The statistics of meta-analysis consist of quantifying experimental outcomes to achieve these goals (Lajeunesse, 2010). Experimental outcomes—often pooling research from different taxa—provide research summaries and to test hypotheses on moderators of these outcomes with effect sizes, assigning a weight to each effect size among effect sizes from related taxa. The covariances necessary to account for phylogenetic correlations 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)].

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) along with phylogenetic versions of all the traditional meta-analytical statistics designed to help ecologists, evolutionary biologists and conservationists 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.

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 polymorphies; 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 \( k \) effects into an overall average effect \( \bar{\delta} \):

\[
\bar{\delta} = (X'^{-1}X)^{-1}X'^{-1}E,
\]

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:

\[
W = DPD^T.
\]

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 taxa 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)].
text file of the hypothesized phylogeny in NEWICK format. This
NEWICK tree is converted into a correlation matrix (P) that is
integrated into the GLS weighted regression models (Lajeunesse,
2009). Users are prompted for the names of each file on each run,
and all analyses (e.g. Q-tests, fixed- and random-effects models)
are executed automatically. As a console program, phylolMeta also
accepts these two file names as command line arguments; this
facilitates the calling of phylolMeta in R for rapid visualization
of results or for simulation analyses.

After each run, phylolMeta saves all the results in a single text
file. Finally, phylolMeta can analyze data based on any effect size
metric (e.g. Hedges' $d$, log ratio response, correlations) as long as
these data are paired with valid variance estimates. By definition,
variances are required for meta-analysis and are used as weights in
a weighted regression (Hedges, 1992).

I currently compile phylolMeta with an early version of MS VC++
(6.0) to avoid use of the Windows.Net framework. This allows
for a broad portability among early and later releases of Microsoft
Windows (i.e. NT, XP, Vista, Windows 7) without any additional
installation from the user.

4 PUBLISHED APPLICATIONS
Several published meta-analyses have already used a beta version
of phylolMeta for pooling and testing hypotheses with effect size
data in a phylogenetic context. I highlight below a few of these
studies to emphasize the potential broad applications of phylolMeta
ecological synthesis. These studies also serve as illustrative examples on how to use and report the output of phylolMeta,
and provide important information on how to acquire or construct
phylogenetic trees for meta-analysis.

For example, Carmona et al. (2011) pooled correlations among
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 (Webb and Donoghue,
2004) with internal branch length distances based on divergence
times found on the timetree website (Hedges and Kumar, 2009).
Meunier et al. (2011) also pooled correlations with phylolMeta,
but here focused on testing hypotheses of the adaptive function of
coloration in 26 bird species. In this meta-analysis, they used a molecular phylogeny estimated from gene sequence
data publically available online at GenBank. In another meta-
analysis, results from traditional and phylogenetically independent
meta-analysis were compared among studies based on 87 plant
species to evaluate correlations between fitness and flowering
synchrony (Munguia-Rosas et al., 2011). Finally, Ord et al. (2011)
broadly surveyed published research on amphibians, birds, fish,
and insects to test how animals respond to encounters with conspecific or heterospecific species in their environments. For
their meta-analysis, they used a composite phylogenetic tree with
a topology derived from public web databases (e.g. Encyclopedia
of Life, eol.org) and published phylogenies.

5 CONCLUSION AND PROSPECTUS

phylolMeta 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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