Package: Rphylopars (via r-universe)

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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.

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Depends ape

License GPL (>= 2)

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`Rphylopars-package` *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.

Details

Package:	Rphylopars
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Version:	0.3.10
Date:	2024-01-17
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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
...	Further arguments passed to or from other methods.

`fast.SSC` *Fast Phylogenetic Signal Using Sum of Squared Changes (SSC)*

Description

This function uses a fast ancestral state reconstruction algorithm (anc.recon, Goolsby, In review) to calculate the sum of squared changes bewteen 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 'comp1'
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)
```

---

logLik.phylopars *Extract Log_likelihood*

Description

Generic S3 method for phylopars

Usage

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

Arguments

object	Fitted phylopars object
...	Further arguments passed to or from other methods.

---

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
...	Further arguments passed to or from other methods.

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 can also be used to fit altnerative 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, get_cov_CIs = FALSE)
```

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-Maximiation prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters).

`EM_Fels_limit` Whether to skip Expectation-Maximiation 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 artifiacts. Prevents artificial convergence.

`EM_verbose` Whether to print the log-likelihood during Expectation-Maximization.

`optim_verbose` Whether to print log-likelihooods 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 ot 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.
get_cov_CIs	Whether to return 95-percent confidence intervals of covariance parameters (default=FALSE).

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*(1 - phenotypic_variance/raw_variance), where raw_variance is the variance of all observations for a given trait across species (var(PPE$trait_data[,2:ncol(PPE$t

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: reorder(tree,"postorder"). 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_verbose = FALSE,optim_verbose = FALSE, npd = FALSE,
nested_optim = FALSE, usezscores = TRUE, phenocov_list = list(),
ret_args = FALSE, ret_level = 1, get_cov_CIs = FALSE)
```

Arguments

formula	Model formula – e.g. Y~X1+X2
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-Maximiation prior to generating starting parameters for BFGS optimization (not recommended unless providing fixed parameters).

`EM_Fels_limit` Whether to skip Expectation-Maximiation 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 artifiacts. Prevents artificial convergence.

`EM_verbose` Whether to print the log-likelihood during Expectation-Maximization.

`optim_verbose` Whether to print log-likelihooods 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 ot 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.

`get_cov_CIs` Whether to return 95-percent confidence intervals of covariance parameters (default=FALSE).

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
`...`	Further arguments passed to or from other methods.

`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
`...`	Further arguments passed to or from other methods.

print.SSC *Print SSC*

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 `fast.SSC`
`...`	Further arguments passed to or from other methods.

simtraits *Simulate traits for phylopars estimation*

Description

Simulates traits for `phylopars` 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
...	Further arguments passed to or from other methods.

---

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
...	Further arguments passed to or from other methods.

---

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

```
## 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)
```

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