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rapid global warming. In so doing, comparative phylogeographic inference will increasingly be able to predict and identify climatically stable landscapes that harbor divergent lineages below the species level.

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Edited by Michael N Dawson

## symposium summary

# Analytical advancements in macroecology and biogeography

A symposium at the 5th International Biogeography Society Conference – Heraklion, Greece, 7–11 January 2011

Macroecology analyzes patterns and processes of biological diversity at broad scales, both in space and time, based on an integration of distinct fields of ecology, physiology, behavioural sciences, evolution and biogeography. Common definitions of macroecology (e.g., Brown 1995, Gaston & Blackburn 2000) emphasize two sets of contrasting issues: “patterns and processes” and “scale”. In that context, we can ask not only how ecological and evolutionary processes at local scales—such as selection, drift, dispersal and competition—affect individuals and populations, but also how they may lead to geographic range dynamics

(extinction, contraction and fragmentation) at the species level. We can then contemplate how the patterns derived from ecological and evolutionary processes may shape broad-scale patterns of diversity, and also how other emergent processes or properties contribute to diversity patterns.

To achieve this synthetic, integrative view, and understand the roles of different processes and emergent properties at distinct scales, it is important to think about which methods could be used. The continuous development of computing capacity and increasing data generation allow ever more sophisticated analyses, enabling novel in-

sights into macroecological and biodiversity patterns. These methodological developments are interesting for biogeography and macroecology mainly from a theoretical perspective. To answer complex questions and test hypotheses using large data sets, we might find use for complex analytical tools developed or used in other research fields of ecology and evolutionary biology, or science in general. Bringing together researchers with different backgrounds and working with different methods that may be potentially useful for macroecologists and biogeographers was the main purpose of the symposium on *Analytical Advancements in Macroecology and Biogeography*.

The symposium started with Andy Purvis (Imperial College at Silwood Park, UK) showing how new macroevolutionary approaches and phylogenetic comparative methods can be projected into geographical space and used to test niche conservatism, which he illustrated with global data on mammals and amphibians (e.g., Olalla-Tárraga et al. in press). Pedro Peres-Neto (University of Montreal, Canada) followed the same trend of unifying the analytical frameworks for geographical and evolutionary processes. He showed many simulation results, comparing methods for dealing with spatial and phylogenetic autocorrelation, contrasting Moran's eigenvector methods (see Griffith & Peres-Neto 2006) with generalized least-squares approaches. His talk was followed by Robert Colwell (University of Connecticut, USA) and Thiago F. Rangel (Universidade Federal de Goiás, Brazil) who showed how mid-domain models, originally developed as null models for macroecological patterns in species richness, could be expanded into mechanistic models that account for the roles of various processes causing latitudinal and altitudinal gradients in species richness (e.g., Colwell & Rangel 2010).

At a finer evolutionary scale, Albert Phillimore (Imperial College at Silwood Park, UK) showed how quantitative models of geographic and temporal variation within a species can be used to study adaptive processes at broad geographical scales, providing an interesting link between quantitative genetics and macroecology (Phillimore et al. 2010). Next, Marcel Cardillo

(Australian National University, Australia) presented an analysis of phylogenetic diversity and structure of Carnivora assemblages (Cardillo 2011). Finally, Richard Ree (Field Museum of Natural History, USA) provided models for analyzing speciation, extinction and range dynamics using phylogenies (e.g., Ree & Sanmartín 2009).

Each speaker provided a fresh perspective on methods that were developed in different fields in recent years and which are useful for answering a variety of questions in macroecology. It is important to note that some of the methods and procedures are still under development, and their application to new problems will require more research and deeper evaluation of statistical properties and computational facilities. This is certainly a stimulus to young as well as older researchers and many exciting advances and insightful applications may be expected in the years to come. There seems to be a clear trend towards using tools that simultaneously evaluate phylogenetic and geographical patterns, adopting an explicit definition of macroecology and biogeography as ways to deal with processes underlying species' dynamics in space and time.

In that context, the recent paper by Jonathan B. Losos on the limitations of phylogenies in comparative biology is a reminder to us all that patterns are not to be confused with processes (Losos 2011), and that while a new tool provides exciting new insights it may not necessarily be the best way to hammer an old nail. Also, methodological advances are not a substitute for conceptual and theoretical development. The symposium speakers insightfully illustrated how new methods can aid conceptual advances, via better-defined questions, hypotheses and predictions.

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Edited by Joaquín Hortal

## symposium summary

# Marine biogeography

A contributed session at the 5th International Biogeography Society Conference – Heraklion, Greece, 7–11 January 2011

How does life in the sea compare or contrast with life in or above its land, lakes, rivers, and streams? By asking questions about geographic patterns of marine speciation (Renema, Tellier et al., Tyberghein et al.), how well landscape metrics describe saltwater systems (Wedding et al.), and how patterns of human use impact the marine biota (Davidson et al., Tittensor and Worm), one might begin to intuit some answers.

Willem Renema's study of the distinctive *Cycloclypeus*, the largest living benthic foraminifera (10–12 cm diameter), which occupies a very well characterized niche on tropical coral reefs, provides a well-constrained fossil series, of a quality rare in any realm, for examining patterns and rates of speciation. He found that long-distance dispersal events from the Indo-West Pacific culminate in extinction in the Mediterranean, and that morphological disparity increases regionally but not globally during the Middle Miocene following range contraction and re-expansion. The region of speciation may vary among taxa, even if speciation is contemporaneous. These results suggest patterns of marine species diversity can be influ-

enced by local 'species pumps' (that is, vacuum pumps drawing species in, rather than pressure pumps pushing species outward) causing regional dispersal and diversification, and that evolutionary ecological dynamics of at least some taxa may play out as a series of taxon cycles.

Florence Tellier and colleagues also found evidence of geographically variable evolutionary dynamics along the intertidal rocky shore of the southeastern Pacific. Their comparative phylogeographic study of two low-dispersal co-distributed species, an isopod (*Excirologa hirsuticauda*) and a kelp (*Lessonia nigrescens*), revealed genetic discontinuities in both taxa at 30°S, with sub-groups—possibly cryptic species—of one or the other species either side of this well-known biogeographic filter. Their inference is that concordant phylogeographic patterns may arise from significant environmental factors such as vicariance mediated by oceanography. Yet, secondary discontinuities that are geographically incongruent exist in these taxa: at 27°S for the kelp and 33°S for the isopod. Transplant and laboratory experiments with the kelp suggested at least some of