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picante-package *picante: R tools for integrating phylogenies and ecology*

Description

R tools for integrating phylogenies and ecology

Details

Package: picante
 Type: Package
 Version: 0.7-2
 Date: 2009-10-27
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Author(s)

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Maintainer: Steven Kembel <skembel@uoregon.edu>

color.plot.phylo *Color tip labels based on trait*

Description

Plots a phylogeny with tip labels colored to indicate continuous or discrete trait values

Usage

```
color.plot.phylo(phylo, df, trait, taxa.names,
                 num.breaks = ifelse(is.factor(df[,trait]),
                                     length(levels(df[,trait])), 12),
                 col.names = rainbow(ifelse(length(num.breaks) > 1, length(num.b
                 cut.labs = NULL,
                 leg.title = NULL,
                 main = trait,
                 leg.cex = 1,
                 tip.labs = NULL,
                 ...)
```

Arguments

phylo	An object of class phylo
df	A dataframe containing the traits to be plotted
trait	A string representing the name of column in the dataframe to be plotted
taxa.names	A string representing the name of column in the dataframe that contains the names of the taxa
num.breaks	For continuous traits, the number of bins to separate the data into
col.names	A vector of colors to use for tip labels
leg.title	A title for the tip color legend
main	A main title for the plot
cut.labs	A main title for the plot
leg.cex	A main title for the plot
tip.labs	A main title for the plot
...	Additional argument to pass to the plot.phylo function

Details

If `trait` is a factor then each level of the factor is plotted with the corresponding `col.names` value (if `length(num.breaks) > length(col.names)` colors are recycled.) If `trait` is not a factor then it is assumed to be continuous and `trait` is evenly divided into `num.breaks` levels.

Value

The command is invoked for its side effect, a plot of the `phylo` with tips colored based on `trait`

Author(s)

Peter Cowan <pcdc@berkeley.edu>

comdist

Calculates inter-community mean pairwise distance

Description

Calculates MPD (mean pairwise distance) separating taxa in two communities, a measure of phylogenetic beta diversity

Usage

```
comdist(comm, dis, abundance.weighted = FALSE, exclude.conspecifics = FALSE)
```

Arguments

<code>comm</code>	Community data matrix
<code>dis</code>	Interspecific distance matrix
<code>abundance.weighted</code>	Should mean pairwise distances separating species in two communities be weighted by species abundances? (default = FALSE)
<code>exclude.conspecifics</code>	Should conspecific taxa in different communities be excluded from MPD calculations? (default = FALSE)

Details

This function calculates a measure of phylogenetic beta diversity: the expected phylogenetic distance separating two individuals or taxa drawn randomly from different communities.

Value

Distance object of MPD values separating each pair of communities.

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

C.O. Webb, D.D. Ackerly, and S.W. Kembel. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. *Bioinformatics* 18:2098-2100.

See Also

[mpd](#), [ses.mpd](#)

Examples

```
data(phylocom)
comdist(phylocom$sample, cophenetic(phylocom$phylo), abundance.weighted=TRUE)
```

comdistnt

Calculates inter-community mean nearest taxon distance

Description

Calculates MNTD (mean nearest taxon distance) separating taxa in two communities, a measure of phylogenetic beta diversity

Usage

```
comdistnt(comm, dis, abundance.weighted = FALSE, exclude.conspecifics = FALSE)
```

Arguments

comm	Community data matrix
dis	Interspecific distance matrix
abundance.weighted	Should mean nearest taxon distances from each species to species in the other community be weighted by species abundance? (default = FALSE)
exclude.conspecifics	Should conspecific taxa in different communities be exclude from MNTD calculations? (default = FALSE)

Details

This metric has also been referred to as MNND (mean nearest neighbour distance).

This function calculates a measure of phylogenetic beta diversity: the average phylogenetic distance to the most similar taxon or individual in the other community for taxa or individuals in two communities.

Value

Distance object of MNTD values separating each pair of communities.

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

C.O. Webb, D.D. Ackerly, and S.W. Kembel. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. *Bioinformatics* 18:2098-2100.

See Also

[mntd](#), [ses.mntd](#)

Examples

```
data(phylocom)
comdistnt(phylocom$sample, cophenetic(phylocom$phylo), abundance.weighted=FALSE)
```

comm.phylo.cor	<i>Correlations between species co-occurrence and phylogenetic distances</i>
----------------	--

Description

Calculates measures of community phylogenetic structure (correlation between co-occurrence and phylogenetic distance) to patterns expected under various null models

Usage

```
comm.phylo.cor(samp, phylo, metric = c("cij", "checkerboard", "jaccard", "doi"),
  null.model = c("sample.taxa.labels", "pool.taxa.labels",
    "frequency", "richness", "independentswap", "trialswap"), runs = 999, ...)
```

Arguments

samp	Community data matrix
phylo	Phylogenetic tree
metric	Metric of co-occurrence to use (see species.dist)
null.model	Null model to use (see Details section for description)
runs	Number of runs (randomizations)
...	Additional arguments to randomizeSample

Details

Currently implemented null models (arguments to null.model):

sample.taxa.labels Shuffle phylogeny tip labels (only within set of taxa present in community data)

pool.taxa.labels Shuffle phylogeny tip labels (across all taxa included in phylogenetic tree)

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency)

richness Randomize community data matrix abundances within samples (maintains sample species richness)

independentswap Randomize community data matrix maintaining species occurrence frequency and site richness using independent swap

trialswap Randomize community data matrix maintaining species occurrence frequency and site richness using trial swap

Value

A list with elements:

obs.corr	Observed co-occurrence/phylogenetic distance correlation
obs.corr.p	P-value of observed correlation (standard P-value for correlation coefficient, not based on comparison with randomizations)
obs.rank	Rank of observed correlation vs. random
runs	Number of runs (randomizations)
obs.rand.p	P-value of observed correlation vs. randomizations (= obs.rank / (runs + 1))
random.corr	A vector of random correlation calculated for each run

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Cavender-Bares J., D.A. Ackerly, D. Baum and F.A. Bazzaz. 2004. Phylogenetic overdispersion in Floridian oak communities, *American Naturalist*, 163(6):823-843.

See Also

[randomizeSample](#)

Examples

```
data(phylocom)
comm.phylo.cor(phylocom$sample, phylocom$phylo, metric="cij", null.model="sample.taxa.labels")
```

comm.phylo.qr *Quantile regression slopes between species co-occurrence and phylogenetic distances*

Description

Calculates measures of community phylogenetic structure (quantile regression between co-occurrence and phylogenetic distance) to patterns expected under various null models

Usage

```
comm.phylo.qr(samp, phylo, metric = c("cij", "checkerboard", "jaccard", "doi"),
  null.model = c("sample.taxa.labels", "pool.taxa.labels",
    "frequency", "richness", "independentswap", "trialswap"),
  quant = 0.75, runs = 999, show.plot = FALSE, ...)
```

Arguments

samp	Community data matrix
phylo	Phylogenetic tree
metric	Metric of co-occurrence to use (see species.dist)
null.model	Null model to use (see Details section for description)
quant	Quantile of slope to be fit (using rq)
runs	Number of runs (randomizations)
show.plot	Option to display a plot of co-occurrence versus phylogenetic distance with quantile regression slope fit
...	Additional arguments to randomizeSample

Details

This function fits a quantile regression of co-occurrence versus phylogenetic distances separating species, and compares observed patterns to the patterns expected under some null model. The quantile regressions are fit using the [rq](#) function from the [quantreg](#) package.

Currently implemented null models (arguments to null.model):

sample.taxa.labels Shuffle phylogeny tip labels (only within set of taxa present in community data)

pool.taxa.labels Shuffle phylogeny tip labels (across all taxa included in phylogenetic tree)

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency)

richness Randomize community data matrix abundances within samples (maintains sample species richness)

independentswap Randomize community data matrix maintaining species occurrence frequency and site richness using independent swap

trialswap Randomize community data matrix maintaining species occurrence frequency and site richness using trial swap

Value

A list with elements:

obs.qr.intercept Observed co-occurrence/phylogenetic distance quantile regression intercept

obs.qr.slope Observed co-occurrence/phylogenetic distance quantile regression slope

obs.qr.slope.p P-value of observed quantile regression slope significance versus null model
(calculated based on comparison with randomizations)

obs.rank Rank of observed quantile regression slope vs. random

runs Number of runs (randomizations)

random.qr.slopes A vector of quantile regression slopes calculated for each randomization

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Cavender-Bares J., D.A. Ackerly, D. Baum and F.A. Bazzaz. 2004. Phylogenetic overdispersion in Floridian oak communities, *American Naturalist*, 163(6):823-843.

Slingsby, J. A. and G. A. Verboom. 2006. Phylogenetic relatedness limits coexistence at fine spatial scales: evidence from the schoenoid sedges (Cyperaceae: Schoeneae) of the Cape Floristic Region, South Africa. *The American Naturalist* 168:14-27.

See Also

[randomizeSample](#)

Examples

```
data(phylocom)
comm.phylo.qr(phylocom$sample, phylocom$phylo, metric="cij", null.model="sample.taxa.labels")
```

cor.table *Table of correlations and P-values*

Description

Table of correlations with associated P-values and df, can be used with regular or independent contrast data

Usage

```
cor.table(x, cor.method = c("pearson", "spearman"),
          cor.type=c("standard", "contrast"))
```

Arguments

<code>x</code>	Data frame of data points or contrasts at nodes
<code>cor.method</code>	Correlation method (as <code>cor</code>)
<code>cor.type</code>	Are data standard or independent contrast values?

Value

<code>r</code>	Correlation values
<code>df</code>	Degrees of freedom
<code>P</code>	P-values

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Garland, T., Jr., P. H. Harvey, and A. R. Ives. 1992. Procedures for the analysis of comparative data using phylogenetically independent contrasts. *Systematic Biology* 41:18-32.

`evolve.brownian` *Trait evolution under Brownian motion*

Description

Trait evolution under Brownian motion model

Usage

```
evolve.brownian(phy, value = 0, var = 1)
```

Arguments

<code>phy</code>	phylo object
<code>value</code>	mean
<code>var</code>	variance

Value

Vector of trait values with names corresponding to `phylo$tip.label`

Author(s)

David Ackerly <dackerly@berkeley.edu> and Steven Kembel <skembel@uoregon.edu>

Kcalc *K statistic of phylogenetic signal*

Description

Calculates K statistic of phylogenetic signal

Usage

```
Kcalc(x, phy)
```

Arguments

x	Vector or data.frame of trait data (in phylo\$tip.label order)
phy	phylo object

Value

K	K statistic
---	-------------

Warning

Assumes that trait data are sorted in the same order as phylo\$tip.label

Author(s)

Simon Blomberg <s.blomberg1@uq.edu.au> and David Ackerly <dackerly@berkeley.edu>

References

Blomberg, S. P., and T. Garland, Jr. 2002. Tempo and mode in evolution: phylogenetic inertia, adaptation and comparative methods. *Journal of Evolutionary Biology* 15:899-910.

Blomberg, S. P., T. Garland, Jr., and A. R. Ives. 2003. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution* 57:717-745.

See Also

[phylosignal](#)

Examples

```
randtree <- rcoal(20)
randtraits <- evolve.brownian(randtree)
Kcalc(randtraits[randtree$tip.label], randtree)
```

`matrix2sample` *Convert community data matrix to Phylocom sample*

Description

Converts a community data matrix to a Phylocom database-format community sample

Usage

```
matrix2sample(z)
```

Arguments

`z` Community data matrix

Value

Phylocom database-format community sample

Author(s)

Steven Kembel <skembel@uoregon.edu> and Cam Webb <cwebb@oeb.harvard.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

Examples

```
data(phylocom)
matrix2sample(phylocom$sample)
```

`mntd` *Mean nearest taxon distance*

Description

Calculates MNTD (mean nearest taxon distance) for taxa in a community

Usage

```
mntd(samp, dis, abundance.weighted=FALSE)
```

Arguments

`samp` Community data matrix
`dis` Interspecific distance matrix
`abundance.weighted`
Should mean nearest taxon distances for each species be weighted by species abundance? (default = FALSE)

Details

This metric has also been referred to as MNND (mean nearest neighbour distance), and the function was named `mnnd` in `picante` versions < 0.7.

Value

Vector of MNTD values for each community.

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Webb, C., D. Ackerly, M. McPeck, and M. Donoghue. 2002. Phylogenies and community ecology. *Annual Review of Ecology and Systematics* 33:475-505.

See Also

[ses.mntd](#)

Examples

```
data(phylocom)
mntd(phylocom$sample, cophenetic(phylocom$phylo), abundance.weighted=TRUE)
```

mpd

Mean pairwise distance

Description

Calculates mean pairwise distance separating taxa in a community

Usage

```
mpd(samp, dis, abundance.weighted=FALSE)
```

Arguments

samp	Community data matrix
dis	Interspecific distance matrix
abundance.weighted	Should mean pairwise distances be weighted by species abundance? (default = FALSE)

Value

Vector of MPD values for each community

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Webb, C., D. Ackerly, M. McPeck, and M. Donoghue. 2002. Phylogenies and community ecology. *Annual Review of Ecology and Systematics* 33:475-505.

See Also

[ses.mpd](#)

Examples

```
data(phylocom)
mpd(phylocom$sample, cophenetic(phylocom$phylo), abundance.weighted=TRUE)
```

multiPhylosignal *Calculates phylogenetic signal for data.frame of traits*

Description

Calculates phylogenetic signal for data.frame of traits. Traits may have missing values in which case the tree will be pruned prior to calculating phylogenetic signal for each trait.

Usage

```
multiPhylosignal(x, phy, ...)
```

Arguments

x	Data frame of trait data (traits in columns) with row names corresponding to tip.labels
phy	phylo object
...	Additional arguments to phylosignal

Value

Returns a data frame with phylogenetic signal results for each trait

Warning

Assumes that trait data are sorted in the same order as phylo tip.label

Author(s)

Steven Kembel <skembel@uoregon.edu>

pblm

Phylogenetic Bipartite Linear Model

Description

Fits a linear model to the association strengths of a bipartite data set with or without phylogenetic correlation among the interacting species

Usage

```
pblm(assocs, tree1=NULL, tree2=NULL, covars1=NULL, covars2=NULL, bootstrap=FALSE, nreps=1)
pblmpredict(x, tree1.w.novel=NULL, tree2.w.novel=NULL, predict.originals=FALSE)
```

Arguments

assocs	A matrix of association strengths among two sets of interacting species
tree1	A phylo tree object or a phylogenetic covariance matrix for the rows of <code>assocs</code>
tree2	A phylo tree object or a phylogenetic covariance matrix for the columns of <code>assocs</code>
covars1	A matrix of covariates (e.g., traits) for the row species of <code>assocs</code>
covars2	A matrix of covariates (e.g., traits) for the column species of <code>assocs</code>
bootstrap	logical, bootstrap confidence intervals of the parameter estimates
nreps	Number of bootstrap replicated data sets to estimate parameter CIs
maxit	as in <code>optim</code>
pstart	starting values of the two phylogenetic signal strength parameters passed to <code>optim</code>
x	object of class <code>pblm</code>
tree1.w.novel	A phylo tree object or a phylogenetic covariance matrix which corresponds to <code>tree1</code> of <code>x</code> with species to predict associations

tree2.w.novel A phylo tree object or a phylogenetic covariance matrix which corresponds to tree2 of x with species to predict associations

predict.originals if TRUE then the associations of each original species in the two phylogenies is predicted

Details

Fit a linear model with covariates using estimated generalized least squares to the association strengths between two sets of interacting species. Associations can be either binary or continuous. If phylogenies of the two sets of interacting species are supplied, two *phylogenetic signal strength* parameters ($d1$ and $d2$), one for each species set, based on an Ornstein-Uhlenbeck model of evolution with stabilizing selection are estimated. Values of $d=1$ indicate no stabilizing selection and correspond to the Brownian motion model of evolution; $0 < d < 1$ represents stabilizing selection; $d=0$ depicts the absence of phylogenetic correlation (i.e., a star phylogeny); and $d > 1$ corresponds to disruptive selection where phylogenetic signal is amplified. Confidence intervals for these and the other parameters can be estimated with bootstrapping.

The function `pblmpredict` predicts the associations of novel species following the methods given in appendix B of Ives and Godfray (2006).

Value

MSE total, full (each d estimated), star ($d=0$), and base ($d=1$) mean squared errors

signal.strength two estimates of phylogenetic signal strength

coefficients estimated intercept and covariate coefficients with approximate 95 percent CIs for the three model types (full, star, base)

CI.boot 95 percent CIs for all parameters

variates matrix of model variates (can be used for plotting)

residuals matrix of residuals from the three models (full, star and base)

predicted predicted associations

bootvalues matrix of parameters estimated from the `nreps` bootstrap replicated data sets used to calculate CIs

phylocovs phylogenetic covariance matrices scaled by the estimated `d1` and `d2`

cors.1 correlations among predicted and observed associations for species of `tree1`, NA if `predict.originals=FALSE`

cors.2 correlations among predicted and observed associations for species of `tree2`, NA if `predict.originals=FALSE`

pred.novels1 predicted associations for the novel speices of `tree1`

pred.novels2 predicted associations for the novel speices of `tree2`

Note

Covariates that apply to both species sets (e.g., sampling site) should be supplied in the covariate matrix of the set with the most species.

Bootstrapping CIs is slow due to the function `optim` used to estimate the model parameters. See appendix A in Ives and Godfray (2006) for a discussion about this bootstrapping procedure

If `pblmpredict=TRUE` the function does not first remove each species in turn when predicting the associations of the original species as is done in Ives and Godfray (2006).

Author(s)

Matthew Helmus (mrhasmus@gmail.com)

References

Ives A.R. & Godfray H.C. (2006) Phylogenetic analysis of trophic associations. *The American Naturalist*, 168, E1-E14

Blomberg S.P., Garland T.J. & Ives A.R. (2003) Testing for phylogenetic signal in comparative data: Behavioral traits are more labile. *Evolution*, 57, 717-745

pd

Calculate Faith's Phylogenetic Diversity

Description

Calculate the sum of the total phylogenetic branch length for one or multiple samples.

Usage

```
pd(samp, tree, include.root=TRUE)
```

Arguments

<code>samp</code>	Community data matrix
<code>tree</code>	A phylo tree object
<code>include.root</code>	Should the root node be included in all PD calculations (default = TRUE)

Value

Returns a dataframe of the PD and species richness (SR) values for all samples

Warning

If the root is to be included in all calculations (`include.root=TRUE`), the PD of all samples will include the branch length connecting taxa in those samples and the root node of the supplied tree. The root of the supplied tree may not be spanned by any taxa in the sample. If you want the root of your tree to correspond to the most recent ancestor of the taxa actually present in your sample, you should prune the tree before running `pd`:

```
prunedTree <- prune.sample(sample, tree)
```

Note

The data sets need not be species-community data sets but may be any sample data set with an associated phylogeny. PD is not statistically independent of species richness, it positively correlates with species richness across samples. The function `ses.pd` compares observed PD to the values expected under various randomizations and allows a way to standardize for unequal richness across samples.

If the root is to be included in all calculations of PD (`include.root=TRUE`), the tree must be rooted. Single-species samples will be assigned a PD value equal to the distance from the root to the present.

If the root is not included in all calculations by default (`include.root=FALSE`), the tree need not be rooted, but in the case of single-species samples the PD will be equal to NA and a warning will be issued.

Author(s)

Matthew Helmus [⟨mrhelmus@gmail.com⟩](mailto:mrhelmus@gmail.com), Jonathan Davies [⟨davies@nceas.ucsb.edu⟩](mailto:davies@nceas.ucsb.edu), Steven Kembel [⟨skembel@uoregon.edu⟩](mailto:skembel@uoregon.edu)

References

Faith D.P. (1992) Conservation evaluation and phylogenetic diversity. *Biological Conservation*, 61, 1-10.

See Also

[psr](#), [ses.pd](#)

Examples

```
data(phylocom)
pd(phylocom$sample, phylocom$phylo)
```

 phylocom

Phylocom default data

Description

Tree, community and trait data from the Phylocom 4.0 distribution

Usage

```
data(phylocom)
```

Format

A list with three elements:

phylocom\$phylo Phylogenetic tree

phylocom\$sample Community data

phylocom\$traits Trait data

Source

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

 phylosignal

Measure phylogenetic signal

Description

Calculates K statistic of phylogenetic signal as well as P-value based on variance of phylogenetically independent contrasts relative to tip shuffling randomization.

Usage

```
phylosignal(x, phy, reps = 999, ...)
```

Arguments

x Trait vector (same order as phy\$tip.label)

phy phylo object

reps Number of randomizations

... Additional arguments passed to pic

Value

Data frame with columns:

K	K statistic
PIC.variance	Mean observed PIC variance
PIC.variance.P	P-value of observed vs. random variance of PICs
PIC.variance.z	Z-score of observed vs. random variance of PICs

Warning

Assumes that trait data are sorted in the same order as phylo\$tip.label

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Blomberg, S. P., and T. Garland, Jr. 2002. Tempo and mode in evolution: phylogenetic inertia, adaptation and comparative methods. *Journal of Evolutionary Biology* 15:899-910.

Blomberg, S. P., T. Garland, Jr., and A. R. Ives. 2003. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. *Evolution* 57:717-745.

See Also

[Kcalc](#)

Examples

```
randtree <- rcoal(20)
randtraits <- evolve.brownian(randtree)
phylosignal(randtraits[randtree$tip.label], randtree)
```

phylosor

Phylogenetic index of beta-diversity PhyloSor

Description

Fraction of branch-length shared between two communities

Usage

```
phylosor(samp, tree)
```

Arguments

samp	Community data matrix
tree	Object of class phylo

Value

A distance object of the PhyloSor index of similarity between communities, the fraction of PD (branch-length) shared between two samples

Warning

The phylosor of all samples will include the branch length connecting taxa in those samples and the root of the supplied tree. The root of the supplied tree may not be spanned by any taxa in the sample. If you want the root of your tree to correspond to the most recent ancestor of the taxa actually present in your sample, you should prune the tree before running `phylosor`:

```
prunedTree <- prune.sample(sample, tree)
```

Note

The root of the supplied tree is included in calculations of PhyloSor. The supplied tree must be rooted and ultrametric. Single-species samples will be assigned a PD value equal to the distance from the root to the present.

Author(s)

Helene Morlon <morlon.helene@gmail.com> and Steven Kembel <skembel@uoregon.edu>

References

Bryant, J.B., Lamanna, C., Morlon, H., Kerkhoff, A.J., Enquist, B.J., Green, J.L. 2008. Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. *Proceedings of the National Academy of Sciences* 105 Supplement 1: 11505-11511

See Also

[phylosor.rnd, pd](#)

Examples

```
data(phylocom)
phylosor(phylocom$sample, phylocom$phylo)
```

 phylosor.rnd

 Null PhyloSor values of phylogenetic beta-diversity

Description

PhyloSor values obtained by randomization for different choices of null models

Usage

```
phylosor.rnd(samp, tree, cstSor=TRUE, null.model=c("taxa.labels",
  "frequency", "richness", "independentswap", "trialswap"),
  runs=999, iterations=1000)
```

Arguments

samp	Community data matrix
tree	Object of class phylo
cstSor	TRUE if the Sorensen similarity should be kept constant across communities. FALSE otherwise
null.model	Null model to use (see Details section)
runs	Number of randomizations
iterations	Number of iterations to use for each randomization (for independent swap and trial null models)

Details

Currently implemented null models (arguments to null.model):

taxa.labels Shuffle community data matrix labels. Maintains species richness in each community and species shared between communities. Should be used with cstSor=TRUE

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency). Does not maintain species richness in communities nor species shared between communities. Can only be used with cstSor=FALSE

richness With cstSor=TRUE: For each pair of community, maintains species richness in each community and species shared between communities. Sample in the species pool with equal probability; With cstSor=FALSE: Maintains species richness in each community, does not maintain species shared between communities. Sample in the species pool with equal probability

independentswap Randomize community data matrix with the independent swap algorithm (Gotelli 2000) maintaining species occurrence frequency and sample species richness. Can only be used with cstSor=FALSE

trialswap Randomize community data matrix with the trial-swap algorithm (Miklos & Podani 2004) maintaining species occurrence frequency and sample species richness. Can only be used with cstSor=FALSE

Value

A list of length the number of runs. Each element of the list is a distance matrix containing the PhyloSor values of phylogenetic beta-diversity obtained by randomization

Author(s)

Helene Morlon <morlon.helene@gmail.com> and Steven Kembel <skembel@uoregon.edu>

References

Bryant, J.B., Lamanna, C., Morlon, H., Kerkhoff, A.J., Enquist, B.J., Green, J.L. 2008. Microbes on mountainsides: Contrasting elevational patterns of bacterial and plant diversity. Proceedings of the National Academy of Sciences 105 Supplement 1: 11505-11511

See Also

[phylosor](#), [randomizeSample](#)

Examples

```
data(phylocom)
phylosor.rnd(phylocom$sample, phylocom$phylo, cstSor=TRUE, null.model="richness", runs=5)
```

phylostruct	<i>Permutations to Test for Phylogenetic Signal in Community Composition</i>
-------------	--

Description

Randomize sample/community data matrices to create null distributions of given metrics

Usage

```
phylostruct(samp, tree, env=NULL, metric=c("psv", "psr", "pse", "psc", "sppregs"), null.model="richness", "independentswap", "trialswap"), runs=100, it=1000, alpha=0.05)
```

Arguments

samp	community data matrix, species as columns, communities as rows
tree	phylo tree object or a phylogenetic covariance matrix
env	environmental data matrix
metric	if metric="psv", "psr", "pse", or "psc" compares the observed mean of the respective metric to a null distribution at a given alpha; if metric="sppregs" compares the three correlations produced by sppregs to null distributions
null.model	permutation procedure used to create the null distribution, see randomizeSample

runs	the number of permutations to create the distribution, a rule of thumb is (number of communities)/alpha
it	the number of swaps for the independent and trial-swap null models, see randomizeSample
alpha	probability value to compare the observed mean/correlations to a null distribution
fam	as in sppregs

Details

The function creates null distributions for the [psd](#) set of metrics and for the correlations of [sppregs](#) from observed community data sets.

Value

metric	metric used
null.model	permutation used
runs	number of permutations
it	number of swaps if applicable
obs	observed mean value of a particular metric or the three observed correlations from sppregs
mean.null	mean(s) of the null distribution(s)
quantiles.null	quantiles of the null distribution(s) to compare to obs; determined by alpha
phylo.structure	if obs less than (alpha/2), phylo.structure="underdispersed"; if obs greater than (1-alpha/2), phylo.structure="overdispersed"; otherwise phylo.structure="random" and NULL if metric="sppregs"
nulls	null values of the distribution(s)

Author(s)

Matthew Helmus (mrhelmus@gmail.com)

References

Helmus M.R., Bland T.J., Williams C.K. & Ives A.R. (2007a) Phylogenetic measures of biodiversity. *American Naturalist*, 169, E68-E83

Helmus M.R., Savage K., Diebel M.W., Maxted J.T. & Ives A.R. (2007b) Separating the determinants of phylogenetic community structure. *Ecology Letters*, 10, 917-925

Gotelli N.J. (2000) Null model analysis of species co-occurrence patterns. *Ecology*, 81, 2606-2621

See Also

[psd](#), [sppregs](#), [randomizeSample](#)

pic.circular *Phylogenetic independent contrasts for circular data*

Description

Computes the phylogenetic independent contrasts for traits with circular distributions

Usage

```
pic.circular(x, phy, scaled = TRUE, var.contrasts = FALSE)
```

Arguments

x	A vector of class <code>circular</code> , <code>modulo = "2pi"</code> with length equal to <code>length(phy\$edge.label)</code>
phy	An object of class <code>phylo</code>
scaled	logical, indicates whether the contrasts should be scaled with their expected variance (default to <code>TRUE</code>).
var.contrasts	logical, indicates whether the expected variance of the contrasts should be returned (default to <code>FALSE</code>)

Details

If `x` has names, these are matched to the dataframe, otherwise values are expected to be in the same order and an error is issued.

Value

Vector of contrasts for trait `x` on phylogeny `phy`

Author(s)

Peter Cowan <pc@berkeley.edu> based on the `ape` package `pic` function by Emmanuel Paradis

pic3 *Independent contrasts*

Description

Modification of `pic` function from `ape` to return internal node values as well as contrasts and variance of contrasts.

Usage

```
pic3(x, phy, scaled = TRUE, var.contrasts = TRUE)
```

Arguments

<code>x</code>	Trait vector (same order as <code>phy\$tip.label</code>)
<code>phy</code>	phylo object
<code>scaled</code>	TRUE = standardize contrasts by branch lengths
<code>var.contrasts</code>	TRUE = return variance of contrasts

Value

Matrix with three columns:

<code>row.names</code>	node numbers
<code>contrasts</code>	independent contrast value
<code>variance</code>	variance of contrasts (sum of subtending branch lengths)
<code>node.vals</code>	values calculated at internal nodes by contrast algorithm

Warning

Assumes that trait data are sorted in the same order as `phylo$tip.label`

Author(s)

Original `pic` function by Emmanuel Paradis <Emmanuel.Paradis@mpl.ird.fr> modified to return `node.vals` by David Ackerly <dackerly@berkeley.edu>

References

- Felsenstein J (1985) Phylogenies and the comparative method. *American Naturalist* 125: 1-15.
- Garland T, Jr, Harvey PH & Ives AR (1992) Procedures for the analysis of comparative data using phylogenetically independent contrasts. *Systematic Biology* 41: 18-32.

See Also

[pic](#)

Examples

```
randtree <- rcoal(20)
randtraits <- evolve.brownian(randtree)
pic3(randtraits, randtree)
```

prune.sample	<i>Prune tree to match community data or trait data</i>
--------------	---

Description

Prune a phylogenetic tree to include only species present in a community data set or with non-missing trait data

Usage

```
prune.sample(samp, phylo)
prune.missing(x, phylo)
```

Arguments

phylo	phylo object
samp	Community data matrix
x	Vector of trait data

Value

Returns a pruned phylo object

Author(s)

Steven Kembel <skembel@uoregon.edu>

psd	<i>Phylogenetic Species Diversity Metrics</i>
-----	---

Description

Calculate the bounded phylogenetic biodiversity metrics: phylogenetic species variability, richness, evenness and clustering for one or multiple samples.

Usage

```
psv(samp, tree, compute.var=TRUE)
psr(samp, tree, compute.var=TRUE)
pse(samp, tree)
psc(samp, tree)
psd(samp, tree, compute.var=TRUE)
psv.spp(samp, tree)
```

Arguments

<code>samp</code>	Community data matrix
<code>tree</code>	A phylo tree object or a phylogenetic covariance matrix
<code>compute.var</code>	Computes the expected variances for PSV and PSR for each community

Details

Phylogenetic species variability (PSV) quantifies how phylogenetic relatedness decreases the variance of a hypothetical unselected/neutral trait shared by all species in a community. The expected value of PSV is statistically independent of species richness, is one when all species in a sample are unrelated (i.e., a star phylogeny) and approaches zero as species become more related. PSV is directly related to mean phylogenetic distance. The expected variance around PSV for any sample of a particular species richness can be approximated. To address how individual species contribute to the mean PSV of a data set, the function `psv.spp` gives signed proportions of the total deviation from the mean PSV that occurs when all species are removed from the data set one at a time. The absolute values of these “species effects” tend to positively correlate with species prevalence.

Phylogenetic species richness (PSR) is the number of species in a sample multiplied by PSV. It can be considered the species richness of a sample after discounting by species relatedness. The value is maximum at the species richness of the sample, and decreases towards zero as relatedness increases. The expected variance around PSR for any sample of a particular species richness can be approximated.

Phylogenetic species evenness (PSE) is the metric PSV modified to incorporate relative species abundances. The maximum attainable value of PSE (i.e., 1) occurs only if species abundances are equal and species phylogeny is a star. PSE essentially grafts each individual of a species onto the tip of the phylogeny of its species with branch lengths of zero.

Phylogenetic species clustering (PSC) is a metric of the branch tip clustering of species across a sample’s phylogeny. As PSC increases to 1, species are less related to one another the tips of the phylogeny. PSC is directly related to mean nearest neighbor distance.

Value

Returns a dataframe of the respective phylogenetic species diversity metric values

Note

These metrics are bounded either between zero and one (PSV, PSE, PSC) or zero and species richness (PSR); but the metrics asymptotically approach zero as relatedness increases. Zero can be assigned to communities with less than two species, but conclusions drawn from assigning communities zero values need be carefully explored for any data set. The data sets need not be species-community data sets but may be any sample data set with an associated phylogeny.

Author(s)

Matthew Helmus <mrhelmus@gmail.com>

References

Helmus M.R., Bland T.J., Williams C.K. & Ives A.R. (2007) Phylogenetic measures of biodiversity. *American Naturalist*, 169, E68-E83

See Also

[mpd](#), [mnnd](#), [specaccum.psr](#)

randomizeSample *Null models for community data matrix randomization*

Description

Various null models for randomizing community data matrices

Usage

```
randomizeSample(samp, null.model = c("frequency", "richness", "independentswap", "t
```

Arguments

samp	Community data matrix
null.model	Null model to use (see Details section for description)
iterations	Number of independent or trial-swaps to perform

Details

Currently implemented null models (arguments to null.model):

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency)

richness Randomize community data matrix abundances within samples (maintains sample species richness)

independentswap Randomize community data matrix with the independent swap algorithm (Gotelli 2000) maintaining species occurrence frequency and sample species richness

trialswap Randomize community data matrix with the trial-swap algorithm (Miklos & Podani 2004) maintaining species occurrence frequency and sample species richness

Value

Randomized community data matrix

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

- Gotelli, N.J. 2000. Null model analysis of species co-occurrence patterns. *Ecology* 81: 2606-2621
- Miklos I. & Podani J. 2004. Randomization of presence-absence matrices: Comments and new algorithms. *Ecology* 85: 86-92.

Examples

```
data(phylocom)
randomizeSample(phylocom$sample, null.model="richness")
```

readsample	<i>Read Phylocom sample</i>
------------	-----------------------------

Description

Reads a Phylocom sample file and converts to a community data matrix

Usage

```
readsample(filename = "")
```

Arguments

filename Phylocom sample file path

Value

Community data matrix

Author(s)

Steven Kembel <skembel> and Cam Webb <cwebb@oeb.harvard.edu>

References

- Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

sample2matrix *Convert Phylocom sample to community data matrix*

Description

Convert a Phylocom database-format sample to community data matrix.

Usage

```
sample2matrix(x)
```

Arguments

x Phylocom sample formatted data frame, a data frame with three columns:
 Column 1 Community name
 Column 2 Species abundance
 Column 3 Species name

Author(s)

Steven Kembel <skembel@uoregon.edu> and Cam Webb <cwebb@oeb.harvard.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

ses.mntd *Standardized effect size of MNTD*

Description

Standardized effect size of mean nearest taxon distances in communities. When used with a phylogenetic distance matrix, equivalent to -1 times the Nearest Taxon Index (NTI).

Usage

```
ses.mntd(samp, dis, null.model = c("taxa.labels", "sample.pool", "phylogeny.pool", "abundance.weighted=FALSE", runs = 999, iterations = 1000)
```

Arguments

<code>samp</code>	Community data matrix
<code>dis</code>	Distance matrix (generally a phylogenetic distance matrix)
<code>null.model</code>	Null model to use (see Details section for description)
<code>abundance.weighted</code>	Should mean nearest taxon distances for each species be weighted by species abundance? (default = FALSE)
<code>runs</code>	Number of randomizations
<code>iterations</code>	Number of iterations to use for each randomization (for independent swap and trial null models)

Details

The metric used by this function has also been referred to as MNND (mean nearest neighbour distance), and the function was named `ses.mnnd` in `picante` versions < 0.7.

Currently implemented null models (arguments to `null.model`):

taxa.labels Shuffle distance matrix labels (across all taxa included in distance matrix)

sample.pool Randomize community data matrix by drawing species from pool of species occurring in at least one community (sample pool) with equal probability

phylogeny.pool Randomize community data matrix by drawing species from pool of species occurring in the distance matrix (phylogeny pool) with equal probability

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency)

richness Randomize community data matrix abundances within samples (maintains sample species richness)

independentswap Randomize community data matrix with the independent swap algorithm (Gotelli 2000) maintaining species occurrence frequency and sample species richness

trialswap Randomize community data matrix with the trial-swap algorithm (Miklos & Podani 2004) maintaining species occurrence frequency and sample species richness

Value

A data frame of results for each community

<code>ntaxa</code>	Number of taxa in community
<code>mntd.obs</code>	Observed MNTD in community
<code>mntd.rand.mean</code>	Mean MNTD in null communities
<code>mntd.rand.sd</code>	Standard deviation of MNTD in null communities
<code>mntd.obs.rank</code>	Rank of observed MNTD vs. null communities
<code>mntd.obs.z</code>	Standardized effect size of MNTD vs. null communities (= $(mntd.obs - mntd.rand.mean) / mntd.rand.sd$, equivalent to -NTI)
<code>mntd.obs.p</code>	P-value (quantile) of observed MNTD vs. null communities (= $mntd.obs.rank / (runs + 1)$)
<code>runs</code>	Number of randomizations

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

See Also

[mntd](#), [randomizeSample](#)

Examples

```
data(phylocom)
ses.mntd(phylocom$sample, cophenetic(phylocom$phylo), null.model="taxa.labels")
```

ses.mpd

Standardized effect size of mpd

Description

Standardized effect size of mean pairwise distances in communities. When used with a phylogenetic distance matrix, equivalent to -1 times the Nearest Relative Index (NRI).

Usage

```
ses.mpd(samp, dis, null.model = c("taxa.labels", "sample.pool",
  "phylogeny.pool", "independentswap", "trialswap"),
  abundance.weighted = FALSE, runs = 999, iterations = 1000)
```

Arguments

samp	Community data matrix
dis	Distance matrix (generally a phylogenetic distance matrix)
null.model	Null model to use (see Details section for description)
abundance.weighted	Should mean nearest taxon distances for each species be weighted by species abundance? (default = FALSE)
runs	Number of randomizations
iterations	Number of iterations to use for each randomization (for independent swap and trial null models)

Details

Currently implemented null models (arguments to null.model):

taxa.labels Shuffle distance matrix labels (across all taxa included in distance matrix)

sample.pool Randomize community data matrix by drawing species from pool of species occurring in at least one community (sample pool) with equal probability

phylogeny.pool Randomize community data matrix by drawing species from pool of species occurring in the distance matrix (phylogeny pool) with equal probability

frequency Randomize community data matrix abundances within species (maintains species occurrence frequency)

richness Randomize community data matrix abundances within samples (maintains sample species richness)

independentswap Randomize community data matrix with the independent swap algorithm (Gotelli 2000) maintaining species occurrence frequency and sample species richness

trialswap Randomize community data matrix with the trial-swap algorithm (Miklos & Podani 2004) maintaining species occurrence frequency and sample species richness

Value

A data frame of results for each community

ntaxa	Number of taxa in community
mpd.obs	Observed mpd in community
mpd.rand.mean	Mean mpd in null communities
mpd.rand.sd	Standard deviation of mpd in null communities
mpd.obs.rank	Rank of observed mpd vs. null communities
mpd.obs.z	Standardized effect size of mpd vs. null communities (= (mpd.obs - mpd.rand.mean) / mpd.rand.sd, equivalent to -NRI)
mpd.obs.p	P-value (quantile) of observed mpd vs. null communities (= mpd.obs.rank / runs + 1)
runs	Number of randomizations

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

See Also

[mpd, randomizeSample](#)

Value

A data frame of results for each community

<code>ntaxa</code>	Number of taxa in community
<code>pd.obs</code>	Observed PD in community
<code>pd.rand.mean</code>	Mean PD in null communities
<code>pd.rand.sd</code>	Standard deviation of PD in null communities
<code>pd.obs.rank</code>	Rank of observed PD vs. null communities
<code>pd.obs.z</code>	Standardized effect size of PD vs. null communities (= (pd.obs - pd.rand.mean) / pd.rand.sd)
<code>pd.obs.p</code>	P-value (quantile) of observed PD vs. null communities (= mpd.obs.rank / runs + 1)
<code>runs</code>	Number of randomizations

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

Proches, S., Wilson, J.R.U. and Cowling, R.M. 2006. How much evolutionary history in a 10 x 10m plot? Proceedings of Royal Society of London B, Biological Sciences 273:1143-1148.

See Also

[pd.randomizeSample](#)

Examples

```
data(phylocom)
ses.pd(phylocom$sample, phylocom$phylo, null.model="taxa.labels", runs=99)
```

`specaccum.psr`

Phylogenetic Species Richness Sample-Based Rarefaction Curve

Description

Finds a sample-based rarefaction curve for phylogenetic species richness for a set of samples.

Usage

```
specaccum.psr(samp, tree, permutations = 100, method = "random", ...)
```

Arguments

samp	Community data matrix
tree	A phylo tree object or a phylogenetic covariance matrix
permutations	Number of permutations with method method= "random"
method	Species accumulation method, currently only "random" is supported which adds samples in random order.
...	Other parameters to functions

Value

The function returns an object of class "specaccum" with items:

call	Function call.
method	Accumulator method.
sites	Number of sites/samples.
richness	The mean phylogenetic species richness corresponding to number of sites/samples.
sd	The standard deviation of phylogenetic species accumulation curve (or its standard error) estimated from permutations in method = "random".
perm	Permutation results with method = "random" and NULL in other cases. Each column in perm holds one permutation.

Author(s)

Matthew Helmus (mrhasmus@gmail.com) based on the `vegan` package [specaccum](#) function by Roeland Kindt and Jari Oksanen.

References

Gotelli N.J. & Colwell R.K. (2001) Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. *Ecology Letters*, 4, 379-391

Helmus M.R., Bland T.J., Williams C.K. & Ives A.R. (2007) Phylogenetic measures of biodiversity. *American Naturalist*, 169, E68-E83

See Also

[psr](#), [specaccum](#)

species.dist *Species co-occurrence distances*

Description

Compute interspecific distances based on patterns of species co-occurrence in communities.

Usage

```
species.dist(x, metric = c("cij", "jaccard", "checkerboard", "doij"))
```

Arguments

x	Community data matrix
metric	Co-occurrence metric to use (see Details section for description)

Details

Currently implemented co-occurrence measures (arguments to metric):

cij Schoener's index of co-occurrence

jaccard Jaccard index of co-occurrence

checkerboard Checkerboard index of co-occurrence

doij DOij index of co-occurrence

Value

A `dist` object with co-occurrences among all species pairs

Author(s)

Steven Kembel <skembel@uoregon.edu>

References

Hardy, O.J. 2008. Testing the spatial phylogenetic structure of local communities: statistical performances of different null models and test statistics on a locally neutral community. *Journal of Ecology* 96:914-926.

See Also

[vegdist](#)

Description

Fit regressions on species abundance or presence/absence across communities and calculate phylogenetic correlations

Usage

```
sppregs(samp, env, tree=NULL, fam="gaussian")
sppregs.plot(sppreg, rows=c(1,3), cex.mag=1, x.label="phylogenetic correlations",
y.label=c("occurrence correlations w/ env", "occurrence correlations wo/ env", "change"))
```

Arguments

samp	community data matrix, species as columns, communities as rows
env	environmental data matrix
tree	phylo tree object or a phylogenetic covariance matrix
fam	with fam = "gaussian" fits with <code>glm</code> ; with fam = "binomial" fit logistic regressions with Firth's bias-reduction using <code>brglm</code>
sppreg	object from function <code>sppregs</code>
rows	rows = c(1,3) plots in a row; rows = c(3,1) in a column
cex.mag	value for cex in par
x.label	x axis labels
y.label	y axis labels

Details

For each species in `samp`, the function fits regressions of species presence/absence or abundances on the environmental variables supplied in `env`; and calculates the $(n^2-n)/2$ pairwise species correlations between the residuals of these fits and pairwise species phylogenetic correlations. The residuals can be thought of as the presence/absence of species across sites/communities after accounting for how species respond to environmental variation across sites. Each set of coefficients can be tested for phylogenetic signal with, for example, the function `phylosignal`.

The function `sppregs.plot` produces a set of three plots of the correlations of pairwise species phylogenetic correlations versus: the observed pairwise correlations of species across communities, the residual correlations, and the pairwise differences between (i.e., the change in species co-occurrence once the environmental variables are taken into account). The significance of these correlations can be tested via permutation with the function `phylostruct`.

Value

family	the regression error distribution
residuals	the residuals from each species regression
coefficients	the estimated coefficients from each species regression
std.errors	the standard errors of the coefficients
correlations	correlations of pairwise species phylogenetic correlations between: the observed pairwise correlations of species across communities, the residual correlations, and the pairwise differences between the two
cors.pa	the observed pairwise correlations of species across communities
cors.resid	the residual pairwise correlations of species across communities
cors.phylo	the phylogenetic pairwise correlations among species

Note

The function requires the library `brglm` to perform logistic regressions

Author(s)

Matthew Helmus (mrhelmus@gmail.com)

References

Helmus M.R., Savage K., Diebel M.W., Maxted J.T. & Ives A.R. (2007) Separating the determinants of phylogenetic community structure. *Ecology Letters*, 10, 917-925

See Also

[phylostruct](#), [phylosignal](#)

traitgram

Draw phylogeny with nodes at trait positions

Description

Draws a phylogeny where x position of nodes and tips corresponds to value of a continuous trait variable, and y position corresponds to node depth (i.e. age).

Usage

```
traitgram(x, phy, xaxt = 's', underscore = FALSE, show.names = TRUE,
          show.xaxis.values = TRUE, method = c('ace', 'pic'), ...)
```

Arguments

<code>x</code>	Trait vector (same order as <code>phy\$tip.label</code> , or with taxon names in <code>names</code>)
<code>phy</code>	phylo object
<code>xaxt</code>	x axis default type
<code>underscore</code>	if FALSE remove underscore from taxonomic names
<code>show.names</code>	if TRUE show taxon names across tips of phylogeny
<code>show.xaxis.values</code>	if TRUE show values for trait on x=axis
<code>method</code>	method for calculation of internal trait values. 'ace' = ace maximum likelihood method from ape; 'pic' = independent contrasts method. pic option can be used when ace fails to converge or otherwise seems to fail to correctly reconstruct ancestral values
<code>...</code>	Additional arguments passed to plot

Value

Plots a traitgram, no values returned.

Author(s)

David Ackerly <dackerly@berkeley.edu>

See Also

[pic3](#)

Examples

```
randtree <- rcoal(20)
randtraits <- evolve.brownian(randtree)
traitgram(randtraits, randtree)
traitgram(randtraits, randtree, method='pic')
```

utility

Picante utility functions

Description

Picante utility functions for tree and data manipulation

Usage

```
df2vec(x, colID=1)
internal2tips(phy, int.node, return.names = FALSE)
node.age(phy)
pic.variance(x, phy, scaled = TRUE)
sortColumns(x)
sortRows(x)
taxaShuffle(x)
tipShuffle(phy)
```

Arguments

phy	phylo object
x	A data.frame, matrix or dist object
colID	Numeric or character ID of column to include
int.node	internal node number
return.names	TRUE or FALSE
scaled	Scale contrasts by branch length
...	Additional arguments

Details

Various utility functions for manipulating trees, data, etc.

Value

df2vec	A named vector
internal2tips	Vector of tips descended from a node
node.age	Phylo object with phylo\$ages vector of node ages corresponding to phylo\$edge
pic.variance	Variance of independent contrasts
sortColumns	A data.frame or matrix with columns sorted by name
sortRows	A data.frame or matrix with rows sorted by name
taxaShuffle	Matrix with taxa names shuffled
tipShuffle	Phylo object with taxa names shuffled

Author(s)

Steven Kembel <skembel@uoregon.edu>, Peter Cowan <pcdc@berkeley.edu>, David Ackerly <dackerly@berkeley.edu>

writesample *Write a Phylocom community sample file*

Description

Write a community data matrix to a Phylocom community sample file

Usage

```
writesample(community, filename = "")
```

Arguments

community	Community data matrix
filename	Filename path

Author(s)

Steven Kembel <skembel@uoregon.edu> and Cam Webb <cwebb@oeb.harvard.edu>

References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

writetraits *Write a Phylocom traits formatted file*

Description

Write a Phylocom traits formatted file

Usage

```
writetraits(trt, file = "", bin = NULL, sigd = 3)
```

Arguments

trt	Data frame containing trait data
file	Filename path
bin	Vector index of trait columns to be treated as binary
sigd	Significant digits for output

Author(s)

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References

Webb, C.O., Ackerly, D.D., and Kembel, S.W. 2008. Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Version 4.0.1. <http://www.phylodiversity.net/phylocom/>.

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