Modeling Phylogenetic Comparative Methods with Hybridization

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Abstract

Phylogenetic Comparative Methods (PCMs) are statistical methods for analyzing data on a group of related species (called comparative data in the ecology and evolution literature). Questions such as how does brain mass vary with body mass in a group of species, or what are likely ancestral states all involve comparative data. Since 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. Hybrid species are known for sharing some common phenotypes from their parents. If evolution involves ancient hybridizations (reticulate evolutionary events), then we cannot simply use the phylogeny to represent the affinity among species but instead shall use the phylogenetic network (which is a directed acyclic graph, coupled with time constraints). As the rate of variation of the trait between hybrid and its parents is rarely studied by comparative analysis. I develop possible PCMs when there are ancient hybridization events in addition to the speciation events. I then apply the new PCMs to a real data set (body length in cichlid) to investigate if the rate of variation is statistically significant different between the hybrid and other species. Several simulation studies are also performed to access the robustness of the new PCMs.