

Supporting Information for: Estimates of Phylogenetic Signal Based on Lambda are Often Inaccurate

Here we provide additional supporting information referenced in the main document: additional analyses, and simulation results across a wider set of input conditions.

Simulations on differently shaped phylogenies

In addition to using pure-birth phylogenies, we explored the effect of tree shape on our findings using both balanced and pectinate trees. As before, simulations were conducted on a range of tree sizes ($n = 2^5 - 2^{10}$), and across a range of input levels of phylogenetic signal ($\lambda_{in} = 0.0 - 1.0$; in 21 intervals of 0.05 units). For each n and λ_{in} combination, 50 replicates of a continuous trait were simulated using a Brownian motion model of evolution. Using these, we estimated the degree of phylogenetic signal using λ .

Results. As found with pure-birth phylogenies, estimates of λ varied ** FINISH THIS** (Fig. S1, S2).

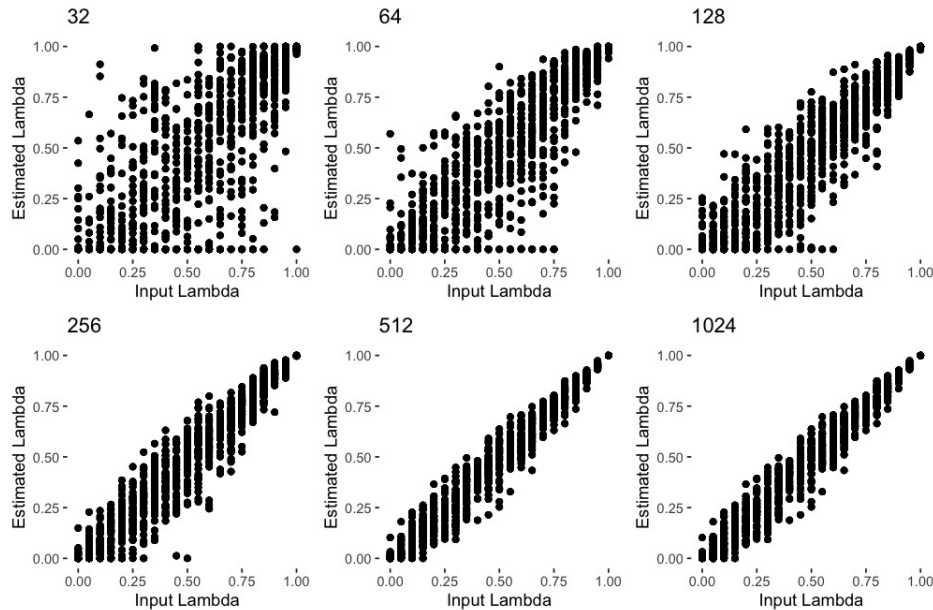


Figure S1. Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. Results obtained using balanced trees.

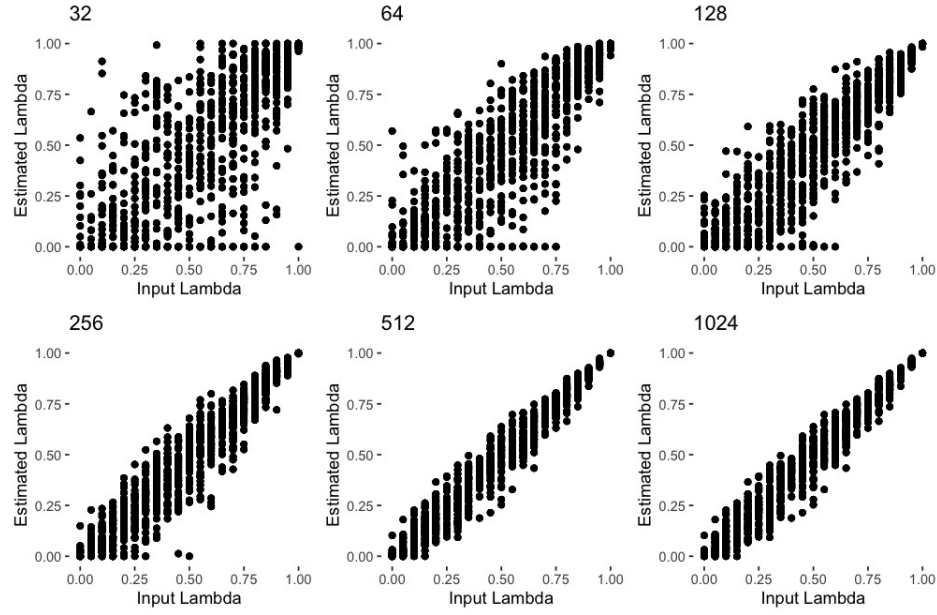


Figure S2. Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. Results obtained using pectinate trees.

Literature Survey

References