

Package ‘Rphylopars’

June 2, 2015

Version 0.1.1

Title Phylogenetic Comparative Tools for Missing Data and Within-Species Variation

Author Eric W. Goolsby, Jorn Bruggeman, Cecile Ane

Maintainer Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

Description Tools for performing phylogenetic comparative methods for datasets with with multiple observations per species (intraspecific variation or measurement error) and/or missing data. Available functions allow ancestral state reconstruction, missing data imputation, phylogenetic regression (phylogenetic generalized least squares), and phylogenetic principal components analysis (pPCA).

Date 2015-06-02

Depends ape

License GPL (>= 2)

Imports Rcpp, doBy, geiger, phylolm, phytools, mvnmlc

LinkingTo Rcpp, RcppArmadillo

NeedsCompilation yes

Repository CRAN

Date/Publication 2015-06-02 08:43:57

R topics documented:

Rphylopars-package	2
anova.phylopars.lm	3
logLik.phylopars	3
logLik.phylopars.lm	4
phylopars	4
phylopars.crossvalidate	7
phylopars.lm	8
phylopars.pca	10
phylopars.predict	11
phylopars.rerun	12
plot.crossvalidate	13

print.crossvalidate	14
print.phylopars	14
print.phylopars.lm	15
simtraits	15
summary.phylopars	16
summary.phylopars.lm	17
write.phylopars	17

Index	19
--------------	-----------

Rphylopars-package	<i>Phylogenetic Comparative Tools for Missing Data and Within-Species Variation</i>
--------------------	---

Description

Tools for performing phylogenetic comparative methods for datasets with with multiple observations per species (intraspecific variation or measurement error) and/or missing data. Available functions allow ancestral state reconstruction, missing data imputation, phylogenetic regression (phylogenetic generalized least squares), and phylogenetic principal components analysis (pPCA).

Details

Package:	Rphylopars
Type:	Package
Version:	0.1.1
Date:	2015-06-02
License:	GPL (>= 2)

Author(s)

Eric W. Goolsby, Jorn Bruggeman, Cecile Ane
 Maintainer: Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Ho, L. S. T. and Ane, C. 2014. "A linear-time algorithm for Gaussian and non-Gaussian trait evolution models". *Systematic Biology* 63(3):397-408.

Examples

```
# simulate data
```

```

sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
  pheno_error = TRUE,phylo_correlated = TRUE,pheno_correlated = FALSE)

PPE

# perform phylogenetic PCA
PPE_pca <- phylopars.pca(PPE)
summary(PPE_pca)

# perform phylogenetic regression
p_BM <- phylopars.lm(V3~V1+V2,trait_data = sim_data$trait_data,tree = sim_data$tree,model = "BM")

# perform ancestral state reconstruction / tip prediction
PPP_ace <- phylopars.predict(PPE)

```

anova.phylopars.lm *Phylopars regression ANOVA*

Description

Generic S3 method for phylopars

Usage

```
## S3 method for class 'phylopars.lm'
anova(object, ...)
```

Arguments

object	Fitted phylopars.lm object
...	

logLik.phylopars *Extract Log_likelihood*

Description

Generic S3 method for phylopars

Usage

```
## S3 method for class 'phylopars'
logLik(object, ...)
```

Arguments

```
object          Fitted phylopars object
...
```

```
logLik.phylopars.lm  Extract Log_likelihood
```

Description

Generic S3 method for phylopars

Usage

```
## S3 method for class 'phylopars.lm'
logLik(object, ...)
```

Arguments

```
object          Fitted phylopars.lm object
...
```

```
phylopars          Estimation of phylogenetic and phenotypic covariance parameters
```

Description

This function estimates parameters for the phylogenetic and phenotypic variance-covariance matrices for datasets with missing observations and multiple within-species observations. This function is a prerequisite for ancestral state reconstruction and missing tip estimation ([phylopars.predict](#)) and phylogenetic PCA ([phylopars.pca](#)).

Usage

```
phylopars(trait_data, tree, model = "BM", pheno_error = TRUE,
  phylo_correlated = TRUE, pheno_correlated = FALSE, calc_pheno = FALSE,
  calc_pheno_auto_n = 20, calc_pheno_phenocovs, use_means=FALSE,
  species_identifier = "species", verbose = FALSE, phylocov_start,
  phenocov_start, theta_start, model_start, skip_optim = FALSE, REML = TRUE,
  optim_limit = 50, BM_first = TRUE, usezscores = TRUE)
```

Arguments

trait_data	A data frame with one column per trait, as well as a column labeled "species" (with species names matching tips on the phylogeny). Each row corresponds to a single observation, and multiple observation for species are allowed. Missing data should be represented with NA.
tree	An object of class phylo
model	Model of evolution. Default is "BM". Also accepts "lambda", "kappa", "delta", "EB", and "OUrandomRoot", "OUfixedRoot",
pheno_error	If TRUE (default), parameters are estimated assuming within-species variation.
phylo_correlated	If TRUE (default), parameters are estimated assuming traits are correlated.
pheno_correlated	If TRUE, parameters are estimated assuming within-species observations traits are correlated (default is FALSE).
calc_pheno	If TRUE, phenotypic error variance is estimated for each species. If the number of observations for a given species is less than calc_pheno_auto_n (default=20), pooled within-species variance is used, unless phenotypic covariance matrices are supplied in the calc_pheno_phenocovs argument.
calc_pheno_auto_n	The minimum number of within-species observations for a given species for which within-species variance is calculated individually for a given species rather than pooled within-species variance. Only relevant if calc_pheno=TRUE and calc_pheno_phenocovs is not supplied.
calc_pheno_phenocovs	User-supplied phenotypic covariance matrix OR a list of phenotypic covariance matrices for each species.
use_means	Whether to use means (as in Ives et al. 2007) or raw data. Default is raw data (use_means=FALSE).
species_identifier	Optional argument. The name of the column in data where species names are stored. The default value is "species", but can be changed for convenience if data has an alternative species column name.
verbose	Optional argument. Whether or not to print the log-likelihood during optimization (NOTE: constants in the likelihood calculation are dropped from the value reported during optimization.)
phylocov_start	Optional starting value for phylogenetic trait variance-covariance matrix. Must be of dimensions n_traits by n_traits.
phenocov_start	Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimensions n_traits by n_traits.
theta_start	Optional starting parameters for theta.
model_start	Optional starting parameters for the evolutionary model.
skip_optim	Optional argument to skip optimization (NOTE: this will produce the WRONG answer unless BM=TRUE, there is no missing data, and pheno_error=FALSE; generally leave set to FALSE).

REML	If TRUE (default), the algorithm will return REML estimates. If FALSE, maximum likelihood estimates will be returned.
optim_limit	Optional: number of extra optimization attempts allowed if convergence is not achieved. Only necessary if convergence failure is suspected.
BM_first	Whether to estimate covariance assuming Brownian motion prior to estimating alternative evolutionary model parameters.
usezscores	Whether to convert data to z-scores during optimization (recommended).

Value

An object of class phylopars.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>, Cecile Ane, Jorn Bruggeman

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15, ntraits = 4, nreps = 3, nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data, tree = sim_data$tree,
  pheno_error = TRUE, phylo_correlated = TRUE, pheno_correlated = FALSE)

PPE

# perform phylogenetic PCA
PPE_pca <- phylopars.pca(PPE)
summary(PPE_pca)

# perform phylogenetic regression
p_BM <- phylopars.lm(V3~V1+V2, trait_data = sim_data$trait_data, tree = sim_data$tree, model = "BM")

# perform ancestral state reconstruction / tip prediction
PPP_ace <- phylopars.predict(PPE)
```

`phylopars.crossvalidate`*Phylopars cross-validation*

Description

This function performs cross-validation of the fitted phylopars object using the leave-one-out method. For each species, all observations for a single trait are temporarily deleted, and the value is phylogenetically imputed using `phylopars.predict()`. A regression between the observed and predicted species means is returned. Also estimated is mean bias and error of the phylopars model, as well as two alternative reference models: mean model and nearest neighbor model.

Usage

```
phylopars.crossvalidate(PPE, plot = FALSE, verbose = FALSE)
```

Arguments

<code>PPE</code>	Fitted phylopars object
<code>plot</code>	Whether or not to plot cross-validation statistics (default is TRUE)
<code>verbose</code>	Whether or not to print progress of cross-validation (default is FALSE)

Value

Returns a summary of cross-validation statistics.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15, ntraits = 4, nreps = 3, nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data, tree = sim_data$tree,
  pheno_error = TRUE, phylo_correlated = TRUE, pheno_correlated = FALSE)
```

PPE

```
phylopars.crossvalidate(PPE)
```

phylopars.lm

Phylopars regression

Description

Performs phylogenetic regression.

Usage

```
phylopars.lm(formula, trait_data, tree, model = "BM", pheno_error = TRUE,
  phylo_correlated = TRUE, pheno_correlated = FALSE, calc_pheno = FALSE,
  calc_pheno_auto_n = 20, calc_pheno_phenocovs, use_means = FALSE,
  species_identifier = "species", verbose = FALSE, phylocov_start,
  phenocov_start, theta_start, model_start, skip_optim = FALSE,
  REML = TRUE, optim_limit = 50, BM_first = TRUE, usezscores = TRUE)
```

Arguments

formula	A model formula.
trait_data	A data frame with one column per trait, as well as a column labeled "species" (with species names matching tips on the phylogeny). Each row corresponds to a single observation, and multiple observation for species are allowed. Missing data should be represented with NA.
tree	An object of class phylo
model	Model of evolution. Default is "BM". Also accepts "lambda", "kappa", "delta", "EB", and "OUrandomRoot", "OUfixedRoot",
pheno_error	If TRUE (default), parameters are estimated assuming within-species variation.
phylo_correlated	If TRUE (default), parameters are estimated assuming traits are correlated.
pheno_correlated	If TRUE, parameters are estimated assuming within-species observations traits are correlated (default is FALSE).
calc_pheno	If TRUE, phenotypic error variance is estimated for each species. If the number of observations for a given species is less than calc_pheno_auto_n (default=20), pooled within-species variance is used, unless phenotypic covariance matrices are supplied in the calc_pheno_phenocovs argument.
calc_pheno_auto_n	The minimum number of within-species observations for a given species for which within-species variance is calculated individually for a given species rather than pooled within-species variance. Only relevant if calc_pheno=TRUE and calc_pheno_phenocovs is not supplied.

calc_pheno_phenocovs	User-supplied phenotypic covariance matrix OR a list of phenotypic covariance matrices for each species.
use_means	Whether to use means (as in Ives et al. 2007) or raw data. Default is raw data (use_means=FALSE).
species_identifier	Optional argument. The name of the column in data where species names are stored. The default value is "species", but can be changed for convenience if data has an alternative species column name.
verbose	Optional argument. Whether or not to print the log-likelihood during optimization (NOTE: constants in the likelihood calculation are dropped from the value reported during optimization.)
phylocov_start	Optional starting value for phylogenetic trait variance-covariance matrix. Must be of dimensions n_traits by n_traits.
phenocov_start	Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimensions n_traits by n_traits.
theta_start	Optional starting parameters for theta.
model_start	Optional starting parameters for the evolutionary model.
skip_optim	Optional argument to skip optimization (NOTE: this will produce the WRONG answer unless BM=TRUE, there is no missing data, and pheno_error=FALSE; generally leave set to FALSE).
REML	If TRUE (default), the algorithm will return REML estimates. If FALSE, maximum likelihood estimates will be returned.
optim_limit	Optional: number of extra optimization attempts allowed if convergence is not achieved. Only necessary if convergence failure is suspected.
BM_first	Whether to estimate covariance assuming Brownian motion prior to estimating alternative evolutionary model parameters.
usezscores	Whether to convert data to z-scores during optimization (recommended).

Value

A fitted phylopars.lm object.

Examples

```
# no missing data
s <- simtraits(ntaxa = 50,ntraits = 3,nreps = 1,nmissing = 0)
p_BM <- phylopars.lm(V3~V1+V2,trait_data = s$trait_data,tree = s$tree,model = "BM")
p_lambda <- phylopars.lm(V3~V1+V2,trait_data = s$trait_data,tree = s$tree,model = "lambda")
summary(p_BM)
summary(p_lambda)

# with missing data
# notice that logLik, AIC, and BIC are not reported if data is missing
s <- simtraits(ntaxa = 50,ntraits = 3,nreps = 1,nmissing = 15)
```

```
p_BM <- phylopars.lm(V3~V1+V2,trait_data = s$trait_data,tree = s$tree,model = "BM")
p_lambda <- phylopars.lm(V3~V1+V2,trait_data = s$trait_data,tree = s$tree,model = "lambda")
summary(p_BM)
summary(p_lambda)
```

phylopars.pca

Phylogenetic principal components analysis

Description

This function, adapted from [phyl.pca](#) in the **phytools** package, performs phylogenetic principal components analysis on a fitted phylopars object. Additionally, fast algorithms are used to avoid large matrix inversions using the [three.point.compute](#) function in **phylolm**.

Usage

```
phylopars.pca(PPE, mode = "cov", pgl_s_means = FALSE)
```

Arguments

PPE	Fitted phylopars object
mode	Either "cov" (default) or "corr"
pgl_s_means	Whether to use raw species trait means of PGLS species trait means in forming the PCA

Value

Returns an object of class `phyl.pca`.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>, Cecile Ane, Jorn Bruggeman

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Revell, L. J. (2009) Size-correction and principal components for interspecific comparative studies. *Evolution*, 63, 3258-3268.

Ho, L. S. T. and Ane, C. (2014) A linear-time algorithm for Gaussian and non-Gaussian trait evolution models. *Systematic Biology*, 63: 397-408.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
  pheno_error = TRUE,phylo_correlated = TRUE,pheno_correlated = FALSE)

PPE

# perform phylogenetic PCA
PPE_pca <- phylopars.pca(PPE)
summary(PPE_pca)
biplot(PPE_pca)
```

phylopars.predict *Ancestral state reconstruction and missing value tip reconstruction*

Description

This function performs ancestral state reconstruction (and missing value tip reconstruction) given a fitted phylopars object.

Usage

```
phylopars.predict(PPE, nodes, tips, verbose = FALSE)
```

Arguments

PPE	Fitted phylopars object
nodes	Optional argument: vector of which internal nodes to reconstruct.
tips	Optional argument: vector of which species values to predict.
verbose	Whether or not to print progress of node reconstruction / tip prediction (default is FALSE).

Value

Returns a list of reconstructed node and tip means, as well as standard deviations for each mean.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
  pheno_error = TRUE,phylo_correlated = TRUE,pheno_correlated = FALSE)

phylopars.predict(PPE)
```

phylopars.rerun

Rerun phylopars optimization

Description

This function reruns parameter optimization for a phylopars object if convergence issues are suspected.

Usage

```
phylopars.rerun(PPE)
```

Arguments

PPE Fitted phylopars object

Value

Returns a fitted object of class phylopars.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
  pheno_error = TRUE,phylo_correlated = TRUE,pheno_correlated = FALSE)

# suspect convergence failure, so optimize parameters again
PPE <- phylopars.rerun(PPE)
```

plot.crossvalidate *Phylopars cross-validation*

Description

Plots cross-validation results

Usage

```
## S3 method for class 'crossvalidate'
plot(x, ...)
```

Arguments

x Crossvalidate object
...

Value

Returns a summary of cross-validation statistics.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

print.crossvalidate *Phylopars cross-validation*

Description

Generic S3 method for crossvalidate objects

Usage

```
## S3 method for class 'crossvalidate'  
print(x, ...)
```

Arguments

x Crossvalidate object
...

Value

Prints cross-validation results.

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

print.phylopars *Print phylopars*

Description

Generic S3 method for phylopars

Usage

```
## S3 method for class 'phylopars'  
print(x, ...)
```

Arguments

x Fitted phylopars object
...

```
print.phylopars.lm      Print phylopars.lm
```

Description

Generic S3 method for phylopars.lm

Usage

```
## S3 method for class 'phylopars.lm'
print(x, ...)
```

Arguments

x Fitted phylopars.lm object
...

```
simtraits             Simulate traits for phylopars estimation
```

Description

Simulates traits for codephylopars estimation.

Usage

```
simtraits(ntaxa = 15, ntraits = 4, nreps = 3, nmissing = 10, tree, v, anc, intraspecific)
```

Arguments

ntaxa Either number of taxa (ntaxa) or a tree can be supplied.
ntraits Number of traits to be simulated.
nreps Number of replicates per trait per species to simulate.
nmissing Number of randomly missing trait values.
tree Either number of taxa (ntaxa) or a tree can be supplied.
v Trait covariance (v) can be optionally supplied; otherwise off-diagonal elements are set to 0.8.
anc Value for ancestral state at root node for [fastBM](#) from the **phytools** package.
intraspecific Optional value for within-species variance.

Value

data Data for phylopars()
tree Tree for phylopars()

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

# estimate parameters under Brownian motion
# pheno_error = TRUE assumes intraspecific variation
# pheno_correlated = FALSE assumes intraspecific variation is not correlated
# phylo_correlated = TRUE assumed traits are correlated

PPE <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
  pheno_error = TRUE,phylo_correlated = TRUE,pheno_correlated = FALSE)

PPE
```

summary.phylopars *Phylopars summary*

Description

Summarizes phylopars

Usage

```
## S3 method for class 'phylopars'
summary(object, ...)
```

Arguments

object Fitted phylopars object
...

summary.phylopars.lm *phylopars.lm summary*

Description

Summarizes phylopars.lm

Usage

```
## S3 method for class 'phylopars.lm'
summary(object, ...)
```

Arguments

object Fitted phylopars.lm object
 ...

write.phylopars *Write data and tree files for Python phylopars compatability.*

Description

Writes data and tree files for Python phylopars compatibility.

Usage

```
write.phylopars(trait_data, tree, data_file, tree_file, species_identifier = "species")
```

Arguments

trait_data A data frame with one column per trait, as well as a column labeled "species" (with species names matching tips on the phylogeny). Each row corresponds to a single observation, and multiple observation for species are allowed. Missing data should be represented with NA.

tree An object of class phylo

data_file Desired path to write data file.

tree_file Desired path to write tree file.

species_identifier
 Title of species column in data file. Defaulted to "species"

Author(s)

Eric W. Goolsby <eric.goolsby.evolution@gmail.com>

References

Bruggeman J, Heringa J and Brandt BW. (2009) PhyloPars: estimation of missing parameter values using phylogeny. *Nucleic Acids Research* 37: W179-W184.

Examples

```
# simulate data
sim_data <- simtraits(ntaxa = 15,ntraits = 4,nreps = 3,nmissing = 10)

write.phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,data_file = "data_path.txt",
tree_file = "tree_path.new")
```

Index

- *Topic **Ancestral state reconstruction**
 - Rphylopars-package, 2
 - *Topic **Intraspecific variation**
 - Rphylopars-package, 2
 - *Topic **Measurement error**
 - Rphylopars-package, 2
 - *Topic **Missing data**
 - Rphylopars-package, 2
 - *Topic **Phylogenetic imputation**
 - Rphylopars-package, 2
 - *Topic **Phylogenetic principle components analysis**
 - Rphylopars-package, 2
 - *Topic **Phylogenetic regression**
 - Rphylopars-package, 2
 - *Topic **Phylogenetic variance-covariance**
 - Rphylopars-package, 2
 - *Topic **Within-species variation**
 - Rphylopars-package, 2
 - *Topic **package**
 - Rphylopars-package, 2
- anova.phylopars.lm, 3
- fastBM, 15
- logLik.phylopars, 3
- logLik.phylopars.lm, 4
- phyl.pca, 10
- phylopars, 4
- phylopars.crossvalidate, 7
- phylopars.lm, 8
- phylopars.pca, 4, 10
- phylopars.predict, 4, 11
- phylopars.rerun, 12
- plot.crossvalidate, 13
- print.crossvalidate, 14
- print.phylopars, 14
- print.phylopars.lm, 15
- Rphylopars-package, 2
- simtraits, 15
- summary.phylopars, 16
- summary.phylopars.lm, 17
- three.point.compute, 10
- write.phylopars, 17