"Modeling phylogenetic comparative methods with hybridization"

Dr. Tony Jhwueng
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Tuesday, January 25, 2011
3:30 p.m.*, Room 403, Blount Hall, 1534 White Ave.

Phylogenetic Comparative Methods (PCMs) are statistical methods for analyzing the data on a group of related species. Questions such as "How does brain mass vary with body mass in a group of species?" and "What are likely ancestral states?" all involve comparative data. While hybrid species are known to share similar phenotypes inherited from their parents, the rate of variation of a trait between the hybrid and its parents is rarely studied by comparative analysis. Because the species are related by shared evolutionary history, it may not be reasonable to view such data as independent, identically distributed realizations of the same stochastic process. Instead, information about the shared evolutionary history, as given by the phylogeny for the species, is often incorporated into the analysis. If evolution involves ancient hybridizations, then we cannot simply use the phylogeny to represent the affinity among species but instead use the phylogenetic network. Dr. Tony Jhwueng develops possible PCMs when there are ancient hybridization events in addition to speciation events. The new PCMs are applied to a real data set to investigate whether the rate of variation is statistically significantly different between the hybrid and other species. Several simulation studies to assess the validity of the new PCMs are also performed. Dr. Jhwueng will discuss his research and findings during the seminar.

*Join us for refreshments in the NIMBioS Lobby on the 4th floor at 3 p.m.