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Title: Embracing the hidden strengths of large (or many) phylogenetic trees for comparative biology

Abstract -- The distribution of diversity within plants can vary considerably from clade to clade. Attempts to understand these patterns often employ state-dependent speciation and extinction models to determine whether the evolution of a particular novel trait has increased speciation rates and/or decreased extinction rates. It is still unclear, however, whether these models are uncovering important drivers of diversification in plants (e.g., high rates of speciation and/or lower rates of extinction), or whether they are simply pointing to more complex patterns involving many unmeasured and co-distributed factors (e.g., flower color correlates with diversification, but the true correlation is with plant height). Here, I will discuss these issues in detail and how they can be solved by extending the popular state-dependent speciation and extinction models to account for the presence of unmeasured factors that could impact diversification rates estimated for the states of any observed trait. I will focus on the important ways in which these new methods provide a more nuanced understanding of trait-dependent diversification. I will also focus on the inherent value of large (or many) phylogenetic trees (e.g., phylogenies with 1000's of species), in general, and discuss ways in which they naturally mitigate against biases with the way many comparative tests are traditionally carried out on any taxonomic group of interest.