

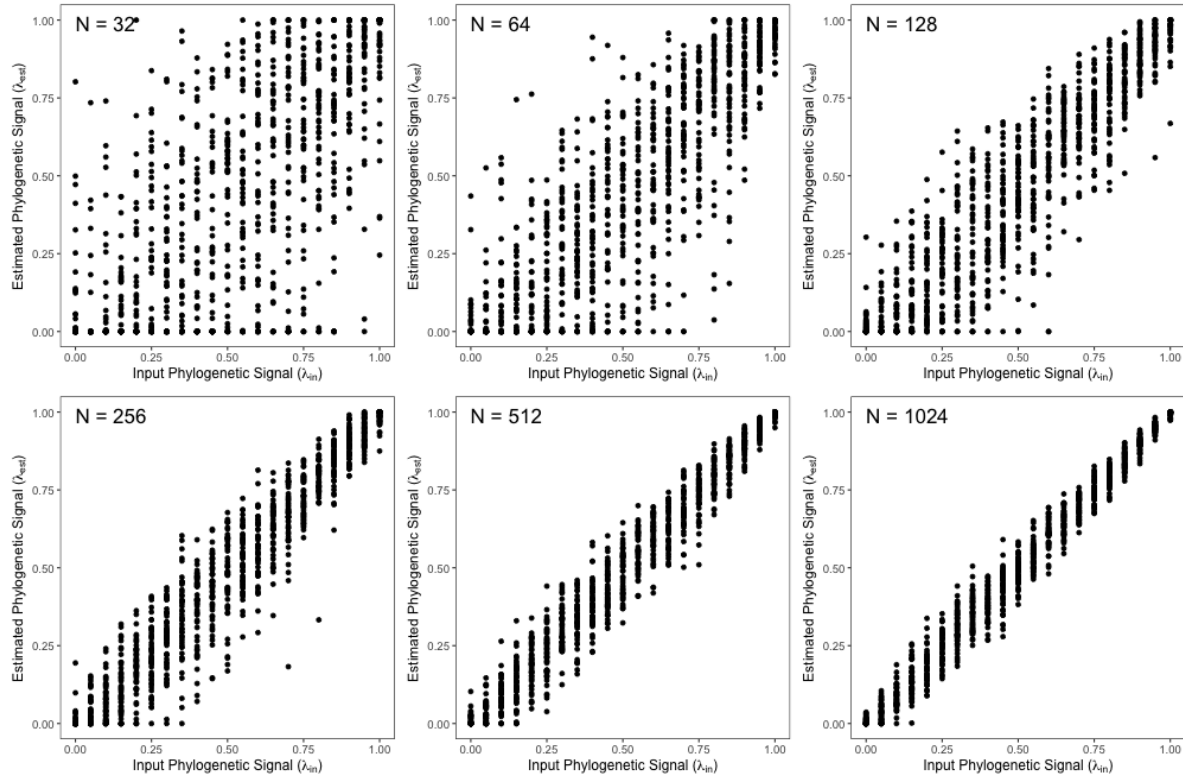
# Supporting Information for: A Standardized Effect Size for Evaluating the Strength of Phylogenetic Signal, and Why Lambda is not Appropriate

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

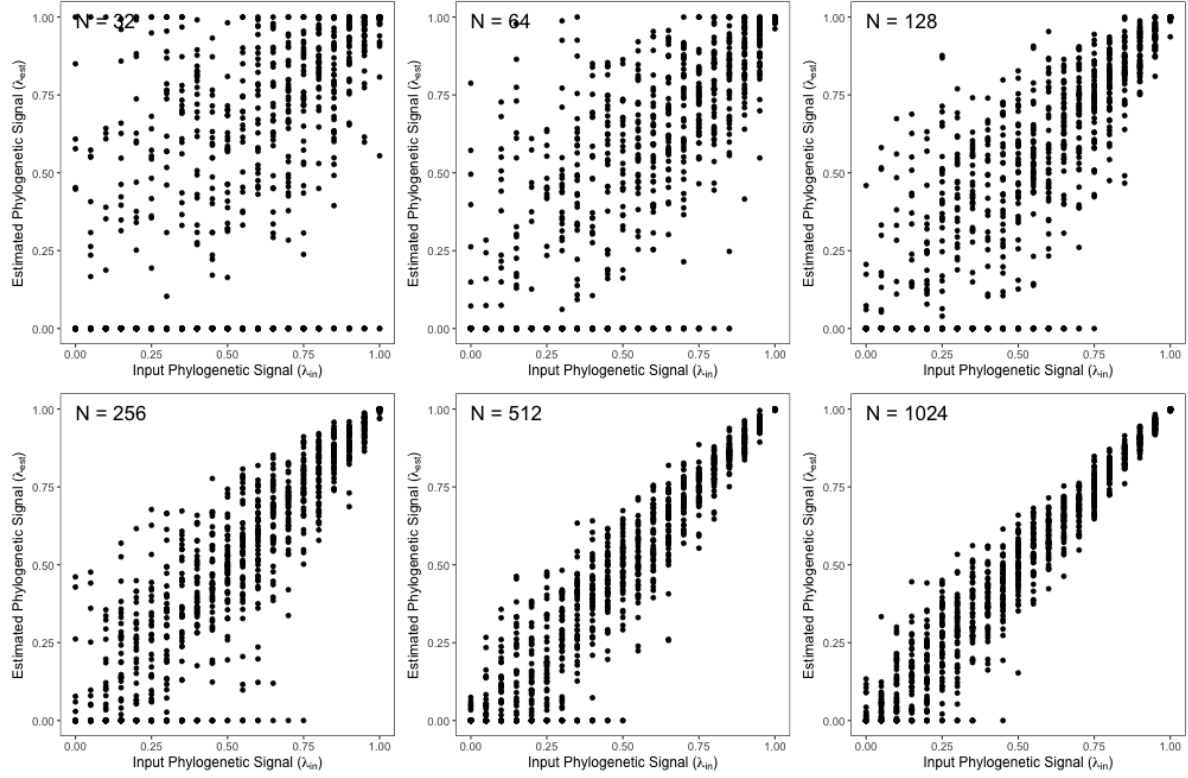
## Simulations on differently shaped phylogenies

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  $\lambda_{in}$  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  $\lambda$ .

*Results.* As found with pure-birth phylogenies, estimates of  $\lambda$  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  $\lambda$  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.

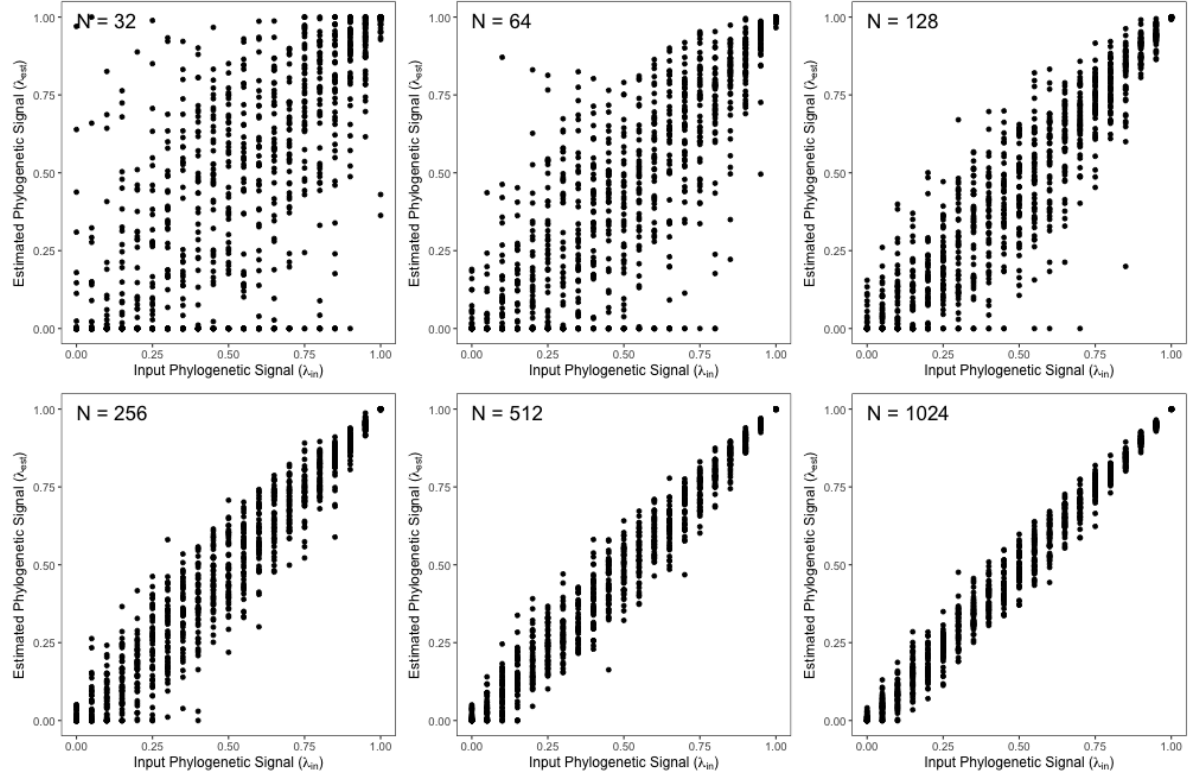


**Figure S2.** Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. Results obtained using pectinate trees.

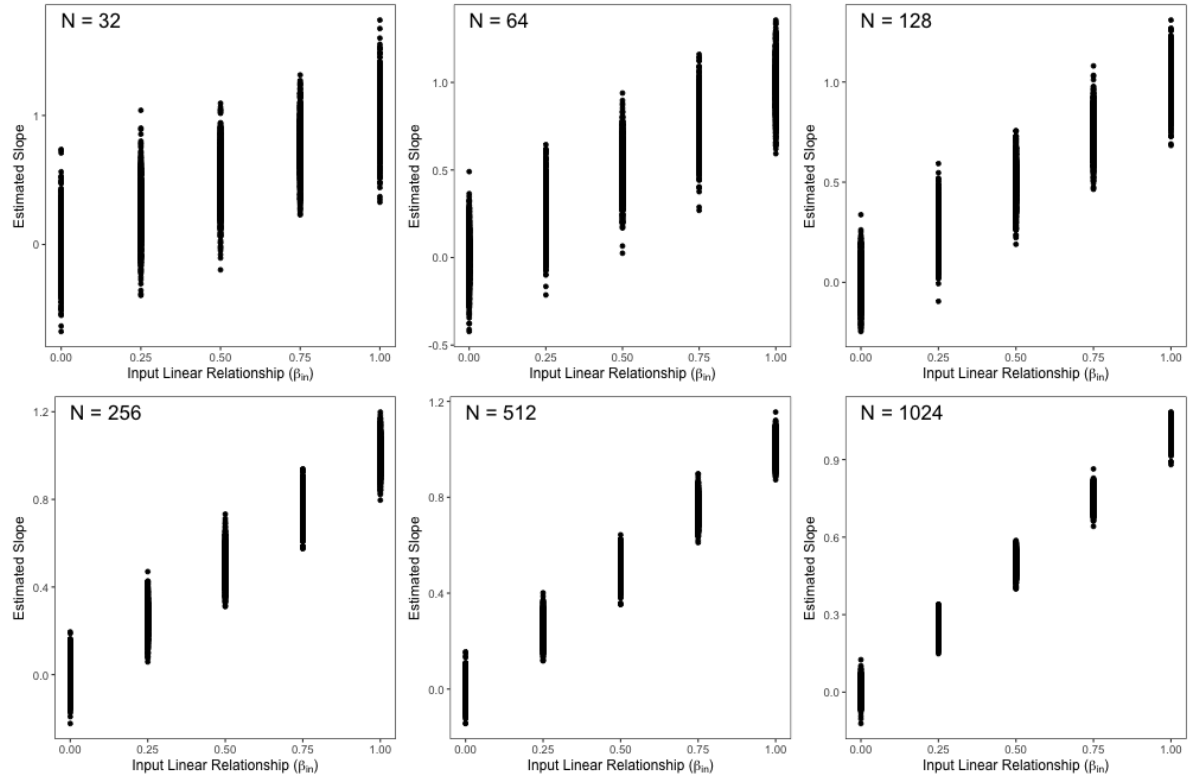
## Simulations of phylogenetic regression and ANOVA

We analyzed the precision of parameter estimation when parameters were obtained in phylogenetic regression and ANOVA. This involved simulations of dependent variables with  $\lambda$  values ranging from 0 to 1 (21 intervals of 0.05 units) across pure-birth trees ( $n = 2^5 - 2^{10}$ ). For each  $\lambda$  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  $\lambda$  was then estimated.

*Results* As with the results from the regression analyses in the main text, we found poor precision of  $\lambda$  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  $\lambda$  values (Fig. S4).



**Figure S3.** Precision of Pagel's  $\lambda$  when incorporated in phylogenetic ANOVA. Results are from input  $\beta$  values of 0.5.

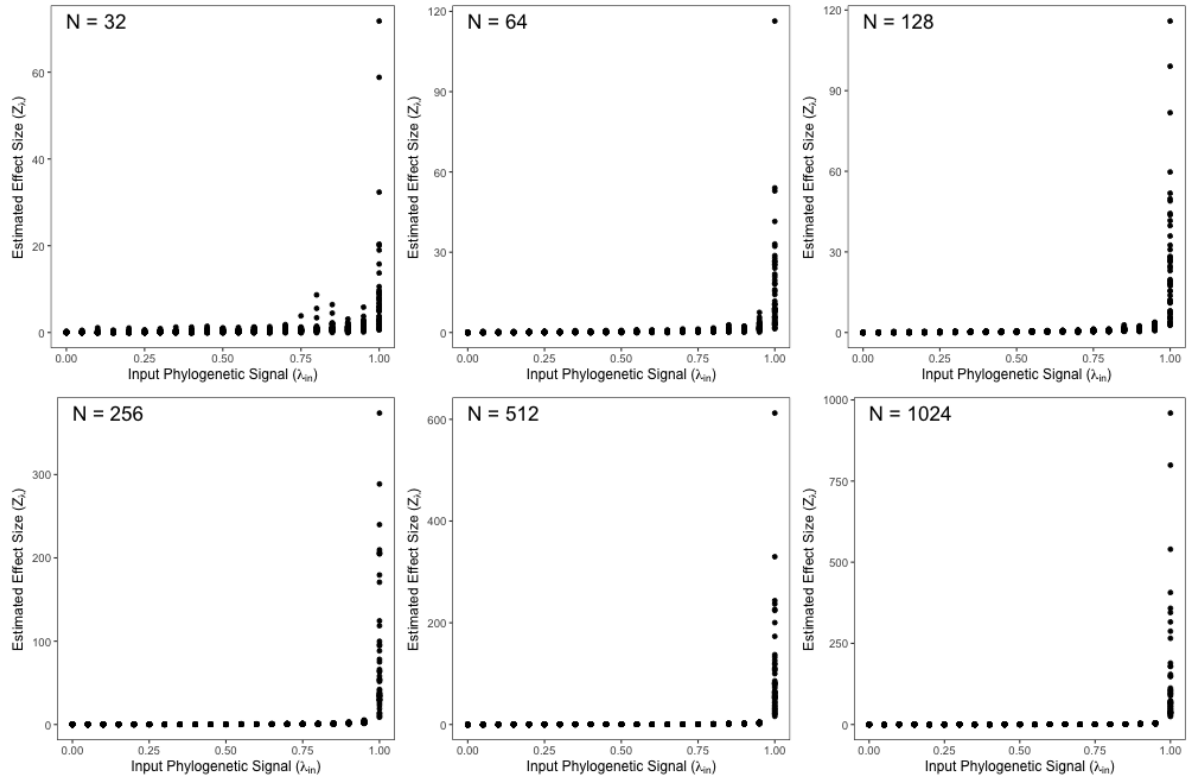


**Figure S4.** Precision of slope estimates across known input  $\beta$  values of phylogenetic regression. Results shown include all input  $\lambda$  values.

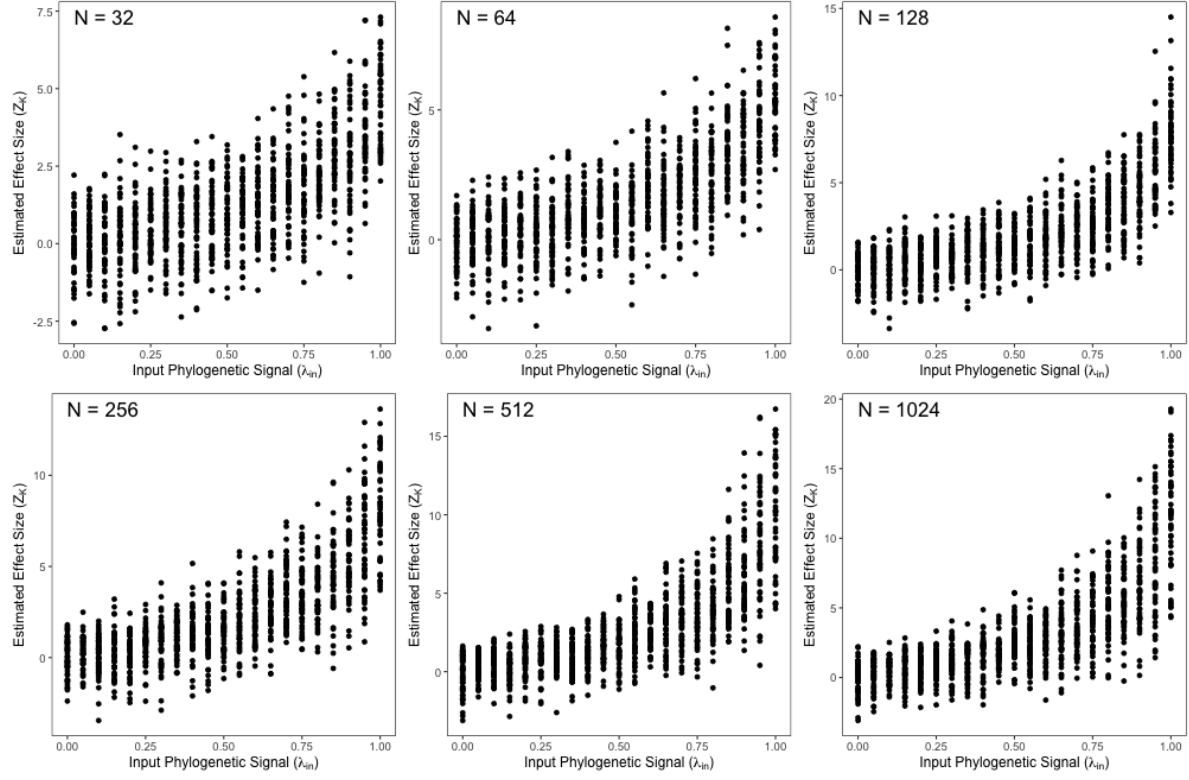
## Effect Sizes of Pagel's Lambda ( $Z_\lambda$ ) and Kappa ( $Z_\kappa$ )

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:  $\lambda$  and  $\kappa$ . The precision of effect sizes  $Z_\lambda$  and  $Z_\kappa$  are summarized in the main text, primarily for simulations where  $n = 32$ . Here we present results from additional simulations.

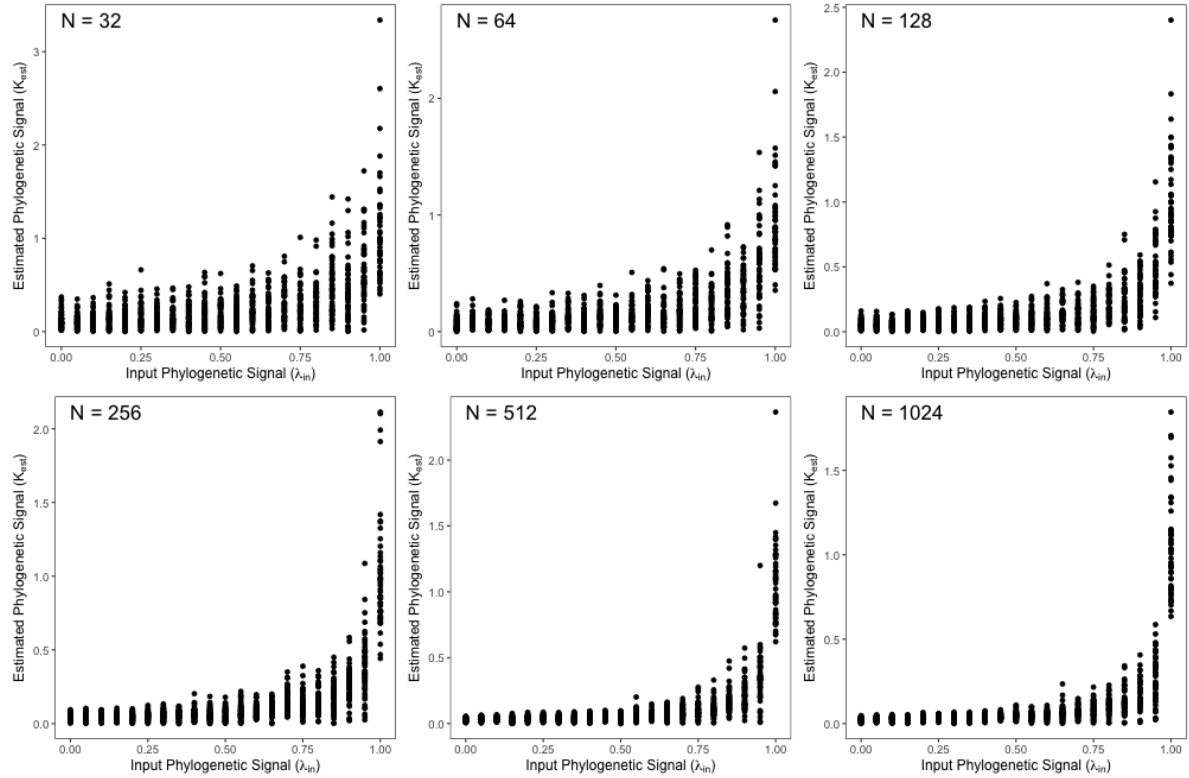
*Results* Effect sizes for Pagel's  $\lambda$  ( $Z_\lambda$ ) scale nonlinearly with input levels of phylogenetic signal, and this pattern is consistent across all tree sizes examined (Figure S5). Further, the precision of  $Z_\lambda$  varied widely across input levels of phylogenetic signal, with decidedly greater variation (less precision) at stronger input levels of phylogenetic signal (Figure S5). By contrast, effect sizes for  $\kappa$  ( $Z_\kappa$ ) 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  $Z_\kappa$  remained constant across input levels of phylogenetic signal (Figure S6). Together these results imply that  $Z_\kappa$  is a more reliable estimate of the strength of phylogenetic signal.



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



**Figure S6.** Variation in effect size ( $Z$  score) of  $\kappa$  across input  $\lambda$  values on various tree sizes.



**Figure S7.** Estimates of phylogenetic signal using  $\kappa$  across known lambda 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 ( $Z_\kappa$ ) is preferred.