

Using phylogenetic information and the comparative method to evaluate hypotheses in macroecology

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It is widely recognized that macroecological patterns are not independent of the evolution of the lineages involved in generating these patterns. While many researchers have begun to evaluate the effect of ancestor-descendant relationships on observed patterns using the phylogenetic comparative method, most macroecological studies only utilize the cross-sectional comparative method to 'remove the phylogenetic history', without considering the option of evaluating its effect without removing it. Currently, most researchers use this method without explicitly evaluating three fundamental evolutionary assumptions of the comparative method: (i) that the phylogeny is constructed without error (which implies evaluating phylogenetic uncertainty); (ii) that more closely related species tend to show more similar characters than expected by chance (which implies evaluating the phylogenetic signal) and; (iii) that the model of the characters' evolution effectively recapitulates their history (whic