

# ***phyloMeta*** User's Guide

Software for Phylogenetically-Independent  
Meta-analysis

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## 1. Installation

*There is no installation required.* PhyloMeta will work in any version of Windows (XP, Vista, Windows 7). However, *phyloMeta* was compiled for XP (see [Compiler and Library Information](#)). To minimize potential of bugs when running analyses on Vista or Windows 7, you should run this program in “compatibility mode” for Windows XP. You can also run *phyloMeta* in R using the `?shell` or `?system` commands for the Windows or Mac versions of R (for further details see: [How to Run](#)).

Also note that *phyloMeta* uses two text files that contain the phylogeny and effect size data for the meta-analysis. These two files should be in the same folder/directory as `phyloMeta.exe`.

## 2. How to Run

*phyloMeta* is a console program, and can be run either by double clicking on `phyloMeta.exe` in Windows, or by using the command prompt to perform text-based (command-line) runs of the program.

When running *phyloMeta* directly, you will be prompted to input two file names. The first is the file containing the phylogeny, and the second the file with the effect size data. For example:

```
DATA FILES. Input two sources: (1) phylogeny and (2) effect size data.
-----
(1) Please enter the filename containing the phylogeny.
    (e.g., phylo.txt): phylogeny_example.txt
(2) Now the filename containing the effect size data.
    (e.g., meta.txt): metadata_example.txt
```

Alternatively, you can input these files using the command prompt (e.g., `C:\`). This will bypass the two inputs above. For example:

```
Microsoft Windows [Version 6.1.7600]
Copyright (c) 2009 Microsoft Corporation. All rights reserved.

C:\phyloMeta phylogeny_example.txt metadata_example.txt
```

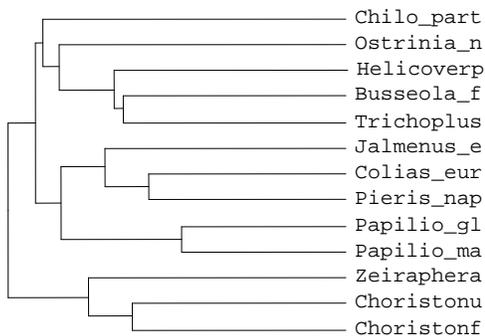
### 3. The Two File Inputs

You will need two text files for phyloMeta:

- a. *A file containing the phylogeny in NEWICK format.* See example: `phylogeny_example.txt`. The format is as follows:

```
((Chilo_part:0.185951,(Ostrinia_n:0.176054,(Helicoverp:0.143093,(Busseola_f:0.136721,Trichoplus:0.136721):0.006372):0.032961):0.009897):0.004756,((Jalmenus_e:0.148224,(Colias_eur:0.121749,Pieris_nap:0.121749):0.026475):0.026837,(Papilio_gl:0.100951,Papilio_ma:0.100951):0.07411):0.015646):0.017501,(Zeiraphera:0.158739,(Choristonu:0.131218,Choristonf:0.131218):0.027521):0.049469);
```

This file should not contain any spaces. If you can run your phylogeny in Treeview (<http://code.google.com/p/treeviewx/>), then you should not have any problems. Note: the phylogeny must be ultrametric (e.g., all tips must be aligned contemporaneously), and should not have branch-length information for the root of the tree. Also note that the number of tips in your tree should be the same as the number of effect size data, and that the names in the phylogeny should also correspond with the effect size data.



The ultrametric phylogeny found in `phylogeny_example.txt`

- b. *A file containing the effect size data.* See example: `metadata_example.txt`. The data should be in column format (either space or tab delimited) as follows:

<i>Chilo_part</i>	-0.041	0.052	0
<i>Ostrinia_n</i>	0.359	0.017	0
<i>Helicoverp</i>	0.304	0.128	1
<i>Busseola_f</i>	0.469	0.082	1
<i>Trichoplus</i>	0.263	0.075	1
<i>Jalmenus_e</i>	0.366	0.071	0
<i>Colias_eur</i>	1.013	0.205	2
<i>Pieris_nap</i>	1.169	0.255	1
<i>Papilio_gl</i>	0.232	0.044	2
<i>Papilio_ma</i>	0.251	0.155	0
<i>Zeiraphera</i>	0.016	0.067	0
<i>Choristonu</i>	1.028	0.037	1
<i>Choristonf</i>	0.137	0.048	0

The order of the columns are as follows: taxa name, effect size, effect size variance, and moderator grouping. The taxa name should be the same as in the phylogeny. The moderator groupings are numbered 0, 1, 2, etc. and indicate the subgroup analyses (ANOVA style tests). If

there are no subgroups, each row should have the same moderator number. Note that phylometa will not run if the effect size variances are zero or negative.

## 4. Description of Output

### a. Phylogeny summary.

PHYLOGENY

```

├── Chilo part
│   ├── Ostrinia n
│   ├── Helicoverp
│   └── Busseola f
│       └── Trichoplus
├── Jalmenus e
│   ├── Colias eur
│   └── Pieris nap
├── Papilio gl
└── Papilio ma
├── Zeiraphera
├── Choristonu
└── Choristonf
    
```

PHYLOGENY SUMMARY.

```

# of tips = 13
ultrametric = true
# of polytomies = 0
    
```

the phylogeny in funny text format (this taxa name alignment should be the same as in the effect size data file.)

number of taxa in tree

Test that evaluates whether the tree tips are aligned and contemporaneous. It assumes that differences in the total branch-length for each tip is not less than 0.0000000000000001.

a count of the number of unresolved bifurcations in the tree

b. Results Section A. Traditional meta-analysis (without phylogenetic information).

RESULTS SECTION A. Traditional meta-analysis.

TABLE 1. Summary of fit statistics.

Source	Q	df	p
Between groups	9.17	1	0.0025
Within groups	14.14	12	0.2919
Within group 0	3.51	5	0.6212
Within group 1	8.18	4	0.0853
Within group 2	2.45	1	0.1176
Total	23.31		
Between groups random-effects	5.83	1	0.0157

Homogeneity tests as defined by Hedges & Olkin (1985) pages 158 through 165.

The following regression equation to evaluate non-zero effects:

$$E^T V^{-1} X (X^T V^{-1} X)^{-1} X^T V^{-1} E$$

where  $E$  is the effect size vector,  $X$  is the design matrix and  $V$  the variance-covariance matrix, which is distributed as a chi-square with 1 degrees of freedom. The Z value is the weighted sum of squares due to the regression model (see Hedges 1992).

TABLE 2. Summary of pooled effect sizes ( $\delta$ ) and variances ( $\sigma^2$ ).

Group	k	$\delta$	$\sigma^2$	95%CI	Is non-zero?		
					Z	df	p
Fixed-effects							
All studies	13	0.373	0.0044	(0.243, 0.503)	31.47	1	0.0000
Group 0	6	0.225	0.0074	(0.056, 0.394)	6.79	1	0.0092
Group 1	5	0.684	0.0156	(0.439, 0.928)	30.07	1	0.0000
Group 2	2	0.370	0.0362	(-0.003, 0.743)	3.78	1	0.0519
Random-effects (between-study $\sigma^2=0.02691$ )							
All studies	13	0.373	0.0072	(0.206, 0.539)	19.19	1	0.0000
Group 0	6	0.197	0.0133	(-0.030, 0.423)	2.90	1	0.0884
Group 1	5	0.651	0.0224	(0.358, 0.945)	18.94	1	0.0000
Group 2	2	0.415	0.0543	(-0.042, 0.872)	3.17	1	0.0750

Pooled effect sizes and variances among all (k number) of effect sizes, and among moderator groups, with 95% confidence intervals (CI), and Z-tests for non-zero effects. Confidence intervals not overlapping with zero indicate a non-zero effect. The Z-test also tests this hypothesis but will generally be more conservative (see Hedges & Olkin 1985).

c. Results Section B. Phylogenetically-independent meta-analysis as described in Lajeunesse (2009).

RESULTS SECTION B. Phylogenetically-independent meta-analysis.

TABLE 1. Summary of fit statistics.

Source	Q	df	p	Adjusted via # polytomies	
				df	p
Between groups	15.50	1	0.0001		
Within groups	14.51	12	0.2691	12	0.2691
Within group 0	3.69	5	0.5948	5	0.5948
Within group 1	6.90	4	0.1411	4	0.1411
Within group 2	2.45	1	0.1176	1	0.1176
Total	30.01				
Between groups random-effects	8.00	1	0.0047		

Here the df's of Q tests are adjusted conservatively due to having unresolved phylogenetic relationships described with polytomies.

For further details see Purvis & Garland (1993).

TABLE 2. Summary of pooled effect sizes ( $\delta$ ) and variances ( $\sigma^2$ ).

Group	k	$\delta$	$\sigma^2$	95%CI	Is non-zero?		
					Z	df	p
Fixed-effects							
All studies	13	0.355	0.0073	(0.188, 0.522)	17.29	1	0.0000
Group 0	6	0.233	0.0091	(0.047, 0.420)	6.00	1	0.0143
Group 1	5	0.767	0.0201	(0.489, 1.044)	29.23	1	0.0000
Group 2	2	0.875	0.0362	(0.502, 1.248)	21.13	1	0.0000
Random-effects (between-study $\sigma^2=0.02691$ )							
All studies	13	0.346	0.0112	(0.138, 0.553)	10.66	1	0.0011
Group 0	6	0.199	0.0154	(-0.045, 0.442)	2.56	1	0.1098
Group 1	5	0.719	0.0286	(0.387, 1.050)	18.05	1	0.0000
Group 2	2	0.830	0.0543	(0.373, 1.287)	12.69	1	0.0004

d. Results Section C. Selection criteria for multiple models used in phyloMeta.

RESULTS SECTION C. Traditional vs. phylogenetically-independent meta-analysis.

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TABLE 1. Summary of model fit.

Meta-analysis	AIC		-2(likelihood)	
	fixed	random	fixed	random
Traditional	39.99	35.18	10.72	10.16
Phylogenetically-independent	42.32	36.64	12.68	10.81

Note. Lowest AIC is best fit.

Akaike's information criterion (AIC) for evaluating the fit of multiple models. Likelihood scores do not penalize models based on the number of parameters included (e.g., no parsimony penalization). Likelihood score based on equation (6) of Butler and King (2004).

### 5. The Output File

The output file (`phyloMeta_output.txt`) will contain all of the above analyses in text format. This file will appear in the same folder as where phyloMeta was run.

### 6. Funding and Support

Early versions of phyloMeta was supported by an NSF grant to the National Evolutionary Synthesis Center (grant # EF-0423641). Current funding for the development of this software is through the College of Arts and Sciences at the University of South Florida (Tampa, FL).

### 7. Release Versions and Updates

phyloMeta v1.3 (05/12/2011)

1. *The evaluation of whether a phylogeny is ultrametric has been corrected.* Previous forms of this evaluation would simply compare the total branch-lengths of all species. But now I include a minimum BL (e.g.,  $< 0.000000000000001$ ) where differences can occur to account for floating point errors when strings are converted to doubles in C.

phyloMeta v1.3 beta (02/10/2011) [NOTE: not officially released, custom modifications for the EEB Rice University course on meta-analysis]

1. *Fixed bug that had "all studies" results differ from within studies groupings when only one moderator variable is coded.* These two types of analyses now yield the same homogeneity

tests and pooled effect sizes. I thank Scott Chamberland et al. (Rice University) for making me aware of this issue.

2. *Added  $-2(\text{likelihood})$  scores along with AIC scores—to help assess which model is the best fit with the data.* Likelihood scores do not penalize models based on the number of parameters included (e.g., no parsimony penalization). Likelihood score based on equation (6) of Butler and King (2004).
3. *Phylometa now reports the value for the between-study variance used in random-effects models.* This value will be the same for both traditional and phylogenetically-independent meta-analysis because I assume that this variance is not phylogenetically correlated (see Lajeunesse 2009).

phylometa v1.2 beta (released 12/05/2010)

1. *Now accepts command-line arguments.* phylometa accepts two command-line arguments: the phylogeny filename and the effect size data filename (in that order). Entering these two filenames bypasses the manual input of these files. Running phylometa without command-lines will prompt the input of these two files.

EXAMPLE IN COMMAND PROMPT: `phylometa phylo.txt metadata.txt`

2. *Now saves all console output into an output file.* All analyses performed with phylometa will be saved in the file `phylometa_output.txt`.
3. *Now reports a phylogeny summary.* These include the number of tips on the tree, the number of polytomies, and whether the tree is ultrametric (tips all aligned contemporaneously).

phylometa v1.0 beta (released 06/05/2009)

1. Originally released for students of a National Evolutionary Synthesis Center (NESCent) course on meta-analysis taught by J. Gurevitch (SUNY Stony Brook), K. Mengersen (University of Queensland) and M.J. Lajeunesse. “An introduction to meta-analysis in ecology and evolutionary biology: NESCent Summer Course 2009”. Durham, NC. June 5–10, 2009

## **8. Compiler and Library Information**

All versions were compiled using Microsoft Visual C++ 6.0 using a modified STL-like template tree class by K. Peeters (2001; `tree_msvc.hh`) and the matrix library `Newmat10D` by R.B. Davies (2006).

## 9. References

- Butler, M.A., and A.A. King. 2004. Phylogenetic comparative analysis: a modeling approach for adaptive evolution. *American Naturalist* 164, 683–695.
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- Purvis, A., and T. Garland, Jr. 1993. Polytomies in comparative analyses of continuous characters. *Systematic Biology*, 42:569–575.

## 10. Known bugs

1. Will sometimes freeze when estimating the likelihood score of analyses with large phylogenies (>120 tips).