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update: Of refugia and colonization, an innovative use of biogeography for climate studies

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Author

Thorne, James H.

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require a careful consideration of exactly what constitutes a "random" and a "structured" matrix with respect to species nesting and spatial turnover. But they should be conducted before attempting a meta-analysis of published empirical matrices.

Second, this index, like most other measures of nestedness and beta diversity, assumes that island censuses are complete and there are no undetected species. Anne Chao and colleagues have recently modified classic similarity indices to take into account undetected shared species. The presence of undetected species biases the unmodified indices towards underestimating shared species (and hence over-estimating beta diversity). It is not yet clear how serious of a problem this is for Baselga's (2009) proposed partition.

Baselga (2009) has made an innovative contribution that deserves further exploration.

Baselga, A. (2009) Partitioning the turnover and nestedness components of beta diversity. *Global Ecology and Biogeography*, doi:10.1111/j.1466-8238.2009.00490.x.

Nicholas J. Gotelli

Department of Biology, University of Vermont, USA

e-mail: Nicholas.Gotelli@uvm.edu
<http://www.uvm.edu/~ngotelli/homepage.html>

Edited by Thiago F. Rangel

update

Of refugia and colonization, an innovative use of biogeography for climate studies

A beautiful sight in Glacier National Park is found along the Trail of the Cedars, a stand of western red cedar (*Thuja plicata*) replete with mossy rocks and cold running waters. This tree, and western hemlock (*Tsuga heterophylla*), are emblematic of the northern coastal temperate rainforests of the western US and Canada. However, they are also found over 160 kilometers to the east, across a large expanse of sagebrush steppe, on the western flank of the Rocky Mountains. This well known disjunct rainforest distribution is the subject of a new biogeographic study titled, "The coastal-disjunct mesic flora in the inland Pacific Northwest of USA and Canada: refugia, dispersal and disequilibrium" by Daniel Gavin, professor of Geography at the University of Oregon. Dr Gavin analyzed the patterns of biodiversity between the coastal populations and northern and southern interior populations of 67 vascular plant species, all components of the temperate rainforest group. He used the biogeographic patterns to explore the possible interactions between species richness, climate change, and glaciation. The study examines how species richness varies with climate; how distribution patterns may have been affected by

glaciated *versus* un-glaciated areas in the interior; and whether life history characteristics such as seed dispersal mode and growth habit help explain the current extent of the species analyzed.

Dr. Gavin mapped each plant's range distribution to 50x50 km grid cells using a variety of reference materials. He then examined patterns of species richness, according to life history characteristics and climate as defined in the PRISM data sets. The study used regression models of species richness as a function of Actual Evapotranspiration (AET) in the coastal regions (most mesic and specious) to develop expected levels of species richness for the AET of more recently suitable interior regions. This permitted regional quantification of the level of disequilibrium from expected species richness, an indication of incomplete colonization by the regional flora. The northern interior was most in disequilibrium, indicating that many species have yet to disperse into the area. Since several sources of colonizers exist, the implication is that some plant species may have a difficult time dispersing into newly suitable habitats across a fragmented landscape under future climate change.

The pattern-based analysis provided an opportunity to test a variety of dispersal and refugia scenarios that have been proposed for the Pacific Northwest, because it has three categorical areas: coastal non-glaciated, southern interior non-glaciated, and northern interior glaciated. Species with the highest dispersal capacity had the largest ranges and were more likely to have dispersed to the northern interior glaciated (recently unglaciated) zone. The study also found that the northern interior zone had been colonized by species from both the coast and from further south in the interior. Less dispersive capable species showed more restricted range, including six endemic species from Idaho, which had not moved to the north.

This last finding led the author to conclude that plant characteristics are likely an important component in the effort to determine what species may be able to successfully shift range across

a fragmented landscape under future climate change. The author points to the importance of including phylogeographies in future work, but has done a remarkable job of identifying vulnerabilities of plant species to climate change using more traditional biogeographic techniques.

Gavin, D.G. (2009) The coastal-disjunct mesic flora in the inland Pacific Northwest of USA and Canada: refugia, dispersal and disequilibrium. *Diversity and Distributions*, 15, 972-982.

James H. Thorne

Information Center for the Environment, University of California at Davis, USA

e-mail: jhthorne@ucdavis.edu

<http://ice.ucdavis.edu/people/jhthorne>

Edited by Lee Hannah

update

More uncertainty with BIOMOD

Species distribution modeling (SDM) has grown in importance over the last decade to become a powerful tool in conservation planning, global change forecasting, ecological hypothesis testing, and characterization of niche properties in phylogenetic analyses. Many scientists have contributed to the conceptual, statistical and technical development of this field. While I believe that further development has asymptoted in many domains of SDM research, it is clear that BIOMOD is a significant contribution.

A decade ago, we faced numerous uncertainties and limitations in building SDMs. Few statistical techniques were available and no comparative studies existed. Generalized Linear Models were a standard method, and key issues included how best to fit response shapes, how to evaluate competing models, and what statistical methods to use to get “the best model” of a target species. Climate change projections were usually established by simply adding 2-4°C to annual mean temperature maps, and “the best model” was then projected into the future. BIOMOD, in its

first version of 2003, was a huge step forward. It included four different statistical methods to model hundreds of species automatically. Further, it used a simple method to identify the model that best fit the general trend among the resulting models.

At the same time modeling and forecasting of a range of scenarios, including the assessment of projection uncertainty, became an important aspect of research on climate change impacts. This has dramatically increased the demand for model building, model averaging, ensemble forecasting, and analysis of complex output. We are no longer interested in identifying “the best model”, but rather the mean and variation of models – currently and when projected to the future.

Ensemble forecasting is so complex that most of us will only include a fraction of the possible uncertainty sources when modeling potential climate change effects upon species distribution patterns. Over the last 6 years BIOMOD has been developed, improved, and extended. It now offers