

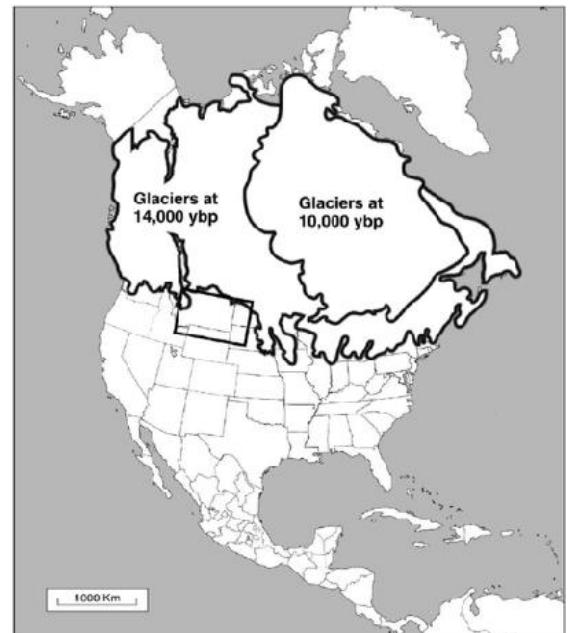
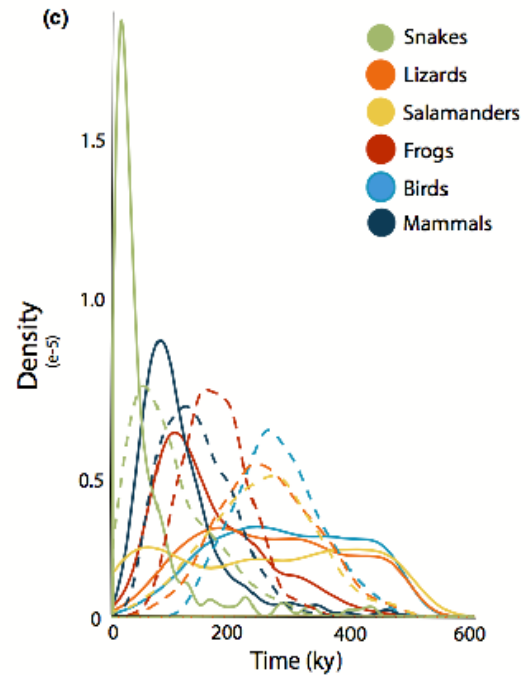
DEPARTMENT OF ECOLOGY & EVOLUTIONARY BIOLOGY

Fall 2016 Seminar Series

Dr. Mike Hickerson - City University of New York
American Museum of Natural History

“Comparative population genomics for inference of community assembly”

Pleistocene climatic cycles altered species distributions, yet the complex temporal and spatial fundamentals underlying the resulting community assemblies remain unknown. To meet this challenge, we have developed several temporal and spatial methods for reconstructing the complex assemblage-level demographic histories that make use of genomic data from non-model organisms within hierarchical Bayesian, composite likelihood and random forest classification frameworks. To illustrate, we first test if population sizes across lineages of snakes, lizards, turtles, mammals, birds, salamanders and frogs in the eastern Nearctic expanded synchronously to Late Pleistocene climate changes. To better accommodate important details in such assembly models, we introduce a new model that directly links forward time processes underlying species abundance distributions under various models of community assembly with backwards genetic processes under the coalescent. Secondly, I present the spatial site frequency spectrum, a new tool for jointly using spatial and genetic data to infer the geographical source areas underlying Late Pleistocene assemblage-level expansion and assembly. Lastly, I present our new technique for using whole-genome data for inference of the cyclical isolation, admixture and divergent selection across co-distributed taxon-pairs.



Friday, November 4, 2016; Room 307, SERF; 3:30 - 4:30PM.
Pre-talk reception: 3:00 PM in Dabney 568