



NIMBioS

National Institute for Mathematical
and Biological Synthesis



NIMBioS Interdisciplinary Seminar

3:30 p.m.*, Tuesday, October 29, 2013

Dr. Nick Matzke
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“Statistical model choice in phylogenetic biogeography: Inference of speciation processes and ancestral range, and prospects for integration with species distribution modeling”

Historical biogeography has been characterized by unresolved debates about which processes, such as dispersal or vicariance, are most important for explaining geographic distributions. Biogeography programs typically make fixed assumptions about which processes are allowed, and these assumptions dominate inference. A new R package, BioGeoBEARS, implements the most popular models in a common likelihood framework, and adds new "+J" models that allow jump dispersal/founder-event speciation. Statistical model choice shows that founder-event speciation is a crucial process in almost every clade, although it is measurably weaker in non-island systems. Simulations indicate that better models estimate ancestral ranges with dramatically greater confidence and higher accuracy. All of these models are special cases of a supermodel implemented in BioGeoBEARS, enabling estimation of the relative importance of different speciation modes given sufficient data. At the conclusion of my talk, I outline a program to expand this research by linking phylogenetic biogeography with species distribution modeling (SDM). Standard SDM is done one-species-at-a-time, ignoring phylogenetic autocorrelation, and typically ignores non-climatic causes of distributions such as dispersal limitation. As a result, all of these factors are confounded in current environmental niche models. With a combined approach, we may be able to untangle these factors.

Location: Room 105 at NIMBioS, Claxton Education Bldg, 1122 Volunteer Blvd.

**Join us for refreshments at 3 p.m.*

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