

Appendix from R. P. Freckleton et al., “Comparative Methods as a Statistical Fix: The Dangers of Ignoring an Evolutionary Model” (Am. Nat., vol. 178, no. 1, p. E10)

Supplemental Information

In this appendix, we include alternatives to figures 1 and 2 in the main text that were generated under alternative models. In figures A1–A4, we describe simulations in which the model of trait evolution was the Ornstein-Uhlenbeck model (e.g., Hansen 1997). This model yields traits exhibiting weaker phylogenetic signals than the Brownian model used in the text. We assumed either a moderate restraining force ($\alpha = 0.1$; figs. A1, A2) or a strong restraining force ($\alpha = 1$; figs. A3, A4). The key results from the main article continue to hold: the performance of the phylogenetic eigenvector regression (PVR) method is worse than that of the generalized least squares (GLS) method in all respects. This includes (1) increased sampling variance of PVR estimates relative to GLS ones (figs. A1, A3), (2) reduced degrees of freedom for hypothesis testing under PVR (figs. A1d, A3d), (3) incomplete accounting for phylogenetic signal by the PVR method (figs. A2a, A4a), and (4) enhanced Type I error rates of the PVR method (figs. A2b, A2c, A4b, A4c).

In figures A4 and A5, we show results obtained when there is no phylogenetic signal in the data. This is the only case in which the variance of the PVR estimates have lower sampling variance than those derived from GLS (fig. A5). However, as shown in figure A6, the PVR method still fails to appropriately control for phylogenetic signal and always has elevated Type I error rates relative to the nominal level. The GLS method also performs poorly when the predictor x has no phylogenetic signal (fig. A6b).

The current recommendation is to test and control for variable levels of phylogenetic signal using a method such as that of Pagel (1997, 1999); for example, see studies by Freckleton et al. (2002), Blomberg and Garland (2002), and Blomberg et al. (2003). As we show in figures A7 and A8, if there is no phylogenetic signal in the data, then applying the lambda statistic of Pagel (1997, 1999) considerably improves the performance of the GLS method, substantially improving it over the PVR method.

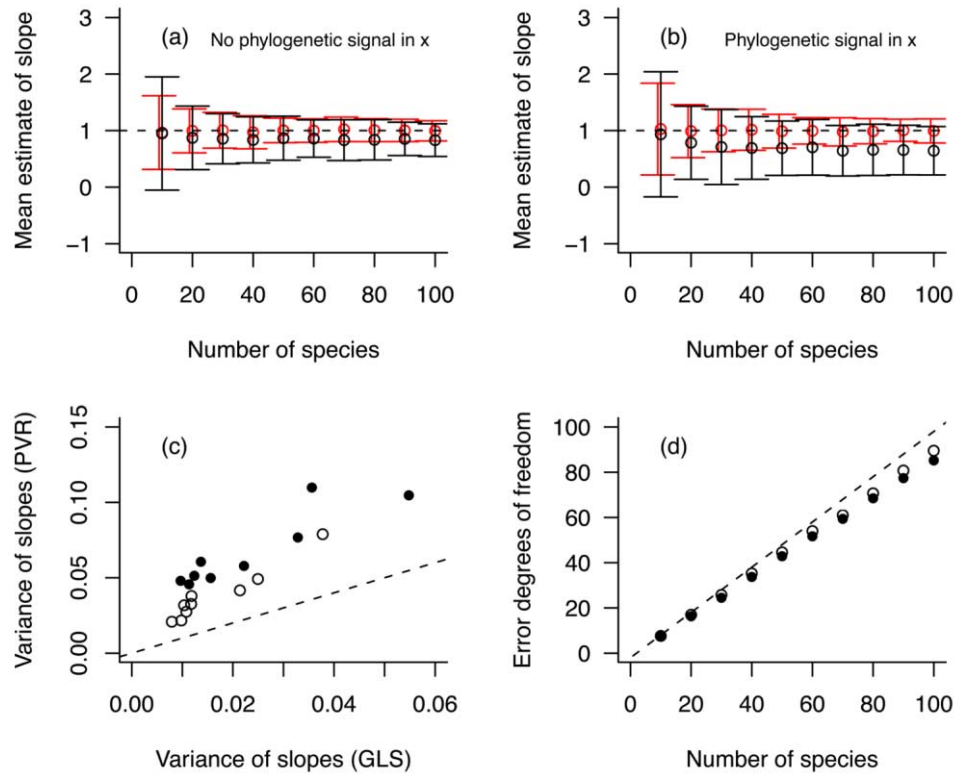


Figure A1: Comparisons of estimates of parameters, their variance, and residual degrees of freedom from generalized least squares (GLS) and phylogenetic eigenvector regression (PVR) regression models under the Ornstein-Uhlenbeck model with a moderate ($\alpha = 0.1$) restraining force. *a*, Estimates of mean value of the slope for the regression of y on x when there is no phylogenetic signal in x , for different-sized phylogenies. Error bars are 95% confidence intervals from 1,000 simulations; PVR estimates are in black, and GLS estimates are in red. *b*, As in *a* but when x possesses a phylogenetic signal. *c*, Variance in parameter estimates in *a* and *b* are compared. The variance in estimates from 1,000 simulations was calculated, and the values obtained from the PVR method were plotted against those from the GLS models. The dashed line represents the 1 : 1 relationship. *d*, Error degrees of freedom from the models. The dashed line is the GLS model; the points are means from the PVR method. In *c* and *d*, the filled circles are estimates from simulations in which there was a phylogenetic signal in x , and the open circles are simulations in which there is no phylogenetic signal in x .

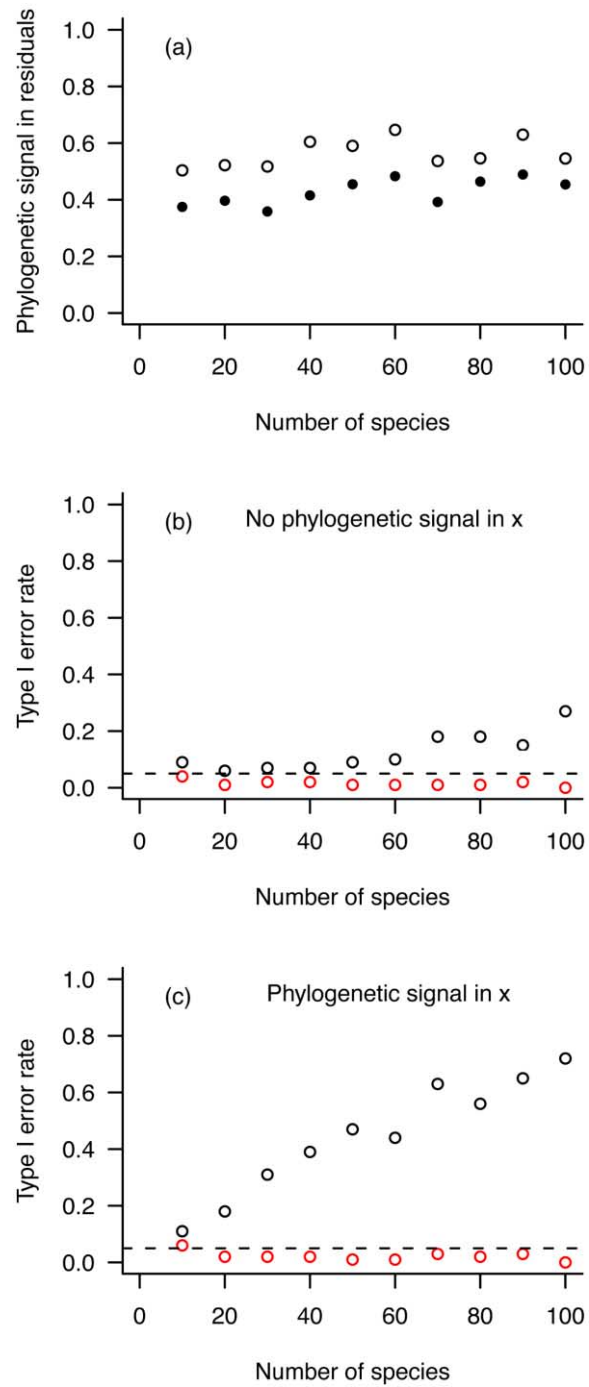


Figure A2: Phylogenetic signal in residuals and Type I error rates of phylogenetic eigenvector regression (PVR) methods under the Ornstein-Uhlenbeck model with a moderate ($\alpha = 0.1$) restraining force. *a*, Estimates of Pagel's λ for residuals of PVR models from models based on phylogenies of different sizes and for data sets in which there is no phylogenetic signal in x (open circles) and in which there is a phylogenetic signal in x (filled circles). *b*, *c*, Type I error rates for generalized least squares (GLS; red) and PVR (black open circles) from data sets of varying sizes. In *b* there is no phylogenetic signal in x , whereas in *c* there is a strong phylogenetic signal in x .

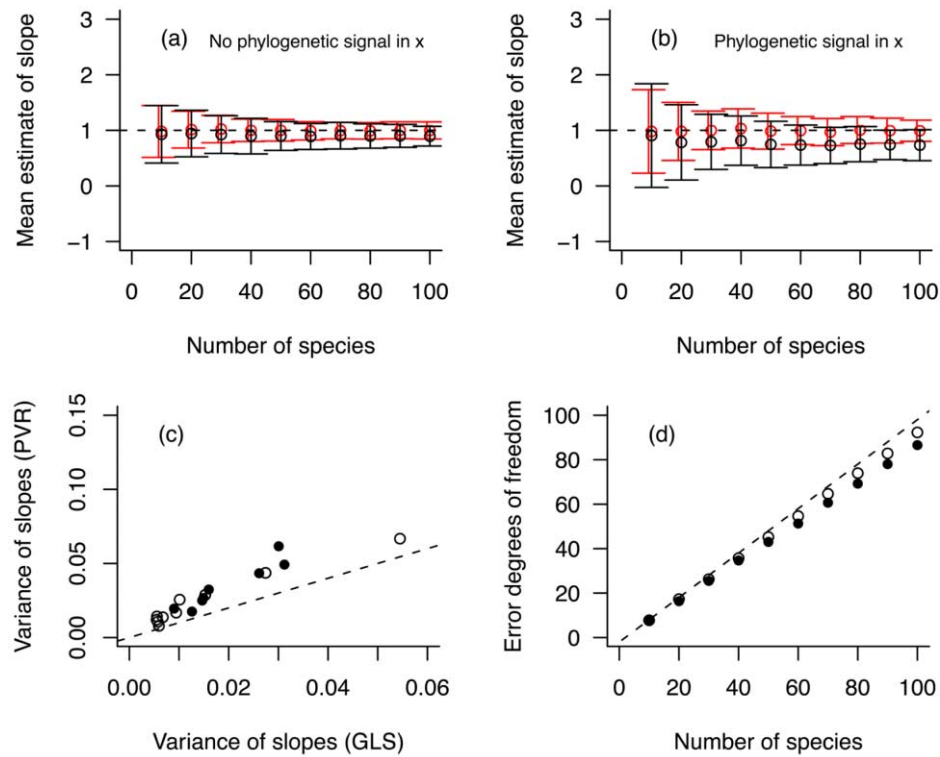


Figure A3: Comparisons of estimates of parameters, their variance, and residual degrees of freedom from generalized least squares (GLS) and phylogenetic eigenvector regression (PVR) regression models under the Ornstein-Uhlenbeck model with a strong ($\alpha = 1$) restraining force. *a*, Estimates of mean value of the slope for the regression of y on x when there is no phylogenetic signal in x for different-sized phylogenies. Error bars are 95% confidence intervals from 1,000 simulations; PVR estimates are in black, and GLS estimates are in red. *b*, As in *a* but when x possesses phylogenetic signal. *c*, Variance in parameter estimates in *a* and *b* are compared. The variance in estimates from 1,000 simulations was calculated, and the values obtained from the PVR method were plotted against those from the GLS models. The dashed line represents the 1 : 1 relationship. *d*, Error degrees of freedom from the models. The dashed line is the GLS model; the points are means from the PVR method. In *c* and *d*, the filled circles are estimates from simulations in which there was a phylogenetic signal in x , and the open circles are simulations in which there is no phylogenetic signal in x .

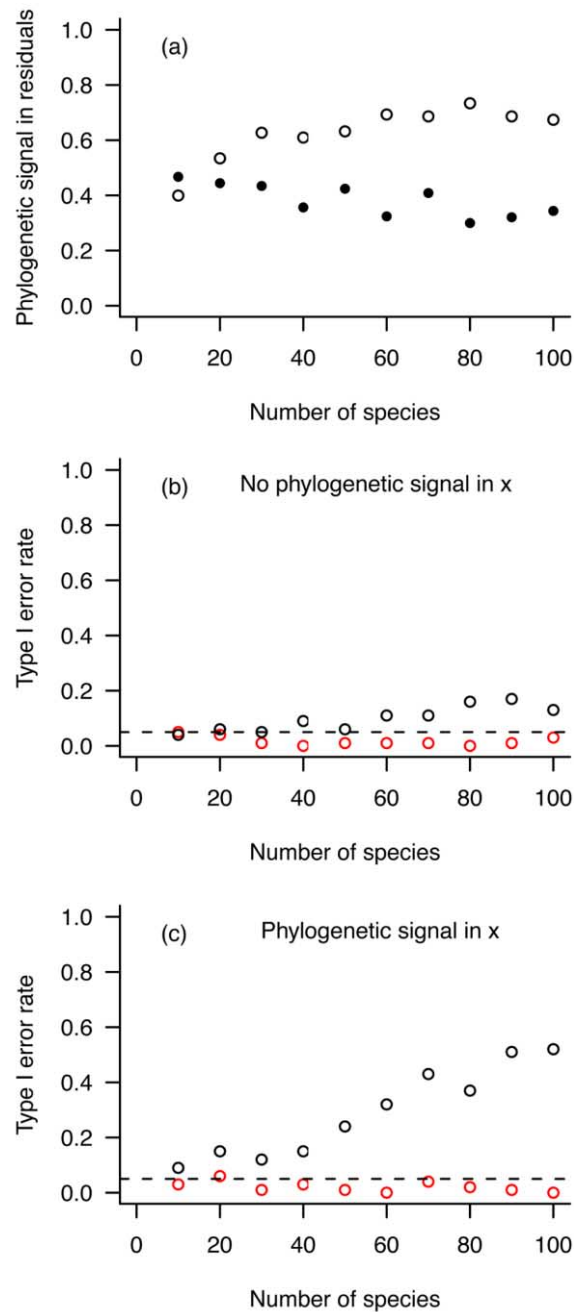


Figure A4: Phylogenetic signal in residuals and Type I error rates of phylogenetic eigenvector regression (PVR) methods under the Ornstein-Uhlenbeck model with a strong ($\alpha = 1$) restraining force. *a*, Estimates of Pagel's λ for residuals of PVR models from models based on phylogenies of different sizes and for data sets in which there is no phylogenetic signal in x (open circles) and in which there is a phylogenetic signal in x (filled circles). *b*, *c*, Type I error rates for generalized least squares (GLS; red) and PVR (black open circles) from data sets of varying sizes. In *b*, there is no phylogenetic signal in x , whereas in *c* there is a strong phylogenetic signal in x .

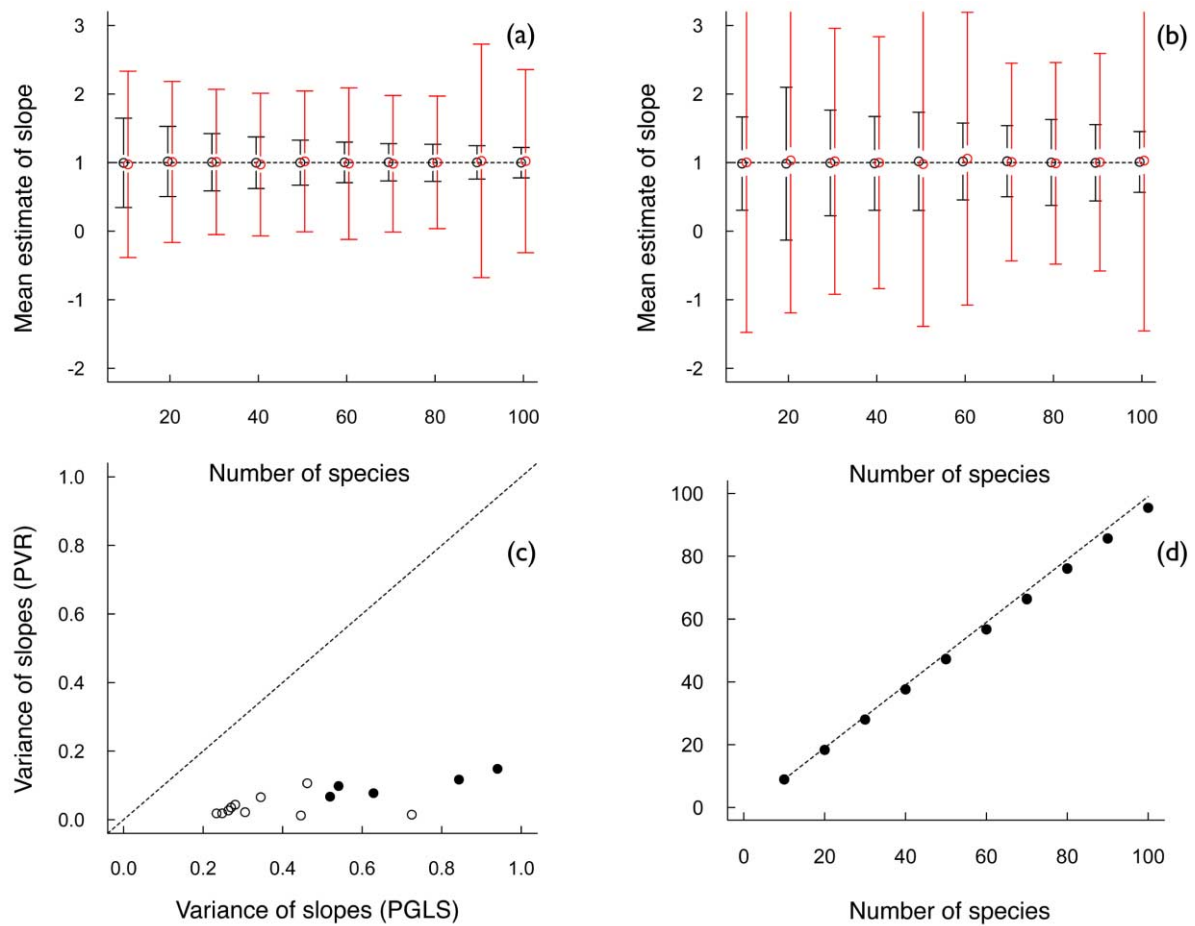


Figure A5: Comparisons of estimates of parameters, their variance, and residual degrees of freedom from generalized least squares (GLS) and phylogenetic eigenvector regression (PVR) regression models applied to data in which there is no phylogenetic signal in the residuals. *a*, Estimates of mean value of the slope for the regression of y on x when there is no phylogenetic signal in x , for different-sized phylogenies. Error bars are 95% confidence intervals from 1,000 simulations; PVR estimates are in black, and GLS estimates are in red. *b*, As in *a* but when x possesses a phylogenetic signal. *c*, Variance in parameter estimates in *a* and *b* are compared. The variance in estimates from 1,000 simulations was calculated, and the values obtained from the PVR method were plotted against those from the GLS models. The dashed line represents the 1 : 1 relationship. *d*, Error degrees of freedom from the models. The dashed line is the GLS model; the points are means from the PVR method. In *c* and *d*, the filled circles are estimates from simulations in which there was phylogenetic signal in x , and the open circles are simulations in which there is no phylogenetic signal in x .

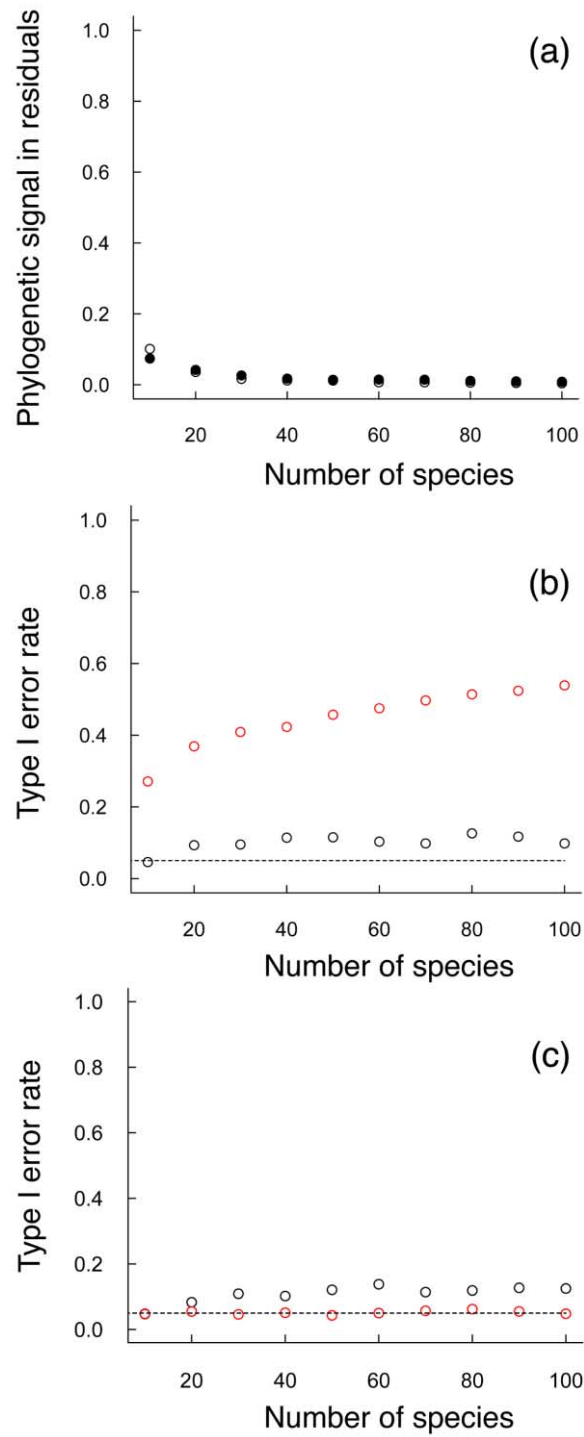


Figure A6: Phylogenetic signal in residuals and Type I error rates of phylogenetic eigenvector regression (PVR) methods applied to data in which there is no phylogenetic signal in the residuals. *a*, Estimates of Pagel's λ for residuals of PVR models from models based on phylogenies of different sizes and for data sets in which there is no phylogenetic signal in x (*open circles*) and in which there is a phylogenetic signal in x (*filled circles*). *b*, *c*, Type I error rates for generalized least squares (GLS) models (*red*) and PVR method (*black open circles*) from data sets of varying sizes. In *b* there is no phylogenetic signal in x , whereas in *c* there is a strong phylogenetic signal in x .

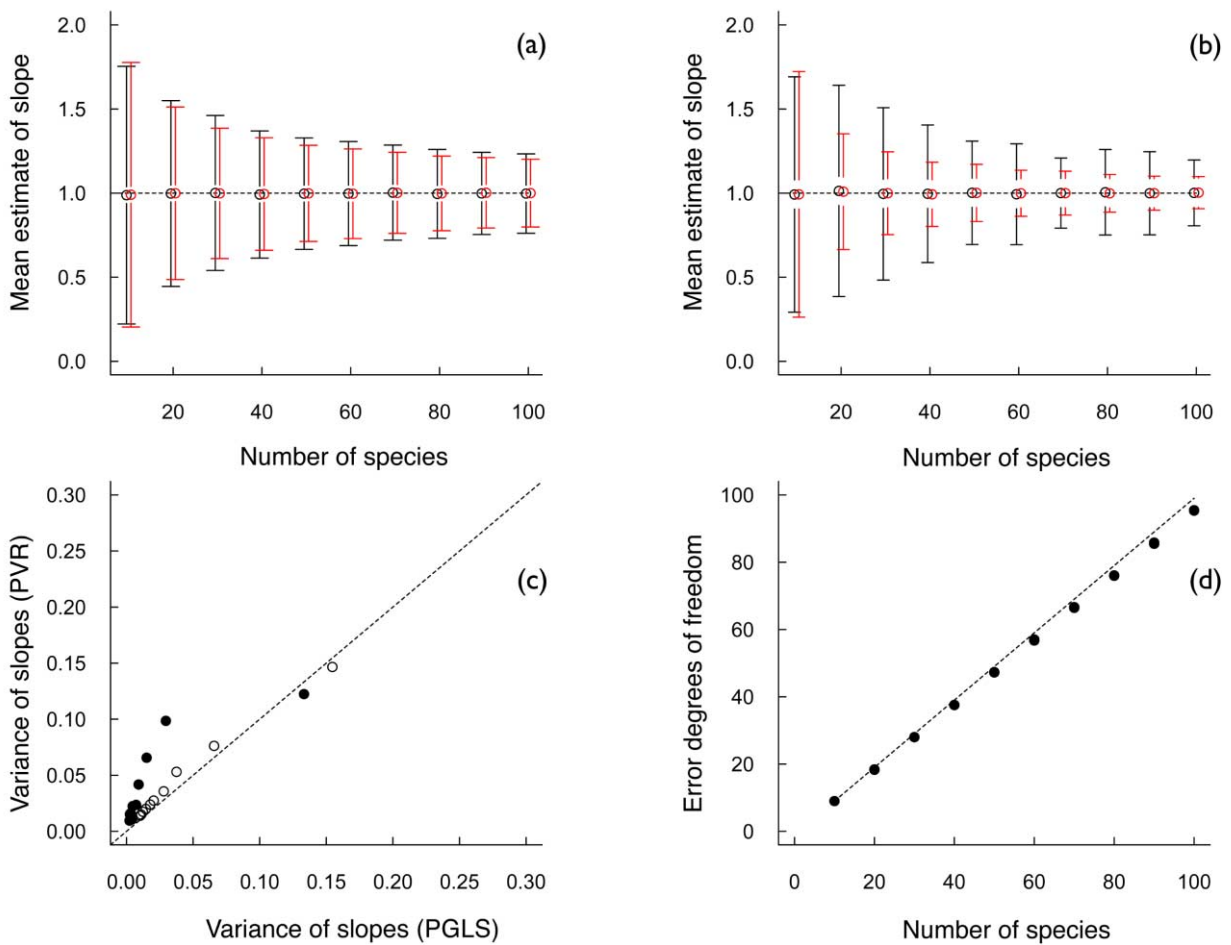


Figure A7: Comparisons of estimates of parameters, their variance, and residual degrees of freedom from generalized least squares (GLS) and phylogenetic eigenvector regression (PVR) regression models applied to data in which there is no phylogenetic signal in the residuals but where Pagel's λ is used to correct the GLS results. *a*, Estimates of mean value of the slope for the regression of y on x when there is no phylogenetic signal in x , for different-sized phylogenies. Error bars are 95% confidence intervals from 1,000 simulations; PVR estimates are in black, and GLS estimates are in red. *b*, As in *a* but when x possesses a phylogenetic signal. *c*, Variance in parameter estimates in *a* and *b* are compared. The variance in estimates from 1,000 simulations was calculated, and the values obtained from the PVR method were plotted against those from the GLS models. The dashed line represents the 1 : 1 relationship. *d*, Error degrees of freedom from the models. The dashed line is the GLS model; the points are means from the PVR method. In *c* and *d*, the filled circles are estimates from simulations in which there was phylogenetic signal in x , and the open circles are simulations in which there is no phylogenetic signal in x .

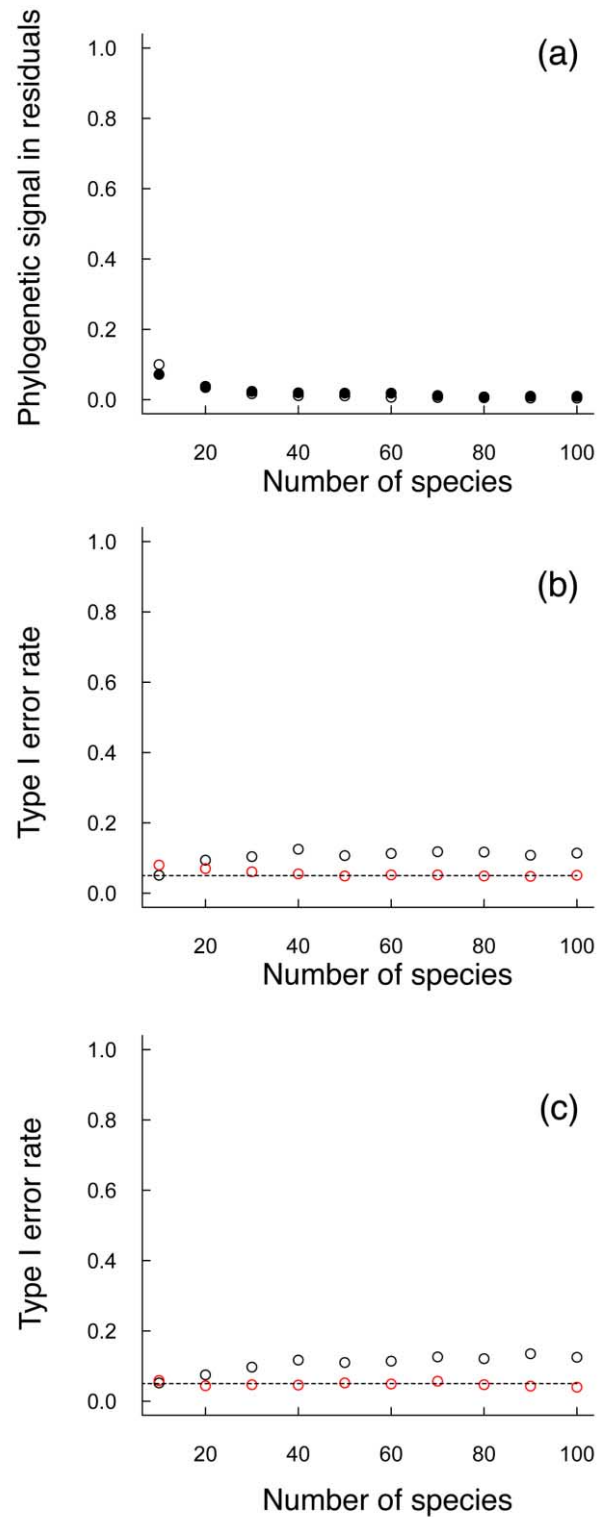


Figure A8: Phylogenetic signal in residuals and Type I error rates of phylogenetic eigenvector regression (PVR) methods applied to data in which there is no phylogenetic signal in the residuals but where Pagel's λ is used to correct the generalized least squares (GLS) results. *a*, Estimates of Pagel's λ for residuals of PVR models from models based on phylogenies of different

sizes and for data sets in which there is no phylogenetic signal in x (*open circles*) and a phylogenetic signal in x (*filled circles*). b , c , Type I error rates for GLS models (*red*) and PVR method (*black open circles*) from data sets of varying sizes. In b there is no phylogenetic signal in x , whereas in c there is a strong phylogenetic signal in x .

Literature Cited Only in the Appendix

- Blomberg, S. P., and T. Garland Jr. 2002. Tempo and mode in evolution: phylogenetic inertia, adaptation and comparative methods. *Journal of Evolutionary Biology*. 15:899–910.
- Blomberg, S. P., T. Garland Jr., and A. R. Ives. 2003. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution* 57:717–745.