification of species distribution and local dynamics requires to address the notion of habitat connectivity, crucial for replenishment, dispersal and gene exchange of populations. This influence can be adressed statistically as an interpretation of the genetical heterogeneity of populations at various spatial scales. Research strategy is developped in this direction, as to precise the distribution limits of both species, and identify potential local environmental barriers separating both species (Chacana, 2002).

## MEOW: MARINE ECOREGIONS OF THE WORLD

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Urgent threats to marine habitats and limited resources have led to the realisation that representative and systematic conservation planning is necessary. A biogeographic approach is vital for providing a framework for assessing current conservation efficacy, and ensuring representation at regional levels in future planning. However, marine biogeography still lags far behind terrestrial and until now no single, widely accepted comprehensive biogeographic classification of the oceans existed. We developed a new global system of biogeographic regions for coastal and shelf waters based on extensive literature and expert review by a team of conservation practitioners and academic biogeographers. It is largely a compilation of existing global (e.g. Bailey, Longhurst, Briggs, LMEs) and numerous regional systems and is designed to be cross-walked into other classifications and be as consistent as possible with those already in use for conservation planning. The bioregionalisation is hierarchical and comprises 12 realms, nested within which are 61 provinces and 229 ecoregions. It is currently restricted to continental shelf regions where the majority of threats and conservation action occur. However, it is clear that other areas need to be included (particularly open ocean, deep benthic and sea mounts). It is our hope that the MEOW will be adopted and used extensively by conservation organisations around the world. We welcome feedback on the system.

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## DEPRESSION OF VICARIANT SPECIATION DURING THE LATE DEVONIAN BIODIVERSITY CRISIS RELATED TO SPECIES INVASIONS

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Combining phylogenetic, ecological niche modeling, and GIS range analysis of fossil brachiopod and bivalve species provides insight into the faunal dynamics of the Late Devonian (Frasnian-Famennian) Biodiversity Crisis, an interval of biotic decline resulting in dramatic overturn in ecological systems approximately 364 million years ago. Species-level phylogenetic analyses of representative taxa provide a framework for calculating rates of biodiversity overturn. Rate analyses indicate moderate rates of speciation in the Middle Devonian which decline to near zero in the Frasnian. Extinction rates are elevated during the crisis interval, but do not exceed rates calculated for pre-crisis time. Speciation decline, therefore, was the key driver of net biodiversity loss. Ranges of individual species reconstructed using GIS and GARP (Genetic Algorithm Using Rule-Set Prediction) for narrow temporal intervals provide a framework for interpreting timing and extent of species invasions (dispersal events) between tectonic basins. Increasing species invasions are correlated with speciation rate decline. Phylogenetic biogeography further reveals an offset in timing between vicariance (Early to Middle Devonian) and geodispersal patterns (Late Devonian) that indicates a fundamental change in the style of biogeographic patterns during the Devonian. The long-term effects of modern invasive species, therefore, may include depression of vicariant speciation thereby hindering recovery and reestablishment of diversity following the present biodiversity crisis.

## TROPHIC STRUCTURE OF FISH ASSEMBLAGES ALONG A SUBTROPICAL – TEMPERATE GRADIENT: GOING BEYOND SPECIES RICHNESS

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We sampled shallow benthic rocky reef fish assemblages along the Gulf of California (ca. 22º to 30º latitude), Mexico, and examined the distribution of trophic guilds along a subtropical – temperate gradient. Different patterns in trophic structure were obtained when looking at species richness vs. abundance. For species richness, the proportion of planktivore (11%) and piscivore (8%) species remained low and constant, while carnivore species richness (and proportion; 55-70%) increased with latitude, and herbivore richness and proportion decreased (25-12%). On the other hand, regarding abundance, planktivores were generally the most abundant fish (density), with relatively constant contributions along latitude (40%), but the main contributors in terms of biomass were carnivores (40%), with highest biomasses at mid latitudes. In the northernmost (i.e. temperate) regions, however, herbivores were the most abundant fish both in terms of density, biomass, and their proportions (40% and 50%, respectively). These patterns are not consistent with the general paradigm of lower abundance of herbivores in temperate regions and highlight the importance of going beyond species richness when examining biodiversity patterns, since other measurements can reveal key functional trends which would go unnoticed otherwise.

## PHYLOGEOGRAPHY OF THE MARINE SPONGE *PHORBAS FICTITIUS* (PORIFERA, POECILOSCLERIDA): INSIGHTS INTO THE COLONIZATION AND GENETIC STRUCTURE AT OCEANIC ISLANDS

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The way that marine species with low dispersal capabilities colonize remote habitats such as oceanic islands and the effect of microevolutionary processes in the genetic structure of such populations constitutes an interesting challenge for the understanding of island evolution. Located approximately 1,200 km off the closest continental landmass the Azores archipelago constitutes an excellent place to perform such studies, in particular for taxa with short-lived, poorly-dispersing larvae, such as sponges. The ongoing project involves the study of 6 selected species with a wide distributional range in the Mediterranean/Atlantic region (*Erylus discophorus, Cliona celata*, *Cliona viridis, Phorbas fictitius, Tedania anhelans* and *Petrosia ficiformis*) and aims to: (1) test for population differentiation in sponge species at different spatial scales and try to determine probable directions of dispersal and common ancestry; (2) assess the genetic structure of island populations (within populations, between populations within the same island, between populations from different islands and different island groups) and compare it with conspecific mainland populations; (3) determine the role played by shallow seamounts (e.g. Gorringe, Ampere) in long distance dispersal of these species. Here we present our results concerning the phylogeography and genetic structure of the poecilosclerid sponge *Phorbas fictitius* populations across two spatial scales: large scale (Iberian Atlantic and Mediterranean) and local or archipelagic scale (Azores Islands). Interestingly the highest haplotypic diversity was found in a continental shelf archipelago followed by two oceanic archipelagos (Azores and Madeira), whereas mainland counterparts showed low haplotypic diversity. Moderate to high genetic differentiation was found at the large scale (pairwise $F_{ST}$ ranging from 0.2398 to 0.7138). At the intra-archipelagic scale (Azorean populations) a very high level of genetic differentiation was found (pairwise $F_{ST}$ ranging from 0.4251 to 1.0000) with a clear split between western and easternmost populations. At both scales a high genetic structure was found with the variation among populations accounting for 50% and 62% of the total variation in Iberia and Azores, respectively. We discuss how historical events at the different scales (glacial maxima, episodical volcanic activity) may have played a role in shaping the contemporary structure of these populations.

## *Symposium 5*

# Separating historical from environmental effects on species distributions

## HISTORICAL CONTROLS OF PLANT DIVERSITY PATTERNS

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A dominant paradigm in ecology has been, and still is, to interpret large-scale patterns in diversity as predominantly a product of contemporary environmental conditions, notably climate. Albeit this view has been most strongly put forward with respect to patterns in species richness, many have also argued for the view that species distributions are largely in equilibrium with climate, at least at subcontinental scales. The main alternative viewpoint has been that current patterns are strongly controlled by past events and cumulative or time-lagged processes, i.e. history. Here, I first discuss in what ways history might potentially affect or control current patterns in plant species richness and distributions. I then present two cases: I provide evidence to support (1) the idea that tree species richness and distributions patterns in Europe to a large extent are determined by the location of glacial refuges and limited postglacial dispersal, and (2) that niche conservatism, diversification rates, and lineage biogeographic history are strong determinants of the observed patterns of species richness in the palm family (Arecaceae) across the Americas. I end the presentation with an attempt to provide some generalizations on the relative importance of modern environment and history and, secondarily, different kinds of historical factors as controls of plant diversity patterns.

## HISTORICAL DETERMINANTS OF CURRENT PATTERNS OF SPECIES RICHNESS

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It is widely contended that energy and water-energy determine large-scale patterns of species richness. An alternative view posits that richness reflects the response of species to past climate changes. In particular, the evolutionary time hypothesis proposes that species are differentially excluded from areas that experience the most severe climate changes, whereas persistence and speciation are favoured by climate stability over time. These competing 'contemporary climate' vs. 'evolutionary time' hypotheses have been forcefully debated without consensus. Here, we use example from the fossil record, phylogenies and palaeoclimate projections to investigate the proposition that species richness of various organisms at global and European levels can be explained by the evolutionary time hypothesis. Our analyses support the view that climate changes over evolutionary time can contribute to current species richness independently of and at least as much as contemporary climate.

# ENVIRONMENTAL AND HISTORICAL EFFECTS ON BROAD-SCALE GRADIENTS OF DIVERSITY

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A number of recent analyses suggest that a large proportion of the geographic variation in species richness can be explained by contemporary environment. Its consistently strong explanatory power may suggest an only minor role for historical processes for which direct evidence is notoriously difficult to establish. However, there is no doubt that history is reflected, in one form or another, in the current distribution of species. The inability to quantitatively separate these effects within one framework is indicative for the divide between ecological and historical approaches that has marked the past forty years of research in the interface of biogeography, ecology and evolution. Here I analyze the global diversity patterns of terrestrial vertebrates and plants and first evaluate the degree to which environmental drivers alone can explain them. I scrutinize the generality of putative determinants across space and phylogenies. I proceed to investigate residual variation and the degree to which it may represent the signature of history. While specific correlates of potential historical processes may co-vary with some aspects of contemporary environment, 'left-over' variation is a powerful handle on effects that are otherwise hard to isolate. Finally, I test for specific importance of the approximate times of origin and dispersal of clades. I attempt a crude synthesis as to the relative statistical and presumed mechanistic importance of contemporary environmental versus historical effects on broad-scale patterns of species richness.

## COMMUNITY RELATEDNESS, SPECIES RICHNESS, AND THE INFLUENCE OF ENVIRONMENTAL FILTERING ON BROAD-SCALE BAT (CHIROPTERA) COMMUNITIES IN THE AMERICAS

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Several related historical hypotheses for diversity gradients (e.g. 'centre of origin' and 'niche conservatism') postulate that diversity gradients arise through a strong effect of environmental filtering. When environmental filtering drives community structure, community members will be phylogenetically clustered, i.e. more closely related than expected by chance, due to shared adaptations to environmental conditions. Linking phylogenies and community ecology has provided valuable insight into the processes that structure communities at local scales. Here, we extend this concept to quantitatively examine the role of environmental filtering in determining community structure at broad scales. We predict that: (1) relatedness will be negatively correlated with species richness; (2) species richness and community relatedness will be best predicted by the same environmental factors; (3) including community relatedness in predictive models of species richness will substantially increase the explained variance. We tested these predictions for bats (Chiroptera) in the Americas (~300 spp.). We found patterns consistent with predictions 1 and 2 but not prediction 3, suggesting that while environmental filtering exerts an important influence on community membership, it is not solely responsible for the contemporary climate-species richness relationship.

## RANGE EDGE DENSITY OF NORTH AMERICAN AND EUROPEAN WOODY TREE SPECIES

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Much work has been done on statistically modelling species richness values that are derived from range maps on a grid-cell basis. However, no studies that we know of have analysed the richness of species' range edges. Range edges are particularly important when considering the potential effects of global environmental change. We investigate the distribution of range edges of woody tree species on two continents, to assess the extent to which climate, history and other factors might relate to range-edge density. We mapped range edge density of all North American and European tree species at four grain sizes (27.5 km, 55 km, 110 km and 220 km) and related the spatial patterns to key climatic and topographic variables. Our findings are intriguing and some are difficult to explain. We find a strong relationship between topography and range-edge richness that could reflect steep environmental gradients and/or dispersal limitation effects. We also find a strong relationship between range-edge richness and species richness. Interestingly, this range-edge richness–species richness relationship varies strongly spatially, producing geographic patterns that were unexpected.

## THE PHYSIOLOGICAL DEPENDENCE OF CLIMATE-INDUCED RANGE SHIFTS: PREDICTIONS FROM A DYNAMIC BIOENERGETIC MODEL

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We present a dynamic bioenergetic model that couples individual energetics and population dynamics to predict current lizard ranges and those following climate warming. The model predictions are uniquely based on first principles of morphology and thermal physiology. We apply the model to 12 lizard species in North America. Comparing actual current ranges to those predicted reveals how dispersal limitations and species interactions influence the occupied portions of thermally suitable ranges. The dynamic model predicts individualistic responses to a uniform 3ºC warming, but a northward shift in the northern range boundary for all species. In contrast to standard, correlative climate envelope models, the extent of the predicted northward shift depends on organism physiology and metabolic rate. Our results highlight the limitations of correlative models and the need for more dynamic models of species' ranges.

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## SYSTEMATIC AND BIOGEOGRAPHIC APPROACH TO *VITEX* L. (LAMIACEAE)

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*Vitex* L. (*Viticoideae*) is a taxonomically complex genus comprising approximately 250 tropical, subtropical and a few temperate *taxa* with a panglobal distribution. In Africa the genus is represented by c. 87 species included in two subgenera, *Vitex* and *Homskioldiopsis*. Despite its taxonomic complexity there are to date no phylogenetic studies published within the genus. Recently, about two-thirds of the genera usually placed within Verbenaceae (including *Vitex*) were transferred to the Lamiaceae in order to make both monophyletic. The present study focuses primarily on African species, with particular emphasis in the Grex *pilosae* (Pieper 1928). In order to test its monophyly we sampled species across the entire distribution of the genus. The molecular markers being used are the ITS (internal transcribed spacers of ribosomal DNA) and the chloroplast *trn*L-F intron/spacer regions. Preliminary results suggest that the genus *Vitex* is not monophyletic, and neither the Grex *pilosae.* The paraphyly of the American species is also indicated, with two distinct clades. Further research will focus on obtaining divergence times using fossil and geological calibration points in order to unravel historic events leading to the present day distribution of the genus.

## BIOGEOGRAPHY OF NEOTROPICAL GLASS FROGS (FAMILY CENTROLENIDAE)

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The American tropics harbor the largest and most endangered amphibian diversity in the world, but our knowledge is very poor. The combined study of the geographic distribution and the phylogeny of glass frogs can provide a better understanding of the mechanisms underlying the Family radiation. Additionally, this offers an excellent opportunity to study the little known consequences of the Quaternary environmental changes in the Neotropics and to examine the different hypotheses on the origins and distribution of the Andean and Guyanese faunas. Due to the limited dispersal capabilities of these species, a number of questions arise: (1) do Centrolenidae have their origin in the pre-Cambrian Guiana Shield or in the Andes?; (2) has the principal communication route between the Andes and the Guiana Shield been the Amazonian forest or the coastal ranges of Venezuela?, what barriers and corridors have influenced this communication?; (3) are the phylogeographic patterns of Centrolenidae consistent with the hypothesized Pleistocene tropical forest refugia?; (4) do congeneric species in each region form monophyletic groups as should be expected if there was only one arrival?

## SPATIAL PATTERNS OF TREE SPECIES RICHNESS IN THE IBERIAN PENINSULA: THE ROLE OF ENVIRONMENTAL FACTORS AND CONTAGIOUS BIOTIC PROCESSES

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In the Iberian Peninsula, macroclimatic factors (mean annual precipitation and annual actual evapotranspiration), topographic relief, percentage carbonate substrates and the interaction between precipitation and substrate emerged as the most important predictors of tree species richness in 100 km x 100 km grid cells. Cumulatively, these environmental variables explain c. 82% of the variation in richness and account for most of the spatial structure in the data when they are fitted simultaneously in a multiple model using ordinary least squares regression. However, even though this model has a high explanatory power, a statistically significant positive spatial autocorrelation remains in the residuals at small distances, which originates not only because of similar richness values from adjacent cells but also because of a similar species composition (low species turnover). We argue that, in addition to environmental factors, contagious biotic processes, such as seed dispersal by animals (endozoochory), and history should be considered for explaining the actual patterns of richness of trees, and advocate the use of spatial regression models.

## RAINFALL GRADIENT AND □ $^{13}C_{PLANT}$ VALUES FOR THE CHARACTERIZATION OF SYRIAN VEGETATION: MODERN PATTERN AND HISTORICAL PERSPECTIVE

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The correlation between rainfall regime and vegetal bio-ecological distribution was inferred also by recent studies on the plant carbon isotopic variation (□ $^{13}C_{plant}$) in different regional areas. We used a similar approach in the Near East (Syria region) for the characterization of plant distribution: ecological transects, based on rainfall gradient, were carried out in the Country from the Mediterranean belt to the desert area. The identification of a regional trend in □ $^{13}C_{plant}$ variation led us to justify the application of this method also in a palaeo-ecological perspective. The correlation between □ $^{13}C_{plant}$ values and $^{14}C$ dates by Accelerator Mass Spectrometry (AMS), applied to the plant remains from the archaeological site of Ebla, were used to study vegetation response to the III millennium BC dry crisis attested in the Near East by other proxy data.

## SIMPLE DISPERSAL MODEL REDUCES UNCERTAINTY IN RANGE SHIFTS PREDICTIONS AND REVEALS RANGE DYNAMICS UNDER CLIMATE CHANGE

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Dispersal is emerging as one of the greatest uncertainties in predictions of biological responses to climate change. To date, studies have generally dealt inadequately with this uncertainty by bracketing the range of potential responses and assuming species will either disperse freely to all suitable locations (full dispersal) or species will not disperse at all (no dispersal). To explore the impact of dispersal assumptions beyond 'no' and 'full dispersal', we assigned a more reasonable dispersal rate (7.5 $km^{-decade}$) to 246 wind-dispersed Proteaceae species endemic to Western Australia. For each decade between 1990 and 2080 and across multiple future climate scenarios, we developed predictions of species distributions using MaxEnt and then linked predicted distributions using a simple adjacent-spread model. Under 'full dispersal', results were driven by several species that greatly expanded their ranges. However, simulated dispersal prevented unlimited range expansion and reduced the range of predicted outcomes across future climate scenarios. Consideration of decadal range dynamics revealed that distributions of species tended to change little by mid century, at which point most species lost range rapidly. By 2070, the rate of range loss slowed, suggesting species may eventually contract to core areas of their range after exhibiting rapid, non-linear responses to climate change.

## USING PREDICTIVE MODELS FOR INFERRING CAUSES OF DISJUNCTION OF THE MACARONESIAN PALAEOENDEMISM *NAVAEA PHOENICEA* (MALVACEAE)

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*Navaea phoenicea* (Vent.) Webb & Berthelot (Malvaceae) is an arborescent palaeoendemic from Tenerife (Canary Islands). This species grows in the northern slopes of the two oldest massifs: Teno on the West and Anaga in the East, lacking populations in the centre of the northern coast of the island. In order to know if this disjunct pattern is mainly due to human influence, we tested the performance of six predictive models (Bioclim, ENFA, Climate Space, Minimum Distance, Average Distance and GARP) based on climatic, topographic and soil data to establish if there are potential distribution areas for *N. phoenicea* along the northern Tenerife façade. The selected models, either by predictability or statistical support, were ENFA and Bioclim as they were able to match the known distribution of the species. Apart from Anaga and Teno massifs, both models also predicted suitable habitats for the plant on localized western cliffs of La Orotava valley. Thus, present Anaga-Teno disjunction seems to be better explained by ecological constraints than by recent human induced extinction, although landslides and/or land reclamation could have contributed to disappearance of potential bridge-populations.

## REGIONAL AND CLIMATIC EFFECTS ON MAMMAL LOCAL SPECIES RICHNESS AT GLOBAL EXTENT

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Current variations in species richness have been related to recent productive energy and ambient energy (i.e. environmental conditions), acting locally in ecological (i.e. contemporary) time. In addition, the past effects of these factors and other contingent historic events (e.g. dispersal, extinctions, etc.) result in differences between regional faunas acting at broad extents. While contemporary factors have been widely studied, and their role in the shaping of species richness patterns has often been highlighted, the regional effects of historical processes are most times undervalued. Here, we characterize global trends in mammal species richness of local assemblages. We explored richness variations in local checklists covering all terrestrial realms except Antarctica. We grouped these checklists according to their area, and then partitioned the variation in each of the resulting groups: (i) between currently-acting contemporary factors and the historical effects under regional differences, and (ii) among water, energy, and regional differences. We also assessed the effect of the regional species pool on local communities, as well as the different relationships between water, energy and richness per region. Our results indicate that the unique history and physiographic characteristics of a particular region produce important differences between the richness of local assemblages. The relationship between species richness and water and energy variables varies among regions, both in shape and strength. Therefore, regional differences should also be taken into account for the development of current species richness-energy hypotheses.

## SPECIES POOL EFFECTS ON THE FUNCTIONAL STRUCTURE OF AFRICAN MAMMAL ASSEMBLAGES

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The assembly of species in local assemblages is known to depend on the species available in the regional pool. However, there is little evidence on how the functional structure of these assemblages is affected by their species pool. We test to what extent such functional structure is a product of the functional characteristics of the species available in the pool in 16 mammal assemblages located in the Paleotropical realm. Different geographic definitions of the regional pool have been proposed, and also of the degree of pertenence of each species to such pool. Therefore, we used seven different definitions of pool (weighted and unweighted circle, biome and dispersal field, and the whole biogeographic region), accounting for different geographic definitions and degrees of pertenence to the pool. Weighted pools provide better approximations to the local structure of African mammal assemblages than unweighted ones. Here, geographic distance describes species assembly better than the biogeographic signal contained in the number of species shared with the studied locality. In addition, our results show that the effect of the species pool on local assemblage structure is high in most localities (median similarities between random assemblages and local checklists above 0.7), providing support for the hypothesis of an important effect of regional species pool in the assembly of African communities. However, some sites located in restricted biomes present deviations from such pattern.

## GLOBAL PATTERN OF DIVERSIFICATION RATES IN FLOWERING PLANTS: THE RELATIVE IMPORTANCE OF ENERGY AND CLIMATE CHANGE

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The cause of the latitudinal gradient in species diversity still remains a puzzle. A distinction is often made between contemporary processes setting limits on coexistence, such as energy availability, and historical processes, usually climate change in the past. We used the largest DNA-based phylogeny of flowering plants to date to evaluate the relative importance of energy and past climate change in explaining global patterns in diversification. Diversification rates increased towards the equator, suggesting that the latitudinal diversity gradient can be explained by differences in diversification rather than post-speciation migration. Measures of past climate change could explain variation in diversification better or equally well compared to energy measures. Energy and climate change measures were strongly intercorrelated, making it difficult to reject either of them as causes for patterns in diversification. Reviewing the hypothesized mechanisms to explain diversification, we show that mechanisms linking plant diversification to measures of energy can either be rejected or evidence is lacking, whereas there is more evidence in favour of the role of climate change. Digitized range maps showed that range-size corrected species richness was highest in the main tropical rainforest blocks, but that diversification uncorrected for phylogenetic relationships was higher in climatically and geologically younger areas, such as arctic and boreal regions and along the Andes.

## REPLICATE CLIMATIC VICARIANCE, NICHE CLEAVAGE AND SPECIATION IN THE *EPHIPPIGER* GENUS OF BUSHCRICKETS

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Evolutionary/biological diversification most often occurs within a context of vicariance. Ecological niche models are increasingly being used to investigate patterns of niche evolution as well as to provide independent evidence for vicariant events inferred from phylogeographic pattern. However, empirical evidence for the role of niche diversification in speciation remains limited because few analyses clearly distinguish between the roles of geographical, ecological and biotic factors in defining ranges and hence niche models. We used classification and regression trees (CART) to identify climatic isolines that delineate multiple disjunct populations, subspecies and species ranges within the *Ephippiger* genus of European bushcrickets. Two temperature isolines were found to partially define the extent of multiple population, subspecies and species ranges. Importantly, these isolines divide both parapatric and allopatric ranges of sister taxa. The geographical position of the isolines at the last glacial maximum provides a historical shapshot of historical climate pattern and potential species and subspecies ranges. Synthesis of the occupancy of climatic space by all taxa within the genus leads us to propose an extension of the Hewittian model of Pleistocene divergence in the southern European peninsula and across mountain ranges that includes biotic exclusion and explains the observed patterns of 'paraclimate' niche adjacency between sister taxa. If correct, niche divergence does not necessarily fit into the simple 'primary' or 'secondary' divergence dichotomy; instead it may result from multiple temporally spaced interactions between diverging range entities driven by the structuring of climate by landscape.

## RARE PALMS AROUND IQUITOS, PERU

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Diversity hotspots often attain their high species richness through skewed abundance distributions with many rare species. Looking into the reasons for rarity thus contributes to explain large-scale diversity patterns. One of the world's most diverse palm communities exists in the western part of the Amazon around Iquitos, Peru. Here we investigate the reasons for rarity by quantifying how species can be categorized according to three different types of rarity: (1) widespread, but sparse, (2) habitat specialist, and (3) endemic to the Iquitos area. In 59 transects (5 × 500 m, with each palm individual identified to species level as either seedling, juvenile, sub-adult or adult) we found 75 species in total, with abundances ranging from only one individual in one transect to numerous individuals in nearly all transects. Species are ranked according to two abundance criteria, density and frequency, and the least abundant 25% of all species in either one of the rankings defined as rare. Preliminary results point to low abundance of species that are otherwise wide-spread as the most common type of rarity among palms in the Iquitos area. However, all three rarity types were represented. E.g., *Itaya amicorum* provides an example of a very rare local endemic, and *Mauritiella aculeata* an example of a habitat specialist (here encountered outside its previously known range).

## HOW DOES THE STRAIT OF GIBRALTAR AFFECT PLANT SPECIES DISTRIBUTION AND SPECIATION?

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Understanding the ecological and evolutionary mechanisms that shape biodiversity distribution is a pivotal topic of modern biogeography. The Strait of Gibraltar (SG) is a major hotspot of biodiversity within the Mediterranean Basin that harbors a large number of paleorelict and endemic plant species. The SG has experienced a complex geological history with recurrent closing and opening of the Strait until the late Tertiary (5.5 Myr ago), and may thus have strongly shaped biodiversity distribution by influencing both species dispersal and local speciation. Here we tested whether the SG has acted as a significant barrier for plant species dispersal between South Iberia and North Morocco, and whether it has triggered evolutionary diversification on each of both sides. We performed a phylogenetic analysis of the angiosperm flora of the SG Biodiversity hotspot (ca. 2,100 species). We tested the hypotheses that species distributed on both sides of the SG are more likely to (i) display adaptations for long distance seed dispersal and/or pioneer strategies ('filter-bridge' mechanism), and (ii) belong to families with low speciation rate in the region (with low 'niche pre-emption'). This analysis provides a mechanistic description of how historical processes of dispersal and speciation shaped the biodiversity distribution in a biodiversity hotspot.

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## USING MODELLING TO EXPLAIN RECENT CHANGES IN THE DISTRIBUTION OF THE MARINE GASTROPOD *PATELLA RUSTICA*

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Modelling species distributions can be used to monitor and predict community responses to long-term environmental changes. *Patella rustica* has gradually been expanding its distribution in northern Iberia, and in the late 1990s an historical gap in distribution in northern Portugal was bridged. It is thought that during that period a coincidence of several factors, including sea temperature, provided exceptional conditions which allowed the geographical expansion of this species. Since sea temperature is expected to rise at higher rates in the following decades, changes in the distribution of this species are likely to continue. The present work aimed to investigate possible climate-driven explanations for the observed change in the distribution of *P. rustica*. Based on a predictive model of the species distribution built from historical surveys and climatic/oceanographic data, present range was nowcasted by feeding the model with contemporary environmental data.

## BIASES AND COMMON MISTAKES IN DISTRIBUTION MODELS: WHAT ARE WE PREDICTING?

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The accomplishment of predictive models of species distribution requires the use of good quality biological data. However, many sources of uncertainty in the biological used data dramatically influence the reliability of such kind of models. The spatial bias in the collecting presence localities of a species, the level of false absences, the type and number of absences (or pseudo-absences), and the ratio between the area of the species distribution and the whole extent of the modelled territory are generally unconsidered factors that decisively influence the accuracy of predictive model results. Using a virtual species several analysis demonstrate that: (i) to select the absence information at random between the localities without presence information is a bad practice because presence information is frequently spatially biased and model techniques are unable to discriminate false absence information; (ii) balanced designs (with similar number of presence and absence data) diminish the likelihood of representing all truly negative environmental regions increasing the rate of overprediction; and (iii) the extent of the analyzed area highly influences both the probability of selecting reliable absence data and validation results. The relevance of these sources of uncertainty in delimiting realized and potential distributions was assessed.

## COULD THE BARBARY GROUND SQUIRREL INVADE THE CANARY ISLANDS? MODELLING ITS ABUNDANCE IN FUERTEVENTURA AND PREDICTING COLONIZATION SUCCESS

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Understanding variables that affect the distribution of invasive species is crucial to figure out the ecology of invasions. The Barbary ground squirrel (*Atlantoxerus getulus*), endemic to Morocco and some areas of Algeria, was introduced into Fuerteventura Island in 1965. Being the most desert island and the nearest to squirrels' African native range, this island seem to provide an optimal environment for squirrels to colonize. We analyze the relevance of four different groups of variables (environmental, food resource, interaction and refuge variables) in determining the presence and abundance of squirrels in Fuerteventura, as well as, by using data on the species native distribution and climate-based models, predict the rest of the Canarian islands environmental capacity for housing the invasive rodent. Variables related with shelters are the most relevant to explain the abundance of squirrels in Fuerteventura. Although food resources are less explicative, the presence of certain plant species seems to be correlated with the squirrel abundance. General environmental and other-mammal-interaction variables are irrelevant to explain rodent distribution in Fuerteventura Island. Not all the archipelago and its diverse environments are suitable to house this invasive squirrel.

## DIRECT AND INDIRECT EFFECTS OF CLIMATE AND HABITAT FACTORS ON SPECIALIST AND GENERALIST BUTTERFLY DIVERSITY

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Using structural equation modeling (SEM), we investigated direct and indirect effects of climate variables, host-plant richness and habitat diversity on butterfly species richness across Britain. Climate variables had strong effects on habitat generalists, whereas host-plant richness and habitat diversity contributed relatively more for habitat specialists. Climate constrains species richness of generalist butterflies largely by direct, perhaps physiological, effects; while climate influences the species richness of specialist butterflies by both direct and indirect effects *via* resource and habitat availability.

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## WORLD MOUNTAIN SYSTEMS AND GLOBAL CLIMATE WARMING DURING XXI^TH^ CENTURY

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Current climate models have been applied to the whole world, as well as to many areas at local, regional or continental scale. Also have been applied to different biomes, among them to some mountain areas and even to entire mountain ranges. But to our knowledge, this is the first time that different climate models are run at a global scale, over all the mountain systems of the world. We provide assessments of surface temperature change in mountain areas of the world using a set of projections at 0.5º resolution for two thirty-year periods (2040-2069 (2050) and 2070-2099 (2080)) using four IPCC emission scenarios and five AOGCM. Projected average temperature changes varied between +2.1ºC and +3.2ºC for 2050, and +2.8ºC and +5.3ºC for 2080. The temperature is expected to rise more in polar and boreal mountains than in mountains located in temperate and tropical zones. The rate of global warming specifically in mountains is projected to be three to five times higher than that recorded in the 20th century.

## EXPLORING PATTERNS OF FUNCTIONAL DIVERSITY IN AFRICAN TERMITES

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Termites can be considered in general a tropical taxon, their occurrence extending from subtropical to tropical latitudes. In these regions they play a major role as ecosystem engineers, by modifying the interactions between plants, animals and microbial components of the soil biota and by changing the physical properties of soils (e.g. structural heterogeneity, stability, distribution of organic matter, water infiltration and retention). The pattern of termite diversity in the tropics is characterized by a decrease in diversity from the equator towards the poles. This decrease takes place at a slower pace at more southern latitudes. However, no studies have yet assessed whether a similar pattern is present for the distribution of the different functional types (i.e. feeding guilds). The aim of this work was to determine the main factors that shape the distribution of the termites' functional types (e.g. wood-litter, live grass, soil and dung feeders) and assess the hot spots of functional diversity of termites in the African continent. Our results showed that extreme environmental events related to precipitation and temperature are the main divers shaping species distributions, and therefore biological and functional diversity. In particular, we found the closed canopy tropical forests in the Ethiopian region, followed by the tropical savannas in the Riff valley to be the functional and biological diversity hotspots in continental Africa.

## MEASURED SUCCESS IN PREDICTING PLANT DISTRIBUTIONS OVER SIX MILLENNIA: AMONG-SPECIES VARIABILITY IN NICHE CONSERVATISM?

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Assessing the accuracy of predictions of the response of species to ongoing climate change is difficult because there have been few opportunities to confirm the performance of predictive models over time. We use independent data on present- and past climate and plant distributions to test predictive models by 'hindcasting' past distributions and forecasting present distributions. We estimated species occurrence and distribution of seven species in Europe at 6,000 ybp ± 500 yrs using pollen records. We estimated mid-Holocene climate anomalies with data from the Paleoclimate Modelling Intercomparisons Project Phase II (PMIP2) UBRIS-HadCM3M2 general circulation model. Data on current plant distribution was taken from the Atlas Florae Europapeae. Current climate was estimated for Europe with the WorldClim dataset. We developed models of species distributions with the Gradient Boosting Machine, implemented in R. Ten-fold cross validation, bootstrap and jackknife of AUC showed that models fit well the calibration data from both the present and the past. Accuracy of bidirectional model predictions varied among species. These results suggest that prediction accuracy of the response of plant distributions to climate change will also vary greatly among species. Variation in the degree of niche conservatism is one likely reason, but there are others.

## PHYLOGEOGRAPHY AND FLOWER BIOLOGY OF THE WINTER FLOWERING *NARCISSUS PAPYRACEUS* ACROSS THE STRAIT OF GIBRALTAR

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'Paper white' daffodil, *Narcissus papyraceus,* is distributed throughout the Mediterranean Basin where it presents an uncommon winter flowering season. The species is particularly abundant, in terms of population number and size, in marl and clay lowlands close to the shores of the Strait of Gibraltar (SG), whereas it becomes rarer towards inland. A study with AFLP markers was carried out on 116 individuals from 26 populations across the SG. A Neighbour-Joining tree based on Nei & Li genetic distance rendered a well-supported group of large coastal populations on both shores of the SG and other coastal areas. These populations are dimorphic for style length and have both nocturnal, long-tongued, and diurnal, short-tongued pollinators acting from December to January. The rest of populations are distributed peripherically to that group and include mostly monomorphic populations pollinated by diurnal, short-tongued insects in February-March. We discuss the effect of flowering phenology, pollinator type and probably seed and bulb dispersal on the reported pattern of genetic differentiation across populations and regions.

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## OMBROTYPIC MAP OF THE PENINSULAR AND BALEAR SPAIN AND THE JOINED DISTRIBUTION ITS BIOCLIMATES, ITS VARIANTS AND THE OMBROTYPES

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Based on more of 4,400 metheorological stations, selected from a total number of over 6,000 given by CIF –Phytosociological Research Center- the first Ombrotypic Map of the Peninsular and Balear Spain has been worked out. Seven, out of the nine Ombrotypes worldwide considered, have representation in the considered area: Arid, Semiarid, Dry, Subhumid, Humid, Hyperhumid and Ultrahyperhumid. The Ombrotypes with larger area are: Dry, Subhumid and Humid, which in total sum up approximately 88% of the territory; the one with the smaller area is Ultrahyperhumid, with only minor areas at the top of Cantabrian and Pyrenean ranges. Within the Mediterranean Macrobioclimate all Ombrotypes appear with the exception of the Ultrahyperhumid; on the contrary, only four Ombrotypes, Subhumid, Humid, Hyperhumid and Ultrahyperhumid have been found in the Temperate Macrobioclimate. Taking into account Bioclimates and its Variants, together with Ombrotypes, thirty different bioclimatic situations have territorial representation in the considered area: Mepo_Dry and Mepo_Shu, with more of the 60% of the territory, are the more widespread bioclimatic combinations; on the contrary, Teco_Stp_Shu and Teoc_Stp_Hum, have the more restricted distribution, with an extensión of 43 $km^2$ for both. Maps of Ombrotypes and of Bioclimates, its Variants and the Ombrotypes have been drawn.

## ECOLOGY MATTERS: ATLANTIC-MEDITERRANEAN DISJUNCTION IN THE SAND-DUNE SHRUB *ARMERIA PUNGENS*

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This study aims at finding the cause(s) for the occurrence of a West Iberian-Sardinian disjunction in a sand-dune shrub species with a linear (coastal) distribution range. Predictive models based on climatic data were carried out to assess the potential distribution of *Armeria pungens*. Two approaches were followed. To explore whether the current distribution of the species covers most of its environmental envelope or, alternatively, suitable sites are found elsewhere, all presence data were used to construct the model. To explore if different climatic profiles could be identified in the areas harbouring the two main genetic lineages within *A. pungens*, subsets of the data were used. Conditions in Corsica-Sardinia were found to be more similar to SW Portugal and less so to the Gulf of Cadiz (the closest geographically). This finding is very is consistent with the previously obtained genetic structure of the species based on nuclear and chloroplast markers, which reveals a recent long-distance dispersal of *A. pungens* from Portugal into Corsica-Sardinia. Altogether, our data suggest that the climate is one of the main factors shaping the current genetic structure of the species.

## NULL-MODELS FOR SIGNIFICANCE TESTING OF SPECIES' DISTRIBUTION MODELS DEVELOPED WITH PRESENCE-ONLY DATA

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Species' distribution models relate species presence data to climatological and environmental variables. A crucial step in species' distribution modelling is to assess model accuracy. The most robust, threshold and sampling prevalence independent, single measure of accuracy is the area under the curve (AUC) of receiver-operating characteristic (ROC) plot. However, when applied to species' distribution models developed with presence-only data, the required absences are lacking. This is solved by introducing pseudo-absences. Pseudo-absences are points randomly drawn from the geographical area of interest, representing its environmental variation. Consequence is that the maximum achievable AUC value is no longer 1, but $1 - a/2$ (where $a$ is the fraction of the area covered by a species' true distribution, which typically is not known). Therefore, an AUC value > 0.7 indicating useful models, no longer applies. We solved this problem by introducing null-models. Null models are pattern-generating models that deliberately exclude a mechanism of interest, and allow for randomization tests of ecological and biogeographic data. The way we implied null-models in species' distribution modeling, is by testing whether AUC values of species' distribution models are significantly larger than can be expected from 999 times randomly drawn and modeled points. Thereby we exclude the mechanism of an ecological niche.

## BIOTIC INTERACTIONS MAY LIMIT THE SOUTHERN DISTRIBUTION OF BOBCATS *LYNX RUFUS*

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Bobcats *Lynx rufus* are opportunistic felids occurring in a diverse range of habitats and with a widespread distribution from southern Canada to southern Mexico. We modeled the ecological niches of the felid community in southern Mexico to explore why the bobcat distribution stops abruptly at the Isthmus of Tehuantepec (IT). The IT, a lowland region with subtropical swamp habitat, is unlikely to serve as a geographic and ecological barrier to bobcats. Mammal inventories conducted for over a century rejects the hypothesis that bobcats are present but have not yet been recorded south of the IT. No evidence of fossil records south of the IT provides little support for a past presence of bobcats in that region. We show that the ecological niche of bobcats extends south of the IT, suggesting that ecological conditions exist for the establishment of populations in that region. The overlap of the bobcat geographic niche was lowest with margay and ocelot, both felids with similar size and feeding habits. Moreover, an independent analysis computing an index of 'geographic avoidance' between all felids' collecting localities showed high values between bobcats with margay, ocelot and jaguar, but not with puma. We propose that biotic interaction with other felids limits the southern distribution of bobcats, preventing dispersal to a suitable but geographically reduced niche south of the IT.

## POTENTIAL *VS*. REAL DISTRIBUTION OF IBERIAN FORESTS: THE RANDOM FOREST ALGORITHM FOR MODELLING FORESTS DISTRIBUTION

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The study of potential distribution areas of species is a discipline of great interest to many researchers, due to the difficulty involved in establishing these areas in highly modified environments like Europe. As a result of the efforts made in modeling habitat suitability, predictive techniques have become more numerous and have been improved in recent years, with a direct effect upon their quality and credibility. Lately greater use has been made of machine learning methods. These techniques does not require assumption of normality of the variables and can deal with non-linear relationships. We present the potential distribution of 6 tree species on the Iberian peninsula by means of a relatively new machine learning method for predicting species habitat suitability: the Random Forest algorithm. The 6 species has been chosen from the whole Iberian forest types. They inhabit in all the Iberian forestall environments: As Mediterranean ones *Quercus suber* and *Pinus pinea* has been chosen. As Submediterranean, *Pinus nigra* and *Quercus faginea* subsp. *faginea*. Finally, to study the behavior of the model working with mountain coniferous forest and with temperate broadleaves forest we have chose *Pinus uncinata* and *Fagus sylvatica*. To facilitate the interpretation of the results, a presence/absence map has been derived from the provability map. To improve the biological significance of the model, we propose to validate the results with available biological data. This biological validation can be grounded by the use of historic data on the presence of species in the past available in the bibliography.

## IMPACT OF CLIMATE CHANGE ON MIGRATORY BIRDS: EVOLUTION VERSUS SORTING OF SPECIES

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Across Europe, the proportion of migratory birds in bird communities declines with increasing temperature. On the one hand, fewer migratory species are found in warmer areas. On the other hand, many migrants show intra-specific variation in migratory behaviour, with migratory activity being weaker at higher temperatures. Accordingly, if temperature increases with climate change, the proportion of migrants at a specific site is expected to decline. This should be caused by shifts in geographic ranges, i.e. sorting of species, and by changes in migratory activity, i.e. evolution. In order to predict the consequences of climate change, we inferred the magnitude of sorting effects from spatial variation in the proportion of migratory species and of evolutionary effects from spatial variation in the proportion of these species that actually migrate at a specific site. Our results suggest that a 1°C increase of winter temperature causes a 1.9% decrease in the proportion of migratory birds. This is caused by a decrease in migratory species (-0.3%) and a decrease in migratory activity (-2.3%). Accordingly, climate change is expected to change the proportion of migratory birds at a specific site more through evolutionary changes in migratory activity than through sorting of species.

## MATE CHOICE AMONG CLOSE AND DISTANT SEXUAL AND ASEXUAL POPULATIONS OF THE GEOGRAPHIC PARTHENOGEN OSTRACOD *EUCYPRIS VIRENS* (CRUSTACEA: OSTRACODA)

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Among non-marine ostracods, there are some species with sexual reproduction, some with asexual (parthenogenetic) reproduction, and some species show both types of reproductive strategies. One of these last cases is the widespread *Eucypris virens,* commonly found in temporary pools across Europe, but with males (bisexual populations) distributed only around the Mediterranean, where parthenogenetic populations can also be found frequently. In order to assess the importance of mate recognition between males and (sexual or asexual) females, on the coexistence of both types of reproductive strategies, we carried out behavioural experiments using marked individuals from four populations (4 sexual, 1 asexual) of *Eucypris virens* from Morocco and Spain, and females of another but similar species, *Heterocypris incongruens* from Spain. The results show that: (i) Males preferentially copulate with females of the same species from sexual sites when both sexual and asexual females are available and (ii) males copulate more frequently with females from their original pond or another nearby pond (geographical preference) than with females from a sexual population of distant origin. Quantitative analysis of sperm content in the experimental females allowed for a very accurate assessment of mating success, and largely confirmed the patterns of the observed mating events.

## BRYOPHYTE DISTRIBUTION MODELS TO PREDICT THE EFFECTS OF CLIMATIC CHANGE: EXAMPLES AT THE EUROPEAN LEVEL

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Attention in climate change has significantly increased in the past 10 years, both within and outside the scientific community. The reason for this interest is related to the anticipated global warming in global scale. As a result of this interest, several studies have been raised relative to climate warming based in species distribution changes. Bryophyte species have, in generality, a wide tolerance range to temperature, atmospheric humidity, total annual rainfall and duration of dry periods are much more important constraints of climate than temperature. However each species has an optimum temperature range, reflected by the geographic distribution and on the altitudinal preferences. The recent extension of geographical distribution, gradually towards northern latitudes of bryophyte with thermophilic affinities, as Macaronesian and Mediterranean species, could provide opportunities for simulate and test the use of bryophytes as indicators of future climate changes. In this work it will be applied distribution models to suggest future climatic changes in Europe, based in actual Iberian and/or Macaronesian distribution of several bryophyte species, almost exclusively restricted to the Mediterranean, warm-temperate or oceanic areas. Future distributions of species, as *Sematophyllum substrumulosum* (Hampe) E. Britton, will be built based on different Intergovernmental Panel on Climate Change (IPCC) scenarios for climate alterations. Models will be based on Ecological niche modelling tools like Maxent, Garp and Enfa. These methods identify favorable climate and environmental conditions for species occurrence, based on actual distributions, allowing to pursuit areas where major changes in the distribution of these species would serve as early indicators of potential changes in vegetation composition in Europe.

## THE FUTURE OF AFRICA'S PLANT DIVERSITY – POTENTIAL EFFECTS OF CLIMATE CHANGE ON SPECIES DISTRIBUTIONS

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To fulfil the Convention on Biological Diversity's 2010 targets to "achieve by 2010 a significant reduction of the current rate of biodiversity loss", we need sound information on the distribution of species and on the patterns of biodiversity. Already today, many species are threatened due to habitat fragmentation. The Gran Canaria Declaration highlights the relevance of climate change for plant conservation, which will further increase the pressure on habitats. We mapped distribution patterns for more than 4500 plant species (c. 10% of the flora) in the continental Africa at a spatial resolution of c. 50 km x 50 km (0.5° grid cells). First, environmental niche models were generated that predict species ranges on the basis of documented distributions and climate parameters, assuming that the extent of species ranges depends predominantly on climate. Second, species distributions were modeled under predicted climate conditions until the year 2100, using different future scenarios derived from the Intergovernmental Panel on Climate Change (IPCC). We used two different dispersal scenarios, supposing either no or full ability of species to invade new suitable areas. The vast majority of species ranges may markedly decrease in size by 2100. Even if species will be able to invade new geographic regions, a large proportion of climatically suitable habitats may be lost during the next century, especially in dry lowland areas. However, some areas may serve as biodiversity refuges, especially in the tropical wet lowlands and the afrotropical mountains. These areas are of particular priority for the setup of sustainable conservation strategies.

## A NOVEL METHOD TO EXPLAIN SPECIES RICHNESS FROM ENVIRONMENTAL HETEROGENEITY ACROSS THE ALPS AND CARPATHIANS

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Conservation biologists and bio-geographers increasingly rely on empirical biodiversity distribution models for decision-making. Even though it is widely accepted that species richness increases with increasing habitat variability, most species richness models use single climatic and other environmental predictors usually at the same spatial resolution of the response variable. In our study on the high mountain flora of the Alps and Carpathians, we developed a novel method to incorporate the spatial heterogeneity within sample grids of 23 km x 25 km, for which the species richness data were available. Our method starts from climate and other environmental variables at 90 m spatial resolution. The predictors are grouped into classes. Varying combinations of these classes lead to small hyper-cubes (potential habitats) which subdivide the environmental hyperspace and thus allow expressing the richness, diversity and area of these potential habitats within sample cells. We tested this method against other approaches that express the environmental variability within sample cells. Results demonstrate that our method explains ca. 70% of the species diversity, which is favorable compared to traditional methods. We suggest that a combination of habitat diversity and climatic predictors will highly improve the present modeling processes.

## ENERGY, RANGE DYNAMICS AND GLOBAL SPECIES RICHNESS PATTERNS: RECONCILING MID-DOMAIN EFFECTS AND ENVIRONMENTAL DETERMINANTS OF AVIAN DIVERSITY

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Spatial patterns of species richness follow climatic and environmental variation. However, they could also reflect random dynamics of species ranges leading to the mid-domain effect (MDE). Using data on the global distribution of birds, we compared predictions based on energy availability (actual evapotranspiration, AET, the best single correlate of avian richness) with those of range dynamics models. MDE operating within the global terrestrial area provides a poor prediction of richness variation, but if it operates separately within traditional biogeographic realms, it explains more global variation in richness than AET. The best predictions, however, are given by a model of global range dynamics modulated by AET, such that the probability of a range origin and subsequent spreading into an area is proportional to its AET. This model also accurately predicts the latitudinal variation in species richness and variation of species richness both within and between realms, thus representing a compelling mechanism for the major trends in global biodiversity.

## SHIFTING RANGES IN PAST AND PRESENT CLIMATE: THE INABILITY OF NORTHERN WHELKS TO DRILL THE RANGE EXTENDING BARNACLE *TETRACLITA RUBESCENS*

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The volcano barnacle *Tetraclita rubescens* is an intertidal invertebrate that has recently expanded its range >300 km northward along the coast of California, consistent with the prediction that increasing global temperatures will permit species to shift poleward. In newly colonized northern habitats, *Tetraclita* has joined an assemblage of intertidal barnacles that are preyed upon by two species of whelks (*Nucella ostrina* and *N. canaliculata*). In field enclosures at Bodega Marine Reserve we exposed small barnacles of three species to whelks (*N. ostrina*) from different northern populations. *Tetraclita* were seldom preyed upon as juveniles, regardless of which region the whelks came from. In laboratory experiments we tested the ability of northern whelks to prey upon larger *Tetraclita*. We also conducted laboratory experiments on the more southern and recently diverged congener *N. emarginata*. This whelk was able to prey on adult *Tetraclita* at significantly higher levels despite the fact it lacks any distinguishing morphological characteristics. These results suggest that northern whelks will have few negative impacts on the range expansion of *Tetraclita* as they have not yet evolved a mechanism to recognize and efficiently prey on *Tetraclita*, unlike their recently diverged southern analogue. We suggest that a comprehensive understanding of climate driven range shifts will incorporate species interactions into a framework similar to that applied to invasive species. Specifically, the success of a population established beyond a species' historical range boundary will be influenced by the functional traits of that species in relation to the composition and evolutionary history of the surrounding community.

## A NOVEL APPROACH TO BIOGEOGRAPHIC DISTRIBUTION AND ABUNDANCE MODELING OF DATA-POOR, MONTANE-OBLIGATE AVIFAUNA IN MESOAMERICA

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Over the past 2 decades, numerous algorithms have been developed that use geographical points as training data, in combination with environmental raster data, to predict species distributions. Unfortunately, sufficient data with which to model distributions for the vast majority of bird species is unavailable and too costly to procure, or of poor or unknown quality, making robust modeling impossible. I developed a GIS-based methodology that circumvents the need for training points, enabling the estimation of both distribution and relative abundance for species that have never been modeled before. The process requires harvesting pixels values from a stack of environmental rasters along fixed transects within the historical range of the species, and deriving summary statistics from them. Mean pixel values from three or more habitat quality categories are used as anchor points from which to interpolate intermediate values from each of the environmental rasters. In turn, these are used to develop continuous geospatial data surfaces of apparent habitat quality ranging from 0-100. The approach is termed the "transect interpolation method" (TIM). A forest density habitat quality factor and an elevation mask are applied to further refine the models for montane forest-obligate bird species. I present TIM results for 2 threatened, data-poor, Galliform species, Bearded Wood-Partridge (*Dendrortyx barbarus*), and Horned Guan (*Oreophasis derbianus*). To assess the quality of the modeling approach, I compare TIM results with those of pre-existing algorithms for the data-rich Ruddy-capped Nightingale Thrush (*Catharus frantzii*).

## USING OF SPECIES-ENERGY THEORY FOR VASCULAR PLANTS FOR IDENTIFICATION OF LARGE SCALE BIODIVERSITY HOTSPOTS IN RUSSIA

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Large-scale vegetation diversity can be predicted to a major extent by the climatically determined latent heat required for evaporation and the geometrical structure of landscape, described as an altitudinal difference (Venevsky and Venevskaia, 2003). National biodiversity hotspots can be mapped from biotic or abiotic data using the quantitative criteria for plant endemism and land use (corrected for the respective country) from the 'global hotspots' approach (Venevsky and Venevskaia, 2005). During the study, the three biodiversity hotspots North Caucasus, South Siberia and the Far East are mapped from abiotic data. Despite the relatively small total area of the three Russian hotspots (they occupy only 3% of the entire Russian territory), these areas are inhabited by 68% of the Russian RDB species belonging to the five taxa (vascular plants, amphibian, reptiles, birds and mammals).

Venevsky, S. & Venevskaia, I. (2003) Large-scale energetic and landscape factors of vegetation diversity, *Ecology Letters* 6: 1004 -1016
Venevsky, S. & Venevskaia, I. (2005) Hierarchical systematic conservation planning at the national level: Identifying national biodiversity hotspots using abiotic factors in Russia. *Biological Conservation* 124, 235-251

## RICHNESS OF WOODY PLANTS IN THE IBERIAN PENINSULA: EVALUATING THE IMPORTANCE OF CLIMATE, TOPOGRAPHY AND SUBSTRATE AT TWO SPATIAL SCALES

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Climate-based models often explain most of the variation in species richness along broad-scale geographic gradients. However, a general consensus on the mechanisms that yield diversity patterns is still lacking. We evaluate the relative importance of macroclimatic factors, topography and substrate for woody species richness in the Iberian Peninsula at two spatial scales of analysis (2,500 and 22,500 km$^2$), using generalized additive models and least squares regression. Elevation range emerged as the most important predictor at both grain sizes. When tested separately, minimum monthly potential evapotranspiration was the best climatic predictor at the largest grain size, whereas annual actual evapotranspiration was most significant at the smallest grain size. Precipitation was fitted together with an interaction term between itself and substrate at both grain sizes, which demonstrated that water availability is also dependent on the substrate, and revealed a complex relationship between richness and precipitation (third-order polynomial). We compare our results with those obtained after fitting the interim general models of O'Brien (1998) and discuss the differences and similarities between the models by considering the proportion of spatially structured pattern explained, the grain size used and the range of the climatic variables.

## DOES CLIMATE DRIVE RANGE SHIFTS IN THE DIANA FRITILLARY?

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Butterflies are key organisms for monitoring biological diversity, and many northern species have been shown to shift their geographic ranges in response to global climate change. There have been no documented effects of global warming on butterflies in the southern Appalachian Mountains. However, even small temperature increases in this southern region can have dramatic effects on high elevation species that have nowhere to go. We are investigating the conservation status of the Diana fritillary, (*Speyeria diana*), a butterfly species of concern that has disappeared for unknown reasons from low elevations in the South-eastern United States. As the first part of this research, we collected over 1,500 records of this species' occurrence from 1896-2006 in order to document any shifts in range or phenology that have occurred over the past 110 years. Records were obtained from university and museum collections, state agencies, national parks, and private collectors. All location data were entered into a GIS and were mapped to the county level. We are next using these data to model future distributions of *S. diana* and members of its mimicry complex under predicted climate change scenarios to better manage and protect this species.

## NOVEL AND DISAPPEARING CLIMATES IN THE 21ST CENTURY: DISTRIBUTION AND ECOLOGICAL IMPLICATIONS

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By the end of the 21st century, the Earth system likely will include climate regimes with no modern analog and, possibly, no good analog to any Quaternary climates. No-analog climates challenge ecological forecasting, because most climate niche models are parameterized using modern observational data. Conversely, the likely disappearance of some 20th-century climates threatens species with narrow climatic distributions. Here we analyze global multi-model ensembles for the A2 and B1 greenhouse gas emission scenarios produced for the fourth assessment report of the Intergovernmental Panel on Climate Change (IPCC AR4), with the goal of identifying regions projected to experience (1) high rates of local climate change, (2) development of novel 21st-century climates, and/or (3) disappearance of extant climates. Novel climates are projected to develop primarily in the tropics and subtropics, whereas disappearing climates are concentrated in tropical montane regions and the poleward portions of continents. Under the high-end A2 scenario, 12-39% and 10-48% of the earth's terrestrial surface may respectively experience novel and disappearing climates by 2100AD. Corresponding projections for the low-end B1 scenario are 4-20% and 4-20%. These estimates increase after accounting for dispersal limitations of plant species. Paleoecological records show that novel species associations tend to form in areas with novel climate regimes, raising the risk of unexpected species interactions and other future ecological surprises. Conversely, disappearing climate regimes challenge conservation planning, because standard approaches to maintaining biological diversity in the face of climate change (e.g. connected reserve networks, assisted migration) cannot accommodate the total disappearance of some climates.

## MODELLING PINK-FOOTED GOOSE WINTERING DISTRIBUTION FOR THE YEAR 2050: POTENTIAL EFFECTS OF LAND USE CHANGE IN EUROPE

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Since the 1980's the Svalbard population of pink-footed geese (*Anser brachyrhynchus*) has switched from its natural grassland habitat to more nutritious and widely available agricultural crops. Along with increased protection from hunting, this switch has increased goose survival, and given rise to an agricultural conflict along their north western European flyway. We forecasted the potential distribution of the species at a fine spatial resolution (1 km) using generalised additive models (GAM) and three potential land use scenarios for the year 2050.GAM analyses showed that probabilities of goose occurrence were significantly correlated with proximity to coast, elevation, degree of habitat closure, and the presence of cropland and grassland. GAM predictions to the 2050 scenarios revealed noticeable shifts in the suitability of goose habitat evident at the local and regional scale in response to future shifts in land use. In particular, as grasslands and croplands give way to unsuitable land use types (e.g. woody biofuel crops and increased urbanisation), our models predict a decrease in habitat suitability for geese. If coupled with continued goose population expansion, we expect that conflict with agricultural interests will intensify under these future scenarios.

## EFFECTS OF SAMPLE SIZE ON THE PERFORMANCE OF SPECIES DISTRIBUTION MODELS

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A wide range of species distribution models (SDMs) exists, but the amount of locality data available for generating predictions is often limited. To explore how the predictive power of SDMs changes with data availability we developed predictions for 46 species (from 6 different regions of the world) at 3 sample sizes (100, 30 and 10 records) using 12 different SDMs, and evaluated these using independent presence-absence data. Across SDMs, performance generally increased with increasing sample size, while variability in predictive accuracy decreased. An SDM based on maximum entropy (MAXENT) generally outperformed others across all sample sizes. DOMAIN and a genetic algorithm (OM-GARP) had an intermediate performance at 100 records but often performed better than the remaining algorithms at 10 records. Novel modelling methods that incorporate both interactions between predictor variables and complex response shapes (e.g. GBM, MARS-INT, BRUTO) performed best at large sample sizes but not at small sample sizes. Acoss SDMs, a few highly accurate predictions were obtained with only 10 records. While this finding lends some support to the use of small data sets in exploratory modelling, no SDM predicted every species well at small sample size, and such predictions should be considered preliminary.

# Other abstracts

## PHYLOGEOGRAPHY AND TAXONOMY OF THE GENUS BERBERIS (BERBERIDACEAE) FROM NEPAL HIMALAYA

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*Berberis* is the largest genus of the Berberidaceae, with at least 500 species globally, with the major centre of diversity in the Sinohimalayan region and a secondary centre in South America. The closely related genus *Mahonia* is distinguished from *Berberis* s.s. primarily by the presence of compound leaves. Based on geographical location, Schneider (1905) divided Berberis into the Septentrionales of Eurasia and the South American Australes and likewise split Mahonia into the Asian Orientales and North American Occidentales. There are currently thought to be 32 species of *Berberis s.l.* in Nepal. ITS studies (Kim et al 2004) have given new insights into the taxonomy and biogeography of the genus, demonstrating that *Mahonia* is paraphyletic with respect to the *Berberis*, and that the Australes are nested within the paraphyletic Septentrionales, and indicating a complex history including dispersal and vicariance. The addition of 21 Nepalese taxa to Kim's matrix confirms that Schneider's infrageneric classification is invalid. The most recent revision of *Berberis* was by Ahrendt (1960), but it is problematic, with Landrum (1999) reducing the number of species in Chile from 60 to 20. There is a clear need for further revisions of *Berberis* throughout its range, combined with molecular studies to elucidate relationships within the genus and clarify its biogeography. The current study focuses on the Nepalese species, clarifying their taxonomy and investigating their speciation and hybridisation to understand the origin and maintenance of diversity within this region. As ITS sequence divergence is rather low for use at the species level, we will also use AFLPs to examine these relationships.

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## BRIDGING THE PAST AND THE FUTURE – PHYTOGEOGRAPHIC RESEARCH IN THE EASTERN ARC MOUNTAINS, TANZANIA

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The Eastern Arc Mountains, thirteen forest-capped mountain blocks stretching from southern Kenya through Tanzania, harbour one of the highest unit area densities of endemic species worldwide. The origins of this striking biodiversity, and the potential impacts of future environmental change, have been subject of much debate. Research within the York Institute for Tropical Ecosystem Dynamics (KITE) is analysing Eastern Arc taxa at a range of spatial levels, within and between different mountains blocks, to shed light on phytogeographic patterns. Identified patterns will be analysed at numerous ecological levels: on a population/species level with respect to species specific dispersal modes and ecological tolerance amplitudes; and on a plant community level with respect to present-day environmental correlates. This analysis will draw upon all botanical data from the area, constituting the most comprehensive study of its kind. Key methodological challenges include data gaps and incomparability. Results will have temporal implications, and bridge research focussed on the past, the present and the future, *viz.* the KITE research strands palaeoecology, phylogeography and modelling. Overall research outputs will be applicable to conservation management, i.e. through the development of responsive strategies in the face of climate change projections, and in quantifying the botanical targets of recent declines in forest cover.

## THE BRYOPHYTE FLORA OF SÃO TOMÉ ISLAND PROJECT. COMMUNITIES' ANALYSIS OF THE DISTRIBUTION PATTERN OF THE GENUS *PINUS* (SUBSECTION *PONDEROSAE*)

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One of the major goals of Biogeography is to detect how much of the diversity and distribution patterns between species are attributable to ecological factors, and how much of the variation is attributable to historical factors. Mexico represents the second center of diversification of the genus *Pinus* with near to 45% of the species currently described. The subsection *Ponderosae* is one of the most important due to biological, economical and ecological properties. This subsection represents a monophyletic group, probably originated in Western North America, where 12 of the 17 species are distributed in Mexico. The goal of this work was to assess how many chorological patterns are present in Mexican species of the subsection *Ponderosae.* 1,519 records from 21 national and international herbariums were collected. ArcGis 8.2 and DIVA GIS 5.4 were used to construct single distribution patterns and richness patterns. 35 enviromental variables (climatic and edaphic) were used in the discriminant analysis of the four chorological patterns defined. Wilks lambda ($\lambda = 0.3217$, $P<0.0001$) allow discriminate only one group, rest of them show high levels of overlapping.

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## *PRUNUS LUSITANICA* L. SSP. *HIXA* (WILLD.) FRANCO, INDICATOR OF THE DYNAMIC STATE OF THE ANAGA FORESTS (TENERIFE ISLAND, CANARIES, SPAIN)

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Studies of *Prunus lusitanica* L carried out over the last six years on the Iberian Peninsula have acknowledged the transcendence of this taxon's clonal sprout reproduction. The analyses of its population dynamics have shown that vegetative reproduction is essential to the survival of this species and to the increase in the number of specimens in each population; it also explains why it is found in relatively few locations despite the high number of specimens. In contrast to the localised presence of *Prunus lusitanica* ssp. *hixa* in the other islands of the Canary Archipelago, this species, which is endemic to the Canaries and Madeira, dominates the Anaga laurisilva both in terms of number of specimens and the wide area that it covers. The importance of its vegetative reproduction in relation to canopy gaps and its frequent spatial association with *Erica scoparia* ssp. *platycodon* and *Erica arborea* scrubs, traditionally used for charcoal making, make it a good indicator of immature stages of the Anaga laurisilva. This hypothesis is being tested by analysing the distribution of forest species by age in various study parcels.

## THE CONTRIBUTION OF CHOROLOGY TO THE STUDY OF THE DYNAMICS OF LAURISILVA IN THE SOUTHERN SECTOR OF GARAJONAY NATIONAL PARK (LA GOMERA ISLAND, CANARIES, SPAIN)

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The forest in the southern area of Garajonay National Park contains a mosaic of communities that are directly related to the old agricultural, pasture and forestry uses of this region. Thanks to the gentle topography of the leeward sector of the forest, the laurisilva growing in this area has traditionally been a valuable economic resource for the subsistence economy of the rural population. After the declaration of the national park the proportions of different arboreal species in this forest have changed in such a way as to indicate an increase in the maturity of the forest. Five taxons have been selected for this work based on their significance to the dynamics of the forest: *Erica arborea, Myrica faya, Ilex canariensis, Persea indica* and *Ocotea foetens*. The location and quantity of each species is established by chorological cartography. These maps provide essential systematic spatial information, as well as an understanding of the population ecology of the taxons, in order to identify and evaluate the level of spontaneous recuperation and the change in the internal geography of the laurel forest over the last 25 years.

## THE DISTANCE DECAY OF SIMILARITY IN BOREAL STREAM COMMUNITIES

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The similarity between two communities often decays as the distance between them increases, a pattern mostly recognized in terrestrial animal and plant communities. A decay of similarity in ecological communities can result from a decrease in environmental similarity with distance or by the spatial configuration and the nature of the landscape. Variation in distance decay rates among different species groups will also arise if the groups have a different dispersal ability. We examined the relationship between community similarity and environmental and geographical distance in three freshwater taxa (bryophytes, insects and diatoms) across Finland using Mantel tests. We also examined the slope and the intercept of the distance decay rates for each group. Our results showed that community composition was more strongly related to environmental than to geographical distance. Differences in decay rates with environmental distance were observed between taxa, implying that these groups are responding differently to stream environmental variation. Moreover, decrease in community similarity with geographical distance was relatively low and rather similar between these taxa, implying that dispersal differences between these taxa are not as important as expected a priori.

## TRUMPETER FINCH COLONIZATION PATTERNS OF EUROPE

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Border populations are usually founded by few individuals, and after colonization, populations typically experience a bottleneck that results in a fast genetic differentiation from the original population together a decrease in genetic variability. However, due to the immigration from source populations such effects can be diminished or even lacking. Trumpeter Finch (*Bucanetes githagineus*) is a semidesert species recently established (1960s-70s) in the Iberian Peninsula and currently carrying out an expansion process northwards. Our goal is to study the colonization pattern of Trumpeter Finch by comparing the genetic variability of populations from North Africa with several Iberian populations distributed along the recently colonized area at different expansion steps. In addition we compare the genetic variability found in such populations with two well long-time established populations in Canary Islands (around 7,000 years). We used a set of seven polymorphic microsatellite to test for genetic differences among populations. Our results suggest an incipient divergence between Iberian and North African populations. Nevertheless, two Iberian populations seem to be at length made up of African specimens suggesting a high genetic flow. Canary Islands populations were genetically well differenced from the rest of studied populations. The results confirm the North African populations as the source of the Iberian ones.

## NUTRIENT AVAILABILITY IN A SUBSTRATE AGE GRADIENT ACROSS PINUS CANARIENSIS FORESTS: TESTING OF A BIOGEOCHEMICAL MODEL

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Walker and Syers (1976) suggested that plant growth in ecosystems on young soils might be expected to be limited by nitrogen, while growth on old soils should be limited by phosphorus. Because phosphorus is present in rocks and lacks a significant gas phase, ecosystems developing on new substrates contain all the phosphorus that they will ever have. When rock is exposed to water and acidity, it weathers and releases phosphorus as biologically available phosphate. Over time, therefore, the available and total phosphorus in the system as a whole should decline. In contrast, nitrogen is absent from most primary substrates, so biologically available nitrogen should be in relatively short supply early in soil development. Total soil nitrogen increase with time and ecosystem development. This model has been tested from arid to boreal ecosystems. Here we show a substrate age gradient in *Pinus canariensis* forests in the Canary Islands. This soil chronosequence ranges in age from few hundred years to four million years old. Our first results show different control of nitrogen of phosphorus through the ecosystem development.

## PLIOCENE VS. ANTHROPOCENE – EVOLUTION OF BIOGEOGRAPHIC PATTERNS AND PROCESSES IN MARINE BRYOZOA

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Because most cheilostomatous Bryozoa possess short-lived larvae, dispersal is dependent on habitat-parallel currents and the covered distance per generation is generally short. The expected, relatively restricted range of geographic distribution of bryozoan species is corroborated by a comparison of Pliocene faunas from the North Sea Basin (NSB) with contemporaneous Mediterranean ones, which revealed that only 6 (4%) of the 141 species present in the NSB also occurred in the Mediterranean Sea. These regions were thus separated by oceanographic barriers during the Pliocene and an exchange of bryozoan taxa was rather by chance (e.g. rafting) than the rule. In contrast, Recent faunas from the same areas share a much greater number of species (97 = 63% of 155 species recorded off SE England). The discrepancy between fossil and Recent faunal similarities and species ranges cannot be explained by changes in natural oceanographic processes. It is therefore concluded that (1) since the beginning of seafaring, shallow marine (bryozoan) faunal compositions and geographic species ranges have been drastically altered; (2) analysis of only Recent biogeographic species distributions is likely not to reflect the natural pre-nautical pattern and consulting the fossil record may prove to be indispensable for certain taxa and regions; (3) the restricted geographic distribution of bryozoans allows to reveal palaeobiogeographic patterns and to reconstruct oceanographic pathways at a very fine scale.

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## OLIGO-MIOCENE ORIGINATION OF THE ATLANTIC-MEDITERRANEAN AND INDO-PACIFIC BIOGEOGRAPHIC PROVINCES

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The Early Miocene witnessed the collision of the African-Arabian and Eurasian tectonic plates and, as a consequence, the termination of the circumtropical Tethys Ocean. The associated compartmentalisation of a single large biogeographic unit into the Atlantic-Mediterranean and Indo-Pacific provinces marks a significant oceanographic and biogeographic turning point in the Cenozoic. The aim of our project is to understand the origin and composition of the modern biogeographic regions by examining latitudinal and longitudinal patterns of the palaeogeographic distribution of benthic organisms. Mollusks, echinoids, larger foraminifers and scleractinian corals collected from the Oligo-Miocene of the Middle East, located in the centre of the narrowing Tethyan Seaway, were compared with records from the western and eastern Tethyan regions. The results suggest that a significant part of the taxa originated in the western Tethys and migrated towards the east, contributing to the regional diversity of the (proto-) Indo-Pacific. For instance, tridacnid bivalves appear to have displayed a diversity centre in the western Tethys during the Paleogene before vanishing in this region and diversifying in the Indo-West Pacific during the Neogene. These findings contrast with some recent interpretations concerning the Indo-Pacific as a historical centre of origin, including those based on genetic studies, and highlight the need to integrate palaeontological data in broader biogeographic analyses.

## ECOREGIONAL APPROACH TO IDENTIFY CONSERVATION PRIORITIES IN MEXICO

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Ecoregions capture numerous features of biological diversity. We performed a gap analysis to assess how well represented are the 72 terrestrial ecoregions identified for Mexico on the 405 natural protected areas (NPA), which cover 11% of its territory. A first step consisted in evaluating representativity of PA for each vegetation type and geographical features defining elevational gradients within ecoregions. The second step consisted in developing three indices to characterize ecoregions and identify priorities for conservation: (1) biological importance, considering variables such as primary vegetation types, species richness and endemic, (2) degree of threats, considering stressors for biodiversity such as potential fire points, population increase, unsustainable management practices and endangered species, and (3) actions and responses, which consider mainly areas that are already protected by the current nature reserve system, among other instruments. These indices are a useful quantitative instrument to rank ecoregions according to prioritisation values and provide a framework for strengthening conservation activities. Indices values ranked in ascending importance from two to 100, showing that the ecoregions that exhibited the highest prioritization values are located in the western region, mainly across the Pacific Coast of the country which are characterized by dry forests, xerophytic vegetation, and oak and pine forests. Assessing ecoregion gaps provide a framework for strengthening conservation activities.

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## TERRESTRIAL PRIORITY SITES FOR CONSERVATION IN MEXICO: AN ANALYSIS OF KEY TARGETS AND MAJOR THREATS

Coordinated by CONABIO, CONANP, FCF-UANL, FC-UNAM, IB-UNAM, IE-UNAM, PRONATURA, TNC & SEMARNAT

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In the context of bringing together conservation efforts to generate strategies at a national level, numerous researchers and institutions performed a multiple-approach analysis to detect terrestrial priority areas for conservation. We compiled data for several conservation objects, including potential areas of distribution of terrestrial vertebrates, occurrence data of some plant groups, crucial habitats and plant vegetation types, together with some threats such as main roads, human population increase, rate of vegetation change, and urban areas growth. Workshops were carried out to define the criteria to prioritize the conservation objects (such as endemism, rarity, etc.), and existing or potential threats to biodiversity (such as agriculture, fragmentation, fires, etc.) were identified and included in the study. We used different software to enrich and complement the identification of priority sites and possible conservation networks. A high beta diversity country like Mexico implies challenges and practical difficulties in identifying all biodiversity elements of concern in a small number of area. Therefore, criteria were re-defined to count with different scenarios that might provide a national vision of hotspots (most diverse and most endangered sites). Results show Mexico's high biodiversity and complexity to achieve the goal to preserve representative areas of most endangered species and habitats; which are discussed in a national framework.

## PRIORITY CONSERVATION AREAS FOR MEXICAN MARINE BIODIVERSITY

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Mexico has assumed the goal to increase marine protected areas by 2012, following CBD programmes of work. We organized an expert's workshop to identify priority areas for the conservation of coastal and oceanic environments. The methodology was to first select priority areas at a national scale for groups (fishes, bentic organisms, seagrasses, mangroves, macroalgae, birds, turtles, mammals) and to overlap all layers. Each pre-selected site was revised in a regional perspective and evaluated with criteria such as endemism, species richness, endangered species, flag species, economic value, sustainable use programs, habitat heterogenity, environmental services, ecological integrity, biological relevance, oceanic processes, impact on the habitats such as pollution, over-exploitation, shipping traffic and presence of invasive or alien species. The selected priority areas were then compared with the protected areas to find the gaps. A comparison was made also considering other priority sites such as Ramsar, important bird areas, and previous exercises of marine prioritisation. We created a web page to have a validation and feedback process with the participants and abroad specialists. Total coverage of these 110 priority sites is 34,158,421.34 ha and only 17.61% of this area (50 sites) overlap with 40 NPA of a total of 127 NPA. Not all priority areas determined are thought as future protected areas, but as places that need monitoring efforts and sustainable management.

## HOW TO BUILD A NATIONAL AGENDA FOR CONSERVATION? A META-ANALYSIS WITH A MULTI-INSTITUTIONAL EFFORT

Coordinated by CONABIO, CONANP, TNC, UANL, PRONATURA, KU, IB-UNAM, FC-UNAM, IE-UNAM & SEMARNAT

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Mexico has been recognized as a megadiverse country because of its exceptional biodiversity in number of species, endemics, habitats, landscapes, and ecosystems, a frame that forces to have a multi-scale analysis approach. A number of gap analyses in the literature are focused on some specific groups of species, or units such as ecoregions, usually mean for a given environment. To generate a comprehensive vision at a country level, the National Commission for the Knowledge and Use of Biodiversity (CONABIO), the National Commission for Protected Areas (CONANP), and several institutions and specialists developed an integrated approach to integrate different results for marine, island, freshwater and terrestrial priority areas, to identify key sites for endemic, rare, and threatened habitats and species. We propose a five steps conceptual model: (1) Determine critical ecoregions for conservation; (2) Identify high priority sites for conservation, emphasising species level; (3) Identify gaps in the Natural Protected Areas System; (4) Identify important areas for connectivity and ecological resilience, and (5) Develop a first approach to an interface between terrestrial and marine priority areas for conservation. We present the results for the first three steps while the last ones remain to be developed. Despite natural protected areas are essential for *in situ* conservation, a plethora of complementary instruments are considered to achieve the goal of conserve and provide sustainable use to our natural heritage.

## BIOGEOGRAPHY OF *CINERARIA* (ASTERACEAE - SENECIONEAE)

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The distribution, centres of diversity and endemism, and possible origins of the afromontane genus *Cineraria* L. (Asteraceae - Senecioneae) were investigated, as well as incidence and causes of rarity. *Cineraria* exhibits an ‘African track’ distribution, occurring mainly on the mountains of Africa but extending to sea level in the Western Cape of South Africa. Outside of Africa, one species is endemic to Madagascar and another extends from Ethiopia into Yemen and Saudi Arabia. The centre of diversity for *Cineraria* is in the KwaZulu-Natal Midlands in South Africa, part of the Maputaland-Pondoland Centre of Endemism. Molecular phylogenetic analyses reveal that reticulation has played a major role in driving speciation in *Cineraria* and that the genus originated in the Western and/or Eastern Cape, with *Bolandia* the putative sister group. In contrast, numerous convergent morphological features place *Cineraria* sister to *Pericallis*, a Macaronesian endemic, in phylogenetic analyses based on morphological data alone. Fifteen species of *Cineraria* are endemic to specific mountains or regions of endemism and five are near-endemic. Rare species were identified and categorised according to Rabinowitz’s criteria of geographic range, habitat specificity and local population size. Rare species number at eleven, with causes of rarity in *Cineraria* linked to narrow habitat specificity, particularly soil or rock type and/or altitudinal range.

## OPTIMIZING MONITORING UNDER DIFFERENT VASCULAR PLANTS INVENTORY SCHEMES IN THE MEDITERRANEAN CLIMATE ZONE

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Currently inventory schemes (Atlases, Biodiversity Databases, etc.) are important tools to detect significant trends in biodiversity losses and to assess present conservation measures. But there is a vast variability among inventory methods and aims. In fact, at present data collection methodology in plant field surveys can be considered highly idiosyncratic. Nevertheless, range distribution is a central theme in all inventories, and virtually all threatened plant classifications (CNPS, IUCN, etc.) strongly rely on species range measurements as a first approach for conservation status. We use plants databases coming from three different Atlases to optimize plant monitoring. In this way we employ data from rare plants in California (California Natural Diversity Database), from threatened Spanish plants (Atlas de Flora Amenazada) and from the family Proteaceae in South Africa (Protea Atlas). We explored several statistics – arithmetic mean (AM) and geometric mean (GM) – to identify good estimators for change in species ranges. We employed bootstrapping techniques to estimate bias. California has very similar coefficient of variation (V) for both statistics regardless of sample effort. For Spain, GM seems to be less variable in each subsample size. Proteas dataset produces the largest V by sample effort. Similarly to Spanish case, GM performs better than AM. But differences among coefficient of variation for AM and GM in South African data set are smaller.

## SIZE-DISTANCE ANALYSIS OF SHRUB SPECIES IN CANARY ISLANDS COASTAL SCRUB

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Coastal scrub is one of the most peculiar and typical ecosystems we can find in Canary Islands. This ecosystem is dominated by *Euphorbia* species, mainly *E. canariensis* and *E. balsamifera*; these and other species in this ecosystem are adapted to high temperatures and water stress. In some zones we have an annual average rainfall of less than 100 mm; water is the limiting factor of this ecosystem. When it is a limiting factor, it is usual to find competence relationships, among and within species. As this ecosystem is an open scrub, light is not supposed to be the principal limiting factor for growth, and competence is expected to occur mainly around ground resources like water and nutrients. On the other hand, in extreme environments it is proved that facilitation relationships (one species facilitates establishment, survival or growth of other) are even more important than competence relationships. The aim of this research is to determine what kind of relationships we can find between the most abundant species in this ecosystem, using nearest-neighbour technique and plant size data.

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## IMPROVING PUBLIC UNDERSTANDING OF BIOGEOGRAPHY

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Communicating biogeography to non-scientists is difficult because as the field has become more specialized and technical, the public has come to feel that the subject matter is accessible only to experts. Students enthusiastically participate in school-based science; all but a few do not retain understanding or interest in science into adulthood. School reforms can go only so far because, in the absence of other role models, students will tend to adopt the values of their peers, families and popular culture. Though it is necessary to continue to improve science education, school based reforms tend to reinforce the idea that science is limited to academic settings and the result is a society that is increasingly ignorant, indifferent, or hostile toward science. Successful collaborations between biogeographers and informal science institutions, like the New Mexico Museum of Natural History and Science can illustrate to the wider populace how biogeography is a vital part of life. Field-based outreach programs, like the Student Ecology Research Program, can allow people of all ages to become involved in the scientific process. These citizen science programs can not only help biogeographers gather valuable data, but also help foster an increased understanding of and support for scientific research and create a population who is able to intelligently participate in political discourse and policy making.

## IDENTIFYING SHIFS IN GEOGRAPHIC RANGES FROM REGIONAL DATA-BASES: IBERIAN BUTTERFLIES

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Trend surface analysis was used for determining date-dependent shifts in the centroid distributions of 170 species of Iberian butterflies along the period 1850-2006. Five regression models were fit to the whole data set to account for the large- and local-scale temporal patterns in the whole data set. Residuals from these models were then used to identify species-specific trends. Based in the most conservative criterion, 13 species showed significant temporal trends in all the analyses, while congruent negative evidence was found for 19 species. The results identify correctly three examples of recent range expansion that might be obvious on an intuitive basis. However, there was little agreement between the species trends detected and those proposed on intuitive or other grounds by former authors in the study area, or in south Europe. There was also a low degree of congruence between the latitudinal patterns detected and the altitudinal shifts recently reported by other researchers. In spite of some limitations of the method, it may work efficiently whenever the spatial pattern of the data matrix is reasonably accounted for by the regression model, hence it may represent a useful first step in studies concerning potentially shifting geographic distributions of terrestrial organisms.

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## POPULATION MONITORING OF AN ENDEMIC BAT SPECIES IN RESPONSE TO ERADICATION OF *RATTUS RATTUS* ON ISLA SAN PEDRO MÁRTIR, SEA OF CORTÉS, MEXICO

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Introduced species on islands have had devastating effects on native insular faunas across the globe. Currently, the effects of exotic predators on populations of the endemic fish-eating bat (*Myotis vivesi*) in northwestern Mexico are unknown. *M. vivesi* is an insular endemic bat species that forages for small surface fish and forms maternity colonies under rocks on islands in the Sea of Cortés. Its ground-dwelling roosting habits may make it particularly susceptible to predation by introduced *Rattus rattus.* The predation effects of *R. rattus* on ground-nesting seabird colonies have raised conservation concerns and eradication efforts have been implemented on islands to protect breeding bird colonies in the region. This study will monitor *M. vivesi* populations sampled at night roosts to determine how population levels change after eradication of *R. rattus* on Isla San Pedro Mártir in the Sea of Cortés. The monitoring project will include one pre-eradication sample and two years of post-eradication monitoring to evaluate population dynamics. Using mark-recapture and Pollock's robust design model, we aim to estimate both abundance and survival rates of *M. vivesi* during the two year study. Our project will aid in future island conservation efforts by determining whether this endemic species is vulnerable to exotic predation.

## NO LATITUDINAL GRADIENTS IN LOCAL STREAM MACROINVERTEBRATE DIVERSITY

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Latitudinal gradients in biodiversity have been found to exist in many, if not most, organism groups. However, some organism groups have received little attention in this respect. I examined the relationships of local stream invertebrate diversity to latitude and explanatory variables at local, catchment and geographical scales across Finland (60ºN – 70ºN, 20ºE – 32ºE). The examined diversity indices were species richness, Margalef's index, Pielou's evenness, and Shannon's diversity. No diversity index was significantly related to latitude. Variation in biodiversity was most strongly related to the same suites of local environmental variables (e.g. stream width, acidity), catchment characteristics (e.g. catchment size, altitude), as well a few terms of the polynomial describing spatial location. However, diversity and evenness were not significantly related to spatial variables. In general, catchment variables were most important in affecting species diversity indices, followed by local environmental variables, and spatial variables. The finding that there were no significant relationships between the species diversity indices and latitude may be due to the fact that the responses to latitude and co-varying climatic gradients vary among major stream macroinvertebrate groups. There was nevertheless significant spatial variation in species richness, suggesting that different regions in the study area harbour communities with differing biodiversity. However, catchment characteristics and local environmental variables were generally more influential than spatial variables in accounting for variability in biodiversity.

## AMPHISBAENIAN PALEOBIOGEOGRAPHY: EVIDENCE OF VICARIANCE AND GEODISPERSAL PATTERNS IN FOSSORIAL REPTILES

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Paleobiogeographic patterns within the Amphisbaenia were evaluated using the modified Brooks Parsimony Analysis (BPA) and published morphological and molecular phylogenies. Extant amphisbaenians are present in Africa, South America, North America, Europe, and the Middle East. Modified BPA was used to determine the relative effects of Pangean breakup, sea-level change, and climate change on evolutionary and distributional patterns within the Amphisbaenia. The morphological and molecular analyses resulted in different biogeographic hypotheses. The morphological analysis indicated three biogeographic regions for the Amphisbaenia: (1) Africa, South America, and the Caribbean, (2) western Asia, and (3) North America. The molecular analysis indicated two biogeographic regions: (1) Africa, western Asia, and North America, and (2) South America. The morphological biogeographic pattern corresponds with the known timing of the breakup of Pangea and the resulting paleogeographic reconstructions of the Mesozoic and early Cenozoic. While the molecular pattern is similar to patterns recovered from dinosaurian biogeographic studies, the closer connection of Africa with North America rather than South America does not match well-constrained geologic evidence for the sequence of Pangean breakup. Both analyses resulted in congruent patterns of speciation through vicariance and geodispersal. This suggests that in addition to the breakup of Pangea, such cyclical Earth history processes as sea-level and climate changes played an important role in the biogeographic patterns of the Amphisbaenia.

## COMPARATIVE PHYLOGEOGRAPHIC META-ANALYSIS USING HIERARCHICAL BAYESIAN MODELS

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Testing for biogeographic concordance across co-distributed species is of central importance in evolutionary biology, and community ecology. Such inferences inform processes underlying speciation, community composition, range delineation, and the biotic consequences of climatic changes. In practice, tests of such ecological and/or biogeographic hypotheses always result in parameter estimate differences across species, and practitioners often interpret these differences to be the result of unshared histories stemming from ecologically deterministic processes (e.g. assembly rules and/or ecological differences). Instead, such studies should use models that incorporate inherent variance to better test hypotheses of uniformity across species. Here we provide a way to pool information across datasets within a hierarchical coalescent model in order to test such hypotheses while implicitly accounting for inherent variance in genetic data across species. Such hierarchical models are natural because they allow for uncertainty in 'nuisance' parameters across species while making efficient use of the data to test for complex hypotheses of species concordance. To demonstrate, we use our method to perform a test for simultaneous vicariance across taxon-pairs of reptiles and mammals that are co-distributed across Baja California. The method utilizes the computational power and flexibility of approximate Bayesian computation (ABC) and is implemented in our msBayes software pipeline.

## PHYLOGENETIC RELATIONSHIPS OF THE 'CROWN CORVIDAN' FAMILIES CAMPEPHAGIDAE, PACHYCEPHALIDAE, AND ALLIES IN SEARCH OF BIOGEOGRAPHIC DISPERSAL PATTERNS 'OUT OF AUSTRALIA' AND ACROSS WALLACE'S LINE

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The systematic relationships among basal 'Crown Corvidan' families have been poorly studied so far and as such been useless for biogeographic interpretations. The group has its origin in Australia and colonized Africa and the New World via Asia. The dispersal out of Australia probably began some 35 Mya when terranes of Australian origin collided with Asian landmasses. Recent detailed tectonic mapping of the origin of land masses in the region around Wallace´s Line have revealed a particularly complex movement of terranes over the last 20-30 Myr. Thus the biogeographic dispersal pattern of 'Crown Corvida' is a particularly exciting case for linking speciation history and dispersal events with Earth history. We included 86 taxa covering a broad range of genera belonging to the basal radiations within 'Crown Corvida' which are distributed in all geographical areas within Southeast Asia, Wallacea, Western Pacific islands, the Australo-Papuan region and Africa. Bayesian analyses of nuclear DNA sequence data were used to assess inter-generic systematic affinities. The phylogeny provides a unique opportunity to assess general dispersal patterns across Wallace's Line and furthermore indicates where particularly interesting dispersal scenarios have taken place and where more detailed research should be focused.

## GEOPHYLOBUILDER 1.0: PUTTING THE GEOGRAPHY INTO PHYLOGEOGRAPHY

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Geographical Information systems (GIS) are a system of hardware and software used for storage, retrieval, mapping, and analysis of geographic data. Despite the inherent spatial nature of population genetic, phylogeographic and historical biogeographic data GIS is only just beginning to be employed in these fields. *GeoPhyloBuilder 1.0* is an ArcGIS tool that creates a GIS data structure by combining phylogenetic and biogeographic models. Phylogenetic models may be pairwise distance matrices, reticulate networks or trees. Biogeographic models may be from a variety of sources including fossil distributions, dispersal-vicariance analysis, Brooks parsimony or ecological niche model projections. The GIS data structure is a spatial network that connects point, line or polygon geographical entities, which represent observed or inferred distributions. Storage of data within GIS facilitates archiving and dissemination of data, interclade comparative analysis, quantitative analysis of clades to climate and landscape models and visualization. Here we describe the existing and proposed functionality of GeoPhyloBuilder and illustrate the use of ArcScene to visualize phylogenetic trees in 3D using the z-dimension to represent time.

## CHANGES IN COMPOSITIONAL PATTERNS OVER SPACE AND TIME ALONG AN OCCURRENCE–ABUNDANCE GRADIENT

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Changes in compositional patterns over space and time due to the influence of human activities have been examined primarily with occurrence data. To address this deficiency, we examined changes in compositional patterns along an occurrence–abundance gradient for 443 species of breeding avifauna in North America from 1970 to 2005. Our findings suggest that distance decay in similarity transitioned from a long-lived decay pattern and well defined sill at the occurrence end of the gradient to a rapid decay pattern and no sill at the abundance end of the gradient with dissimilarity peaking at intermediate distances. Compositional similarity increased over time at all points along the gradient with the magnitude and spatial extent increasing with the increasing influence of abundance. The structure of the abundance–occupancy relationship and the geographic expansion of widespread species likely played primary roles in defining these patterns. Our findings suggest that the ecological and evolutionary implications of biotic homogenization are more substantial when abundance is included in the assessment.

## HOW DOES THE EXOTIC COMMON REED (*PHRAGMITES AUSTRALIS*) SPREAD? A HISTORICAL AND GENETIC ANALYSIS

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An exotic genotype of common reed (*Phragmites australis*; Poaceae) has been invading North American wetlands since the beginning of the 20th century. This invader is a major threat for plant and animal species colonizing marshes. We hypothesized that the road network contributed to the spread of the species. Using historical (herbarium) and modern plant specimens, we reconstructed the spread of the exotic genotype – identified with molecular tools – in Québec (Canada). The first exotic common reed colony found in Québec (1916) was located on the shores of the St. Lawrence River. The exotic reed rapidly spread through the St. Lawrence Lowlands only from the 1970's. This spread coincided with the development of the highway network in the province. Today, in Québec, only 5% of reed colonies are native (92% before 1950). Along the road network (and in the marshes located nearby), common reed colonies are almost exclusively (99%) exotic. Our study suggests that the road network strongly contributed to the spread of the exotic genotype, acting as conduit and as habitat, the exotic reed tolerating de-icing salts spread on roads during winter.

## HOW DO TROPICAL FORESTS RESPOND TO DROUGHT? A SPATIAL ANALYSIS OF LEAF TRAITS AND DROUGHT RESISTANT GENERA ACROSS THE AMAZON BASIN.

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The ecological consequences of drought conditions are becoming increasingly significant as evidence mounts for global anthropogenic climate change. Tropical rainforests may be especially vulnerable to shifts in water availability as some tree genera are adapted to narrow precipitation regimes. Geographic variation in plant functional traits, such as leaf structure, forest structure and plant distribution, could provide important clues to how tropical forests are responding, and have responded, to drought conditions. In this respect, possession of compound leaves may be of particular interest as they are thought to be an adaptation to dry conditions. Equally, the process by which plant distributions are constrained by climate is important in terms of forest structure and composition and exploring this may inform our understanding of forest dynamics under future scenarios of climate change. Here, we use two potential community metrics of drought resistance, frequency of trees with compound leaf structure and relative abundance of drought resistant tree genera, to explore biogeographical patterns of tree-water relationships across the Amazon basin. We use multivariate statistics to uncover trait-environment correlations in 139 permanent plots, and discuss our findings in the context of the observed spatial relationships between plant functional traits and drought conditions.

## HABITAT TYPE PREDICTS GENETIC DIVERSITY IN FRESHWATER ANIMALS: RESULTS OF A GLOBAL SURVEY

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A basic challenge in biology is to establish links between ecology and evolution. One important link is the habitat template. The spatial and temporal settings of a habitat strongly influence the evolution of species dispersal. Here, we evaluate the importance of the habitat on genetic diversity of freshwater invertebrates. Freshwater habitats are either lentic or lotic. On average, lotic habitats are more stable and predictable for organisms than lentic habitats. Accordingly, lentic habitats favour the evolution of stronger dispersal propensity with more gene flow. To test this prediction, we used extensive data on genetic population differentiation of freshwater invertebrates taken from published allozyme studies. Controlling for several experimental, biological and geographical confounding effects, we always found that on average lentic invertebrates exhibit lower genetic population differentiation than lotic species. This pattern was consistent across insects, crustaceans and molluscs. Our results imply fundamental differences in genetic diversity among species adapted to different habitat types. We propose that such differences should also occur in other habitat types that differ in their spatio-temporal stability. Furthermore, our results highlight that stable habitats harbour a considerable amount of genetic diversity with the potential for rapid speciation. Thus, biogeographic studies dealing with species richness should consider ecological traits –such as habitat preferences- of the species investigated.

## INTEGRATED APPROACHES, MULTIPLE SCALES: SNAG DYNAMICS IN BURNED VERSUS UNBURNED LANDSCAPES

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Integrating landscape ecology from a biogeographical perspective with GIScience practices offers new ways to study how landscapes change over time and space, including how they can be measured, analyzed, and modeled for management needs. This poster presents methodologies and selected results of analyzing spatial patterns from field data across multiple scales by examining standing dead tree (snag) processes across wildfire-disturbed landscapes in Arizona, USA. Our primary motivation is to illustrate a particular type of work benefiting from the coalescing of landscape ecology and GIScience: that functioning at the methodological and practical overlap of these two contributing fields. Our management goals are to: (1) describe spatial patterns and characteristics of snags in pairs of burned and unburned ponderosa pine forests of Arizona in four recent (< 10 yrs) wildfires, (2) document bird response to wildfires by combining landscape ecology and GIScience methods, and (3) link these patterns to snag monitoring plots and cavity-nesting bird use to predict the probability of snag use by birds and cavity nesters based on snag characteristics (snag use model). The methods and results demonstrate how integration of landscape ecology with GIScience improves the ways to study landscapes and land management issues, in this case offering guidelines for retention of snags that provide habitat for wildlife.

## THE PALMETUM OF SANTA CRUZ DE TENERIFE: THE BIOGEOGRAPHY OF PALMS RECREATED ON A LANDFILL

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The Palmetum of Santa Cruz de Tenerife is a botanical garden, mainly devoted to palms, located on the coast of Santa Cruz, the capital city of the Western Canary Islands. It was started in 1996 on an abandoned landfill bordering the sea. I contributed to its original masterplan by dividing its surface in biogeographical sections. The goal was to recreate the environments of the world regions which are richest in palm species, especially focusing on the island territories, which are home to many interesting and unusual palms. The project run out of funding in 1999 and the whole dream was paralysed. The Palmetum has never been opened to the public and survives with basic maintenance. Ten years passed since the earliest plantings and about 300 palm species resist. I wish to share a recent survey of the garden collections as well as a new map of the gardens. While the Palmetum is still waiting for further developments, some of its biogeographical sections are today ideal outdoor classrooms to teach palm biology and island ecology.

## GLOBAL PATTERNS OF GYMNOSPERM DIVERSITY

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Based on a biogeographical information system for all c. 1,000 gymnosperm species, we present diversity maps of all gymnosperms as well as for several sub-groups. The most important centers of gymnosperm diversity at all taxonomic levels are located in SE Asia. Especially the Chinese provinces of Yunnan and Sichuan with almost 60 species co-occurring on an area size of 10,000 km² are very species rich. Other centers with at least 30 species per 10,000 km² are S China in general, which is as well the most important region at higher taxonomic level, New Caledonia, northern Borneo with Mt. Kinabalu, the central range of New Guinea, southern Mexico, which is an important center on family level as well, and California. Large areas of the southern hemisphere harbor only few (or no) gymnosperm species. Exceptions are New Caledonia, eastern Australia, Tasmania, and New Zealand, the South African Drakensberg area, and parts of the South American Andes. The largest contiguous coniferous forests of the world, the northern hemisphere boreal forests or taigas, harbor only few species. The various subgroups (families, genera, etc.) of gymnosperms show highly diverging diversity patterns.

## PREDICTING RICHNESS OF STREAM MACROINVERTEBRATES ACROSS REGIONAL SCALES: THE INFLUENCE OF GEOGRAPHICAL EXTENT ON MODEL PERFORMANCE

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Predictive models have been increasingly used in freshwater bioassessment and conservation planning. These models are routinely applied across broad geographical areas, yet the influence of geographical extent on model performance has not been assessed. We examined the influence of changing geographical extent on the precision of predictive models for macroinvertebrates of boreal headwater streams. Macroinvertebrate data were first clustered and taxa richness was predicted from environmental variables for each site. Separate models were constructed for two hierarchical geographical extents: across five ecoregions covering whole of Finland (60ºN – 70ºN, 20ºE – 32ºE) and within two separate ecoregions. The precision of the models was assessed by examining the distributions of observed to expected taxa ratios (O/E). The importance of geographical location and some large-scale landscape characteristics varied parallel with increasing regional extent, whereas local in-stream variables showed the opposite pattern. The ecoregion-level models were more precise than the broad-scale model, but differences among the models were reduced when richness of only widespread taxa (taxa occurring ≥ 50% of sites) was predicted. However, even then the agreement of the O/E ratios among the models was low, indicating that predicted richness may depend on the underlying cluster groupings and the environmental variables used to predict the site groupings.

## RICHNESS AND ENDEMISM, A MATTER OF SCALES?

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Latitudinal richness gradient is one of the most generalized patterns in biology, however, the majority of analyses have been developed using large scales. The aim of this research is to discern scales where it makes sense talk about a latitudinal general pattern and establish the level where the richness and endemism are related. We use the database of CONABIO and data of 44 national and foreign collections, which contains 441.305 records representing 1197 species of Mexican herps. We debug records, eliminating all inconsistencies to have models as exact and precise as possible. We generate range distribution models based in the niche concept (GARP) through the finest possible resolution (1 km$^2$). Then, we edit models and develop analysis of richness and endemism for all country at different scales (1, $^1/_2$, $^1/_4$ and $^1/_8$ degrees). We found a latitudinal gradient of richness at huge scales, however at the smaller scales we did not find any pattern related with the latitude. Results of the richness-endemism relationships reveal differences between the groups at different scales. Amphibians and reptiles have different phylogenetic constraints that could provide insights in the patterns explanations of richness and endemism from the Mexican herps. Thus different histories produce dissimilar patterns at smaller scales. We suggest being cautious making generalizations mainly when studies have implications in the designing of long-term conservation strategies.

## FATHOMING NEOTROPICAL DIVERSITY: APPROACHING TRUE(R) PATTERNS OF ELEVATIONAL DIVERSITY FOR THE MAMMALS AND BIRDS OF THE MANU BIOSPHERE RESERVE, PERU

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Tropical systems on the eastern slopes of the Andes may be the most diverse ecosystems on earth. We recently completed a three-year inventory of mammals and birds along an elevational gradient from 450-3,450 m in Manu Biosphere Reserve in southeastern Peru. Our report (*Fieldiana: Zoology*, 2006) lists 222 species of mammals (12 of them new, including undescribed species of marsupials, bats and rodents) and 1005 species of birds. The reserve is the world's richest protected area for both vertebrate groups. It is remarkable, as well as humbling, that so many additions could be made to the supposedly well-known fauna during three years of standardized sampling. We consider how recent discoveries have altered several diversity patterns described previously (*J. Biogeogr.* 25:593; 1998) and present revised patterns of richness, range amplitude, range boundaries, and nestedness for these faunas. The relationships of these patterns to ecological and historical explanations are discussed.

## PERSISTENCE IN THE REAR EDGE: IS THE POPULATION RESPONSE CONSISTENT ACROSS EUROPEAN TREE SPECIES?

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Many Northern Hemisphere tree species have experienced range shifts since the last glacial maximum, a trend that have been shown to be exacerbated by recent climate change. As a result, a *rear edge* and a *leading edge* can be defined according to the prevalent direction of geographical shifts. Range reshaping in marginal populations have been analyzed almost exclusively in relation to climatic oscillations, whereas the explanatory role of biotic or anthropogenic variables has been largely neglected. We investigated the relative importance of biotic and abiotic interactions as explanations for the performance of populations located in the rear edge of the distribution of five European cool temperate (*Taxus baccata*, *Betula alba*, *Quercus robur*, *Sorbus torminalis*) or subtropical (*Prunus lusitanica*) tree species. Population sensitivity to abiotic stress in our Mediterranean, drought prone locations was hypothesized to be species-specific as a result of differential biotic attenuation of abiotic effects. Almost all study populations showed regeneration failure. Though exposure to summer drought caused moderate to high reproductive losses due to fruit abortion (rowan and yew) or seedling mortality (all species), the whole-cycle recruitment success strongly depended on early- or late-acting biotic (including anthropogenic) factors. Overall, our results indicate that the potential for abiotic stress to influence population persistence in the rear edge is species-specific and that it could be limited by the effects of biotic factors acting solely or interacting with climate.

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## SPECIES RICHNESS AND EVOLUTIONARY NICHE DYNAMICS: A SPATIAL PATTERN-ORIENTED SIMULATION EXPERIMENT

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Evolutionary processes underlying spatial patterns in species richness remain largely unexplored, and correlative studies lack the theoretical basis to explain these patterns in evolutionary terms. In this study, we developed a spatially explicit simulation model to evaluate, under a pattern-oriented modeling approach, whether evolutionary niche dynamics (niche conservatism and niche evolution processes) can provide a parsimonious explanation for patterns in species richness. We model the size, shape, and location of species' geographical ranges in a multivariate heterogeneous environmental landscape by simulating an evolutionary process in which environmental fluctuations create geographic range fragmentation that regulates speciation and extinction. We applied the model to the South American domain, adjusting parameters of species' niche center and breadth conservatism/evolution, and probability of extinction as function of geographic range size, in order to maximize the correspondence between observed and predicted patterns in richness of 3,088 bird species. Predicted spatial patterns, which closely resemble observed ones, proved sensitive to niche dynamics processes. Our simulations allow evaluation of the role of both evolutionary and ecological processes in explaining spatial patterns in species richness, revealing the enormous potential of the link between ecology and historical biogeography under integrated theoretical and methodological frameworks.

## FUZZY MODELLING OF EXOTIC VERTEBRATE SPECIES IN SPAIN

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We identified seven significant chorotypes (groups of species whose distributions overlap more than expected at random) among the thirteen exotic terrestrial vertebrate species inhabiting mainland Spain, using the 50 km x 50 km UTM grid. We modelled each species separately using a favourability function based on a GLM and 32 variables related with climatic stability, energy availability, water availability, productivity, disturbance, topography, space, and human influence. We avoided using highly correlated variables related to the same factor to diminish multi-colinearity, and controlled the false discovery rate during the variable selection procedure. We identified favourable areas for every species and considered the favourability value as the degree of membership to the fuzzy set of cells favourable for the species. We also modelled each multi-species chorotype considering presences the UTM squares where any of the species belonging to the chorotype was present. We performed the fuzzy logic operations of union and intersection of the favourability values of the species belonging to multi-species chorotypes. The result of union was roughly equivalent to modelling the chorotype whereas the result of intersection detects hotspots for each chorotype. We downscaled the models to a grid of 10 km x 10 km UTM cells and assessed the performance of the models using the data in the distribution atlases.

## RE-EVALUATING HUMMINGBIRDS' DISTRIBUTIONS: AN APPROACH WITH THE GENUS *COELIGENA* (AVES: TROCHILIDAE)

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The biogeography of tropical birds has been an important theme during last years. In all recent studies of hummingbirds about taxonomy, phylogeny, and biogeography, high resolution tools has been used with the purpose of obtaining the best resolution analysis and the correct inferences. These tools include from the quantitative analysis of plumage coloration to the DNA sequencing, all of those improve the support of the phylogenetic hypotheses. However, the biogeography and speciation scenario reconstruction based on these hypotheses, needs to be supported by high resolution areas of current distribution for the species. *Coeligena* species were probably radiated into high-Andean habitats during the orogenic formation activity, making it a good indicator of the Andean biogeographic history. In this research we used the most recent topology for the genus introducing high resolution predictive models for species distribution in the biogeographic analysis in order to compare our results with the studies that have used distribution models based on low resolution polygons. The last uplift of the northern Andes, and subsequent Pleistocene climatological changes, influenced the populations' subdivision and isolation, therefore vicariance processes were assumed to be the main factors modelling the speciation events. This work discusses the influence of species distribution maps produced using distinct methodologies over the identification of protection areas and the establishing of conservation plans.

## A TEST OF THE NICHE CONSERVATISM HYPOTHESIS ON GLOBAL SPECIES RICHNESS PATTERNS

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Climate and energy variables are consistenly good predictors of global diversity patterns, although mainly for the segment of more widespread species. While a statistical correlation has been established for decades, a convincing mechanism for why contemporary tropical climate should generate and maintain more species has sofar proven elusive. Other hypotheses have unsuccesfully tried to explain the pattern by highlighting the greater extent of the tropical biome in contemporary space or evolutionary time. A novel hypothesis, niche conservatism, combines the space and time aspects by suggesting that the global diversity gradient is created by clades that have remained predominately tropical in spite of global climate cooling. We test this hypothesis by analysing variation in tropical affinity among taxa originated in different geological ages. The vast majority of organisms have had their origin and basic radiation on a globe that was predominantly tropical, and they have strong tropical affinities. In contrast, our data clearly show that taxon groups radiated in colder ages have no particular affinity for the tropical biome. Current climatic conditions may therefore simply constrain the possible distribution of the vast majority of taxa, which on the clade level have been unable to modify their basic environmental niche during late Tertiary and Quarternary global cooling.

## DISTRIBUTION OF THE IBERO-BALEARIC BUTTERFLIES. SELECTION OF AREAS FOR THEIR CONSERVATION

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The distribution of 223 species of butterflies belonging to the superfamilies Papilionoidea and Hesperioidea has been studied in the Iberian Peninsula and Balearic islands using 10 x 10 km UTM squares. Sixteen out of 223 species are considered threatened, 33 rare and 16 are endemic to the Iberian Peninsula. Two squares in the Pyrenees had the highest number of species, with 139 species each. A square in the Pyrenees and one in Sierra Nevada had the highest number of threatened species (five), three squares host seven endemic species each in the Pyrenees and Sierra Nevada and one Pyrenean square had the highest number of rare species (11). The coincidence between the existing network of protected areas and the number of butterfly species was tested. We obtained as a result that five species were not covered by the network. Subsequently selections of areas were performed to determine the necessary number of UTM squares which would altogether include: all the species, all the threatened species and all the endemic or rare species. These selections resulted in a total of 16, eight, five and 13 squares respectively. The selected areas are especially concentrated in the Pyrenees, the Cantabrian mountains, and in the mountain systems Central, Ibérico and Penibético.

## A NEW CLINE CONCEPT : THE VARIABLE-FREE CLINE

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The classical concept of cline refers to the gradation of a measured variable, and is used to quantify aspects of systematics like geographical variation, polymorphism, and speciation dynamics. One drawback of this method is the presence of as many clines as variables defining them, hence the risk of studying the variation of the parameters of the organisms instead of studying the variation of the organism itself.

Best-known cases of clines are Bergmann's and Allen's rules, which are synthetic as they deal with the variation of organisms but put forward empirically rather than assessed with computations. In order to fit these synthetic clines with the cline notion based on measured variables, the usual practice is the choice of one representative variable among several, or a couple of variables known to share the same trend, which could depict the searched features. I propose to assess a cline by means of the eigenvectors (factor axes) calculated from multivariable statistical analyses on databases defining for each individual, variables involved in body size and appendage size. These analyses were carried out on two avian species complexes, the Chiffchaffs and the Giant Petrels. My poster shows, from large samples of birds, that the first and second factor axes are respectively correlated to variables describing body size (e.g. wing and tarsus lengths), and appendage length (e.g. tarsus and bill lengths).

## GLOBALIZATION OF HUMAN INFECTIOUS DISEASE

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Globalization has facilitated the spread of infectious diseases to all corners of the planet. Analysis of the Global Infectious Disease Epidemiology Network Database illustrates for the first time that the globalization of human infectious diseases depends significantly on the range of hosts utilized. Infectious diseases specific to humans are broadly and uniformly distributed whereas zoonotic diseases are far more localized in their distribution. Moreover, these patterns vary depending on transmission mode and disease taxonomy. This dichotomy is unlikely to persist if certain aspects of globalization and environmental change continue unabated. This raises a serious concern for public health and leaves nations with the task of determining the infectious diseases that have the greatest potential to establish within their borders. At the advent of a century characterized by an apparent increase in emerging infectious diseases, these results have critical implications for public health policy and future research pathways of infectious disease emergence.

## mtDNA PHYLOGEOGRAPHY OF THE ALPINE NEWT (*TRITURUS ALPESTRIS*, SALAMANDRIDAE, CAUDATA)

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In this study, we performed phylogenetic analyses of numerous *T. alpestris* populations all over Europe, using fragments of two mtDNA genes, cytochrome *b* (309 bp) and 16S rRNA (~500 bp). Results reveal the existence of a relict lineage (Clade A) of late Miocene origin, comprising populations from south-eastern Serbia. This lineage is proposed to be ancestor to a western and an eastern lineage, which diverged at early-middle Pliocene. The western lineage (Clade B) is further divided in two subclades of middle Pliocene origin that represent populations from Italy (B1) and populations from central Europe and Iberia (B2). Further subdivision, dated back to middle Pliocene, was found within the eastern lineage (Clades C, D), representing southern and central-northern Balkan populations respectively. The extent of divergence indicates cryptic speciation in the Balkans, while paedomorphic lineages were found to have been evolved during early Pleistocene probably as a response to the ongoing dramatic climatic oscillations. Extensive sequence divergence, implying greater isolation in multiple refugia, is found within eastern clades, while the western clades seem to have been involved in the colonization of central, western and north-eastern Europe from a refugium in the Alps.

## SELECTING POPULATION TARGETS FOR PRESERVING THE GENETIC VARIATION OF THE NARROW CANARIAN ENDEMICS *CRAMBE TAMADABENSIS* AND *C. PRITZELII* IN A SEED BANK

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We used the information in 9 enzymes of 727 individuals belonging to 4 populations of *Crambe tamadabensis* and 8 populations of *C. pritzelii* to (i) estimate the levels and apportionment of genetic variation of these endemics from the island of Gran Canaria, and (ii) design a sampling strategy to capture their genetic variation for storage in the seed bank of the JBCVC. We interpreted 12 putative allozyme loci and a total of about 60 alleles. In accordance with the emerging picture of higer levels of genetic variation in Canarian endemics than those reported in other oceanic archipelagos, the genetic variability detected is substantially high and similar in both species, despite the more restricted distribution range of *C. tamadabensis*. Interpopulation diversity for both *C. tamadabensis* and *C. pritzelii* is only moderate ($F_{ST}$ = 0.1205 and $F_{ST}$ = 0.1204, repectively). Spatial analysis of these genetic data allows us to select target populations for sampling which maximize the percentage of captured genetic variability while minimizing collection effort and seed storage space in the seed bank. The data discussed are part of the Phd. of MES.

## PHYLOGENY AND BIOGEOGRAPHY OF *CRYPTOTAENIA* AND RELATED TAXA, WITH EMPHASIS ON MACARONESIAN ENDEMICS (MAGNOLIOPHYTA, FAMILY APIACEAE)

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The northern hemispheric angiosperm genus *Cryptotaenia* exhibits an anomalous distribution pattern, with five of its eight species being narrow endemics geographically isolated from their presumed relatives, including *C. elegans* from the Canary Islands. We examined the monophyly of the genus using nuclear rDNA ITS sequence variation and ascertained the phylogenetic placements of its constituent members in order to explain their distribution patterns. Biogeographic scenarios were inferred using dispersal-vicariance analysis (DIVA). Our results indicate that *Cryptotaenia* is polyphyletic and includes three distant lineages: (1) *Cryptotaenia* sensu stricto (*C. canadensis*, *C. japonica*, *C. flahaultii*, and *C. thomasii*) is maintained within tribe Oenantheae and exhibits a Holarctic distribution pattern with its members occurring in regions that were important glacial refugia. The genus probably originated in Asia and from there dispersed to Europe and North America. (2) *Cryptotaenia elegans* is placed among members of tribe Scandiceae that have their distribution centre in the Mediterranean. *Cryptotaenia elegans* is probably related to *Monizia edulis* and *Melanoselinum decipiens* from Madeira and distantly related to *Tornabenea* from Cape Verde. The latter is nested within *Daucus carota*. (3) The African members of *Cryptotaenia* (*C. africana*, *C. calycina,* and possibly, *C. polygama*) comprise a clade with some African and Madagascan umbellifers which is sister group to Eurasian *Pimpinella*.

## GBIF DATA PORTAL – A SOURCE FOR BIOGEOGRAPHY DATA

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Since 2004, the Global Biodiversity Information Facility (GBIF, http://www.gbif.org/) has been operating a prototype data index and web portal for biodiversity data from around the world. These tools have provided basic mechanisms for users to discover relevant data on the occurrence of individual species from anywhere in the network. Currently (Oct. 2006) more than 70 million geo-referenced records are accessible through the GBIF portal. This prototype data portal has allowed GBIF to learn a great deal about the characteristics of available data and about integrating such data. During 2006, GBIF is completely redeveloping the portal infrastructure based on lessons learned, and plans to release a new data portal early in 2007. Key innovations in the new architecture will include: (1) greater flexibility in linking to data resources using new data formats; (2) dynamic evaluation of potential inconsistencies and overall characteristics of each data resource (during indexing); (3) improved management of descriptive metadata for each data resource; (4) a wide range of web service interfaces; (5) improved and more flexible search options through the HTML user interface; (6) user interface components enabled for inclusion within other web sites (accessing GBIF data through web services); and (7) open interfaces for developing visualisations and analyses of GBIF data. The new GBIF data portal will permit biogeography scientists to easily access millions of geo-referenced records documenting species distributions.

## IS SEED RESISTANCE TO SOIL PATHOGENS AN INVASIVE TRAIT IN GARLIC MUSTARD?

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Although invasive species are a leading cause of extinction, the cause of invasiveness is still debated. Invasiveness can be explained by: (1) external factors, such as the absence of natural enemies to check population growth in introduced regions, and (2) internal factors, which focus on the adaptations of species. Needed are studies on candidate traits for invasiveness, which may eventually lead to the discovery of genes that control the spread of certain species. Using quantitative genetics, we examined genetic variation in a population of *Alliaria petiolata* introduced to southeastern Wisconsin. Applying the invasive trait hypothesis, which states that invasive traits are under strong selection and therefore have low genetic variation, we tested whether seed resistance to a fungal pathogen *Alternaria* was a potential cause of invasiveness. We compared seed resistance to a non-candidate trait, seed size. There was no significant difference in genetic variation between seed resistance and size. Our results therefore do not support the invasive trait hypothesis. A more rigorous test of the hypothesis will come from studies that test more traits and that are able to compare introduced and native populations.

## TAXONOMIC DECOMPOSITION OF LATITUDINAL DIVERSITY GRADIENTS IN NEW WORLD VASCULAR PLANTS

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The latitudinal gradient in species richness is a pervasive pattern that has prompted historical, evolutionary, macroecological, and random explanations. Here we quantitatively and qualitatively describe the latitudinal gradient of New World vascular plant species richness. As this single gradient is the aggregate of numerous independently evolving plant clades, we describe the latitudinal gradient in species richness for each of the terrestrial vascular plant families (~monophyletic clades). Using a simple metric (sum of squared deviations) on standardized data, we compare the richness gradient of each family against the overall richness gradient.

## CANOPY DYNAMICS AND INVASION OF A SHADE-TOLERANT SPECIES

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Species that compete in a closed canopy rely on shade tolerance and timing for space. In southeastern Wisconsin, quadrat and transect designs were used to determine patterns of two plant communities threatened by shade tolerant invasive non-native species. In a fire-adapted oak savanna, sites managed with frequent fire had lower canopy cover (51%) than unmanaged sites (97%). *Quercus macrocarpa* dominated the canopy in managed sites, but was suppressed in unmanaged sites (88% vs 16%). In the understory, species such as *Echinecea purpurea* and *Solidago canadensis* were abundant in managed sites, but shade associated species such as *Thalictrum dasycarpum* and *Geranium maculatum* dominated the unmanaged site. More recently, shade-tolerant *Alliaria petiolata* invaded the unmanaged site and can contribute to oak suppression. In a mesic closed canopy site, *A. petiolata* has invaded the area for two decades. Certain tree species and understory composition were influenced by invasion. Seedlings and saplings of *Fagus grandifolia* were suppressed while *Acer saccharum* regeneration increased near *A. petiolata*, and the earliest herbaceous species, such as *Isopyrum biternatum* and *Smilacina racemosa* were limited. Future research will determine if invasion alters community development after control efforts are conducted.

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