

Pagel's Lambda Estimates are Often Inaccurate

Keywords: Pagel's lambda, phylogenetic signal

Short Title: Inaccuracies in Pagel's Lambda

Abstract

conclusion holds: interpreting the regression is not appreciably different (in terms of slopes and f values)

Introduction

Investigating macroevolutionary patterns requires a phylogenetic approach as species are non-independent by nature of their shared ancestry. Since the first appropriate method was introduced by Felsenstein (phylogenetic independent contrasts; [Felsenstein1987]), dozens of other methods have been developed and applied to increasingly complex questions in macroevolutionary biology (e.g. [AdamsNason2019]). Understanding the degree of phylogenetic signal present in a dataset is paramount, and identifies the mode with which a trait has evolved. High measures of phylogenetic signal indicate a Brownian motion process, whereas lower levels of phylogenetic signal indicate natural selection or some other evolutionary force has influenced the traits evolutionary history.

Several approaches to quantify phylogenetic signal exist. For continuous data, the most common parameters used in the literature include Pagel's lambda [Pagel1997] and Blomberg's kappa [Blomberg1900]. Pagel's lambda has the advantage of being couched in the likelihood framework and thus has also been utilized to incorporate phylogenetic signal while doing phylogenetic regressions and ANOVA. However, the accuracy of the lambda estimation methods have not been fully evaluated, and thus it remains unknown the degree to which lambda estimates appropriately represent degree of phylogenetic signal.

An earlier study [BoettigerEtAl2012], briefly addressed this topic by showing how uninformative smaller phylogenies could be using estimation methods for various parameters. That paper concluded that a measure of power must be considered when quantifying Pagel's lambda. Here we take a more comprehensive approach to demonstrate the scenarios under which estimated lambdas accurately reflect known lambdas as well as the effect of these at times dubious estimation methods on significance testing when used in a pgls framework.

Methods and Results

Simulated trait

To assess the accuracy of Pagel's lambda estimations, we simulated pure-birth phylogenies with known lambdas. We _____ by scaling simulated phylogeny with the scaling parameter and . We also did this with other tree shapes (symmetrical and ladder).

Simulated ANOVA and Regressions

To ascertain the statistical performance of pgl

Meta-Analysis of Empirical Results

Despite the urging of Boettiger and colleagues to publish confidence intervals with all lambda parameter estimates, only 18% of papers published in 2019 do so.

All analyses were performed in R 3.6.2 [R-Base] using the packages `geomorph` (Adams and Otárola-Castillo 2013; Adams et al. 2019), `RRPP` (Collyer and Adams 2018).

Discussion

Using the estimated lambda values from pgl are not useful. The questions of whether or not signal exists is appropriate, but inferring more from lambda *magnitude* is inappropriate.

More discussion paragraphs

References

- Adams, D. C., and E. Otárola-Castillo. 2013. Geomorph: An r package for the collection and analysis of geometric morphometric shape data. *Methods in Ecology and Evolution* 4:393–399.
- Adams, D., M. Collyer, and A. Kaliontzopoulou. 2019. Geomorph: Software for geometric morphometric analyses. *r* package version 3.1.1.
- Collyer, M. L., and D. C. Adams. 2018. RRPP: An R package for fitting linear models to high-dimensional data using residual randomization. *Methods in Ecology and Evolution* 9:1772–1779.

Figure Legends

Figure 1. Accuracy of Pagel's lambda estimations across known lambda inputs on various tree sizes. As trees increase in size, the estimates more closely resemble the input lambdas, however considerable and concerning variation is apparent in trees smaller than those with 256 tips.

Figure 2. Figure 2 legend here

Figure 3. (A) Figure 3 legend (B) Second part of legend.

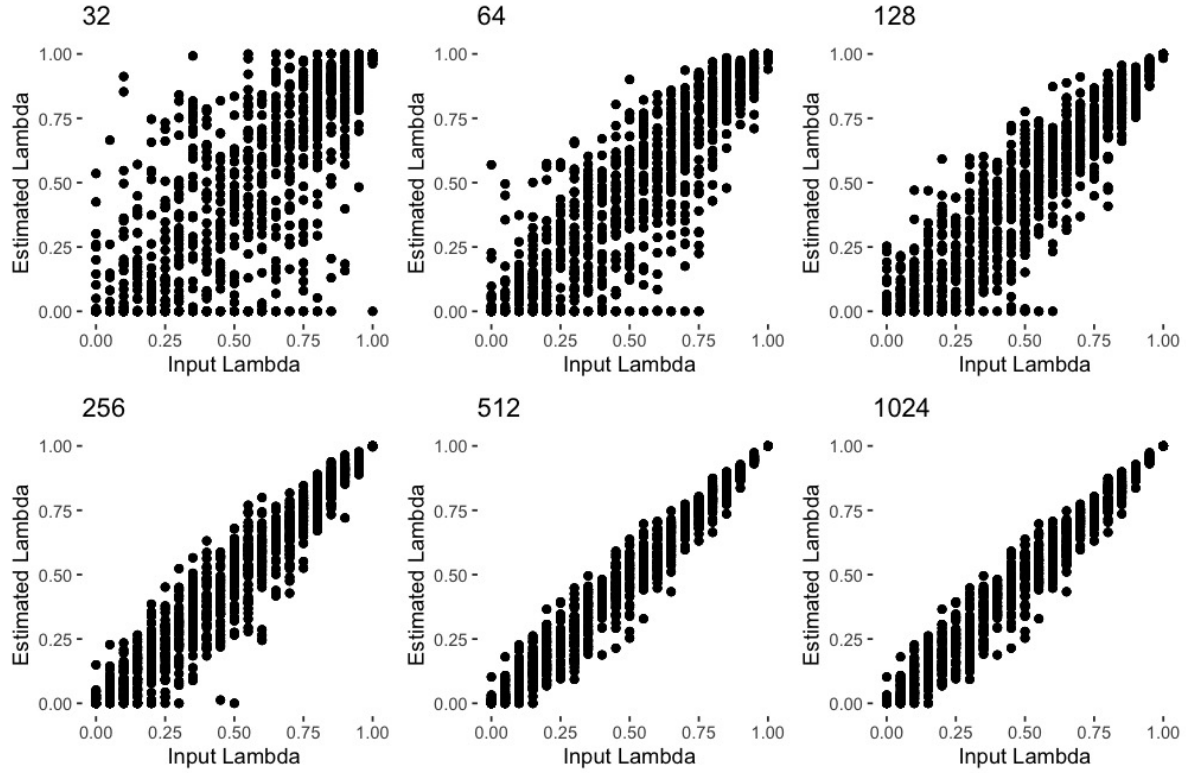


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Other Figures Here