The statistics of meta-analysis consist of quantifying experimental outcomes from multiple published studies (Hedges and Olkin, 1985). Ecologists use these weighted effect sizes to provide an overall synthesis of multiple published studies (Hedges and Olkin, 1985). Ecologists analyze effect size data extracted from published studies for integrating phylogenetic information into meta-analysis. It is designed to help ecologists, evolutionary biologists and conservation biologists analyze effect size data extracted from published studies in a comparative phylogenetic context. This software estimates phylogenetic versions of all the traditional meta-analytical statistics used for pooling effect sizes with weighted regressions; evaluating the homogeneity of these effect sizes; performing moderator tests akin to ANOVA style analyses; and analyzing data with fixed- and random-effects models. phyloMeta is developed in C/C++ and can be used via command line in MS Windows environments.

Availability: phyloMeta can be obtained freely as an executable on the web at http://lajeunesse.myweb.usf.edu/publications

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1 INTRODUCTION

The statistics of meta-analysis consist of quantifying experimental outcomes with effect sizes, assigning a weight to each effect size that is inversely proportional to its variance, and then averaging these weighted effect sizes to provide an overall synthesis of multiple published studies (Hedges and Olkin, 1985). Ecologists and evolutionary biologists rely heavily on these statistics to provide research summaries and to test hypotheses on moderators of experimental outcomes—often pooling research from different taxa to achieve these goals (Lajeunesse, 2010).

However, pooling effect size data from multiple taxa can potentially bias the outcome of meta-analysis because of the non-independence of effect sizes due to the shared phylogenetic history of taxa (Lajeunesse, 2009). phyloMeta fills a gap in the statistical tools needed to assess and account for this form of non-independence when performing a meta-analysis on ecological research. This software reports all the familiar statistics of meta-analysis (e.g. pooled effect sizes paired with 95% confidence intervals and homogeneity tests) along with phylogenetic versions of these statistics (as reported in Lajeunesse, 2009; Lajeunesse et al., 2011). My intention with this software is to overcome the current limitations of widespread meta-analytical software such as metaWin (Rosenberg et al., 2000) and the emerging metafor package in R (Viechtbauer, 2010). These tools are unable to integrate the covariances necessary to account for phylogenetic correlations among effect sizes from related taxa.

2 STATISTICAL METHODS

The statistical methods reported by phyloMeta are based on the generalized least squares (GLS) approach to meta-analysis described by Lajeunesse (2009) and Lajeunesse et al. (2011). These include: weighted regressions to pool effect sizes paired with confidence intervals; homogeneity statistics (Q-tests) used for evaluating whether effect size should be pooled without bias; conservative adjustments of homogeneity tests should the phylogeny contain polytomies; analyses for both fixed- and random-effects models; ANOVA style moderator analyses, based on partitioning within- and between-group homogeneity tests; calculation of model selection criteria (AIC scores) to evaluate the relative fit of competing regression models. These methods are modifications of the regression models of Hedges and Olkin (1985) and Hedges (1992).

Briefly, for example, in a fixed-effects meta-analysis of $k$ number of effect sizes, the following GLS regression equation in matrix notation is used to pool all these $k$ effect sizes into an overall average effect $\bar{\delta}$:

$$\bar{\delta} = (X'W^{-1}X)^{-1}X'W^{-1}E$$  \hspace{1cm} (1)

where $X$ is a $k \times 1$ column vector of ones, $E$ is a $k \times 1$ column vector of the effect sizes, and $W$ is the variance–covariance matrix that defines how effect sizes are to be weighted and how they relate to one another, and is defined as:

$$W = DPD$$  \hspace{1cm} (2)

This variance–covariance matrix contains the weights due to sampling error as required by meta-analysis (these are defined in $D$, a $k \times k$ diagonal matrix of the SDs of each effect size) and the phylogenetic correlations. The phylogenetic correlations $P$ is a $k \times k$ diagonal matrix containing the shared branch length distances of each taxon on a phylogenetic tree. See Rohlf (2001) for an example of this correlation matrix. In a traditional meta-analysis, $P$ is simply defined as an Identity matrix—indicating that effect sizes are independent (Lajeunesse, 2009). Currently, phyloMeta ($v. 1.3$ as of 05/12/2011) assumes, as in Felsenstein’s (1985) phylogenetically independent contrasts, that branch lengths are proportional to the expected change (e.g. a Brownian motion model of evolution). Future releases will include diagnostics of this assumption [as described in Lajeunesse (2009)].

3 IMPLEMENTATION

The software requires no installation and little input from the user other than a text file containing the meta-analytical data and second
Windows (i.e. NT, XP, Vista, Windows 7) without any additional installation from the user. For a broad portability among early and later releases of Microsoft (6.0) to avoid use of the Windows .Net framework. This allows a weighted regression (Hedges, 1992).

variances are required for meta-analysis and are used as weights in a metric (e.g. Hedges’ phyloMeta
results or for simulation analyses. For their meta-analysis, they used a composite phylogenetic tree with conspecific or heterospecific species in their environments. For example, Carmona et al. (2011) also pooled correlations among 40 plant species to test the importance of secondary metabolites but here focused on testing hypotheses of the adaptive function of anti-herbivore defense. They found no significant differences between the traditional and phylogenetically independent meta-analyses, and chose to report only the latter. Their phylogenetic tree for ecological synthesis. These studies also serve as illustrative examples on how to use and report the output of phyloMeta, and provide important information on how to acquire or construct phylogenetic trees for meta-analysis.

For example, Carmona et al. (2011) pooled correlations for 40 plant species to test the importance of secondary metabolites over other plant characteristics (e.g. life history traits) as predictors of anti-herbivore defense. They found no significant differences between the traditional and phylogenetically independent meta-analyses, and chose to report only the latter. Their phylogenetic tree of plants was estimated using phylogenetic trees for meta-analysis. These studies also serve as illustrative examples on how to use and report the output of phyloMeta, and provide important information on how to acquire or construct phylogenetic trees for meta-analysis.

5 CONCLUSION AND PROSPECTUS

phyloMeta is a stand-alone software for assessing and accounting of phylogenetic non-independence of meta-analytical data. I am continuously developing this software and custom versions can be made upon request for specific research requirements. Further developments of the software will include optimizations via maximum likelihood for different models of evolution [e.g. Ornstein-Uhlenbeck processes; Lajeunesse (2009)], and integration of diagnostics useful for evaluating phylogenetic bias and publication bias in effect size data.

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