

Package ‘Rphylopars’

February 6, 2021

Version 0.3.2

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

Description Tools for performing phylogenetic comparative methods for datasets with with multiple observations per species (intraspecific variation or measurement error) and/or missing data (Goolsby et al. 2017). Performs ancestral state reconstruction and missing data imputation on the estimated evolutionary model, which can be specified as Brownian Motion, Ornstein-Uhlenbeck, Early-Burst, Pagel's lambda, kappa, or delta, or a star phylogeny.

Date 2021-02-04

Depends ape

License GPL (>= 2)

URL <https://github.com/ericgoolsby/Rphylopars/wiki>

Imports Rcpp, doBy, geiger, phylolm, phytools, Matrix, MASS

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 7.1.1

NeedsCompilation yes

Author Eric W. Goolsby [aut, cre],
Jorn Bruggeman [aut],
Cecile Ane [aut]

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

Repository CRAN

Date/Publication 2021-02-06 07:20:17 UTC

R topics documented:

| | |
|---------------------|---|
| Rphylopars-package | 2 |
| anc.recon | 3 |
| anova.phylopars.lm | 4 |
| fast.SSC | 5 |
| logLik.phylopars | 6 |
| logLik.phylopars.lm | 6 |

| | |
|--------------------------------|----|
| phylopars | 7 |
| phylopars.lm | 10 |
| print.phylopars | 13 |
| print.phylopars.lm | 13 |
| print.SSC | 14 |
| simtraits | 14 |
| summary.phylopars | 15 |
| summary.phylopars.lm | 16 |
| write.phylopars | 16 |

| | |
|--------------|-----------|
| Index | 18 |
|--------------|-----------|

| | |
|--------------------|---|
| 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 (Goolsby et al. 2017). Performs ancestral state reconstruction and missing data imputation on the estimated evolutionary model, which can be specified as Brownian Motion, Ornstein-Uhlenbeck, Early-Burst, Pagel's lambda, kappa, or delta, or a star phylogeny.

Details

Package: Rphylopars
 Type: Package
 Version: 0.3.2
 Date: 2021-02-04
 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.

Goolsby EW, Ane C, Bruggeman J. 2017. "Rphylopars: Fast Multivariate Phylogenetic Comparative Methods for Missing Data and Within-Species Variation." *Methods in Ecology & Evolution*. 2017. 8:22-27.

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 = TRUE)

PPE

PPE$anc_recon # Ancestral state reconstruction and species mean prediction
PPE$anc_var # Prediction variance

###NOT RUN
# estimate parameters under multivariate OU
# PPE_OU <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
#   model="mvOU",pheno_error = TRUE,phylo_correlated = TRUE,
#   pheno_correlated = TRUE)
#
# PPE
```

anc.recon

Ultra-fast maximum likelihood ancestral state reconstruction

Description

This function performs ancestral state reconstruction using a fast algorithm based on Ho and Ane (2014).

Usage

```
anc.recon(trait_data, tree, vars = FALSE, CI = FALSE)
```

Arguments

| | |
|------------|---|
| trait_data | A vector or matrix of trait values. Names or row names correspond to species names. Data cannot have any missing data or within-species variation (this type of data can be handled by the phylopars function). |
| tree | An object of class phylo. |

| | |
|------|---|
| vars | Whether to return the variances of the restricted maximum likelihood estimates |
| CI | Whether to return 95% confidence intervals of the restricted maximum likelihood estimates |

Value

A named vector of maximum likelihood ancestral states (with names corresponding to node names if available or node numbers from the tree rearranged in postorder, as obtained by the command `reorder(tree, "postorder")`). If `vars` or `CI` is set to `TRUE`, a list is returned with these values included.

Author(s)

Felsenstein, J. (1985) Phylogenies and the comparative method. *American Naturalist*, 125, 1-15.

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

Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, 3, 217-223.

See Also

[fastAnc](#), [ace](#), [pic](#)

Examples

```
require(ape)
tree <- rtree(10000) # random tree with 10,000 taxa
x <- setNames(rnorm(1e4), tree$tip.label) # random trait data
recon <- anc.recon(trait_data=x, tree=tree)
```

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
...

```

| | |
|----------|--|
| fast.SSC | <i>Fast Phylogenetic Signal Using Sum of Squared Changes (SSC)</i> |
|----------|--|

Description

This function uses a fast ancestral state reconstruction algorithm ([anc.recon](#), Goolsby, In review) to calculate the sum of squared changes between ancestral and descendant nodes/tips, as described in Klingenberg and Gidaszewski (2010). Significance is assessed via phylogenetic permutation.

Usage

```
fast.SSC(trait_data, tree, niter = 1000)
```

Arguments

| | |
|------------|--|
| trait_data | A vector or matrix of trait values. Names or row names correspond to species names. Data cannot have any missing data or within-species variation. |
| tree | An object of class phylo. |
| niter | Number of iterations for hypothesis testing (default=1000). |

Value

| | |
|------------|--|
| pvalue | Description of 'compl' |
| scaled.SSC | Scaled sum of squared changes. A value less than 1 indicates less phylogenetic signal as measured by SSC than expected under Brownian motion, and a value greater than 1 indicates greater phylogenetic signal as measured by SSC than expected under Brownian motion. |
| SSC | Total sum of squared changes (SSC) |

Author(s)

Eric W. Goolsby

References

Goolsby E.W. 2016. Likelihood-Based Parameter Estimation for High-Dimensional Phylogenetic Comparative Models: Overcoming the Limitations of 'Distance-Based' Methods. *Systematic Biology*. Accepted.

Blomberg SP, Garland T, Ives AR. 2003. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution*, 57:717-745.

Klingenberg, C. P., and N. A. Gidaszewski. 2010. Testing and quantifying phylogenetic signals and homoplasy in morphometric data. *Syst. Biol.* 59:245-261.

Adams, D.C. 2014. A generalized K statistic for estimating phylogenetic signal from shape and other high-dimensional multivariate data. *Systematic Biology*. 63:685-697.

Examples

```
sim_dat <- simtraits(ntaxa = 100, ntraits = 4)
fast.SSC(trait_data = sim_dat$trait_data, tree = sim_dat$tree)
```

| | |
|-------------------------------|-------------------------------|
| <code>logLik.phylopars</code> | <i>Extract Log_likelihood</i> |
|-------------------------------|-------------------------------|

Description

Generic S3 method for phylopars

Usage

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

Arguments

| | |
|---------------------|-------------------------|
| <code>object</code> | Fitted phylopars object |
| <code>...</code> | |

| | |
|----------------------------------|-------------------------------|
| <code>logLik.phylopars.lm</code> | <i>Extract Log_likelihood</i> |
|----------------------------------|-------------------------------|

Description

Generic S3 method for phylopars

Usage

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

Arguments

| | |
|---------------------|----------------------------|
| <code>object</code> | Fitted phylopars.lm object |
| <code>...</code> | |

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 can also be used to fit alternative evolutionary models, including Ornstein-Uhlenbeck, Early-Burst, star phylogeny, or Pagel's lambda, kappa, or delta. Reconstructed ancestral states and predicted species means (i.e., for missing data), along with prediction variances, are also provided.

Usage

```
phylopars(trait_data, tree, model = "BM", pheno_error, phylo_correlated = TRUE,
  pheno_correlated = TRUE, REML = TRUE, full_alpha = TRUE, phylocov_start,
  phenocov_start, model_par_start, phylocov_fixed, phenocov_fixed, model_par_fixed,
  skip_optim = FALSE, skip_EM = FALSE, EM_Fels_limit = 1000, repeat_optim_limit = 1,
  EM_missing_limit = 50, repeat_optim_tol = 0.01, model_par_evals = 10, max_delta = 10000,
  EM_verbose = FALSE, optim_verbose = FALSE, npd = FALSE,
  nested_optim = FALSE, usezscores = TRUE, phenocov_list = list(), ret_args = FALSE,
  ret_level = 1)
```

Arguments

| | |
|------------------|---|
| trait_data | A data frame with the first column labeled "species" (with species names matching tips on the phylogeny) and one column per trait. Each row corresponds to a single observation, and multiple observations for species are allowed. Missing data should be represented with NA. |
| tree | An object of class phylo |
| model | Model of evolution. Default is "BM". Alternative evolutionary models include "mvOU" (for the multivariate Ornstein-Uhlenbeck), or univariate tree transformations: "OU" "lambda", "kappa", "delta", "EB", "star". |
| pheno_error | If TRUE (default, unless <=1 observation per species is provided), parameters are estimated assuming within-species variation. |
| phylo_correlated | If TRUE (default), parameters are estimated assuming traits are correlated. |
| pheno_correlated | If TRUE (default), parameters are estimated assuming within-species observations traits are correlated. |
| REML | If TRUE (default), the algorithm will return REML estimates. If FALSE, maximum likelihood estimates will be returned. |
| full_alpha | Only applicable for the multivariate OU (model="mvOU"). If TRUE (default), a fully parametrized alpha matrix is fit. If FALSE, a diagonal alpha matrix is fit. |
| phylocov_start | Optional starting value for phylogenetic trait variance-covariance matrix. Must be of dimension n_traits by n_traits. |

| | |
|--------------------|--|
| phenocov_start | Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimension n_traits by n_traits. |
| model_par_start | Optional starting parameters for the evolutionary model. For model="mvOU", must be of dimension n_traits by n_traits. Otherwise, must be a single value. |
| phylocov_fixed | Optional fixed value for phylogenetic trait variance-covariance matrix. Must be of dimension n_traits by n_traits. |
| phenocov_fixed | Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimension n_traits by n_traits. |
| model_par_fixed | Optional fixed parameter for the evolutionary model. For model="mvOU", must be of dimension n_traits by n_traits. Otherwise, must be a single value. |
| skip_optim | Whether to skip BFGS optimization (not recommended unless all parameters are fixed). |
| skip_EM | Whether to skip Expectation-Maximization prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters). |
| EM_Fels_limit | Whether to skip Expectation-Maximization prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters). |
| repeat_optim_limit | The number of times to repeat numerical optimization (default is 1). |
| EM_missing_limit | Maximum number of iterations for EM. |
| repeat_optim_tol | Maximum tolerance for repeated numerical optimization (only relevant if repeat_optim_limit>1). |
| model_par_evals | Number of times to evaluate univariate tree transformation models along the range of possible parameter values. Used to generate informed starting values for alternative evolutionary models if nested_optim=TRUE. |
| max_delta | Maximum allowed difference between the log-likelihood for EM-generated starting parameters and new parameters tried under numerical optimization. Extremely large deltas are likely to be numerical artifacts. Prevents artificial convergence. |
| EM_verbose | Whether to print the log-likelihood during Expectation-Maximization. |
| optim_verbose | Whether to print log-likelihoods during numerical optimization. |
| npd | Whether to find the nearest positive-definite matrix for all covariance matrices during numerical optimization (slow – only set to TRUE if converging to singular matrices). |
| nested_optim | Only relevant if fitting a univariate alternative evolutionary model. Tries multiple tree transformation parameter values along the range of possible values to make informed starting parameters. Slower than the default (nested_optim=FALSE), in which all parameters are estimated simultaneously. |

| | |
|---------------|---|
| usezscores | Whether or not to use centered and standardized data during numerical optimization (recommended). |
| phenocov_list | An optional named list of species-specific within-species covariance matrices to be held fixed, as in Ives et al (2007). This option forces pheno_error and pheno_correlated to be FALSE, and uses mean species values instead of raw data. Raw variance should be divided by the number of observations per species (i.e., squared standard errors). See Ives et al (2007) for more details. |
| ret_args | For internal use only. |
| ret_level | For internal use only. |

Value

An object of class phylopars. For models with phenotypic (within-species) covariance, the estimated percentage of variance explained by the phylogeny is provided as $100 \times (1 - \text{phenotypic_variance}/\text{raw_variance})$, where raw_variance is the variance of all observations for a given trait across species (`var(PPE$trait_data[, 2:ncol(PPE$`

| | |
|------------|--|
| logLik | The log-likelihood of the model |
| pars | A list composed of phylogenetic trait covariance and phenotypic (within-species) trait covariance, if estimated |
| model | The model of evolution (e.g., BM, OU, lambda, etc.), and any additional evolutionary model parameters estimated. For OU models, stationary covariance is calculated from both phylogenetic covariance (Sigma) and alpha (see Supplement 1 of Clavel et al. 2015). |
| mu | The estimate ancestral state at the root of the tree. |
| npars | The total number of parameters estimated by optimization (used for AIC and BIC). |
| anc_recon | Reconstructed ancestral states and species means. Row names correspond to species names (for the first 1:nspecies rows), and the remaining row names correspond to node numbers on a tree with edges in postorder: <code>reorder(tree, "postorder")</code> . Or, if node labels were included on the original tree, row names correspond to node labels. |
| anc_var | Variance of reconstructed ancestral estimates and imputed species means. |
| anc_cov | Covariance of estimates among variables. |
| tree | The phylogenetic tree supplied to phylopars |
| trait_data | The trait data supplied to phylopars |
| REML | TRUE if REML, FALSE if ML. |

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. Clavel, J., Escarguel, G. & Merceron, G. (2015) mvmorph: an r package for fitting multivariate 261 evolutionary models to morphometric data. *Methods in Ecology and Evolution*, 6, 131-1319. Felsenstein, J. (2008) Comparative methods with sampling error and within-species variation: contrasts revisited and revised. *American Naturalist*, 171, 713-725. Ho L.S.T., Ane C. 2014. A linear-time algorithm for Gaussian and non-Gaussian trait evolution models. *Syst. Biol.* 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 = TRUE)

PPE

PPE$anc_recon # Ancestral state reconstruction and species mean prediction
PPE$anc_var # Prediction variance

###NOT RUN
# estimate parameters under multivariate OU
# PPE_OU <- phylopars(trait_data = sim_data$trait_data,tree = sim_data$tree,
#   model="mvOU",pheno_error = TRUE,phylo_correlated = TRUE,
#   pheno_correlated = TRUE)
#
# PPE
```

phylopars.lm

Rphylopars regression

Description

Performs phylogenetic regression.

Usage

```
phylopars.lm(formula, trait_data, tree, model = "BM", pheno_error,
  phylo_correlated = TRUE, pheno_correlated = TRUE, REML = TRUE,
  full_alpha = TRUE, phylocov_start, phenocov_start, model_par_start,
  phylocov_fixed, phenocov_fixed, model_par_fixed, skip_optim = FALSE,
```

```
skip_EM = FALSE, EM_Fels_limit = 1000, repeat_optim_limit = 1,
EM_missing_limit = 50, repeat_optim_tol = 0.01, model_par_evals = 10,
max_delta = 10000, EM_verbos = FALSE, optim_verbos = FALSE, npd = FALSE,
nested_optim = FALSE, usezscores = TRUE, phenocov_list = list(),
ret_args = FALSE, ret_level = 1)
```

Arguments

| | |
|------------------|---|
| formula | Model formula – e.g. $Y \sim X_1 + X_2$ |
| trait_data | A data frame with the first column labeled "species" (with species names matching tips on the phylogeny) and one column per trait. Each row corresponds to a single observation, and multiple observations for species are allowed. Missing data should be represented with NA. |
| tree | An object of class phylo |
| model | Model of evolution. Default is "BM". Alternative evolutionary models include "mvOU" (for the multivariate Ornstein-Uhlenbeck), or univariate tree transformations: "OU" "lambda", "kappa", "delta", "EB", "star". |
| pheno_error | If TRUE (default, unless ≤ 1 observation per species is provided), parameters are estimated assuming within-species variation. |
| phylo_correlated | If TRUE (default), parameters are estimated assuming traits are correlated. |
| pheno_correlated | If TRUE (default), parameters are estimated assuming within-species observations traits are correlated. |
| REML | If TRUE (default), the algorithm will return REML estimates. If FALSE, maximum likelihood estimates will be returned. |
| full_alpha | Only applicable for the multivariate OU (model="mvOU"). If TRUE (default), a fully parametrized alpha matrix is fit. If FALSE, a diagonal alpha matrix is fit. |
| phylocov_start | Optional starting value for phylogenetic trait variance-covariance matrix. Must be of dimension n_{traits} by n_{traits} . |
| phenocov_start | Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimension n_{traits} by n_{traits} . |
| model_par_start | Optional starting parameters for the evolutionary model. For model="mvOU", must be of dimension n_{traits} by n_{traits} . Otherwise, must be a single value. |
| phylocov_fixed | Optional fixed value for phylogenetic trait variance-covariance matrix. Must be of dimension n_{traits} by n_{traits} . |
| phenocov_fixed | Optional starting value for phenotypic trait variance-covariance matrix. Must be of dimension n_{traits} by n_{traits} . |
| model_par_fixed | Optional fixed parameter for the evolutionary model. For model="mvOU", must be of dimension n_{traits} by n_{traits} . Otherwise, must be a single value. |
| skip_optim | Whether to skip BFGS optimization (not recommended unless all parameters are fixed). |

| | |
|--------------------|---|
| skip_EM | Whether to skip Expectation-Maximization prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters). |
| EM_Fels_limit | Whether to skip Expectation-Maximization prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters). |
| repeat_optim_limit | The number of times to repeat numerical optimization (default is 1). |
| EM_missing_limit | Maximum number of iterations for EM. |
| repeat_optim_tol | Maximum tolerance for repeated numerical optimization (only relevant if repeat_optim_limit>1). |
| model_par_evals | Number of times to evaluate univariate tree transformation models along the range of possible parameter values. Used to generate informed starting values for alternative evolutionary models if nested_optim=TRUE. |
| max_delta | Maximum allowed difference between the log-likelihood for EM-generated starting parameters and new parameters tried under numerical optimization. Extremely large deltas are likely to be numerical artifacts. Prevents artificial convergence. |
| EM_verbose | Whether to print the log-likelihood during Expectation-Maximization. |
| optim_verbose | Whether to print log-likelihoods during numerical optimization. |
| npd | Whether to find the nearest positive-definite matrix for all covariance matrices during numerical optimization (slow – only set to TRUE if converging to singular matrices). |
| nested_optim | Only relevant if fitting a univariate alternative evolutionary model. Tries multiple tree transformation parameter values along the range of possible values to make informed starting parameters. Slower than the default (nested_optim=FALSE), in which all parameters are estimated simultaneously. |
| usezscores | Whether or not to use centered and standardized data during numerical optimization (recommended). |
| phenocov_list | An optional named list of species-specific within-species covariance matrices to be held fixed, as in Ives et al (2007). This option forces pheno_error and pheno_correlated to be FALSE, and uses mean species values instead of raw data. Raw variance should be divided by the number of observations per species (i.e., squared standard errors). See Ives et al (2007) for more details. |
| ret_args | For internal use only. |
| ret_level | For internal use only. |

Value

A fitted phylopars.lm object.

Examples

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

phylopars.lm(V4~V1+V2+V3,trait_data=sim_data$trait_data,tree=sim_data$tree)
```

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
...

| | |
|-----------|------------------|
| print.SSC | <i>Print SSC</i> |
|-----------|------------------|

Description

Generic S3 method for objects returned by the function `fast.SSC`

Usage

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

Arguments

| | |
|-----|--|
| x | Object returned by <code>fast.SSC</code> |
| ... | |

| | |
|-----------|---|
| simtraits | <i>Simulate traits for phylopars estimation</i> |
|-----------|---|

Description

Simulates traits for codephylopars estimation.

Usage

```
simtraits(ntaxa = 15, ntraits = 4, nreps = 1, nmissing = 0, tree, v, anc,
intraspecific, model="BM", parameters, nsim, return.type="data.frame")
```

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. |
| intraspecific | Optional value for within-species variance. |
| model | Model of evolution (default="BM"). Other options include "OUfixedRoot", "OUrandomRoot", "lambda", "kappa", "delta", "EB". |
| parameters | List of parameters for the model. alpha for the selection strength in the OU model, lambda, kappa, delta, or rate for the EB model. |
| nsim | Number of simulations to perform (default is 1) |
| return.type | Default is "data.frame". Can also specify "matrix" if nreps=1. |

Value

| | |
|------------|--|
| trait_data | Data for phylopars() |
| tree | The original phylogenetic tree (either provided to the function or generated internally) |
| sim_tree | The transformed tree on which trait simulations were performed (identical to tree if model="BM") |
| original_X | If within-species variation is simulated, original_X is the original species mean values before adding within-species variation. |

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.

Harmon Luke J, Jason T Weir, Chad D Brock, Richard E Glor, and Wendell Challenger. 2008. GEIGER: investigating evolutionary radiations. *Bioinformatics* 24:129-131.

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 compatibility.*

Description

Writes data and tree files for Python phylopars compatibility.

Usage

```
write.phylopars(trait_data, tree, data_file, tree_file, species_identifer = "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_identifer 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

```
## Not run:  
# 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")  
  
## End(Not run)
```

Index

- * **Ancestral state reconstruction**
 - Rphylopars-package, 2
 - * **Intraspecific variation**
 - Rphylopars-package, 2
 - * **Measurement error**
 - Rphylopars-package, 2
 - * **Missing data**
 - Rphylopars-package, 2
 - * **Phylogenetic imputation**
 - Rphylopars-package, 2
 - * **Phylogenetic variance-covariance**
 - Rphylopars-package, 2
 - * **Within-species variation**
 - Rphylopars-package, 2
 - * **package**
 - Rphylopars-package, 2
- ace, 4
- anc.recon, 3, 5
- anova.phylopars.lm, 4
- fast.SSC, 5
- fastAnc, 4
- logLik.phylopars, 6
- logLik.phylopars.lm, 6
- phylopars, 3, 7
- phylopars.lm, 10
- pic, 4
- print.phylopars, 13
- print.phylopars.lm, 13
- print.SSC, 14
- Rphylopars-package, 2
- simtraits, 14
- summary.phylopars, 15
- summary.phylopars.lm, 16
- write.phylopars, 16