

A Standardized Effect Size for Evaluating and Comparing the Strength of Phylogenetic Signal

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Macroevolutionary studies frequently characterize the phylogenetic signal in phenotypes, and wish to compare the strength of that signal across traits. However, analytical tools for such comparisons have largely remained underdeveloped. Here we evaluate the efficacy of one commonly used parameter (Pagel's λ) to estimate the strength of phylogenetic signal in phenotypic traits, and evaluate the degree to which λ correctly identifies known levels of phylogenetic signal. We find that λ behaves as a Bernoulli random variable, and that estimates are increasingly skewed at larger and smaller input levels of phylogenetic signal. Further, the precision of λ in estimating actual levels of phylogenetic signal is often inaccurate, and biological interpretations of the strength of phylogenetic signal based on λ are therefore compromised. We propose a standardized effect size based on κ , (Z_κ), which measures the strength of phylogenetic signal more reliably than does λ , and places that signal on a common scale for statistical comparison. We develop tests based on Z_κ to provide a mechanism for formally comparing the strength of phylogenetic signal across datasets, in much the same manner as effect sizes may be used to summarize patterns in quantitative meta-analysis. Our approach extends the phylogenetic comparative toolkit to address hypotheses that compare the strength of phylogenetic signal between various phenotypic traits, even when those traits are found in different evolutionary lineages or have different units or scales.

phylogenetic signal | macroevolution | lambda | kappa

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Significance Statement

Evolutionary biologists wish to quantify and compare the strength of phylogenetic signal across traits, but analytical tools for these comparisons are generally lacking. Here we develop a standardized effect size based on κ (Z_κ), which measures the strength of phylogenetic signal on a common statistical scale, and provides a mechanism for formally comparing the strength of phylogenetic signal across datasets. Additionally, we find that a commonly used parameter (Pagel's λ) is unsuitable for this purpose. Our procedure enables biologists to quantitatively address hypotheses that compare the strength of phylogenetic signal between various phenotypic traits, even when those traits are found in different evolutionary lineages or have different units or scales.

D.C.A. designed the research; D.C.A., E.K.B., and M.L.C. performed the research and wrote the paper.

The authors declare no conflict of interest.



Fig. 1. Placeholder image of a frog with a long example caption to show justification setting.

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