SCHOOL OF GEOGRAPHY AND THE ENVIRONMENT

UNIVERSITY OF OXFORD

Advances in Biogeography: Early Career Conference

23- 25th September, 2011

Conference Programme and Abstract Booklet

Biodiversity Institute of Oxford

IBS Advisory Panel

Laurence Heaney – President
Michael Dawson – V.P. for Public Affairs
Catherine Graham – Director-at-large
Kenneth Feeley – Upcoming meeting host
Kathy Willis – Director-at-large
Robert J Whittaker – Past President
Ana Margarida C Santos – Student-at-large

Organising Committee

Karen Faller
Sandra Nogué
Leticia M Ochoa-Ochoa
Michele Sanders
Ana Margarida C Santos

IBS gratefully acknowledges support from

School of Geography and Environment of Oxford

Biodiversity Institute of Oxford

Biogeography Research Group of the Royal Geographical Society (with The Institute of British Geographers)

CONFERENCE PROGRAM OVERVIEW

Friday 23 September 2011

	Lecture Theatre "Halford Mackinder"
13:00	Registration opens
14:00	Workshop
17:00	Opening Ceremony & Keynote Addresses I, II
18:15	Welcoming Reception - AJ Hertberson Room

Saturday 24 September 2011

	Lecture Theatre "Halford Mackinder"	"HO Beckit Room"
09:00		
09:15	**Session 1**	
09:30		
09:45	**Macroecology: large-scale patterns**	
10:00		
10:15		
10:30	**POSTER SESSION** & COFFEE/TEA - "AJ Hertberson Room"	
11:00		
11:15	**Session 2**	**Session 3**
11:30		
11:45	**Macroecology: models and processes**	**Palaebiogeography**
12:00		
12:15		
12:30	LUNCH - "AJ Hertberson Room"	
13:30		
13:45	**Session 4**	**Session 5**
14:00		
14:15	**Macroecology: regional patterns**	**Island Biogeography**
14:30		
14:45		
15:00	**POSTER SESSION** & COFFEE/TEA - "AJ Hertberson Room"	
15:15		
15:30	**Session 6**	**Session 7**
15:45		
16:00	**Phylogeography**	**Evolutionary Biogeography**
16:15		
16:30		
16:45		
17:00	Keynote Addresses III, IV	
18:00	**POSTER SESSION** - "AJ Hertberson Room"	

Sunday 25 September 2011

	Lecture Theatre "Halford Mackinder"	"HO Beckit Room"
09:00		
09:15	**Session 9**	**Session 8**
09:30		
09:45	**Conservation Biogeography I:**	**Topics in Biogeography**
10:00	**from DNA to species**	
10:15		
10:30	**POSTER SESSION** & COFFEE/TEA - "AJ Hertberson Room"	
11:00		
11:15	**Session 10**	
11:30	**Conservation Biogeography II:**	
11:45	**a changing World**	
12:00		
12:15		

12:30	Discussion
13:00	**CLOSE OF MEETING**

Friday September 23th 2011, Lecture Theatre "Halford Mackinder"

13:00	REGISTRATION OPENS **"AJ Hertberson Room"**	
14:00	**Robert Whittaker**	**Research ethics, practice and dissemination in biogeography. A workshop focused on preparation, writing and peer review.**
17:00	Opening ceremony	
17:15	**Kenneth Feeley**	**Advances in predicting the impacts of climate change on the distributions and diversity of tropical species**
17:45	**Catherine Graham**	**Untangling the mechanisms influencing hummingbird assemblages: new tools to answer old questions**
18:15	DRINKS RECEPTION **"AJ Hertberson Room"**	

Saturday September 24th 2011, Lecture Theatre "Halford Mackinder"

	SESSION 1: Macroecology: large-scale patterns ***Chair: Leticia Ochoa-Ochoa***	
09:00	*Belmaker J & Jetz W*	Global scaling of functional turnover in birds and mammals
09:15	*Dobrovolski R et al.*	Climatic history and dispersal ability explain the relative importance of turnover and nestedness components of beta diversity
09:30	*Múrria C et al.*	How is genetic diversity structured geographically? Testing the influence of disturbance regimes and dispersion of aquatic insects at local and regional scales
09:45	*Wüest RO et al.*	Available niches canalize climatic diversification in the grass subfamily Danthonioideae
10:00	*O'Brien JD*	The worldwide migration patterns of *Plasmodium falciparum* through its organelles
10:15	*Picazo F et al.*	Local and regional diversity patterns in lentic and lotic freshwater habitats across the Western Palaeartic
10:30	POSTER SESSION (TEA/COFFEE) **"AJ Hertberson Room"**	
	SESSION 2: Macroecology: models and processes ***Chair: Marc Macias-Fauria***	
11:00	*Early R & Sax DF*	Independent data reveal that bioclimate niche models consistently underestimate species climatic tolerances
11:15	*Sarmento Cabral J & Kreft H*	Emerging community properties and single-species range dynamics: lessons from a mechanistic model integrating demographic processes with biotic interactions and speciation under metabolic constraints
11:30	*Vaclavik T & Meentemeyer RK*	Equilibrium or not? Modelling potential distribution of invasive species in different stages of invasion
11:45	*Laube I et al.*	Niche availability in space and time: migration in *Sylvia* warblers
12:00	*Merow C & Silander Jr. JA*	Building better models with Maxent: new techniques and simpler models motivated by ecological hypotheses
12:15	*Pliscoff P*	Predicting the past, present and future of plant biodiversity in Chile: A species distribution modeling approach
12.:30	LUNCH **"AJ Hertberson Room"**	
	SESSION 4: Macroecology: regional patterns ***Chair: Cristina Ender***	
13:30	*Decu V et al.*	Endemic fauna in Serbia with distribution of some cave-living taxa
13:45	*Sánchez-Fernández D et al.*	Habitat type mediates equilibrium with climatic conditions in the distribution of Iberian diving beetles
14:00	*Ochoa-Ochoa LM*	Short-term changes in the amphibian meta-community structure in

		two Mexican fragmented landscapes
14:15	*Chefaoui et al.*	Species distribution models of threatened Iberian invertebrates
14:30	*Pearse WD*	Community structure in Barro Colorado island has two spatial and one phylogenetic scale
14:45	*Monroy F et al.*	Regional patterns of *Collembola* diversity as a result of functional adaptation to local environmental conditions
15:00	POSTER SESSION (TEA/COFFEE) **"AJ Hertberson Room"**	
	SESSION 6: Phylogeography ***Chair: Sarah Jones***	
15:30	*Boston ESM et al.*	New perspectives on postglacial colonisation in Western Europe: the phylogeography of the Leisler's bat (*Nyctalus leisleri*)
15:45	*Moreno-Letelier A et al.*	The effects of Pleistocene glaciations on three montane pine species: hibridisation, shared polymorphism and niche evolution
16:00	*Álvarez-Presas M et al.*	Molecular phylogeography of land flatworms from the Brazilian Atlantic Forest biodiversity hotspot
16:15	*Dexter K & Chave J*	Phylogeography of Amazonian trees with implications for Amazonian biogeography
16:30	*Cooke EL et al.*	Phylogeography of the emerging model plant *Cardamine hirsuta* L.
16:45	*Hughes AC et al.*	Cryptic clues to a complex problem
17:00	**Michael Dawson**	**Advances in Marine Biogeography**
17:30	**Lawrence Heaney**	**Oceanic island biogeography: emerging perspectives and questions**
18:00	POSTER SESSION (DRINKS) **"AJ Hertberson Room"**	

Saturday September 24th, "HO Beckit Room"

	SESSION 3: Palaebioogeography ***Chair: Sandra Nogué***	
11:00	*Morris JL*	Linking historical observations with paleoenvironmental reconstructions using lake sediments
11:15	*Nogué S et al.*	Vegetation dynamics through time: an inter-island comparison on the Canary Islands
11:30	*Dool SE et al.*	The importance of the Balkan refuge for the post-glacial recolonization of Europe by *Rhinolophus hipposideros*
11:45	*García-Amorena I et al.*	Palaeobotanical based species distribution models in ecosystem management: lessons from rear edge pine populations in Spain
12:00	*Nodoka N, William H*	The Japanese hotspot redefined by bioquality approach
12.:30	LUNCH **"AJ Hertberson Room"**	
	SESSION 5: Island biogeography ***Chair: Philipp H. Boersch-Supan***	
13:30	*Santos AMC*	Diversity and structure of island parasitoid communities worldwide
13:45	*Jones K et al.*	What explains the Azores diversity enigma?
14:00	*Särkinen T et al.*	Evolutionary islands in the Andes: persistence, isolation and endemism in Andean dry tropical forests
14:15	*Karger DN et al.*	Patterns of fern diversity in the southeast Asian archipelago
14:30	*Papadopoulou A et al.*	Lineage diversification and community differentiation in a continental archipelago: the case of the Aegean darkling beetles
15:00	POSTER SESSION (TEA/COFFEE) **"AJ Hertberson Room"**	
	SESSION 7: Evolutionary Biogeography ***Chair: Nicolai Roterman***	
15:30	*Pigot AL et al.*	Speciation, extinction and the illusion of range size trajectories in phylogenies and the fossil record
15:45	*Beatty CD & Ware JL*	Biogeography, population genetics and life history of a "living fossil" dragonfly (Insecta: Odonata)
16:00	*Gamisch A et al.*	The evolution of auto-pollination in tropical orchids: morphological, experimental, and phylogenetic studies in *Bulbophyllum thouars* from Madagascar.
16:15	*Mcinnes L et al.*	Untangling the drivers of monocot diversity: can we determine the relative roles of phylogeny, geography and history?
16:30	*Gratton P & Gandolfi A*	Composing the evolutionary puzzle of the last remains of trout (*Salmo trutta* complex) diversity in Italy
16:45	*Kirschel AN et al.*	The extent of trait similarity at contact zones influences range overlap and the trajectory of multidimensional character displacement in African tinkerbirds (*Pogoniulus* spp.)

Sunday September 25th 2011, "HO Beckit Room"

	SESSION 8: Topics in Biogeography ***Chair: Sandra Nogué***	
09:15	*Matzke NJ*	Moving from historical biogeographic inference in discrete space to historical biogeographic inference in continuous space, by moving from species distribution modeling to phylogenetic lineage distribution modeling
09:30	*Dalsgaard B et al.*	Specialization in plant-hummingbird networks is associated with quaternary climate-change velocity
09:45	*Todisco V et al.*	New refugial model for alpine invertebrates: a case study of the *Parnassius phoebus* complex
10:00	*Noriega JA*	Biogeographic provinces and endemicity areas analysis of the dung beetles (Coleoptera: Scarabaeidae) in Colombia
10:15	*Vila-Farré M et al.*	The biogeography of the genus *Crenobia* in Europe
10:30	POSTER SESSION (TEA/COFFEE) **"AJ Hertberson Room"**	

Lecture Theatre "Halford Mackinder"

	SESSION 9: Conservation Biogeography II: from DNA to species ***Chair: Kathleen Buckingham***	
09:15	*Cunningham SW*	Patterns of molecular genetic variation among *Crocodylus suchus* populations throughout West and Central Africa
09:30	*Cottee-Jones HED*	Birds of the Banyan: *Ficus* use by birds in a tropical countryside landscape, Assam
09:45	*Capinha C et al.*	Disentangling the relative influence of human, biological and environmental factors in shaping the invasion of the Signal and the Red swamp crayfish in Europe
10:00	*Borges LMS et al.*	Biogeography of Wood Borers in European coastal waters: a tale of two distinct taxa Sharing the same niche
10:15	*Shipway R et al.*	An invasive species of teredinid, *Teredothyra dominicensis* (Teredinidae, Bivalvia), in the Mediterranean Sea
10:30	POSTER SESSION (TEA/COFFEE) **"AJ Hertberson Room"**	
	SESSION 10: Conservation Biogeography I: a changing World ***Chair: Ashley Massey***	
11:00	*González J-C et al.*	Defying Wallace: Phylogeography and conservation of insular Asian hornbills
11:15	*Abrahamczyk, S et al.*	Impact of climatic seasonality on the diversity of hummingbird assemblages and their food plants: what can we deduce for climate change?
11:30	*Lander TA et al.*	The effect of landscape heterogeneity and anthropogenic land-uses on pollination patterns for wild cherry trees in northern France
11:45	*Rosauer DF & Jetz W*	Geography, predictors and conservation consequences of global centres of mammal phylogenetic endemism
12:00	*Hula MA*	Modelling farming practice as a driver of vegetation change in Benue State, Nigeria
12:15	*Rodríguez-Sánchez , F.*	Investigating biodiversity responses to climate change: the benefits of hindsight
12:30	**Discussion**	
13:00	**WRAP UP AND CLOSE**	

TALKS SESSIONS AND ABSTRACTS

Saturday September 24th 2011, Lecture Theatre "Halford Mackinder"

SESSION 1: Macroecology: large-scale patterns

09:00 Jonathan Belmaker & W Jetz. **Global scaling of functional turnover in birds and mammals**

Department of Ecology and Evolutionary Biology, Yale University, USA
Email: jonathan.belmaker@yale.edu

Traits-based community assembly is receiving increasing attention as an important way to understand processes driving diversity across scales. Here, we quantify multivariate trait ('functional') turnover of birds and mammals between spatially nested assemblages (varying from 3,140,000 to ~400k^2 in size). We separated total functional turnover to the turnover originating from reducing the entire species pool to the ecological species pool, the subset of species with traits that allow existence within the local habitat, and to the turnover originating from reducing the ecological pool to the actual local assemblages. Between the regional pool and the ecological pool assemblages functionality changes across scales much more rapidly than expected from null models and trait combinations at fine scales are clustered relative to larger scales. However, the reverse is true between the ecological pool and local assemblages where functional turnover is lower than expected. We conclude that across a wide range of scales functional diversity is jointly determined by processes causing low functional turnover, such as ecological assembly rules, and processes causing high functional turnover, such as environmental filters.

09:15 Ricardo Dobrovolski, AS Melo, FAS Cassemiro & JAF Diniz-Filho. **Climatic history and dispersal ability explain the relative importance of turnover and nestedness components of beta diversity**

Programa de Pós-Graduação em Ecologia e Evolução, ICB, Universidade Federal de Goiás, Brazil
Email: rdobrovolski@gmail.com

We tested whether the geographic variation in the proportion of beta diversity attributed to nestedness or turnover components was explained by the effect of past glaciation events. Additionally, we tested if the variation was influenced by thermal tolerance and the dispersal ability of species. We used presence/absence data for amphibians, birds and mammals of the New World. We calculated beta diversity among each 1° x 1° cell and the adjacent cells using the Sorensen dissimilarity index that expresses the total beta diversity. Furthermore, we partitioned it into turnover and nestedness components. The relative importance of the two latter components was expressed as the proportion of total beta diversity explained by nestedness (βratio). We calculated the correlation between βratio and the time each cell was free of ice since last glaciation (cell age). To control the overestimation of degrees of freedom due to spatial autocorrelation, we applied the correction method suggested by Clifford *et al.* (1989). The proportion of beta diversity attributed to nestedness was negatively correlated with cell age. Moreover, this effect was stronger for amphibians than mammals, and stronger for mammals than birds. Our results are in accordance with the hypothesis that the nestedness component of beta diversity is more important in areas affected by glaciations until recent time (lower ice age). The beta diversity in high latitudes is the result of past extinctions and recent recolonization, which result in higher levels of nestedness. This process is more evident for vertebrates with lower dispersal ability and lower temperature tolerance.

09:30 Cesc Múrria[1,2*], N Bonada[1], C Zamora-Muñoz[3], CE Sáinz-Cantero[3], J Garrido[4], R Acosta[1], J Alba-Tercedor[3], AP. Vogler[2, 5]. **How is genetic diversity structured geographically? Testing the influence of disturbance regimes and dispersion of aquatic insects at local and regional scales**

[1]Department of Ecology, University of Barcelona, Catalonia; [2]Department of Entomology, Natural History Museum, UK; [3]Department of Animal Biology, University of Granada, Spain; [4]Department of Ecology and Animal Biology, University of Vigo, Spain; [5]Division of Biology, Imperial College London, UK
Email: cmurria@ub.edu

Abstract: Species exist in a dynamic matrix of habitat patches that differ in connectivity and stability. The structure of the diversity is a function of movement of organisms among these patches, while habitat instability affects extinction risk. We used a "community genetic" approach to elucidate the effect of variable disturbance regimes (habitat stability) and dispersal capacities (different taxa) on patterns of genetic and species diversity at local and regional spatial scales. The hierarchical spatial design of the study included 10 permanent headwater aquatic insect communities in 6 regions of 200x200 km (local scale) along a latitudinal gradient from Morocco to Sweden (regional scale). For each community we sequenced the mitochondrial cox1 gene of ≥10 individuals of all species in co-existing

lineages of Trichoptera (*Hydropsyche*), Ephemeroptera (*Baetis*) and Coleoptera (*Elmis*, *Hydraena*) to measure haplotype diversity and turnover related to geographical distance. Different slopes of distance-decay of similarity were detected among regions and taxa suggesting the influence of local disturbance (instream floods) and dispersal abilities. α- and β-diversity were low in northern latitudes, presumably related to large-scale habitat disturbance during Pleistocene glaciations. Patterns of genetic diversity for low-dispersion taxa at local scales resembled patterns of species distribution in high-dispersion taxa at regional scales, i.e. the scale of assemblage similarity depends on the dispersal propensity of lineages (and the stability of the respective habitat). We also show a correlation between genetic and species diversity that further indicates a uniform evolutionary process generating predictable patterns of diversity at multiple spatiotemporal scales.

09:45 Rafael O Wüest, A Antonelli, NE Zimmermann & HP Linder. **Available niches canalize climatic diversification in the grass subfamily Danthonioideae**

Swiss Federal Research Institute WSL, Switzerland.
Email: rafael.wueest@wsl.ch

Abstract: We explore the patterns and processes that influence niche evolution in the Danthonioid grasses, a clade of 281 species occurring in temperate habitats that originated in Southern Africa during the Oligocene and since then colonized every continent on earth. We assess how the differences in the available climatic niche on each of the continents affect the evolution of Danthonioid climatic niches. We show that the evolution of climatic niche parameters is phylogenetically constrained. Although the grass clade occupies temperate habitats on all continents, there are significant niche differences between the continents. Our results indicate that these differences are the result of adaptation to available niches, as the reconstructed selective regimes correlate with the available climatic niches on these continents. We suggest three processes that influenced the evolution of climatic niches in Danthonioideae. The first is niche truncation, where the potential range of the lineage cannot be expressed due to the current absence of suitable climates. The second is evolutionary canalization, where niche evolution is shifted towards the available niche space. And the third is accelerated niche evolution associated with the colonization of new continents.

10:00 John D O'Brien. **The worldwide migration patterns of *Plasmodium falciparum* through its organelles**

Centre for Genomics and Global Health, Wellcome Trust Centre for Human Genetics, University of Oxford
Email: jobrien@well.ox.ac.uk

The blood-borne parasite Plasmodium falciparum is the causative agent of most severe malaria in the world, inflicting an enormous public health burden. Together with a consortium of clinical institutions, we have collected and genotyped hundreds of field isolates of the parasite. Like many parasites, P. falciparum has both a mitochondria and an organelle descended from an algal chloroplast. Since this genetic information exhibits little or no recombination and a slow mutation rate, it provides a perfect set of data for using Bayesian phylogeographic inference. We consider several of the issues specific to this data, such as mixtures of infection. We show how our results compare against 'Out-of-Africa' hypotheses for malaria origins and how they might be used for public health surveillance.

10:15 Félix Picazo, D Sánchez-Fernández, A Millán & I Ribera. **Local and regional diversity patterns in lentic and lotic freshwater habitats across the Western Palaeartic**

University of Murcia, Spain.
Email: fpicazo@um.es

It is well known the drastic climatic changes occurred during the Pleistocene have profoundly shaped diversity gradients in the Western Palaearctic (i.e. the existence of southern ice-age refuges and the subsequent recolonisation process). Habitat stability and species dispersal ability have been recently highlighted as key factors when determining patterns of species distributions in freshwater ecosystems, i.e. there should be a negative relationship between the habitat persistence and the propensity for dispersal of its inhabitants. Since lentic habitats have been generally considered to be more ephemeral than lotic ones, we can expect species living in lentic habitats have conserved a higher dispersal capacity than species living in lotic habitats.Thus, we hypothesize this fact could have caused important differences in the current geographic ranges between lotic and lentic species. Water beetle check-lists from 11 regions in the Western Palaearctic (from South Morocco to North Sweden) were compiled, 647 species belonging to 14 families being classified into lotic and lentic specialist, generalist species not being took into account. We analyse the variation of water beetle species richness across latitude at different scales. In particular, to test our central hypothesis, as a main novelty supplied by this work, we compare the contribution of local to regional diversity across latitude in 181 sampling sites spread on the 11 regions referred above, looking for differences between lotic and lentic habitats. We also assess beta-diversity (in terms of species turnover or nestedness) between species adapted to lotic and lentic habitats.

Saturday September 24th 2011, Lecture Theatre "Halford Mackinder"

SESSION 2: Macroecology: models and processes

11:00 Regan Early & DF Sax. **Independent data reveal that bioclimate niche models consistently underestimate species climatic tolerances**

Universidade de Évora, Portugal. Email: regan.early@gmail.com

Bioclimate models of species niches are one of our most relied-upon tools for predicting the ecological impacts of climate change. However, a major uncertainty is whether species' climatic tolerances can be reliably evaluated by observing the climatic conditions species occupy. A comprehensive evaluation of this uncertainty requires independent distribution data, which are rarely obtainable. To address this shortcoming we test the bioclimate approach for 280 plant species in their native range (Europe) against the species' distributions in their exotic range (the USA). The majority of species are capable of living in hotter, cooler, wetter and / or drier conditions than are observed in any part of their native range. Interestingly, many species appear to have been capable of tolerating these apparently novel climatic conditions as soon as they were introduced into the USA. Thus, species climatic tolerances may be consistently broader than currently measured by bioclimate models. Our results imply that required range shifts under climate change may be less severe than previously thought, but suggests an even greater degree of uncertainty in predictions.

11:15 Juliano Sarmento Cabral & H Kreft. **Emerging community properties and single-species range dynamics: lessons from a mechanistic model integrating demographic processes with biotic interactions and speciation under metabolic constraints**

Free Floater Research Group Biodiversity, Macroecology & Conservation Biogeography, Georg-August University of Göttingen, Göttingen, Germany. Email: jsarmen@uni-goettingen.de

We present a multi-species stochastic model that simulates demography, biotic interactions and speciation in a metabolic framework. With this model we tested the following hypotheses: 1) Integrating demography and interspecific competition enables coexistence of different life-history strategies within spatially-structured communities, with realistic single-species' range and abundance distributions. 2) Evolving species avoid competition with ancestors. 3) Ecosystem engineers influence species richness as well as range and abundance distributions. We implemented stage-structured populations of species with different traits and habitat requirements that competed for space in a hypothetical gridded mountain. Scenario with temperature feedback of ecosystem engineers were performed to test the third hypothesis. The hypotheses were confirmed by several analyses. Surviving communities consisted of species spread heterogeneously within the parameter space. Species richness decreased towards higher altitudes. Altitudinal ranges increased with altitude, confirming the altitudinal Rapoport's rule. Several species had their abundances shifted towards suboptimum conditions and/or were not able to fill their potential range. Reasons for this included species traits not related to climate and species richness (i.e. competition pressure). Endemics were ecologically similar but spatially distant to their ancestors, supporting Darwin's hypothesis that competition pressure is greater between close relatives. Scenarios with ecosystem engineers showed higher total richness and altitudinal species turnover, abundance shifts mostly towards lowlands and smaller realized ranges. Results suggest potential bias of correlative habitat models and of single-species mechanistic approaches if interspecific competition is neglected. Our approach combines Grillenian and Eltonian niche concepts and enables simultaneous investigations about range dynamics and emerging community properties.

11:30 Tomas Vaclavik & RK Meentemeyer. **Equilibrium or not? Modelling potential distribution of invasive species in different stages of invasion**

Center for Applied GIScience, University of North Carolina at Charlotte, USA
Email: tvaclavi@uncc.edu

The assumption of equilibrium between organisms and their environment is a standard working postulate in species distribution models (SDMs). However, this assumption is typically violated in models of biological invasions where range expansions are highly constrained by dispersal and colonization processes. Here we examined how stage of invasion affects the extent to which occurrence data represent the ecological niche of organisms and in turn influence spatial prediction of species' potential distributions. We compiled occurrence data from 697 field plots collected over a nine-year period (2001–2009) of monitoring the spread of the invasive forest pathogen *Phytophthora ramorum* in Oregon, USA. Using these data we applied ecological niche factor analysis to calibrate models of potential distribution across different years of colonization. We accounted for natural variation and uncertainties in model evaluation by comparing findings for *P. ramorum* with three scenarios of varying equilibrium in a simulated virtual species, for which the "true" potential distribution was known. We confirm our hypothesis that SDMs calibrated in early stages of invasion are less accurate than models calibrated under scenarios closer to

equilibrium. SDMs that are developed in early stages of invasion tend to underpredict the potential range compared to models that are built in later stages of invasion. A full environmental niche of invasive species thus cannot be effectively captured with data from the realized distribution that is restricted by processes preventing full occupancy of suitable habitats. If SDMs are to be used effectively in conservation and management, stage of invasion needs to be considered to avoid underestimation of habitats at risk of future invasion spread.

11:45 Irina Laube, CH Graham & K Boehning-Gaese. **Niche availability in space and time: migration in Sylvia warblers**

Biodiversity and Climate Research Centre (BiK-F) and Johann Wolfgang Goethe University, Frankfurt, Germany
Email: irina.laube@senckenberg.de

The rise of species distribution modelling in ecology has sparked a renewed focus on the niche concept. Frequently, the niches quantified from species distribution models and the environments used to calibrate the models have been regarded as static entities. However, the environmental conditions available to a particular species are spatially and temporally dynamic on a variety of scales (e.g. circadian, weather, seasons, climate change). We develop a conceptual framework to understand how species may respond to dynamic niche availability. Organisms have two basic options for coping with variation in environmental conditions: they can track suitable conditions spatially or they can stay in one place and tolerate the change in occupied niche, i.e. their fundamental niche has to encompass the environmental variation. Assuming that both spatial tracking and the ability to tolerate a wide variety of environmental conditions are costly for species, we can derive a number of predictions regarding the relationship of niche characteristics and spatial movement behaviour from the framework. One fascinating example of the strategies organisms evolve to deal with spatially and temporally dynamic environments is migration. We evaluate migratory behaviour in the bird genus *Sylvia* with the goal of testing the predictions derived from our general framework. We explore how variation in spatial movement of *Sylvia* warblers relates to overlap and breadth of their breeding, wintering niches and availability of suitable environmental conditions across continents and seasons.

12:00 Cory Merow & JA Silander Jr. **Building better models with Maxent: new techniques and simpler models motivated by ecological hypotheses**

University of Connecticut, USA. Email: cory.merow@gmail.com

Ecological Niche Models (ENMs) have seen a recent explosion in popularity in an attempt to forecast species' distribution in changing environments. The advent of a highly successful presence-only modeling strategy, Maxent, has extended the application of ENMs to a plethora of data sets that are not amenable to statistical presence/absence modeling. While Maxent has fared favorably when compared to other ENM techniques, little guidance exists for building and evaluating models in this novel framework. The vast majority of existing studies use Maxent's default settings, and there has been relatively limited evaluation of different ways of constructing models and how these alternatives relate to specific ecological questions. For example, variable selection methods explored to date derive almost exclusively from machine learning perspectives, which focus more on complex pattern recognition than on producing easily interpreted models. While existing approaches to variable selection can be valuable for exploratory analyses, especially with large data sets, this is not a panacea for all niche modeling problems. I outline a more general approach, based on constructing simpler models motivated by specific ecological questions, and provide guidelines for their use. To explore Maxent's assumptions, I demonstrate the variability in model output that can result from altering model settings and offer suggestions for choosing these settings. I present new techniques for variable selection using appropriate randomization techniques. Finally, I show how to incorporate prior information into Maxent models, and demonstrate this with (1) a model accounting for dispersal limitation and (2) predicting invasive ranges using native range data.

12:15 Patricio Pliscoff. **Predicting the past, present and future of plant biodiversity in Chile: A species distribution modeling approach**

Spatial Ecology Lab, Department of Ecology and Evolution, University of Lausanne, Switzerland
Email: Patricio.Pliscoff@unil.ch

Abstract: The question of what controls the distribution of species has been the main focus on which the field of Biogeography was founded. Four main processes have been hypothesized to control the distribution of organisms; Climate, Habitat, Species interactions and Dispersal. Climates make this control at broader spatial scales and had been used historically by ecologist and biogeographers to explain distribution patterns of plants and animals. Based on Hutchinson niche Theory and novel statistical methods, Species Distribution Modeling (SDMs) techniques allow the definition of climatic "envelope" which represent their more suitable areas for a species to survive and grow. SDMs have become one of the most important tools of Conservation Biogeography and Climate Change Biology. Chile has been historically identified as a natural laboratory to address biogeography questions. Four of the five macroclimates existing in the world, can be found in Continental Chile. This vegetation diversity plus presence of high rates of endemism in different groups (vascular plants, amphibians, reptiles), associated with historical isolation of Chilean biota explain the interest to understand their key biogeographical process. These backgrounds make Chile an interesting area for SDMs analysis which currently is limited to only few animals' species or broader scale studies.

The general goal of this study is to generate a framework for SDMs in Chile and applying to understand the processes underlying past, present and future distribution patterns of Chilean biota to address evolutionary and conservation biogeography questions.

Saturday September 24th 2011, HO Beckit Room

SESSION 3: Palaebioogeography

11:00 Jesse L Morris. **Linking historical observations with paleoenvironmental reconstructions using lake sediments**

University of Helsinki, Finland
Email: jesse.morris@helsinki.fi

Abstract: Preserved pollen and macroscopic charcoal from lake sediments provides useful information about the influence of long-term climate variability on ecological structure and disturbance regimes. Wildfire and bark beetles (*Dendroctonus* spp.) are the most important disturbance agents in conifer-dominated landscapes occurring in western North America. An analysis of lake sediments corresponding to the historical period reveals that spruce beetle (*D. rufipennis*) outbreaks have pronounced impacts on pollen accumulation rates. Similarly, known fire events observed during the historic period aid in establishing quantitative thresholds for determining fire episodes in charcoal reconstructions. Findings from the historic era were then applied to Holocene-length lake sediment records. The resulting research provides new insights into the environmental history and climate-driven disturbance regime variability in subalpine forests in south-central Utah, USA. As these ecosystems evolved from the relatively cool temperatures of the late Pleistocene to the comparatively warmer mid-Holocene, the forest structure transitioned from spruce parkland to closed-canopy spruce/fir forest. Coincident with greater stand density and fuel/host continuity, wildfire and spruce beetle disturbance events became more frequent. Our records suggest that epidemic spruce beetle events recur at multicentennial intervals and that the mean fire return interval for significant fire episodes is similarly long, ranging between 300-500 years.

11:15 Darren Jeffers & KJ Willis. **Glacial to glacial palaeoclimate and vegetation dynamics of the southern Bekaa Valley, Lebanon**

Long-term Ecology Laboratory, Biodiversity Institute, University of Oxford, UK
Email: darren.jeffers@stcatz.ox.ac.uk

Many predictions for future climate change indicate that the Mediterranean region will experience a combination of higher temperatures and a reduction in rainfall. There is still little detailed information, however, on how biotic communities in the eastern Mediterranean-Levant region will respond to these predicted changes. An ideal timeframe in order to reconstruct the biotic changes during warmer and drier conditions than exist today is the last interglacial (LI). This study presents the results of new sedimentary sequences from the Southern Bekka Valley, Lebanon which spans the last interglacial (≈130-110 ka). High temporal resolution analyses for pollen, isotopes of carbon, total organic carbon and sediment lithology has been undertaken and reveals dramatic shifts in the vegetation composition during the LI. At the onset of the LI an environmental threshold was crossed with the development of steppe dominated by Chenopodiaceae and *Artemisia* probably indicative of a significant reduction in moisture availability. The arid conditions lead to the loss of the deciduous arboreal species (*Betula*, *Alnus* and *Corylus*) and significant reduction in the populations of *Cedrus libani* and *Pinus*. The aridity of the LI in Lebanon suggests that the eastern Mediterranean mountainous regions ecosystems are likely to be especially affected by climate change.

11:30 Sandra Nogué[1], L de Nascimento[2], JM Fernández-Palacio[2], R Whittaker[3] & KJ Willis[1]. **Vegetation dynamics through time: an inter-island comparison on the Canary Islands**

[1]Long-Term Ecology Laboratory, Biodiversity Institute, Department of Zoology, University of Oxford, UK, [2] Island Ecology and Biogeography Research Group, University of La Laguna, Canary Islands, Spain.[3] School of Geography and the Environment, University of Oxford, Oxford, United Kingdom
Email: sandra.noguebosch@zoo.ox.ac.uk

It is increasingly recognized from long-term environmental records that prehistoric and historic human impact has played an important role in shaping many of our present biodiverse landscapes. The Canarian archipelago (Spain) with over 30% endemic plant species is one of the world's biodiversity hotspots. Here, we reconstructed pre-human contact baseline ecological conditions and climate sensitivity of the forest on Tenerife and La Gomera. We will pay special attention on comparing the two islands in order to improve our understanding and to obtain a comprehensive description of the vegetation changes in the last 5000 years. Some key questions that need to be addressed are: what role did fire play in the Canarian landscape prior to human colonization? Were the human impacts synchronous and equivalent on both islands? Finally, although these islands have been considered well-buffered from past climate change, by dint of their location in the Atlantic and their elevational range, concern has been raised as to the viability of the forest formations in the event of substantial future climate change, so how sensitive are these ecosystems to climate change? This study provides the first inter-island picture of vegetation

dynamics through time of this important biodiverse region of Europe.

11:45 Serena E. Dool, SJ Puechmaille, C Dietz, J Juste, P Hulva, S Roué, E Petit, G Jones, SJ Rossiter & EC Teeling. **The importance of the Balkan refuge for the post-glacial recolonization of Europe by *Rhinolophus hipposideros***

University College Dublin, Ireland
Email: serena.dool@gmail.com

Climate cooling during the Tertiary peaked during the Quaternary ice-ages; a time during which much of Northern Europe was covered in ice-sheets or deep in permafrost. The three Mediterranean Peninsulas have emerged from multiple phylogeographic studies as the main but not exclusive areas used as refugia by European biota during the last glacial maximum. The demographic history of the lesser horseshoe bat (*Rhinolophus hipposideros*) in Europe following the most recent glaciation was investigated using a multiple marker dataset. Combining the results of a nuclear intron, mtDNA and microsatellite loci we have shown that an ancient colonization event took place into Europe from the East of the species range and that during the last glacial maximum this species diverged into at least three refugia located in Spain/Morocco, the Balkans and a location east of Turkey. The Balkan refuge was found to have seeded the recolonization of Europe excluding the Iberian Peninsula and possibly Italy. There is loss of genetic diversity following the path of colonization from high diversity in the Balkans to the lowest genetic diversity in Britain and Ireland. Secondary contact between the three clades has occurred but is very limited in the case of the clade found in Spain/Morocco. These findings add further evidence that the Balkan region in particular has played the most significant role in the postglacial recolonization of Europe when compared to the remaining two Mediterranean peninsulas.

12:00 Ignacio García-Amorena, I Alberdi, JM Rubiales & E Moreno. **Palaeobotanical based species distribution models in ecosystem management: lessons from rear edge pine populations in Spain**

Universidad Politécnica de Madrid, Escuela Superior de Ingenieros de Montes, Departamento de Silvopascicultura, Spain
Email: ignacio.garciaamorena@upm.es

Abstract: In recent years numerous predictive techniques have been developed that help determining the ecological limits and expected variations in the distributions of particular species in Southwest Europe. However, outputs of different studies show controversial results. Up to date, although different initiatives are carried out to reduce uncertainties in predictive models, there is still a strong need of further research dealing with problems such as spatial and temporal autocorrelation to validate their outputs. Here, palaeoecology stands out as a strong validation tool. It provides information about the vegetation that existed in the past, with which to validate the output of these models. In this work, by analysing the vulnerability of the *Pinus uncinata*, *P. sylvestris* and *P. nigra* Western most populations to climate change, we exemplify a palaeobotanical-based distribution model at an appropriate forest-management scale (1 km^2). The Spanish Meteorological and Forest Inventory Data, the Iberian palaeobotanical data, and palaeoecological independent palaeo-climate reconstructions from the Paleoclimate Modelling Intercomparison Project have been put together with the MaxEnt program.

12:15 Elizabeth S Jeffers & KK McLauchlan. **Testing the progressive nitrogen limitation hypothesis with long-term data: a global synthesis of long-term changes in terrestrial nitrogen availability associated with increasing CO_2 concentrations**

Biodiversity Institute, Department of Zoology, University of Oxford, UK
Email: elizabeth.jeffers@zoo.ox.ac.uk

The progressive nitrogen limitation (PNL) hypothesis states that declines in nitrogen availability are the result of increased ecosystem nitrogen storage with increased atmospheric CO_2. Thus far, the evidence for and against the PNL has derived from short-term, experimental studies from Free-Air Carbon Enrichment (FACE) sites. Palaeoecological evidence of changes in nitrogen availability (inferred from stable isotope analysis of lake sediments) extends the observational record for testing the PNL from decades to millennia. A global synthesis of nitrogen isotope records from lake sediments is being undertaken in order to look for evidence of PNL during periods of increasing CO_2. We will present preliminary results from recent observations (i.e. past 150 years) and from the late-glacial/early postglacial transition – two periods of rapid increases in CO_2.

Saturday September 24th 2011, Lecture Theatre "Halford Mackinder"

SESSION 4: Macroecology: regional patterns

13:30 Vasile Decu, J Christian, NB Curcic & BPM Curcic. **Endemic fauna in Serbia with distribution of some cave-living taxa**

Geographical Institute "Jovan Cvijic", SASA, Belgrade
Email: ninacurcic@yahoo.com

The paper presents a review of cave-dwelling fauna in Serbia known to date. Karst features, geography of karst, caves and other subterranean habitats are also presented. Further, hydrology of ground waters of Serbia is described. Main species of aquatic and terrestrial environments were described. Serbian karst is an important habitat of many relict and endemic subterranean animals. Present distributions of some taxa (pseudoscorpions, diplopods, carabids and arachnids) are shown in UTM maps. The aim of this study is to offer a more complete review of cave-dwelling inhabitants in Serbia with additional data on a number of new species.

13:45 David Sánchez-Fernández, JM Lobo, A Millan & I Ribera. **Habitat type mediates equilibrium with climatic conditions in the distribution of Iberian diving beetles**

Institut de Biología Evolutiva (CSIC-UPF); Museo Nacional de Ciencias Naturales (CSIC); Universidad de Murcia
Email: davidsan@um.es

We aim to test for differences between species typical of either running or standing water (habitats with different long-term persistence) in the degree of climate-equilibrium (i.e. in their potential vs. realized distribution) in recently deglaciated (Europe) and refuge areas (Iberian Peninsula). For this, a total of 99 species and well established sub-species of Iberian diving beetles were used. At a continental scale we found clear differences in the degree of equilibrium of the geographical distribution between lotic and lentic species. In the Iberian Peninsula differences, if any, were much less pronounced. Our results suggest a stronger influence of geography at continental scale in the distribution of the lotic, less dispersive species. The preference of freshwater invertebrates for standing or running water habitats, a well-known and easy measurable autoecological characteristic, can be linked to large scale geographical patterns (climate-equilibrium) through differences in dispersal ability.

14:00 Leticia M Ochoa-Ochoa. **Short-term changes in the amphibian meta-community structure in two Mexican fragmented landscapes**

School of Geography and the Environment, Oxford University Centre for the Environment, UK
Email: leticia.ochoa@ouce.ox.ac.uk

Habitat fragmentantion is a common ground reality of neotropical forests and it has been estimated that it threatens 89% of Neotropical amphibians. Thus, understanding how amphibian communities respond to fragmentation processes is vital for their conservation. The framework of meta-community ecology focuses on the mechanisms that preserve species richness at local and regional level. As a multi-scale approach attempts to explain the dynamics of entire communities in spatially structure habitats. In this paper the principal aims are: (1) to explore how amphibian communities are structured in two fragmented landscapes with different environmental characteristics; (2) how do the community structure is related to the environment responds and (3) to establish the impact of temporal changes in the environment in community structure. Amphibian communities were sampled in two landscapes (~100km2) in southern Mexico during the rainy seasons of 2009 and 2010. Environmental characteristics (i.e. forest conservation status, temperature, atmospheric pressure, altitude, litter, coverage, body water type, etc.) were also recorded in each sampling unit (~100m^2). Relation between amphibian community structure and environment was analysed using Detrended Correspondence Analysis (DCA), followed by vector analysis. Generalized linear models (GLMs), and mixed models, were performed to analyzed different emergent properties of the community. The two years varied in climatic characteristics (i.e. 2009 was a very dry year, while 2010 had a normal rainy season). Thus, amphibian abundance and diversity characteristics of the sampling units also varied among years, with an obvious effect in the models. The most important factors correlated with the community structure were climatic related, specifically to rainfall pattern.

14:15 Rosa M Chefaoui, JM Lobo & J Hortal. **Species distribution models of threatened Iberian invertebrates**

Museo Nacional de Ciencias Naturales (CSIC), Spain
Email: rosa.chef@gmail.com

Reliable species distribution information on various scales is needed for both biogeographic and conservation purposes. We focused on modeling threatened Iberian invertebrates managing information from atlases and museums, taking advantage of databases and GIS. The poor quality of distributional data on threatened species is a

particularly important problem when working with invertebrates, where the difficulty of developing extensive surveys makes biodiversity databases a necessary alternative. Systematic conservation planning for invertebrate taxa entails modelling species with diverse characteristics and ecological requirements generally using poor quality data, often with no time for detailed "species-by-species" expert assessments. However, it is possible to determine environmental niches of species, those variables that most affect their distribution as well as the potential suitable areas with the purpose of evaluating protected areas, connectivity among populations, and possible reintroductions. There are a variety of predictive techniques and their performances have been widely studied. Although a good modelling method is important, our data quality is crucial for a good model. Assessing the effects of data characteristics and species' ecological traits on the accuracy of SDM, we found that prediction accuracy is mostly affected by the characteristics of the data (sample size and the relative occurrence area). In addition, special care should be taken while modelling species inhabiting inconspicuous habitats or strongly affected by interactions occurring at small spatial scales.

14:30 William D Pearse. **Community structure in Barro Colorado island has two spatial and one phylogenetic scale**

Imperial College London, UK
Email: william.pearse08@imperial.ac.uk

Ecologists have long known that spatial scale matters, but few studies looking at the phylogenetic structure of ecological communities take it into account. Moreover, such studies typically also ignore phylogenetic scale - they look at phylogenetic structure across all species in a community, without considering that subclades may be structured differently. Using spatially-explicit data on plants from Barro Colorado Island together with a new measure of phylogenetic community structure, I show that community phylogenetic structure has two ecologically meaningful spatial scales, and that phylogenetic structure is not consistent among plant clades.

14:45 Fernando Monroy, P Martins Da Silva & MP Berg. **Regional patterns of Collembola diversity as a result of functional adaptation to local environmental conditions**

Vrije Universiteit Amsterdam, Holland
Email: f.monroymartinez@vu.nl

Soils constitute major reservoirs of biodiversity and part of their richness is accounted by the turnover of species across space. However, little is known about the relative contribution of species turnover to the total soil diversity of a certain area and whether it depends on the spatial scale considered. In order to assess the influence of the spatial scale on the species turnover in the soil, we analysed data from 768 Collembola assemblages collected along eight gradients of land use intensity across Europe. The relationship between α and β diversity was calculated at two nested spatial scales: from cm to km (local) and up to 3 10^3 km (regional). In addition to species diversity we used morphological and taxonomic data to calculate functional and taxonomic diversities, respectively. We found that, independently of the land use intensity considered, β diversity was the main source of diversity both at the local and regional scale. The analysis of the relative degree of differentiation between communities revealed that the β component of diversity was significantly greater at the regional scale, suggesting that dispersal limitation processes were responsible for this pattern. Accordingly, species and taxonomic similarity decreased with geographic distance at the regional level, but this relationship was significant only for the latitudinal gradient. There was no taxonomic differentiation between communities on the longitudinal gradient, indicating that dispersal limitation does not necessarily occur at regional scales. Other factors, such as the adaptation to local environmental conditions linked to latitude, may explain the observed pattern of β diversity. This idea was supported by a negative relationship between functional similarity and latitudinal distance. We concluded that in spite of the dispersal potential of Collembola, their communities at the regional scale are characterized by a fast species turnover which is related to their functional adaptation to local environmental conditions.

Saturday September 24th 2011, HO Beckit Room

SESSION 5: Island biogeography

13:30 Ana MC Santos. **Diversity and structure of island parasitoid communities worldwide**

Departamento de Ecologia, Universidade Federal de Goiás, Brazil.
Email: ana.margarida.c.santos@googlemail.com

Islands are natural laboratories for the study of evolutionary and ecological processes due to their discrete and isolated nature. When compared to the mainland, island biotas tend to be species–poor, usually with the absence of entire ecological groups such as predators, parasitoids or pathogens. As a consequence interspecific competition is thought to be relaxed and the ecological space is often not fully saturated. Parasitoids are insects that develop to adulthood by feeding on the body of an arthropod host, eventually killing it. They are a key component of most terrestrial ecosystems, as they are fundamental for the maintenance of the diversity of other animals and plants, being involved in a vast number of trophic interactions and having a regulatory effect on other arthropod populations. Here I investigate the patterns of diversity and community structure of island parasitoid communities worldwide. I used different morphological and ecological traits of two parasitoid families (Braconidae and Ichneumonidae) to assess whether: (i) island parasitoid faunas host proportionally more generalist species than the mainland; and (ii) the functional diversity of island communities deviates from that of its species pool. I also evaluate which climatic, geographical or biological predictor are related to the functional diversity and community structure of island parasitoid faunas. I found that islands host comparatively more generalists than continental areas, and that the most important determinant of island community structure is their source pool. Also, functional diversity correlates with island species richness, area, distance to the mainland and region, and with the richness of the species pool.

13:45 Katy Jones, M Carine & S Hiscock. What explains the Azores diversity enigma?

Natural History Museum, London and Bristol University, UK
Email: katyj@nhm.ac.uk

Macaronesia comprises the volcanic archipelagos of the Azores, Madeira, Canary Islands, Salvage Islands and with very few endemic taxa (c. 60 taxa) and of those, only a small proportion are Single Island Endemics (SIEs; 4%), based on current taxonomic concepts. In contrast, the Canary Islands have an extremely rich endemic flora of c. 607 species with a large proportion of SIEs. Island age, lineage age and habitat diversity alone do not provide satisfactory explanations for these differences. Several new hypotheses have been put forward to explain the differences observed; (i) high levels of undocumented extinctions in the Azores flora, (ii) high dispersal ability of Azorean taxa, (iii) differences in climate across the Macaronesian archipelagos and (iv) inadequacies in the level of taxonomic knowledge of the Azores flora. Molecular analyses of several endemic lineages suggest that there may be a considerable amount of previously undocumented diversity in the flora. This talk presents a preliminary analysis of herbarium collections of Azorean taxa worldwide which suggest that hypothesis (iv) may help to explain the differences in the diversity patterns of endemic taxa between the Azores and the Canary Islands. Future plans for investigations to help resolve the 'Azores diversity enigma' are also outlined.

14:00 Tiina Särkinen, M Simon, T Pennington, M Lavin, & C Hughes. **Evolutionary islands in the Andes: persistence, isolation and endemism in Andean dry tropical forests**

Natural History Museum, Cromwell Road, London, UK
Email: tiina.sarkinen@nhm.ac.uk

The relative contribution of biome history and geological setting to species richness in biodiversity hotspots remains poorly understood. The tropical Andes is one the world's top biodiversity hotspots, and with its diverse biomes and the relatively recent but dramatic mountain uplift, the Andes offers a setting to study the importance of biome stability and geological history in species rich biomes. I will focus on discussing patterns and tempo of species diversification in the tropical Andes, which is comprised of three major biomes: low-elevation seasonally dry tropical forests (SDTF), mid-elevation montane forests (MMF), and high-altitude grasslands (HAG). Using time-calibrated molecular phylogenies of endemic Andean genera, we investigated species diversification patterns in the low-elevation SDTF biome. We also explored sequence datasets with dense sampling of infra-specific variation across multiple genera with Isolation-by-Distance methods. To compare the pattern of species diversification found in SDTF to other Andean biomes, we performed a literature-based meta-analysis. The results show that although comparing phylogenies is not always a straight-forward exercise, comparative phylogenetic approaches can be used to explore large-scale patterns in macro-evolutionary studies.

14:15 Dirk N Karger, VB Amoroso, D Darnaedi, A Hidayat, J Kluge & M Kessler. **Patterns of fern diversity in the southeast Asian archipelago**

University of Zurich, Switzerland
Email: dirk.karger@systbot.uzh.ch

Island systems have long played a crucial role in investigating patterns of biodiversity because they provide comparatively simple systems with clearly defined subunits of usually varying sizes and ecological conditions. Biodiversity, however, can be measured in different ways, representing different levels of diversity (alpha-, beta-, and gamma-diversity), and all levels are influenced by different biotic and abiotic factors. How these factors influence the different levels of diversity and how the different levels of biodiversity are linked to each other are highly debated throughout the scientific world. Most studies focusing on island biodiversity use only one level of biodiversity, but to get an accurate measure of the status of biodiversity on islands and to detangle the links between different biodiversity measures, it is important to investigate all levels of biodiversity as well as the influencing factors. We present initial results from a study that investigates fern diversity on all these different levels of biodiversity in the Southeast Asian archipelago of Indonesia and the Philippines. The Southeast Asian archipelago provides us with a large number of islands of varying sizes and environmental conditions, allowing us to get a first insight into processes linking diversity levels with island conditions.

14:30 Anna Papadopoulou, I Anastasiou & AP Vogler. **Lineage diversification and community differentiation in a continental archipelago: the case of the Aegean darkling beetles**

Institut de Biologia Evolutiva (CSIC-UPF), Spain
Email: anna.papadopoulou@ibe.upf-csic.es

Continental archipelagos of recent origin have traditionally received less attention by biogeographers and evolutionary biologists than oceanic islands, although they represent excellent 'natural laboratories' to study the effects of dispersal limitation on population and community structure. The process of 'relaxation', i.e. the decrease in species number that follows island isolation, provides a unique opportunity to investigate the effect of ecological drift on alpha- and beta-diversity patterns. At the same time, continental islands offer a very intuitive setting to study the evolutionary consequences of population subdivision and restricted gene flow, which is one of the main mechanisms that can drive species formation through genetic drift and local adaptation. We studied the phylogeographic, genetic diversity and species richness patterns of the darkling beetles (Coleoptera: Tenebrionidae) of the central Aegean islands, which we consider as a potential 'textbook example' of diversification in a continental archipelago. We conducted a dense sampling across 30 central Aegean islands and the corresponding coasts of Greece and Turkey, and a thorough survey of DNA sequence variation in the tenebrionid communities. Over 1,500 individuals belonging to 30 genera were sequenced for a mitochondrial and a nuclear gene marker. The generated sequence data were used to reconstruct phylogenies, calculate population genetic parameters, apply DNA-based species-delineation methods, estimate divergence times and assess macroecological patterns. Based on these results we discuss how palaeogeography, contemporary geography and habitat stability interact with stochastic processes at population and community level to shape the observed diversity patterns.

Saturday September 24th 2011, Lecture Theatre "Halford Mackinder"

SESSION 6: Phylogeography

15:30 Emma SM Boston, WI Montgomery & AP Prodöhl. **New perspectives on postglacial colonisation in Western Europe: the phylogeography of the Leisler's bat (*Nyctalus leisleri*)**

Queen's University Belfast/University College Dublin, Ireland
Email: emma.boston@ucd.ie

Despite advances in resolving the interplay of a dynamic physical environment and phylogeography in Europe, the origin of western European biota, especially in Ireland remains uncertain. The Leisler's bat (*Nyctalus leisleri*) is distributed throughout Europe but, with the exception of Ireland, is generally rare and considered vulnerable. Here we present results examining the phylogeographic relationships of Irish *N. leisleri* populations in relation to those across Europe, including the closely related species *N. azoreum*, using a combination of phylogeographic analyses, ecological niche modelling (ENM) and palaeo-climatic reconstructions. Our results reveal distinct and diverse mtDNA lineages, which likely diverged in separate glacial refugia. A western lineage, is restricted to Ireland, Britain and the Azores, and comprised of Irish and British *N. leisleri* and *N. azoreum* specimens. An eastern lineage is distributed throughout Europe. Palaeo-climatic ENM projections indicate suitable habitats during the LGM, including well established refugia, in addition to potential novel refugia along the western fringe. It is concluded that populations on the western edge of Europe may have originated from two or more refugia and are composed of more than one evolutionarily significant lineage, results which may be applicable to populations of many species.

15:45 Alejandra Moreno-Letelier, A Ortiz-Medrano & D Piñero. **The effects of Pleistocene glaciations on three montane pine species: hibridisation, shared polymorphism and niche evolution**

Division of Biology, Imperial College London, UK
Email: a.moreno-letelier@imperial.ac.uk

Temperate flora from subtropical regions went through significant changes in distribution during glacial cycles. Even in the absence of glacial caps, lower temperatures caused altitudinal and latitudinal migrations and the assemblage of new communities. These changes also promoted fragmentation and hybridisation, which together with changes in population sizes, left a genetic imprint on species. One of the species groups that went through dramatic range changes during glaciations is the *Pinus flexilis*, *Pinus strobiformis*, and *Pinus ayacahuite* species complex from Mexico and Western United States. These three species diverged recently, are non-sympatric, and show shared polymorphism in several molecular markers. The later, together with high intraspecific morphological variation has made it difficult to establish species boundaries. Using phylogeographic methods and ecological niche modeling for present and Last Glacial Maximum conditions, we found key ecological and slight genetical differences among the species, as well as evidence of a broad hybridisation zone in Eastern Mexico during the Last Glacial Maximum. These results suggest that speciation is still an ongoing process in this group, where conflicting forces like habitat fragmentation, hybridisation and adaptation to different ecological conditions, have acted at different times since the beginning of the Pleistocene 2.5 million years ago.

16:00 Marta Álvarez-Presas, A Sánchez-Gracía, F Carbayo, J Rozas & M Riutort. **Molecular phylogeography of land flatworms from the Brazilian Atlantic Forest biodiversity hotspot**

Universitat de Barcelona, Spain
Email: onaalvarez@ub.edu

The Atlantic Forest of Brazil (AF) is one of the richest biodiversity hotspots and one of the most damaged by human activities; indeed, only ~11-16% of its original biodiversity is currently preserved. Biological corridors, geographically designed based on inventories of flora and fauna, have been introduced to protect the area and restore ecosystem functionality. Palaeoclimatic modeling studies predicted two stable regions in the central AF, while southern regions might have been unstable during glaciations resulting in an impoverishment of their biota. However, molecular phylogeography and endemism studies show contradictory results: some data support these predictions, while others indicate that palaeoclimatic models fail to predict southern stable areas. Most studies have used species with high dispersal rates leading, likely, to a lack of fine-scale resolution. We have shown that terrestrial planarians, with low dispersal ability, are good predictors of habitat stability even for small populations. Here, we analyse the patterns and levels of nucleotide diversity in 11 populations (inside and outside the Serra do Mar corridor in the AF) of two flatworm species. Although we find that both species harbour high levels of variability for nuclear and mitochondrial markers, they have dissimilar distribution patterns. We tested different demographic scenarios to get insights into the evolutionary processes shaping their levels and patterns of genetic variability. Our results support the existence of ancient stable areas, older than the last glaciations even in the southern AF, showing the limitations of palaeoclimatic models for such studies.

16:15 Kyle Dexter & J Chave. **Phylogeography of Amazonian trees with implications for Amazonian biogeography**

University of Leeds, UK Email: kgdexter@gmail.com

We review our own and other studies on the phylogeography of Amazonian trees and discuss the implications of our results for Amazonian biogeography. The principal debate at one time in Amazonian biogeography concerned whether or not rainforests were contracted into isolated refugia. This has given way to a more nuanced view where different parts of the Amazon may have experienced different climates at different times and species may have responded individualistically to climatic events. Our phylogeographic studies of *Inga* species (Fabaceae) in the western Amazon basin have not shown a pattern of equilibrium isolation by distance. Instead, the distribution of alleles in many species reveals a history of range displacement, extinction, and recolonization. Likewise, our phylogeographic studies of 50 tree species from diverse taxonomic families in French Guiana have found evidence for dynamic histories. Many species show genetic homogeneity over large areas, interspersed with phylogeographic breaks, which sometimes occur over very short spatial distances. Other studies of Amazonian trees have also shown high phylogeographic structure and evidence for non-equilibrium dynamics. In short, tree species in the Amazon basin appear to have very dynamic biogeographic histories, yet there appears to be little correspondence among species' histories. Our results are in agreement with a Gleasonian view of Amazonian biogeography, where climatic and other environmental changes may have driven changes in the distribution of species, but each species seems to have responded in a different manner, presumably depending on their own particular adaptations and evolutionary history.

16:30 Elizabeth L Cooke[1], RW Scotland[1], Robert W.1, MA Carine[2], & M Tsiantis[1]. **Phylogeography of the emerging model plant *Cardamine hirsuta* L.**

[1]Department of Plant Sciences, University of Oxford, [2]Department of Botany, The Natural History Museum, UK
Email: elizabeth.cooke@plants.ox.ac.uk

Cardamine hirsuta (Brassicaceae) is an emerging plant model system in developmental genetics. Studies use natural variation in morphology within *C. hirsuta* to investigate the genetic basis of morphological traits. Yet currently, there is limited knowledge on the extent of genetic and morphological variation within *C. hirsuta* and its genealogical and spatial history. Little genetic variation or structure has previously been found within *C. hirsuta*, despite range wide sampling. This is perhaps unsurprising given that the species is a garden weed and thus there is potential for human mediated dispersal to have obscured or destroyed any phylogeographic structure. Here, by identifying chloroplast regions with suitable levels of intraspecific variation and sampling widely from across the native range of *C. hirsuta*, primarily using DNA extracted from herbarium specimens, geographic structuring of genetic variation has been found in *C. hirsuta*. A haplotype network shows si x major groups, four are geographically restricted in their distribution, to: the Ethiopian highlands, the Atlas Mountains, the Atlantic fringe and the Middle East, and two are widespread, co-occurring across Europe. This presentation will outline these patterns and put forward possible scenarios for their origin.

16:45 Alice C Hughes, C Satasook, P Soisook, PJJ Bates & S Bumrungsri. **Cryptic clues to a complex problem**

University of Bristol, Prince of Songkla University, UK
Email: ah3881@bristol.ac.uk

Recent research has highlighted the genetic diversity of Southeast Asian bat species. However no attempts to map these patterns of genetic diversity have previously been made and therefore there is no knowledge of current biogeographic patterns, or any understanding of the factors which have led to their development. Here we model the distribution of two Hipposiderid and one Rhinolophid bat species during the Last-interglacial period, last glacial maximum and the present, and look for possible geographic isolation between populations. We analysed patterns of acoustic variability within species in relation to both past distributions and the distribution of karsts throughout Southeast Asia (SEA). Morphological variability was also assessed relative to acoustic variability using sPCA. Genetic variation was also assessed relative to past distributions and karsts, and the use of different climatic niches by different populations explored using sPCA. 97 "species" were analysed using TCS, and an additional 118 potential cryptic species suggested using parsimony analysis. Additionally Over 62.9% of currently described species display over 2% sequence divergence. Of the three species spatially analysed each genetic network was found to use different climatic areas and constant morphological features were found to be associated with acoustic groups, therefore localised adaptation during allopatry may have driven speciation. Genetic patterns fitted with geographic isolation during previous time periods, and the locations of karsts throughout the region. Our study suggests that there are sufficient genetic, acoustic and morphologic differences to warrant the elevation of a number of these sub-species to full species status, though further research will be required to formally describe these species. Many regions were projected to show highly fragmented suitable areas in past projections, and these areas showed greatest genetic diversity. If species diversity is to be conserved under potential future climatic

changes then the preservation of this genetic diversity may prove essential.

Saturday September 24th 2011, HO Beckit Room

SESSION 7: Evolutionary Biogeography

15:30 Alex L Pigot, IPF Owens & CDL Orme. S**peciation, extinction and the illusion of range size trajectories in phylogenies and the fossil record**

Department of Zoology. University of Oxford
Email: alex.pigot@zoo.ox.ac.uk

Speciation and extinction define the start and end of a species' life, but what happens in between these events remains poorly understood. A number of models propose that the range size of a species follows a predictable path over the course of its life and this appears to be supported by studies of both the fossil record and molecular phylogenies. Using stochastic models of range evolution we show that the evidence provided by these previous studies is likely to be illusory. Even when range sizes have evolved completely at random the effects of speciation and extinction lead to the appearance of deterministic range size trajectories. We compare the patterns of range evolution predicted by these stochastic models to those observed in phylogenies of birds and mammals and from the fossil record of marine molluscs. We show that, despite the appearance of deterministic trends, in all cases the patterns are instead consistent with geographic range sizes evolving according to a random walk through time.

15:45 Christopher Beatty CD & JL Ware. **Biogeography, population genetics and life history of a "living fossil" dragonfly (Insecta:Odonata)**

Santa Clara University, USA
Email: cbeatty@scu.edu

The dragonfly family Petaluridae, known also as "Petaltails", is extremely old, with fossil species found as far back as the Jurassic. Eleven species exist today distributed in Australia, New Zealand, Japan, Chile, and the Pacific Northwest and Appalachian regions in North America. These species have ecologies quite different from other dragonflies: their larval stage, which is aquatic, lives in flooded burrows in boggy areas, often high in the mountains. The larva takes as many as five years to develop into an adult, but adults fly for only a few weeks. With this life history pattern, individuals from different cohorts within the same bog are not likely to interbreed (as their adult stages emerge in different years), but individuals from the same cohort in different bogs might be able to mate, if the adults can disperse between larval habitats. We are then left with the question: what is a 'population' in this group? We address this question through population genetic analysis of the species *Tanypteryx hageni*, found in northern California and Oregon in the US. We also assess adult dispersal directly through radiotracking. We present the results of these experiments and their implications for our understanding of population structure in this unique group of dragonflies.

16:00 Alexander Gamisch, GA Fischer & HP Comes. **The evolution of auto-pollination in tropical orchids: morphological, experimental, and phylogenetic studies in *Bulbophyllum thouars* from Madagascar.**

University of Salzburg, Salzburg, Austria
Email: alexander.gamisch@stud.sbg.ac.at

The shift from outcrossing to selfing is one the most common evolutionary transitions in flowering plants. Selfing in orchids is typically assumed to provide reproductive assurance under conditions of pollinator and/or mate limitation, especially at northern latitudes. However, in tropical orchids, little is known about the frequency and evolutionary consequences of shifts in mating system. Here, we investigate shifts from outcrossing to selfing ('auto-pollination') over evolutionary time in a clade of self-compatible *Bulbophyllum* orchid species from Madagascar (sects. *Bifalcula*, *Humblotiorchis*, *Calamaria*; c. 30 species). We address this issue by pollination experiments, floral micro-morphological studies, and molecular phylogenetic analyses, including character-mapping procedures and diversification analyses. Our preliminary data indicate that seven out of 28 species surveyed are polymorphic for the (non-)capacity of autonomous fruit set, depending on the absence (or presence) of the rostellum, a structure separating the anthers from the stigma. Phylogenetic evidence suggests that rostellum presence (viz. outcrossing) is the ancestral state of this relatively old clade (Late Miocene), whereas the transition to selfing has occurred multiple times independently, but almost exclusively at the tips of the phylogenetic tree. This pattern clearly accords with the hypothesis that selfing is an evolutionary 'dead end', but may also reflect an adaptation in response to climate-induced range fragmentation and population isolation during the (Late) Pleistocene.

16:15 Lynsey Mcinnes, FA Jones & V Savolainen. **Untangling the drivers of monocot diversity: can we determine the relative roles of phylogeny, geography and history?**

Imperial College London, UK
Email: lynsey.mcinnes01@imperial.ac.uk

Explaining diversity differences among clades is a major goal of macroevolutionary research. A bewildering array of hypotheses has been put forward as potential drivers of heightened diversification or greater species numbers including key innovations, biogeographic opportunity, environmental conditions and time for diversification. Nevertheless, there has been remarkably little quantification of the relative importance of these different factors. Part of the problem has been a lack of a suitably large group with data available such that multiple replicate radiations can be treated within the same statistical framework. Monocots are a diverse and monophyletic group representing approximately a quarter of all flowering plant species including grasses, orchids, palms, gingers, lilies and important crops such as oats, bananas and pineapples. With robust trait and distribution data available, they make an ideal group to pursue an integrated approach. As part of the project, we have also generated a genus-level phylogeny of 73 % monocots. In this talk, I will present preliminary results from our analyses aimed at untangling the relative importance of phylogeny, geography and history in determining contemporary monocot diversity patterns.

16:30 Paolo Gratton & A Gandolfi. **Composing the evolutionary puzzle of the last remains of trout (*Salmo trutta* complex) diversity in Italy**

Department of Biodiversity and Molecular Ecology, IASMA Research and Innovation Centre, Fondazione E. Mach, S. Michele all'Adige , Italy
Email: paolo.gratton@iasma.it

Mediterranean trout populations display a diversity of forms, representing a valuable model for the study of adaptation and a puzzling dilemma for taxonomists and biogeographers, rendered even more problematic by the widespread introgression of allochthonous (Atlantic) genes. Current Bayesian methods allow complex evolutionary models to be treated, offering the opportunity to statistically evaluate explicit hypotheses about the evolutionary relationships of Mediterranean trout populations. We used Approximate Bayesian Computation to test among competing evolutionary scenarios for the main trout lineages autochtonous in the Italian basins ('marble' and Mediterranean 'brown' trout), involving the roles of geographical barriers and climate change in shaping the historical distribution of distinct lineages, and accounting for allochthonous introgression. Our main results were that: i) the gene pool of the Adriatic endemic 'marble' trout started diverging earlier than the separation of Atlantic and Mediterranean lineages of 'brown' trout. ii) a relatively complex model of divergence, involving gene flow into the ancestral gene pool of marble trout from Mediterranean 'brown' trout is most consistent with the genetic data. iii) autochthonous gene pools of 'brown' trout in the Tyrrhenian and Adriatic basins of the Italian peninsula most likely diverged around the Last Glacial Maximum, indicating that movement along the coasts of southern Italy was made possible by climate/salinity conditions. Our approach has, for the first time, allowed to set an explicit model for the evolution of the main trout lineages autochthonous in Italy, which we are currently using to test the hypothesis of speciation by hybridization in the Lake Garda endemic *Salmo carpio*.

16:45 Alexander N Kirschel, N Seal & GF Grether. **The extent of trait similarity at contact zones influences range overlap and the trajectory of multidimensional character displacement in African tinkerbirds (*Pogoniulus* spp.)**

Edward Grey Institute, Department of Zoology, University of Oxford, UK
Email: alexander.kirschel@zoo.ox.ac.uk

The role of character displacement in evolutionary diversification is attracting renewed interest with several recent studies identifying patterns of displacement attributed to either ecological or reproductive processes. As well as the prediction of divergence between sympatric forms, character displacement may also account for divergence among populations of the same species in sympatry and allopatry or among populations at different contact zones. Together, these processes could help explain complex, trait-specific patterns of diversification. There is, however, very little evidence of divergence along different trajectories between interacting species among contact zones. Here we show how traits of two Pogoniulus tinkerbird species vary among contact zones across sub-Saharan Africa. Specifically, we find evidence for character displacement in song and morphology in Central and East Africa where the species coexist widely, with displacement in either species or both. In West Africa, however, greater similarity in plumage coloration could result in competitive or reproductive exclusion. With divergence along different trajectories among contact zones, allopatric populations of the same species might become reproductively isolated. Our findings suggest that interactions between species play an important role in explaining patterns of species diversification.

Sunday September 25th 2011, HO Beckit Room

SESSION 8: Topics in Biogeography

09:15 Nicholas J Matzke. **Moving from historical biogeographic inference in discrete space to historical biogeographic inference in continuous space, by moving from species distribution modeling to phylogenetic lineage distribution modeling**

University of California, Berkeley, USA. Email: matzke@berkeley.edu

In recent decades, historical biogeography has experienced several methodological revolutions. With the growth of phylogenetics, the field has moved from pattern-based methods (cladistic biogeography) to event-based methods (parsimony approaches such as DIVA) to parametric, likelihood-based methods such as Lagrange. What all of these methods share is the coding of geographic range as a discrete character state, resulting in inference of ancestral ranges from the same suite of discrete character states. Discrete biogeographic approaches have many advantages, including speed and simplicity, and they are able to take advantage of the extensive literature and associated algorithms that have have been developed by the phylogenetics community for discrete characters in morphology and molecular evolution. However, discrete-range methods all suffer from some weaknesses, such as the subjectivity of encoding complex biogeography into a few discrete states in the first place, the difficulty of including obviously relevant variables such as climatic preference in ancestral range estimates, the problem of changes in the available states themselves in geological time (e.g. the merging of two geographical areas into one as the result of climate change or tectonics), the appropriate inclusion of fossils, and the limits imposed on the complexity of analyses by the strict computational limits on the size of transition matrices. Parallel to the development of discrete-state historical biogeography, ahistorical biogeographers have created an entire family of methods for species distribution modeling. The purpose of these techniques is to estimate the geographic range of extant species or the ranges of species in the recent past or near future under the influence of climate change. These methods have the advantage of working in continuous space, taking advantage of GIS raster tools, and making extensive use of climatic and other environmental data. However, all species distribution models to date are entirely non-phylogenetic, which seems very strange given the spread of phylogenetic methods in ecology, macroecology, conservation biology, and nearly all forms of comparative biology. I propose that the disadvantages of the above techniques can be avoided by merging phylogenetic methods and species distribution modeling into what I call phylogenetic lineage distribution modeling (PLDM). This takes advantage of phylogenetic methods used for ancestral inference of continuous characters to account for evolutionary conservation and change in lineage climatic preference, and spatial statistical methods such as kriging to account for spatial autocorrelation in lineage distributions. Given sufficient paleoenvironmental data, the range of any lineage at any point on a phylogeny can, in principle, be estimated and mapped in continuous space, as can the uncertainty in these predictions. PLDM has the potential for improving science in several areas. First, phylogenetic information may improve extant species distribution estimates, particularly when extrapolations need to be made from limited point data that does not fully describe the species' environmental niche. Second, the same method can be applied to the ranges of fossil species, where point data is almost always sparse. Third, having estimates of ancestral geographic ranges across a phylogeny enables the calculation of the likelihood of fossil occurrence data, which finally makes "strato-likelihood" an operational possibility. This means that the stratigraphic distribution of fossils can be used in a statistically rigorous way to improve estimates of phylogenetic topology, branch lengths, and divergence times.

09:30 Bo Dalsgaard, E Magård, J Fjeldså, AM Martín González, C Rahbek, JM Olesen, J Ollerton, R Alarcón, AC Araujo, PA Cotton, C Lara, CG Machado, I Sazima, M Sazima, A Timmermann, S Watts, B Sandel, WJ Sutherland & J-C Svenning. **Specialization in plant-hummingbird networks is associated with quaternary climate-change velocity**. University of Cambridge, UK. Email: b.dalsgaard@zoo.cam.ac.uk

Large-scale geographical patterns of biotic specialization and the underlying drivers are poorly understood, but it is widely believed that climate plays an important role in determining specialization. As climate-driven range dynamics should diminish local adaptations and favor generalization, one hypothesis is that current biotic specialization is determined by the degree of past climatic instability, primarily Quaternary climate-change velocity. Other prominent hypotheses predict that either contemporary climate or species richness affect biotic specialization. To gain insight into geographical patterns of biotic specialization and its drivers, we use network analysis to determine the degree of specialization in plant-hummingbird mutualistic networks sampled at 31 localities, spanning a wide range of climate regimes across the Americas. We found greater biotic specialization at lower latitudes, with latitude explaining up to 23% of the spatial variation in plant -hummingbird specialization. Potential drivers of specialization - contemporary climate, Quaternary climate-change velocity, and species richness - had superior explanatory power though, together explaining up to 71% of the variation in specialization. Notably, although specialization was associated with high precipitation and comparatively low temperatures, strong biotic specialization was mainly linked to species-rich networks and low Quaternary climate-change velocity. Our data thus provides empirical evidence for the hypothesized roles of species richness and Quaternary climate-change velocity as key predictors of biotic specialization, whereas contemporary climate seems less important in determining specialization. These results suggest that evolutionary processes at Quaternary time scales can be important in driving large-scale geographical patterns of biotic specialization, at least for co-evolved systems such as plant-hummingbird networks.

09:45 Valentina Todisco, P Gratton, F Sperling & V Sbordoni. **New refugial model for alpine invertebrates: a case study of the *Parnassius phoebus* complex**

University of Rome "Tor Vergata", Rome, Italy. Email: valentina.todisco@libero.it

Our study provides the first comprehensive description of the mitogenetic structure of Holarctic alpine butterflies of the Parnassius phoebus complex. A fragment (824 bp) of the mitochondrial COI gene was sequenced in 203 samples (72 locations), and combined with previously available but geographically restricted COI sequences (499 samples), to obtain full coverage of the Holarctic distribution of the species complex. A global Species Distribution Model (SDM) was calculated by the MAXENT approach, allowing assignment of samples into geographically consistent 'operational' units. Phylogenetic and coalescent methods were applied to describe the global mitogenetic structure and estimate population genetics parameters. Our results show that Eurasian (including Alaskan) and North American populations form two distinct mitochondrial clades. In contrast with its presently scattered distribution within each of Eurasia and North America, the mitogenetic structure of the P. phoebus complex in both continents is shallow and weak, showing no evidence of geographic structure dating back earlier than the last glacial cycles. We argue that mtDNA data are consistent with recent (Würm/Wisconsin) radiations within each of the two continents, and with persistent glacial long-range gene-flow which ceased during the Holocene. P. phoebus may represent a model for Holarctic alpine invertebrates with moderate dispersal abilities, in that its genetic structure at a continental scale reflects extensive connectivity during the most recent glacial phases.

10:00 Jorge A Noriega. **Biogeographic provinces and endemicity areas analysis of the dung beetles (Coleoptera: Scarabaeidae) in Colombia**

Laboratory of Zoology and Aquatic Ecology - LAZOEA, University of Los Andes, Bogota, Colombia
Email: jnorieg@hotmail.com

Dung beetles of the subfamily Scarabaeidae provide several key functions that maintain ecological functional processes. In Colombia, the knowledge of its diversity and distribution patterns have increased in the last years, allowing an approach to the biogeographic analysis of its distribution. By means of compiling the information contained in the main entomological collections of the country and in scientific publications, a presence/absence matrix of species was constructed, in quadrants of 0.5 x 0.5 grades. A cladistic analysis was done using PAE (Parsimony Analysis of Endemicity) with the TNT software. A total of 16940 specimens were reviewed, with validated information for 232 species, finding 583 new departmental records and 155 new registries of extension of altitude intervals. The localities with greater species richness are in proximities to the big cities. Among these, the Amazonian region and the North-western flank of the Sierra Nevada of Santa Marta are worthy of mention as the zones of higher endemicity. The analyses establish 97 equally parsimonious trees. In the tree of strict consensus seven areas of association were identified in agreement with the biogeographic provinces. This close association can be related to the ecological dependency that settles down with mammals. It is necessary to raise strategies for the conservation of the Amazonian region and those areas surrounding the Sierra Nevada of Santa Marta. For future researches, including the totality of species of the Colombian territory, and completing the records of some under sampled zones is highly recommended.

10:15 Miquel Vila-Farré, S Nieto, R Sluy, R Romero, X Ferrer & D Vieites.**The biogeography of the genus Crenobia in Europe**

Universitat de Barcelona, Departament of Genetics, Spain. Email: mvilafarre@gmail.com

The use of software for modelling the distribution range of a species is an emerging technique. We apply the program Maxent to the study of the distribution of the triclad genus *Crenobia*, which is considered to be monospecific by the last taxonomic authorities. Our work joins informatics and molecular approaches to explain the distribution of *Crenobia* in Europe and the Iberian Peninsula. The final output has been validated in the field. It confirms that the combination of these techniques opens new possibilities to the study of the biogeography of triclads.

Sunday September 25th 2011, Lecture Theatre "Halford Mackinder"

SESSION 9: Conservation Biogeography I: from DNA to species

09:15 Seth W Cunningham, M Shirley & E Hekkala. **Patterns of molecular genetic variation among *Crocodylus suchus* populations throughout West and Central Africa**

Fordham University, NY, USA
Email: slypig72@gmail.com

Understanding the phylogeographic history of widespread species is vital to implementing effective conservation and management strategies. Of primary importance, is the recognition of genetically differentiated populations as local management units. The Nile crocodile (*Crocodylus niloticus*) has been found to contain substantial biogeographic sub-structuring corresponding with major river drainages throughout Eastern Africa and Madagascar. This taxon was recently discovered to contain a cryptic species (*Crocodylus suchus*) in Central and Western Africa. Due to heavy exploitation for the leather industry, and ongoing habitat degradation, these African crocodiles must be properly managed if they are to persist into the foreseeable future. In order to better understand the distribution of genetic variation in *C. suchus*, we analyzed specimens, corresponding to major river drainages throughout Central and Western Africa, using multilocus genotyping. Preliminary survey efforts indicate that *C. suchus* is declining or extirpated in much of its range underscoring the need to evaluate population substructuring of this newly identified taxon for conservation planning.

09:30 H Eden W Cottee-Jones. **Birds of the Banyan: *Ficus* use by birds in a tropical countryside landscape, Assam**

University of Oxford, UK
Email: henry.cottee-jones@seh.ox.ac.uk

Recognising that trees of the *Ficus* genus act as keystone species in tropical landscapes around the world, and that scattered trees act as keystone structures in disturbed ecosystems, this study analysed the role fig trees play in supporting frugivorous bird communities beyond protected areas in Assam, India. Data were collected over a six week period in a 20 x 40 km study area. The results suggested that the distance from the nearest protected area and the size of the fig tree were the most important determinants of bird occurrence. Meanwhile, forest vspecialists of conservation concern, such as the Great Indian Hornbill and Hill Myna, were rarely found more than a few hundred meters from the forest edge.

09:45 César Capinha, L Brotons & P Anastácio. **Disentangling the relative influence of human, biological and environmental factors in shaping the invasion of the Signal and the Red swamp crayfish in Europe**

Universidade de Évora, Portugal
Email: capinha@uevora.pt

A major goal of invasion ecology is to identify which factors enable non-native species to establish viable populations. Here we test the relative importance of human, biological and environmental factors in shaping the current distribution of two of the most widespread aquatic invaders of Europe, the Signal crayfish and the Red swamp crayfish. We collected a set of spatially explicit variables specifically related to four well known invasion hypotheses: propagule pressure, climate matching, human disturbance and the Darwin's naturalization hypothesis. Using boosted regression trees we built predictive models by relating these variables with the current distribution of the two invaders in Europe. The models showed a very good predictive ability for the two invaders (mean ROC-AUC ≥ 0.95), with two variables consistently shown as the most relevant: political borders and climatic suitability. Political borders largely define the level of propagule pressure made across the Continent, thus evidencing the importance of this factor. For the Red swamp crayfish the climatic suitability model based on native occurrences showed lower relative influence than those using occurrences from other invasive ranges, providing a limited support to the climate matching hypothesis. The reduced influence of the remaining variables was also not supportive of the human disturbance and the Darwin's naturalization hypothesis. In face of these results it is expected that in the absence of effective measures impeding their dispersal these invaders will increasingly occupy the many climatically suitable areas still available in the European Continent.

10:00 Luisa MS Borges, SM Cragg, LM Merckelbach, I Sampaio & FO Costa. **Biogeography of Wood Borers in European coastal waters: a tale of two distinct taxa Sharing the same niche**

Centre of Molecular and Environmental Biology (CBMA), Department of Biology, University of Minho, Campus de Gualtar, Portugal
Email: luisa.borges@bio.uminho.pt

The most destructive marine wood borers are bivalves of the family Teredinidae and isopods of the family Limnoriidae. In this study we investigated patterns of distribution of wood boring species in Europe by combining

data from a field survey carried out in 15 European sites, ranging from Iceland to Turkey, and from primary literature. For ease of visualization we used Geographical Information Systems ArcMap 9.3. to georeference species occurrence. Furthermore, species were mapped on sea surface temperature and salinity data obtained from the Research Data Archive at the National Center for Atmospheric Research, to indicate the ranges of salinity and temperature tolerated by the organisms. Morphology-based identification of teredinids and limnoriids revealed the occurrence of six teredinid and three limnoriid species. The most widespread teredinid was *Teredo navalis* which is eurythermic and euryhaline. *Lyrodus pedicellatus* was the most abundant teredinid in Southern waters. The distribution patterns of limnoriids also matched closely their limits of tolerance for salinity and temperature. *Limnoria tripunctata* was the not only the most widespread limnoriid species but also the most destructive. In some cases, there was uncertainty in the morphology-based identifications because of damage or sometimes absence of diagnostic characters. Therefore we are using DNA barcoding as an additional tool to improve the accuracy of identifications and uncover potentially overlooked diversity. So far, a reference library of cytochrome oxidase I barcodes made it possible to assign specimens missing diagnostic characters to genus and species level. In addition, barcodes have also uncovered hidden diversity in *L. Pedicellatus*.

10:15 Reuben Shipway, L Borges, J Meuller, M Crockett & S Cragg. **An invasive species of teredinid, *Teredothyra dominicensis* (Teredinidae, Bivalvia), in the Mediterranean Sea**

University of Portsmouth, Institute of Marine Sciences
Email: reuben.shipway@port.ac.uk

This report describes the recent discovery of an invasive species of teredinid, *Teredothyra dominicensis*, in the Mediterranean Sea. Sampling was carried out over a period of one week, from the 7 th – 14th of August 2010, at the site of a replica shipwreck, off the coast of Kaş, southern Turkey. Two species of shipworm were found, *Nototeredo norvagica* and the previously unreported *Teredothyra dominicensis*. Its occurrence in the Mediterranean is highly unusually as it was thought to be confined to the Caribbean Sea and the Gulf of Mexico. Variation in the teredinids pallet size show the shipworm have spawned and recruited in the area, suggesting that this species may have established itself in Mediterranean waters. Further research needs to be conducted in order to assess the invasive potential of this teredinid, and the effects it may have on indigenous species.

Sunday September 25th 2011, Lecture Theatre "Halford Mackinder"

SESSION 10: Conservation Biogeography II: a changing World

11:00 Juan-Carlos González, N Collar, B Sheldon, & J Tobias. **Defying Wallace: Phylogeography and conservation of insular Asian hornbills**

Department of Zoology, Edward Grey Institute for Field Ornithology, University of Oxford, UK
Email: juan.gonzalez@zoo.ox.ac.uk

Recent phylogeographic studies postulated different dispersal regimes for organisms distributed across the Indomalayan and Papuo-Australian regions. Some attempted to determine how certain taxonomic groups traversed major biogeographical barriers – Wallace's, Weber's and Lydekker's lines to inhabit fringing archipelagos. Incomplete sampling across the length of these regions provided limited understanding of historical distributions crucial to identifying colonisation routes taken by ancestral forms. Hornbills are an ideal model system for testing hypotheses on when, where and how Wallacea, Philippines and Australasia were colonised. We constructed a comprehensive molecular phylogeny of representative "geo-isolates" of Southeast Asian hornbills to trace their dispersion. Bayesian chronogram estimated divergence around mid-Miocene and early Pliocene coinciding with key tectonic and palaeoecological events driving the diversification of insular hornbills. Results confirm Sundaland as the centre for Asian hornbill radiation, but different clades followed varied invasion scenarios. Borneo served as the jump-off point for dispersal of key genera into the Philippines and Wallacea. Rhyticeros evolved in Wallacea and radiated on both directions to colonise mainland Asia and Australasia. Divergence estimates and clustering of geo-isolates supports proposed separation into diverse conservation units and these shifts implies re-setting of priorities within the region.

11:15 Stefan Abrahamczyk & M Kessler. **Impact of climatic seasonality on the diversity of hummingbird assemblages and their food plants: what can we deduce for climate change?**

University of Zurich, Switzerland
Email: abraha@systbot.uzh.ch

The main food resource of hummingbirds is nectar and they are therefore strongly linked to their food plants. We conducted a survey of hummingbirds and their food plants along a latitudinal gradient in six Bolivian lowland forests. This gradient also represents a gradient of climatic seasonality. At each locality, species numbers of hummingbirds and their food plants such as hummingbird abundance and the numbers of flowers were recorded once in the rainy and once in the dry season. Climatic seasonality appeared to have a strong impact on the diversity of food plant species but not directly on hummingbird diversity or abundance, which are related to the abundance of food sources. Focussing on changes in species richness and assemblage composition between seasons, climatic seasonality was the most important factor. Therefore, we predict that climate change will directly affect the hummingbird food plants. These in turn will have an influence on the diversity and assemblage composition of hummingbirds. However, because the abundance of single food plant species can have far reaching impact on the hummingbirds assemblages, specific responses of hummingbird assemblages to climate change are difficult to predict.

11:30 Tonya A Lander, S Oddou-Muratorio & EK Klein. **The effect of landscape heterogeneity and anthropogenic land-uses on pollination patterns for wild cherry trees in northern France**

Unité Écologie Forestière Mediterranéenne, INRA, Domaine Saint Paul, F-84914 Avignon, France
Email: tonyaalander@gmail.com

Globally ecosystems are increasingly changed and fragmented. Understanding the effects of these changes on functional connectivity between populations is essential for conservation and management. The effect of fragmentation and non-forest land-uses on pollination for wild cherry (Prunus avium) was investigated at fragmented and unfragmented sites. Trees and progeny arrays were genotyped at seven microsatellites and one self-incompatibility locus. Pollination probability based on genetic data and three models of pollinator movement were analysed in the Spatially Explicit Mating Model (SEMM), a maximum likelihood approach: (1) a straight line between each tree pair divided into land-use types, (2) least cost paths (LCP), and (3) a circuit model. The straight line data showed that distance weighted by land-use type explained more of the variation in pollination probability between tree pairs than did simple linear distance. Trees at both the fragmented and unfragmented sites separated by forest were more likely to mate than those pairs separated by agriculture. At the unfragmented site cut forest (post-clearfell low scrub) posed a greater barrier to pollination than agriculture. The LCP analysis was not better than the straight line analysis at the unfragmented site. The circuit model data did not explain pollination probability as well as either the linear paths or LCPs. These results are explained in terms of hypotheses about how pollinators view and use different land-uses, the assumptions of the different model types, and the conservation possibilities that are opened when we look beyond traditionally defined areas of habitat into the wider landscape.

11:45 Dan F Rosauer & W Jetz. **Geography, predictors and conservation consequences of global centres of mammal phylogenetic endemism**

Yale University, USA
Email: dan.rosauer@yale.edu

We identify concentrations of evolutionary diversity for the world's mammals using phylogenetic endemism (PE), a recently proposed metric integrating range sizes and phylogenetic diversity. These areas of high PE matter for conservation because they hold a disproportionate amount of phylogenetic diversity restricted to small areas. We provide a global, cross-scale assessment that overcomes limitations of previous analyses restricted to predefined regions. The greatest concentrations of PE were found in island areas including Madagascar, the Caribbean, Southeast Asia and New Guinea. Central America, the Andes and small areas of Africa, Australia and the Tibetan Plateau also ranked highly. We assessed the potential determinants of PE patterns using null models and topographic and environmental variables. We predicted that above and beyond climatic drivers, PE would be related to isolation (topography, past and current land area) and historical persistence (climate stability, absence of glaciers). The deviation of observed PE from that expected under a null model was geographically heterogeneous, with peaks in Madagascar, parts of the Caribbean and Chile, confirming endemism of deep lineages. Current climate, topography and contiguous land area, emerge as strongest predictors of PE patterns and explain up to 78% of its variation. Interestingly, contiguous land area at the last glacial maximum, when lower sea level linked many current islands, was a significantly stronger predictor of PE than current land area. These findings contribute to the understanding of the biogeography of phylogenetic diversity and its potential implications for conservation priority setting.

12:00 Marcellinus A Hula. **Modelling farming practice as a driver of vegetation change in Benue State, Nigeria**

Benue State University, Makurdi-Nigeria
Email: akamas3@yahoo.com

This study assessed the contribution of farming practice to vegetation change in Benue State. The data used in this study was obtained through triangulation method where 373 sets of questionnaire were systematically administered to farmers among the farming communities in the State. This was augmented by onsite assessment, personal interviews and remotely sensed data. The study revealed that farm sizes were generally not large but scattered (a factor that encourages vegetation degradation). There was also a drastic drift in fallow period from long to short periods while; most of the tree species identified exhibited attractive lumberable characteristics that encourage loggers. The study also identified five major farming systems as bush fallow, slash-and-burn, zero-till, alley farming and shifting cultivation and four dominant cropping systems practised in the study area. Hence, Multiple Regression Analytical Model was used to model farming as driver vegetation change in Benue State where shifting cultivation, bush fallow and farm size were revealed as the most significant drivers at 0.05 significance level. Furthermore, analysis of the remotely sensed data showed that, vegetation covered 72% in 1986 but has shrank to 59% in 2010 giving rise to 13% loss to other land cover types. Finally, the study concludes by recommending that indiscriminate bush clearing and burning, use of herbicides and deforestation as well as unregulated logging should be discouraged while afforestation programme for all vegetation types should be encouraged. The farmers should be encouraged to practise vegetation conservation through farmer's cooperative societies and agricultural extension workers in the state.

12:15 Francisco Rodríguez-Sánchez. **Investigating biodiversity responses to climate change: the benefits of hindsight**

University of Cambridge, UK
Email: fr286@cam.ac.uk

Current climate change is challenging the predictive ability of biogeographers, ecologists and evolutionary biologists. The magnitude of the expected impacts makes it necessary to anticipate changes in order to attempt mitigation and to ensure preservation of organisms and eco-evolutionary processes. Although reliable forecasts of the future dynamics of biodiversity are thus much needed, retrospective studies can provide key insights based on a better knowledge of biodiversity responses to past climate changes. An important distinction with forecasting studies is the possibility of testing predictions by means of historical data, which permits the detection of flawed assumptions and thus theory refinement. However, the integration of different methodologies and data sources (fossil record, phylogeography, species distribution modelling) is critical in order to obtain strong inferences from the past. Furthermore, moving from hindsight knowledge to predicting the future is far from straightforward, and should be done with extreme caution in order to avoid spurious predictions. I will illustrate some of these problems, and the advantages of integrating evidences from the past, using case studies from the literature and ongoing work,

including the climate-driven demise of European laurel forests during the Neogene, as well as the range dynamics of European trees since the Last Glacial Maximum.

POSTER SESSION, AJ Hertberson Room
In alphabetical order

1. Marianne V Asmüssen, JR Ferrer-Paris, CM Zambrana-Torrelio, TL Bogich, P Dazsak, JP Rodríguez & KM Rodríguez-Clark. **The magnitude and impact of global illegal wildlife trade**

EcoHealth Alliance, UK
Email: zambrana@ecohealthalliance.org

After habitat loss, the greatest threat to biodiversity is the over-exploitation of wildlife, which includes commercial trade. CITES regulates the trade of 34,000 species, but illegal wildlife trade (IWT) is still widespread, being reported by 93% of CITES' 175 signatory countries. We present the first quantitative estimate of the number of birds, mammals and reptiles affected by both international and domestic IWT, using an extensive literature and database review. At least 1,687 species of birds, mammals and reptiles were traded illegally worldwide, with a total of ~29 million individuals trafficked per year. North America was the biggest participant in IWT, as the world's foremost importer (64% of seizures) and one of the largest exporters. IWT had a significant negative impact on the wild populations examined, causing on average a 60-70% decline. Illegal domestic trade appeared to be at least of the same magnitude as international trade, such that surveillance focused on the fraction of trade crossing international borders (e.g. CITES) is clearly insufficient for monitoring overall illegal wildlife trade. The main factor driving IWT was the likelihood of crime, violence and contract enforcement with secondary factors associated with supply and demand. In addition to quantifying the global magnitude of IWT and the negative impact of IWT on biodiversity, our analysis is consistent with hypotheses linking IWT and organized crime.

2. Magdalena Bennett, J Marino Jorgelina & C Sillero-Zubiri. **Andean cat biogeography and conservation: an application of a niche model**

Wildlife Conservation Research Unit, University of Oxford, UK
Email: magdalena.bennett@zoo.ox.ac.uk

Models that describe species' responses to the environment provide operational applications of their ecological niches. These are especially useful for threatened species that are rare, difficult to sample, or for which few data are available. The Andean cat (*Leopardus jacobita*) is among the rarest and least known felids in the world, restricted to the highlands of Peru, Bolivia, Chile and Argentina. This study explores the conservation implications of a bioclimatic model developed from Andean cat occurrence data. We identified biogeographical barriers that are common to other Andean species, and gaps in the distribution and ecological knowledge of Andean cats. In combination with land use maps we identified conservation priorities, taking into account the level of human pressure inside and outside protected areas. Suitable habitats for Andean cats are represented in 58 protected areas, covering 8% of the predicted suitable habitat, but only 14 have records of Andean cats to date. Some of these areas are under significant human pressure, particularly in the northern end of the distribution. We prioritise key areas for future surveys, and propose a detailed evaluation of the effectiveness for Andean cat conservation of this protected area network, thus contributing to the growing efforts to protect this rare cat more efficiently.

3. César Capinha & P Anastácio. **Predicting the impact of climate change on the invasive decapods of the Iberian inland waters: an assessment of reliability**

Universidade de Évora, Portugal
Email: capinha@uevora.pt

In an effort to predict the impact of climate change on invasive species distributions, forecasts from niche based models have been increasingly used. Here we investigate the reliability of these models for predicting the future climatic suitability to four highly problematic invasive decapods of the Iberian Peninsula: *Cherax destructor*, *Eriocheir sinensis*, *Pacifastacus leniusculus* and *Procambarus clarkii*. Predictions were made for three future time periods (2030, 2050 and 2080) under a low and a high greenhouse gases emissions scenario using an ensemble of five distinct predictive algorithms: generalized linear models, artificial neural networks, support vector machines, random forests and alternating decision trees. Four parameters were examined to infer the robustness of the forecasts: ability to predict current distributions, inter-model variability, degree of environmental extrapolation and plausibility of range changes considering the current knowledge about the species ecological preferences. Results show an overall decrease of climatic suitability to all four invaders as time progresses. However, while good indicators of reliability were found for *P. clarkii* and *P. leniusculus*, the forecasts for C. destructor showed low inter-model agreement and high levels of environmental extrapolation. For *E. sinensis* we also identified a consistently high predictive variability in most areas of range change. This study found that by simultaneously taking into account previous knowledge about the species ecology and spatially explicit measures of predictive variability and environmental extrapolation one can achieve useful insights on the reliability of forecasts of climate change impact in the distribution of invasive species.

4. Ivis J Chan Aguilar, DJ Golicher & AC Newton. **Analysis of tree beta diversity patterns for conservation planning in the Mesoamerican region**

Bournemouth University, UK
Email: ichan@bournemouth.ac.uk

The planet's biodiversity is increasingly threatened by the effects of rapid environmental change. Biodiversity loss led by expanding anthropogenic activity, combined with the effects of changing climatic regimes, pose a threat to natural communities and the ecosystem services that they underpin. Understanding how communities of species vary across space and the factors that drive such variation is essential to predicting the impacts of human and climate-induced changes on biodiversity and ecosystem services. This knowledge can be used to plan conservation areas that effectively represent the underlying ecological processes that maintain biodiversity and ensure the provision of ecosystem services crucial to human well-being. Beta diversity has been variably defined since the concept was first introduced as a measure of variation in species composition. This has given rise to the development of different measures of beta diversity, and to varying conclusions regarding the variation of species composition across space. This study evaluates variation in floristic species composition (beta diversity) between previously-defined conservation planning units within the Mesoamerican region. Herbarium collection records from across the region were used to conduct a cluster analysis based on the richness-independent Simpson turnover index (β_{Sim} defined by Lennon *et al.*, 2001) in order to evaluate the extent of species turnover between planning units. This analysis highlighted similarity in species composition between units generally considered to be distinct. We discuss the ecological implications of variations in species composition for conservation planning efforts.

5. Chris Cooney, N Seddon & J Tobias. **Examining the link between climatic niche evolution and the production of avian diversity**

University of Oxford, UK
Email: christopher.cooney@zoo.ox.ac.uk

Understanding the processes responsible for the production of new species has always been a central theme in evolutionary biology. Using data from contemporary species within a comparative framework, it is possible ask if factors thought to be important in the generation of diversity are in fact associated with observed instances of diversification. One potentially significant factor may be the extent to which species are able evolve their climatic niche and thereby adapt to novel environments. Two contrasting hypotheses link climatic niche evolution to diversification. One suggests that climatic niche lability within clades may be associated with accelerated rates of diversification, because lineages will be more likely to colonise novel environments or to have large ranges susceptible to vicariance events. Another suggests that low tolerance of climatic variability will drive speciation because climatic variation more readily presents barriers to gene flow. Here, I test these predictions by examining the relationship between rates of climatic niche evolution and lineage diversification across more than 100 avian clades. Using climatic, ecological and phylogenetic data for over 2000 species of birds, this work represents the most comprehensive investigation to date of how avian diversity has been shaped by adaption to novel climates.

6. Katharina Hoppe, H Kreft, R Seppelt & C Dormann. **Geographic variation of species-area relationships improves prediction of extinction rates**

Helmholtz Centre for Environmental Research – UFZ, Germany
Email: katharina.hoppe@ufz.de

Loss of habitat has been identified as one of the major threats to biodiversity. The most prominent way to estimate extinction rates from habitat loss is relating species richness S and sampling area A by applying the power law. A key role in defining the species-area relationship (SAR) is to estimate the z-value accurately. Although area by itself is an important factor this approach ignores mechanisms and conditions (e.g. climate, habitat diversity, evolutionary history, productivity) that determine species range sizes and density. The aim of this study is to fit SAR of vascular plant species richness to a series of biogeographical regions, e. g. floristic kingdoms, realms and biomes, and examine how different land-cover types effect the SAR parameters as well. For the latter we decided to use the HYDE land-cover data set. However, we test the hypotheses that species richness is more effected by biogeographical patterns than by sample size and SARs are signicantly different among land-cover classes. Finally, we exemplify our approach by predicting extinction rates due to land-cover change and compare our results with predictions made without considering land cover. We hypothesize that including varying SARs alters the prediction of extinction rates due to land conversion.

7. Sarah Jones, R Grenyer & T Thornton. **The importance of place: A methodology for evaluating the biocultural diversity of SE Alaska using Tlingit place names as an indicator of cultural diversity**

Department of Geography, University of Oxford, UK
Email: sarah.jones@bnc.ox.ac.uk

Biocultural diversity describes the intimate relationship between biological and cultural diversity found in

environments around the world. Many studies have evaluated biocultural diversity using the number of languages in an area as an indicator of cultural diversity. This study presents a novel approach to evaluating the relationship between biological and cultural diversity by using place names as the frame of analysis of cultural diversity. Place names are embedded within a people's language and are reflective of that people's knowledge and use of their environment. This study develops a methodology for identifying 'hotspots' of biocultural diversity using place names of the Tlingit, an aboriginal peoples in Southeast Alaska, and various indicators of biological diversity using spatial analysis tools in GIS. The results of this study may indicate priority areas for conservation that will protect both cultural and biological diversity, contributing to the sustainability of Tlingit culture and the environment in Southeast Alaska.

8. Yael Kisel, L Mcinnes, NH Toomey & CDL Orme. **How diversification rates and diversity limits combine to create large-scale species –area relationships**.

Imperial College, London, UK
Email: lynsey.mcinnes01@imperial.ac.uk

Species – area relationships (SARs) have mostly been treated from an ecological perspective, focusing on immigration, local extinction and resource-based limits to species coexistence. However, a full understanding across large regions is impossible without also considering speciation and global extinction. Rates of both speciation and extinction are known to be strongly affected by area and thus should contribute to spatial patterns of diversity. Here, we explore how variation in diversification rates and ecologically mediated diversity limits among regions of different sizes can result in the formation of SARs. We explain how this area-related variation in diversification can be caused by either the direct effects of area or the effects of factors that are highly correlated with area, such as habitat diversity and population size. We also review environmental, clade-specific and historical factors that affect diversification and diversity limits but are not highly correlated with region area, and thus are likely to cause scatter in observed SARs. We present new analyses using data on the distributions, ages and traits of mammalian species to illustrate these mechanisms; in doing so we provide an integrated perspective on the evolutionary processes shaping SARs.

9. Sara Manafzadeh, G Salvo & E Conti. **Evolutionary history of *Haplophyllum* (Citrus family) in the Irano-Turanian and Mediterranean floristic regions**

Institute of systematic botany, University of Zurich, Zollikerstrasse 107, CH-8008, Zurich, Switzerland
Email: sara.manafzadeh@systbot.uzh.ch

Haplophyllum (68 herbaceous species) is one of the most species-rich, but least-studied genera of Rutaceae. It reaches maximum species diversity (60% of the species) in the Irano-Turanian floristic region. Thirteen percent of the species are however present in the Mediterranean basin. Many species of *Haplophyllum* are characterized by a small geographical range size, sometimes limited to a single mountain chain, a feature that makes them especially vulnerable to extinction. We intend to carry out an integrated study that will allow us to understand the origin and evolution of *Haplophyllum*, define species boundaries, improve understanding of species diversity, and finally recommend conservation guidelines. Consequently, we generated phylogenies from DNA sequences for 66% of the species of the genus. Moreover, molecular dating, and ancestral range reconstructions analyses were carried out to investigate the extent to which past geological and climatic histories of the Irano-Turanian and Mediterranean floristic regions explain the current distribution of the genus. Our phylogenetic analyses identified both cases of strongly-supported species monophyly and instances of species non-monophyly. Our preliminary results strongly suggest that the genus *Haplophyllum* originated in the Irano-Turanian region and has subsequently colonized the Mediterranean basin. This is one of the first studies on the interaction between two floristic regions via a genus that has originated in one region and colonized the other. Different ecological requirement (desert vs. mountainous), diverse geographical range (widespread vs. narrow endemic) make *Haplophyllum* an excellent model to investigate the correlates of habitat range, and geography of speciation.

10. Carlos Norman, A Garrido & F Hidalgo. **New exotic species in the western Mediterranean sea**

Grenade University, Spain
Email: carlosnorman@uma.es

The main objective of our work is to catalog and understand the current situation alien species of fishes in the western Mediterranean sea. The study area is located in the Alboran Sea, subbasin located between the western Mediterranean Spanish coast, the Maghreb and Algeria, with a clearly individualized marine space. We have tried to check the exotic species inputs from the atlantic waters and the Red sea waters. Our methodoly has been enriched with the datas from an extensive review of scientific literature, from fishermen who brought some species of theirs sells in the fish markets and from our own direct observation on the trawlers. Finally, we have found seven new species which are triying to stablish from other areas to the western Mediterranean waters.

11. Utku Perktas & E Quintero. **Phylogeography and species limits in the great spotted woodpecker *Dendrocopos major***

Department of Ornithology, American Museum of Natural History, New York, USA
Email: uperktas1@amnh.org

We conducted a comprehensive geographic survey of the mitochondrial DNA variation of the Great Spotted Woodpecker (*Dendrocopos major*) throughout its entire distribution range, using partial sequences of ND2 to investigate the genetic structure of this species. We also constructed current and paleoenvironmental niche models (ENM) to understand their current distribution. Although results showed that the degree of genetic variation is low in Eurasia, populations from Japan, Far East Russia, and Iran showed substantial sequence divergence. The populations from Japan and Far East Russia were sister to the rest of Eurasia and North Africa, whereas the population from Iran was the sister species to the remainder of the clade. Our ENM results suggest that postglacial colonization to Europe and Russia could not have occurred from Iran and Far East Russia. Rather, It is plausible to say that multiple refuges located on southern Europe, Turkey, and southeastern Russia might have affected the current genetic structure of the species.

12. Claire L Salisbury, N Seddon & JA Tobias. **River dynamics, species ecology, and the biogeography of Amazonian birds**

Edward Grey Institute, University of Oxford, South Parks Road, Oxford, UK
Email: claire.salisbury@zoo.ox.ac.uk

Numerous hypotheses have been proposed to explain the high biodiversity of the Amazon rainforest. The Riverine Barrier Hypothesis (RBH) proposes that rivers act to separate populations, reducing gene flow between them, leading to divergence and ultimately speciation. The majority of previous studies testing the RBH have been limited in scope to a few species and rivers at a time, and as a result support for the RBH is mixed. This study addresses these shortcomings by looking at the effect of all major rivers on the range distributions of all Amazonian forest bird species and subspecies, in relation to their ecology. We show that the proportion of species and subspecies bounded by rivers strongly relates to river width but not length. Furthermore, the river effect is much greater at the subspecies level, suggesting a role for rivers in facilitating present-day intraspecific diversification. Ecological traits are key predictors of whether a river will act as a barrier for a species or not: understorey and habitat specialist species are more affected by riverine barriers than their canopy and habitat generalist counterparts. Additional ecological traits become important at the subspecies level. Overall, ecological traits associated with poor dispersal make it more likely that a species will be bounded by a river. This results in poorly dispersing Amazonian taxa having higher levels of intraspecific diversity (measured as subspecies richness), in contrast with global patterns showing greater intraspecific diversification in highly dispersive taxa.

13. Ana MC Santos & MN Dawson. **Frontiers of Biogeography**

International Biogeography Society
Email: ana.margarida.c.santos@googlemail.com

Frontiers of Biogeography (ISSN 1948-6596) is the open access journal published by the International Biogeography Society. Frontiers of Biogeography publishes opinions, perspectives, and reviews, symposia proceedings, letters to the editor, book reviews, research updates, interviews, and articles on how to teach, disseminate and/or apply biogeographical knowledge. The journal is published quarterly, and prior issues are archived at http://www.biogeography.org/html/fb.html. We are actively looking for new syntheses advancing the frontiers of biogeographical knowledge.

14. Diana Mastracci. **How do Maps of Land Cover Change Define Landscapes?**

University of Oxford, UK
Email: diana.mastracci.sanchez@gmail.com

As the space around us permeates with unseen ideologies and boundaries formed by culture, socio-economics, language and politics, it is consequential that conservation overlaps with a wide-range of disciplines. By its very nature it is tied into economic and political structures. It should then be inconceivable and counter-productive to think of remote sensing: one of the most powerful and effective tools in detecting land cover change, in isolation. An investigation of published literature, however, indicates that there is a paucity of research that integrates local knowledge with complex remote sensing techniques such as the use of satellite imagery with supervised classifications and groundtruthed, georeferenced indigenous classifications of land cover. In order to fill this gap we need to advance an appreciation of the complex and multiple dimensions of the study of land cover change. How can existing space observation techniques be used to move towards a bio-cultural study of land cover change? And, as a corollary, what kind of technological design and practices should be constructed to aid in such process?

15. Christopher Trisos, H Petchey, L Owen, JA Tobias & N Seddon. **Tests of community assembly across small spatial scales in Andean bird communities.**

University of Oxford, UK
Email: christopher.trisos@zoo.ox.ac.uk

There is strong evidence that both local and regional processes play a role in determining species occurrences within communities. At the local scale, environmental filtering and competitive exclusion are most often referred to as the processes important in community assembly. Competitive exclusion is thought to play a more dominant role at smaller spatial scales, with environmental filtering being stronger at larger spatial scales. However, the spatial scale at which this switch in the relative strengths of competitive exclusion and environmental filtering occurs is not known for many taxa. We use functional trait and phylogeny-based methods to test for the signal of environmental filtering and competitive exclusion in community assembly for insectivorous bird communities across a range of spatial scales (0.75ha-12ha). Preliminary results show that environmental filtering is stronger than competitive exclusion in determining community membership.