

Supporting Information for: A Standardized Effect Size for Evaluating the Strength of Phylogenetic Signal, and Why Lambda is not Appropriate

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 ($\lambda_{in} = 0.0 \rightarrow 1.0$; 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 most dramatically in simulations with fewer species and at intermediate values of lambda (Fig. S1, S2). Pectinate trees showed an interesting tendency to underestimate λ across input values. Most dramatically, some simulations on the largest pectinate phylogeny ($n = 1024$) estimated $\lambda = 0$ for input values as high as 0.5 (Fig. S2).

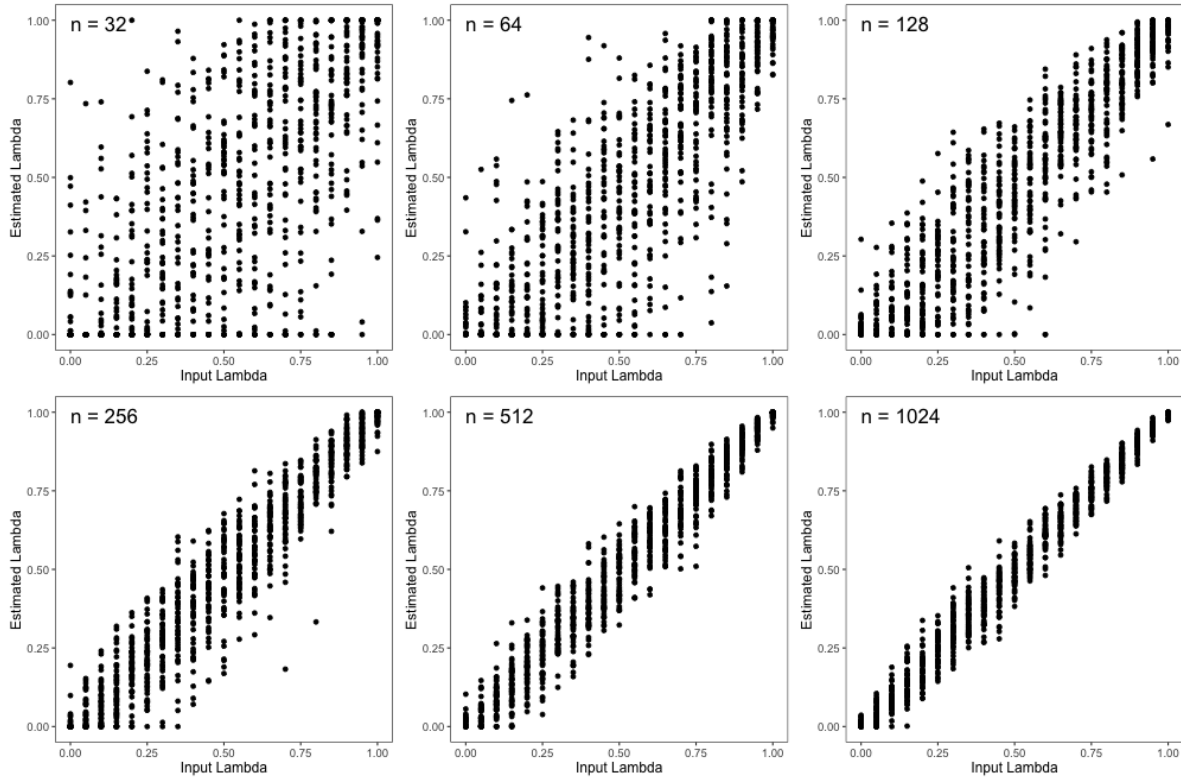


Figure S1. Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. Results obtained using balanced trees.

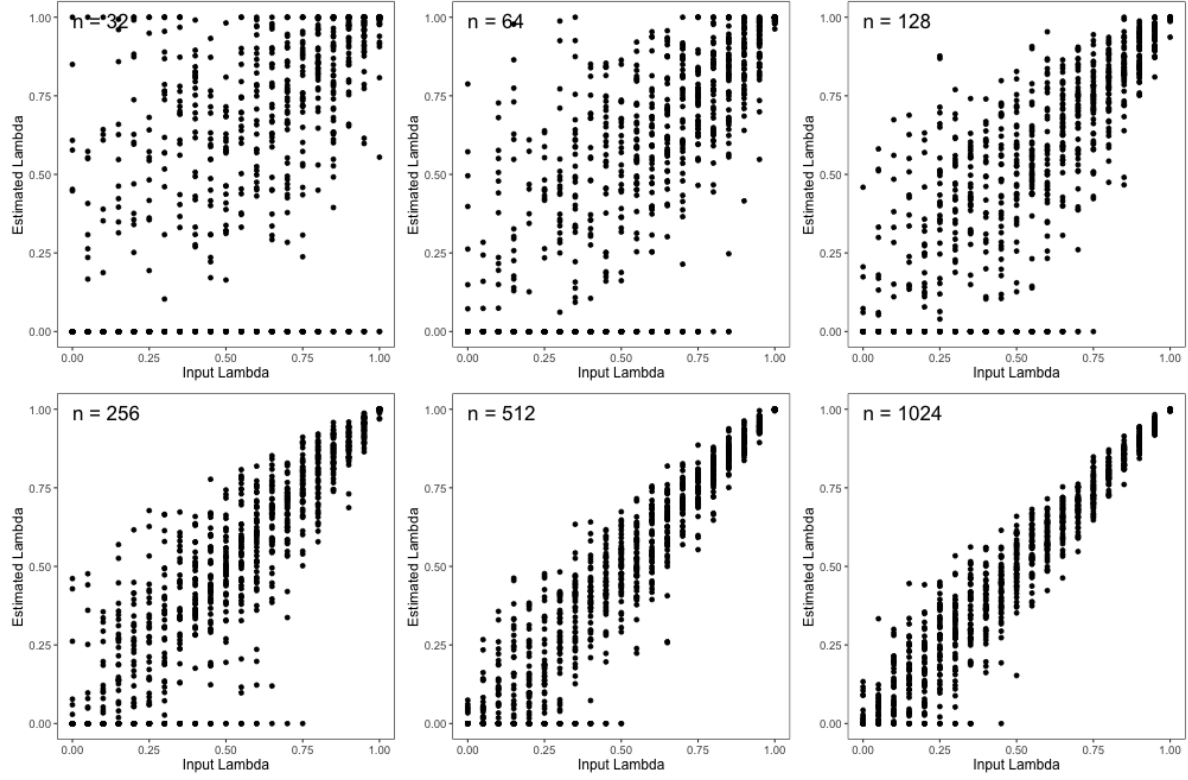


Figure S2. Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. Results obtained using pectinate trees.

Simulations of phylogenetic regression and ANOVA

We analyzed the precision of parameter estimation when parameters were obtained in phylogenetic regression and ANOVA. This involved simulations of dependent variables with λ values ranging from 0 to 1 (21 intervals of 0.05 units) across pure-birth trees ($n = 2^5 - 2^{10}$). For each λ input value, independent variables were then generated with a known relationship to the simulated dependent variable ($\beta = 0, 0.25, 0.5, 0.75, 1.0$), from which λ was then estimated.

Results As with the results from the regression analyses in the main text, we found poor precision of λ estimation in smaller trees and at intermediate levels of phylogenetic signal with phylogenetic ANOVA (Fig. S3). Slope was reliably estimated across tree sizes and known λ values (Fig. S4).

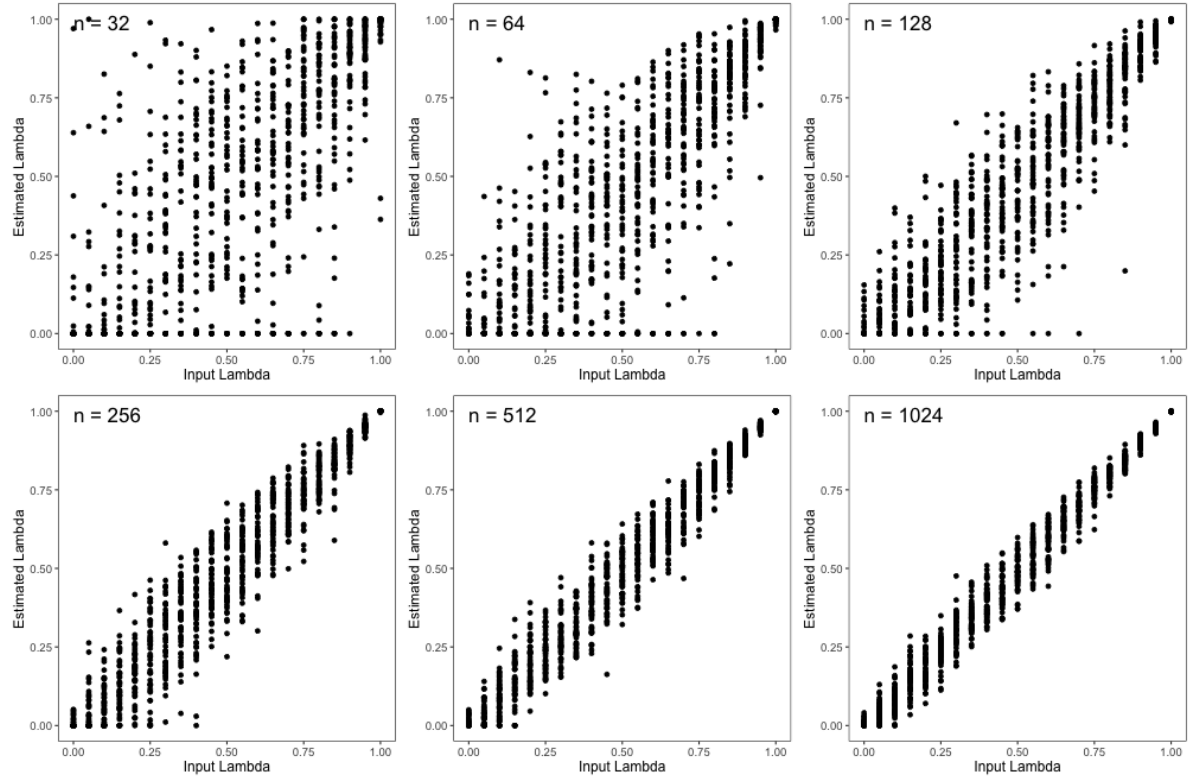


Figure S3. Precision of Pagel's λ when incorporated in phylogenetic ANOVA. Results are from input β values of 0.5.

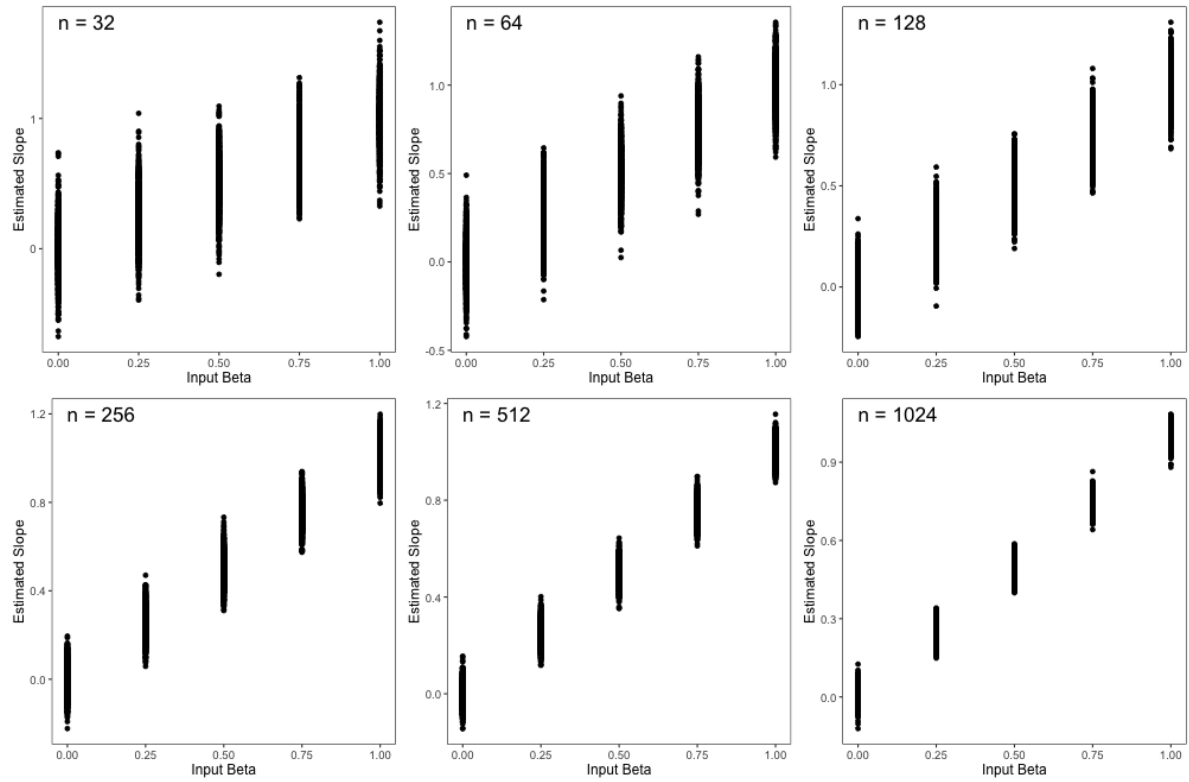


Figure S4. Precision of slope estimates across known input β values of phylogenetic regression. Results shown include all input λ values.

Effect Sizes of Pagel's Lambda (Z_λ) and Kappa (Z_K)

We proposed the use of effect sizes (Z-scores) as a measure of the strength of phylogenetic signal. These were obtained from summary parameters of phylogenetic signal: λ and *Kappa*. The precision of effect sizes Z_λ and Z_K are summarized in the main text, primarily for simulations where $n = 32$. Here we present results from additional simulations.

Results Effect sizes for Pagel's λ (Z_λ) scale nonlinearly with input levels of phylogenetic signal, and this pattern is consistent across all tree sizes examined (Figure S5). Further, the precision of Z_λ varied widely across input levels of phylogenetic signal, with decidedly greater variation (less precision) at stronger input levels of phylogenetic signal (Figure S5). By contrast, effect sizes for *Kappa* (Z_K) displayed a linear increase with increasing input levels of phylogenetic signal, which remained consistent across all tree sizes examined (Figure S6). Additionally, the precision of Z_K remained constant across input levels of phylogenetic signal (Figure S6). Together these results imply that Z_K is a more reliable estimate of the strength of phylogenetic signal.

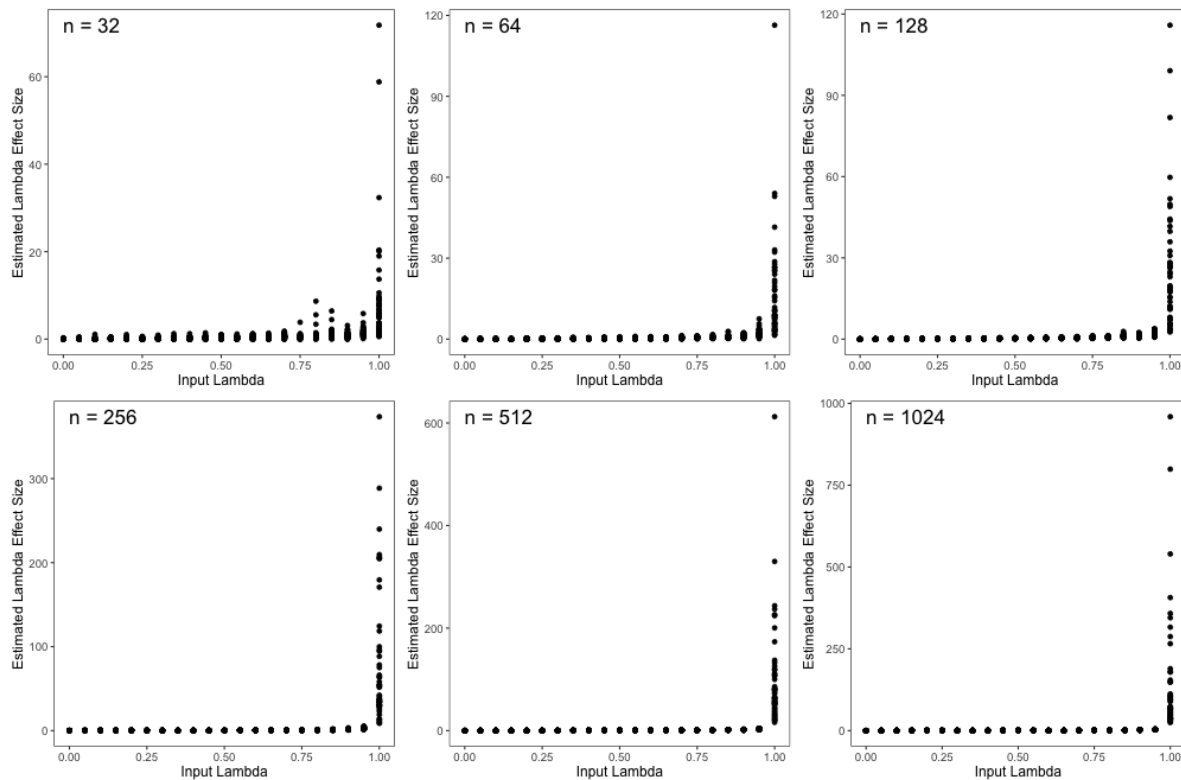


Figure S5. Variation in effect size (Z score) of Pagel's λ across input λ values on various tree sizes.

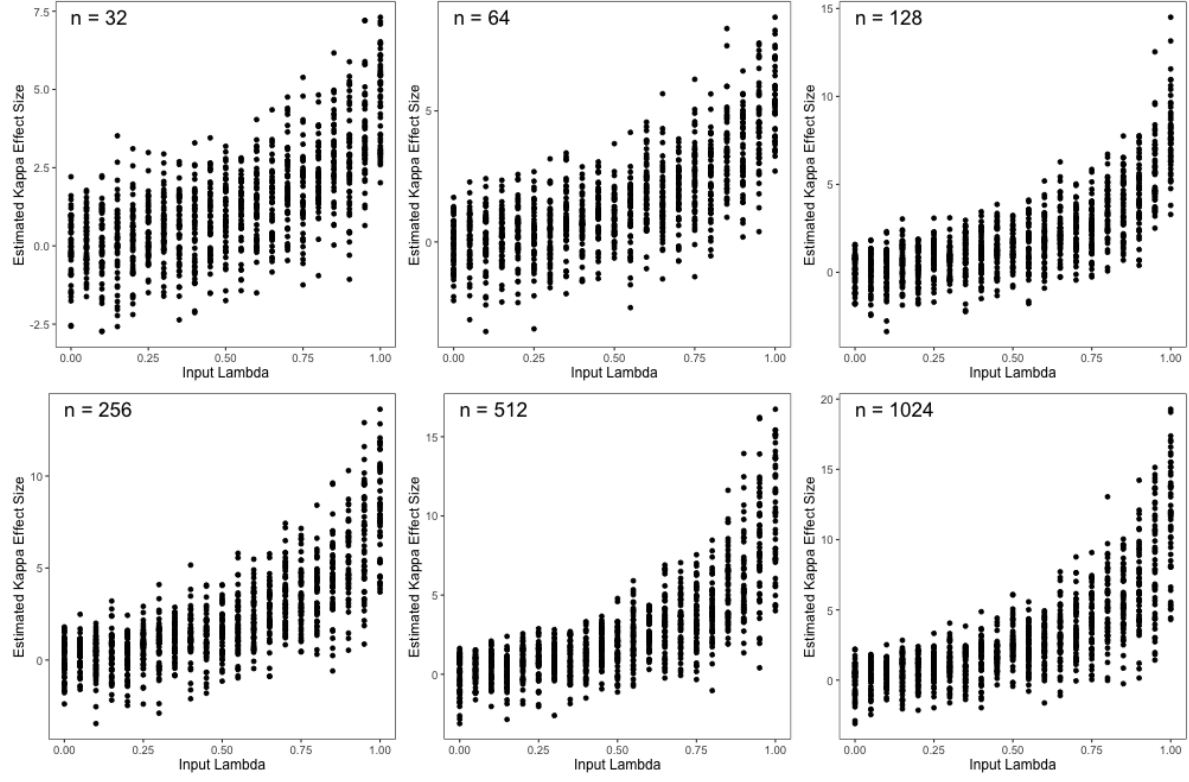


Figure S6. Variation in effect size (Z score) of K across input λ values on various tree sizes.

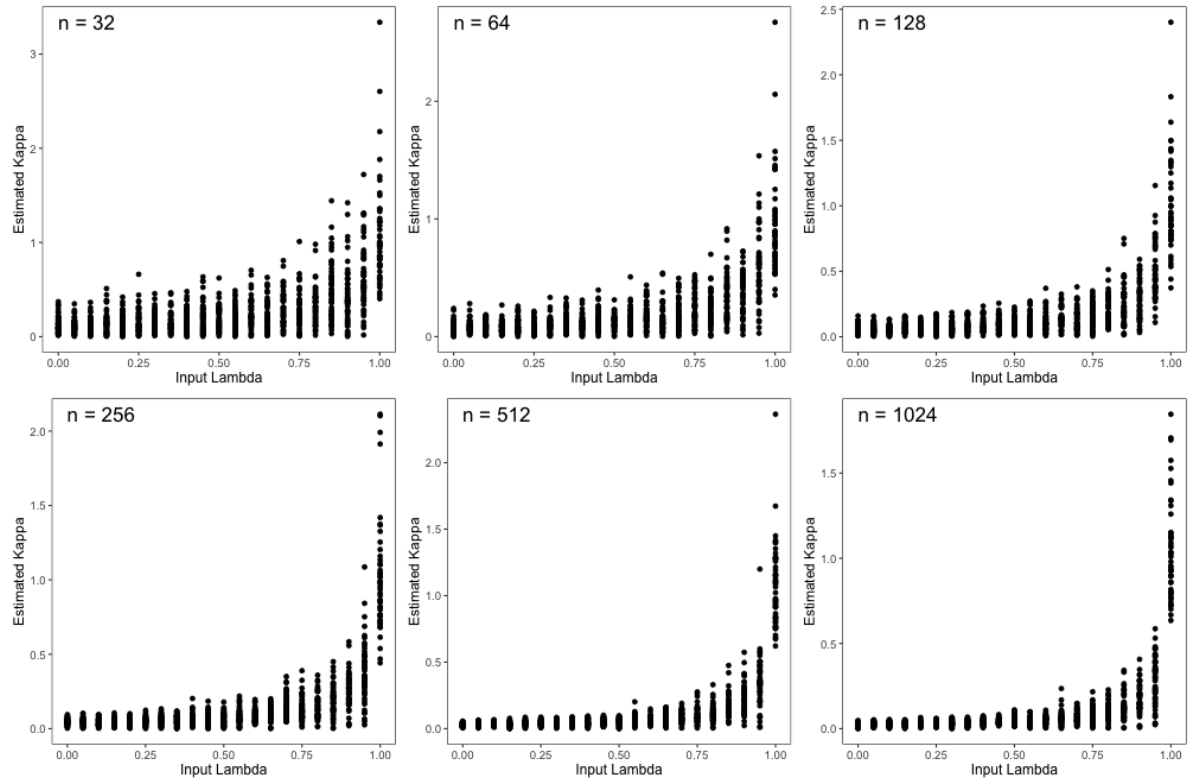


Figure S7. Estimates of phylogenetic signal using $Kappa$ across known λ inputs on various tree sizes.

Plot shows that while *Kappa* increases with increasing phylogenetic signal, the precision of this estimate also varies. Thus, conversion to a standardized effect size (Z_K) is preferred.