

Package ‘phytools’

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Title Phylogenetic Tools for Comparative Biology (and Other Things)

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Depends R (>= 3.2.0), ape (>= 4.0), maps

Imports animation, clusterGeneration, coda, combinat, graphics,
grDevices, methods, mnormt, msm, numDeriv, phangorn (>= 2.1.1),
plotrix, scatterplot3d, stats, utils

Suggests geiger, rgl

ZipData no

Description Package contains various functions for phylogenetic analysis.

This functionality is concentrated in the phylogenetic analysis of comparative data from species. For example, the package includes functions for Bayesian and ML ancestral state estimation; visual simulation of trait evolution; fitting models of trait evolution with multiple Brownian rates and correlations; visualizing discrete and continuous character evolution using colors or projections into trait space; identifying the location of a change in the rate of character evolution on the tree; fast Brownian motion simulation and simulation under several other models of continuous trait evolution; fitting a model of correlated binary trait evolution; locating the position of a fossil or an recently extinct lineage on a tree using continuous character data with ML; plotting lineage accumulation through time, including across multiple trees (such as a Bayesian posterior sample); conducting an analysis called stochastic character mapping, in which character histories for a discrete trait are sampled from their posterior probability distribution under a model; conducting a multiple (i.e., partial) Mantel test; fitting a phylogenetic regression model with error in predictor and response variables; conducting a phylogenetic principal components analysis, a phylogenetic regression, a reduced major axis regression, a phylogenetic

canonical correlation analysis, and a phylogenetic ANOVA; projecting a tree onto a geographic map; simulating discrete character histories on the tree; fitting a model in which a discrete character evolves under the threshold model; visualization of cospeciation; a simple statistical test for cospeciation between two trees. In addition to this phylogenetic comparative method functionality, the package also contains functions for a wide range of other purposes in phylogenetic biology. For instance, functionality in this package includes (but is not restricted to): adding taxa to a tree (including randomly, everywhere, or automatically to genera); generating all bi- and multi-furcating trees for a set of taxa; reducing a phylogeny to its backbone tree; dropping tips or adding tips to special types of phylogenetic trees; exporting a tree as an XML file; converting a tree with a mapped character to a tree with singleton nodes and one character state per edge; estimating a phylogeny using the least squares method; simulating birth-death trees under a range of conditions; rerooting trees; computing a consensus tree under multiple methods, including via minimization of the distance to other trees in the set; a wide range of visualizations of trees; and a variety of other manipulations and analyses that phylogenetic biologists may find useful for their research.

License GPL (>= 2)

URL <http://github.com/liamrevell/phytools>

Repository CRAN

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NeedsCompilation no

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phytools-package	<i>phytools: Phylogenetic Tools for comparative biology (and other things)</i>
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Description

phytools provides functions for phylogenetic comparative biology; as well as several other functions for tree inference, manipulation, and analysis that are not implemented in other R packages.

The complete list of functions can be displayed with `library(help = phytools)`.

More information on **phytools** can be found at <http://www.phytools.org> or <http://blog.phytools.org>.

Author(s)

Liam J. Revell

Maintainer: Liam J. Revell <liam.revell@umb.edu>

References

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

add.arrow	<i>Add an arrow pointing to a tip or node on the tree</i>
-----------	---

Description

This function adds an arrow to a plotted tree.

Usage

```
add.arrow(tree=NULL, tip, ...)
```

Arguments

tree	an object of class "phylo", "contMap", or "densityMap". If not supplied, the function will obtain the last plotted phylogeny from the environmental variable <code>last_plot.phylo</code> .
tip	label of tip or tip or node number. If <code>tree=NULL</code> then the tip or node number must be supplied.
...	optional arguments to control the shape and size of the arrow including: its length (<code>arrl</code>) in the units of the plot; the length of the arrowhead (<code>hedl</code>); the total angle between the wings in the arrowhead (<code>angle</code>); the line width for the plotted lines (<code>lwd</code>); the offset from the tip or end of tip label, in character widths (<code>offset</code>); and the color (<code>col</code>).

Details

This function presently works for radial (type="fan") and right facing square phylograms (type="phylogram"). Trees can be plotted using phytools function plotTree, plotSimmap, contMap, densityMap, and ape method plot.phylo.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[nodelabels](#)

add.color.bar

Add color bar to a plot

Description

This function adds a color bar to a plot created by [plotBranchbyTrait](#). A color bar can be added by clicking on a location within the plot (when prompt=TRUE) or by setting prompt=FALSE and supplying x & y coordinates for the object. This function is also used internally by plot.contMap and plot.densityMap.

Usage

```
add.color.bar(leg, cols, title=NULL, lims=c(0,1), digits=1, prompt=TRUE,
lwd=4, outline=TRUE, ...)
```

Arguments

leg	numerical value for the length of the legend.
cols	colors for the legend.
title	text to plot above the bar.
lims	range for the bar.
digits	digits for plotted numbers.
prompt	logical value indicating whether the location of the legend should be obtained interactively.
lwd	width of the plotted bar.
outline	logical value indicated whether or not to outline the plotted color bar with a 1 pt line.

... optional arguments including: x x-coordinate of the legend (if prompt=FALSE); y y-coordinate of the legend; subtitle optional legend subtitle; direction direction of the color bar (i.e., increase from left to right or from right to left).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J. (2013) Two new graphical methods for mapping trait evolution on phylogenies. *Methods in Ecology and Evolution*, **4**, 754-759.

See Also

[contMap](#), [densityMap](#), [plotBranchbyTrait](#)

add.everywhere *Add tip to all edges in a tree*

Description

This function adds a tip to all branches to the tree and returns a list of trees as an object of class "multiPhylo".

Usage

```
add.everywhere(tree, tip.name)
```

Arguments

tree an object of class "phylo".
tip.name a string containing the name of the tip to add.

Value

A list of trees as an object of class "multiPhylo". Since the tip can be added to any branch, the length of the list is equal to the number of edges in tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also[allFurcTrees](#), [exhaustiveMP](#)

add.random	<i>Add tips at random to the tree</i>
------------	---------------------------------------

Description

This function adds new tips at random to a tree with branch lengths. If no edge lengths are provided, and the tree is ultrametric, then edge lengths are assigned to keep the tree ultrametric. The probability that a new tip is added along any branch is directly proportional to the length of the branch.

Usage

```
add.random(tree, n=NULL, tips=NULL, edge.length=NULL, order=c("random","input"))
```

Arguments

tree	an object of class "phylo".
n	a number of tips to add to the tree. If NULL, will use length(tips).
tips	a set of tip names for the added tips. If NULL, names will be supplied
edge.length	terminal edge length for the added tips. If NULL, and is.ultrametric(tree)==TRUE, then edge lengths will be assigned to keep the tree ultrametric. Note that if edge lengths are assigned and n>1, then the assigned terminal edge lengths are not guaranteed as subsequent random tip addition could occur along the new terminal edge.
order	addition order for the new tips.

Details

Note that sometimes the resultant tree plotted with [plot.phylo](#) or [plotSimmap](#) may display with branches crossing. If so, the tree can be 'untangled' using [untangle](#).

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[allFurcTrees](#), [add.everywhere](#)

add.simmap.legend *Add legend to stochastically mapped tree*

Description

This function adds a legend (by default, interactively) to a plotted stochastic character mapped tree.

Usage

```
add.simmap.legend(leg=NULL, colors, prompt=TRUE, vertical=TRUE, ...)
```

Arguments

leg	states for the discrete character in the order of colors.
colors	colors for the legend in the order of leg, or, if leg=NULL, named vector of colors in which names(colors) are the states of the mapped discrete character.
prompt	logical value indicating whether the location of the legend should be obtained interactively (i.e., by clicking in the plotting area).
vertical	logical value indicating whether to plot the legend vertically (if TRUE) or horizontally.
...	optional arguments including: x x-coordinate of the legend (if prompt=FALSE); y y-coordinate of the legend; and shape which can be shape="square", the default, or shape="circle".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotSimmap](#)

add.species.to.genus *Add species to genus on a phylogeny or bind simulated species subtrees to a backbone genus tree*

Description

add.species.to.genus adds an additional species to a genus on a phylogeny. genus.to.species.tree simulates pure-birth subtrees and then binds them at a random height along the terminal edge leading to each corresponding genus on a genus-level backbone tree.

Usage

```
add.species.to.genus(tree, species, genus=NULL, where=c("root","random"))
genus.to.species.tree(tree, species)
```

Arguments

tree	an object of class "phylo". In the case of genus.to.species.tree this should be a genus-level backbone tree.
species	string contain species name in the format "Genus_species" or "Genus species".
genus	for add.species.to.genus, optional argument containing the genus to which species is to be attached. If NULL then genus will be extracted from species.
where	for add.species.to.genus, the location to attach species to the tree. where="root" will cause the species to be attached to the MRCA of all members of genus. where="random" will cause species to be attached at random to the subtree descended from the MRCA of all members of genus.

Details

For add.species.to.genus, if genus contains only one species and where="root", then species will be attached midway along the branch leading to the one species. If where="random" then species will be added at a random position along the edge. If genus cannot be found in the tree, then the original tree is returned and a warning printed. If the tree is not ultrametric, then the resultant tree may not contain branch lengths and a warning will be printed. If genus is non-monophyletic then species will be attached to the most inclusive group containing members of genus and a warning will be printed.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[add.random](#), [bind.tip](#)

aic.w

Computes AIC weights

Description

This function computes AIC weights for a set of fitted models. It returns an object of class "aic.w" which is just a vector which allows it to be automatically printed with a numerical precision of 8 significant digits.

Usage

```
aic.w(aic)
```

Arguments

`aic` vector of AIC values for different fitted models. If the vector has names, these names will be inherited by the vector returned by the function.

Value

A vector of AIC weights.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

allFurcTrees	<i>Generate all bi- and multifurcating unrooted trees</i>
--------------	---

Description

This function creates all possible unrooted bi- and multifurcating trees and returns a list of trees as an object of class "multiPhylo".

Usage

```
allFurcTrees(n, tip.label=NULL, to.plot=TRUE)
```

Arguments

n	an integer giving the desired number of species.
tip.label	an optional vector of length n containing the tip names.
to.plot	an optional logical value indicating whether or not to plot the trees.

Details

This function should be used with caution for n greater than about 8, as in this case the number of possible trees is extremely large.

Value

A list of trees as an object of class "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. 2004. *Inferring Phylogenies*. Sinauer.

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

See Also

[add.everywhere](#), [exhaustiveMP](#)

anc.Bayes

Bayesian ancestral character estimation

Description

This function uses Bayesian MCMC to sample from the posterior distribution for the states at internal nodes in the tree.

Usage

```
anc.Bayes(tree, x, ngen=10000, control=list())
```

Arguments

tree	an object of class "phylo".
x	a vector of tip values for species; names(x) should be the species names.
ngen	a integer indicating the number of generations for the MCMC.
control	a list of control parameters containing the following elements: sig2: starting value for σ^2 (BM rate); a: starting for the state at the root node; y: starting values for the states at all internal nodes excluding the root (should be labeled with node numbers); pr.mean: means for the prior distributions in the following order - sig2, a, y, note that the prior probability distribution is exponential for sig2 and normal for a and y; pr.var: variances on the prior distributions, same order as pr.mean (but the variance is not used for sig2); prop: variances on the normal proposal distributions in the same order as pr.mean; sample: sample frequency from the MCMC.

Value

A matrix with number of rows ngen/sample+1 containing the posterior sample and likelihoods. Matrix columns are labeled either sig2 or by the node number of the internal node.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ace](#), [anc.ML](#), [anc.trend](#), [evol.rate.mcmc](#), [fastAnc](#)

Examples

```
tree<-pbtree(n=50)
x<-fastBM(tree,sig2=2) # simulate using fastBM
X<-anc.Bayes(tree,x,ngen=10000) # sample ancestral states
estimates<-colMeans(X[21:nrow(X),]) # get estimates, excluding burnin
```

anc.ML

*Ancestral character estimation using likelihood***Description**

This function estimates the evolutionary parameters and ancestral states for Brownian evolution using likelihood. It is also possible (for `model="BM"`) to allow for missing data for some tip taxa.

Usage

```
anc.ML(tree, x, maxit=2000, model=c("BM","OU"), ...)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>x</code>	a vector of tip values for species; <code>names(x)</code> should be the species names.
<code>maxit</code>	an optional integer value indicating the maximum number of iterations for optimization.
<code>model</code>	model of continuous character evolution on the tree. It's possible that only <code>model="BM"</code> works in the present version as <code>model="OU"</code> has not been thoroughly tested & some bugs were reported for an earlier version.
<code>...</code>	other arguments.

Details

Because this function relies on a high dimensional numerical optimization of the likelihood function, [fastAnc](#) should probably be preferred for most purposes. If using [anc.ML](#), users should be cautious to ensure convergence. This has been ameliorated in `phytools` $\geq 0.2-48$ by seeding the ML optimization with the result from [fastAnc](#).

Value

A list with the following components:

<code>sig2</code>	the variance of the BM process.
<code>ace</code>	a vector with the ancestral states.
<code>logLik</code>	the log-likelihood.
<code>convergence</code>	the value of <code>\$convergence</code> returned by <code>optim()</code> (0 is good).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Schluter, D., Price, T., Mooers, A. O., and Ludwig, D. (1997) Likelihood of ancestor states in adaptive radiation. *Evolution* **51**, 1699-1711.

See Also

[ace](#), [anc.Bayes](#), [fastAnc](#), [optim](#)

Examples

```
tree<-pbtree(n=50)
x<-fastBM(tree) # simulate using fastBM
anc.ML(tree,x) # fit model & estimate ancestral states
```

anc.trend

Ancestral character estimation with a trend

Description

This function estimates the evolutionary parameters and ancestral states for Brownian evolution with directional trend.

Usage

```
anc.trend(tree, x, maxit=2000)
```

Arguments

tree	an object of class "phylo".
x	a vector of tip values for species; names(x) should be the species names.
maxit	an optional integer value indicating the maximum number of iterations for optimization.

Details

Note that this will generally only work and produce sensible results for a phylogeny with some non-contemporary tips (i.e., a tree with some fossil species). The function uses [optim](#) with `method="L-BFGS-B"`; however optimization is only constrained for the `sig2` which must be >0.

Value

A list with the following components:

ace	a vector with the ancestral states.
mu	a trend parameter per unit time.
sig2	the variance of the BM process.
logL	the log-likelihood.
convergence	the value of \$convergence returned by optim() (0 is good).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ace](#), [anc.Bayes](#), [anc.ML](#), [optim](#)

Examples

```
tree<-rtree(20)
x<-fastBM(tree,mu=2) # simulate using fastBM with a trend (m!=0)
anc.trend(tree,x) # fit model & estimate ancestral states
```

ancThresh	<i>Ancestral character estimation under the threshold model using Bayesian MCMC</i>
-----------	---

Description

This function uses Bayesian MCMC to estimate ancestral states and thresholds for a discrete character under the threshold model from quantitative genetics (Felsenstein 2012).

Usage

```
ancThresh(tree, x, ngen=1000, sequence=NULL, method="mcmc", model=c("BM", "OU", "lambda"),
control=list(), ...)
```

Arguments

tree	phylogenetic tree.
x	a named vector containing discrete character states; or a matrix containing the tip species, in rows, and probabilities of being in each state, in columns.
ngen	number of generations to run the MCMC.
sequence	assumed ordering of the discrete character state. If not supplied and x is a vector then numerical/alphabetical order is assumed; if not supplied and x is a matrix, then the column order of x is used.
method	only method currently available is "mcmc".
model	model for the evolution of the liability. Options are "BM" (Brownian motion, the default), "OU" (Ornstein-Uhlenbeck), or "lambda" (the lambda model).
control	list containing the following elements: sample, the sampling interval; propliab variance of the proposal distribution for liabilities; propthresh variance on the proposal distribution for the thresholds; propalpha variance on the proposal distribution for alpha (for model="OU"); pr.anc prior probability distribution on the ancestral states for each node, in a matrix - not all nodes need to be supplied; pr.th prior density on the thresholds; burnin number of generations to exclude for burn-in when plotting posterior probabilities on the tree; plot logical value indicating whether or not to plot the posterior probabilities; print logical value indicating whether or not to print the state of the MCMC; piecol colors for the posterior probabilities plotted as pie charts at internal nodes; and tipcol which indicates whether the tip colors should be based on the input data ("input") or sampled tip liabilities ("estimated"). These will only differ if there is uncertainty in the tip states.
...	additional arguments to be passed to <code>plotThresh</code> (called internally).

Value

This function returns as list with four elements:

ace	posterior probabilities for each character state at each internal node, with the burn-in excluded.
mcmc	full posterior sample for the states.
par	full posterior sample for the thresholds, the alpha parameter of the "OU" model (if applicable), and the likelihood.
liab	full posterior sample of the liabilities at internal and tip nodes.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Felsenstein, J. (2012) A comparative method for both discrete and continuous characters using the threshold model. *American Naturalist*, **179**, 145-156.
- Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[anc.Bayes](#), [threshBayes](#)

anoletree	<i>Phylogeny of Greater Antillean anole ecomorph species with mapped discrete character</i>
-----------	---

Description

A phylogeny of Greater Antillean anole species with a mapped discrete character - 'ecomorph class.' Data and tree are from Mahler et al. (2010).

Usage

```
data(anoletree)
```

Format

The data are stored as a modified object of class "simmap" with a mapped discrete character. (E.g., see `read.simmap`.)

Source

Mahler, D. L., L. J. Revell, R. E. Glor, and J. B. Losos. (2010) Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean anoles. *Evolution*, **64**, 2731-2745.

applyBranchLengths	<i>Applies the branch lengths of a reference tree to a target</i>
--------------------	---

Description

This function applies the set of branch lengths from a reference tree to a target tree while reconciling any mappings (as in `read.simmap`) with the new branch lengths.

Usage

```
applyBranchLengths(tree, edge.length)
```

Arguments

tree	target tree.
edge.length	number of digits for rounding. Passed to <code>round</code> .

Value

A tree with branch lengths, or modified "phylo" object with a mapped discrete character.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

as.multiPhylo

Conversion to object of class "multiPhylo"

Description

This function converts between object classes.

Usage

```
as.multiPhylo(x, ...)  
## S3 method for class 'multiSimmap'  
as.multiPhylo(x, ...)
```

Arguments

x object to be converted to "multiPhylo". Presently an object of class "multiSimmap".
... optional arguments.

Value

An object of class "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

ave.rates	<i>Average the posterior rates</i>
-----------	------------------------------------

Description

Primarily used internally by [posterior.evolrate](#).

Usage

```
ave.rates(tree, shift, tips, sig1, sig2, ave.shift, showTree=TRUE)
```

Arguments

tree	a tree.
shift	the shift point for this sample.
tips	tip names tipward of shift.
sig1	rate 1.
sig2	rate 2.
ave.shift	average shift from all samples.
showTree	logical value indicating whether to plot the rate-stretched tree.

Value

A list of the rates.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[evol.rate.mcmc](#), [minSplit](#), [posterior.evolrate](#)

averageTree *Compute an average tree from a set of trees and related operations*

Description

These functions compute average trees or consensus trees by various criteria.

Usage

```
averageTree(trees, start=NULL, method="quadratic.path.difference",
            tol=1e-12, quiet=FALSE, ...)
ls.consensus(trees, start=NULL, tol=1e-12, quiet=FALSE, ...)
minTreeDist(tree, trees, method="quadratic.path.difference", ...)
```

Arguments

trees	object of class "multiPhylo".
tree	object of class "phylo". For minTreeDist the tree on which to find the edge lengths that minimize the distance to the phylogenies in trees.
start	starting tree for optimization.
method	distance criterion for minimization. Options are "symmetric.difference", "branch.score.difference", "path.difference", and "quadratic.path.difference".
tol	tolerance value for optimization.
quiet	logical value indicating whether to run "quietly" or not.
...	other arguments to be passed internally.

Value

An object of class "phylo" with edge lengths.

Author(s)

Liam Revell <liam.revell@umb.edu>

bd *Convert object of class "birthdeath" to raw birth & death rates*

Description

This function converts an object of class "birthdeath" to a vector with the ML birth & death rates.

Usage

```
bd(x)
```

Arguments

x object of class "birthdeath".

Value

A vector.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[birthdeath](#)

 bind.tip

Attaches a new tip to a tree

Description

Functions adds a new tip to the tree. If the tree is ultrametric and no branch length is specified, then edge.length is scaled so that the tree remains ultrametric after the new tip is added.

Usage

```
bind.tip(tree, tip.label, edge.length=NULL, where=NULL, position=0,
         interactive=FALSE, ...)
```

Arguments

tree	receptor tree.
tip.label	a string containing the species name for the new tip.
edge.length	edge length for the new tip (a scalar).
where	node number to attach new tip. If position>0 then then tip will be attached <i>below</i> the specified node. Node numbers can also be tips, in which case the new tip will be added along the terminal edge. To find out the tip number for given species with name " <i>species</i> " type: <code>which(tree\$tip.label=="species")</code> .
position	distance <i>below</i> node to add tip.
interactive	logical value indicating whether or not the species should be added interactively. (Defaults to FALSE.)
...	arguments to be passed to plotTree (for interactive=TRUE.)

Details

Wrapper function for 'ape' [bind.tree](#). Note that interactive=TRUE works only for right-facing phylograms.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

bind.tree.simmap	<i>Attaches a new tip to a tree</i>
------------------	-------------------------------------

Description

This function grafts tree y onto tree x at node where.

Usage

```
bind.tree.simmap(x, y, where="root")
```

Arguments

x	an object of class "simmap". (The receptor tree.)
y	an object of class "simmap". (The tree being grafted.)
where	node number to attach new tip, or the root node if where="root".

Details

This function wraps around [bind.tree](#) for objects of class "simmap"; however it presently only allows y to be grafted at a node of x and it does not allow y to possess a root edge.

Value

An object of class "simmap".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

bmPlot	<i>Simulates and visualizes discrete-time Brownian evolution on a phylogeny</i>
--------	---

Description

This function conducts discrete-time Brownian motion simulation on an input tree, plots the outcome, and returns the tip and internal node states to the user as a named vector. The function will first rescale and round the branch lengths to integer length, if they are not already in integer values. If integer branch lengths are provided, the user should also set `ngen=max(nodeHeights(tree))`. For `type="threshold"` the visualization is of the threshold model (Felsenstein 2012), in which the evolving character is liability and the segments of evolution are colored by their value for the threshold trait. If `type="threshold"` is used, the function requires at least one addition input: `thresholds`, a vector containing the ordered thresholds between states. The user can also provide the colors for plotting in `colors`. Note that one more color than threshold should be provided as one threshold implies two states; two thresholds, three states; etc. If no value for `colors` is provided, the function will recycle a set of four colors up to the number of times required by `thresholds`. Finally, the optional argument `return.tree=TRUE` will tell the function to return a list with the tip and note states and an object of class "phylo" with (for `type="threshold"`), the state for the threshold model through time mapped on the branches of the tree in discrete time.

Usage

```
bmPlot(tree, type="BM", anc=0, sig2=1/1000, ngen=1000, ...)
```

Arguments

<code>tree</code>	a phylogenetic tree in "phylo" format.
<code>type</code>	the type of plot to create. See Description.
<code>anc</code>	the ancestral value for the root node.
<code>sig2</code>	the BM rate (variance of the Brownian evolution process).
<code>ngen</code>	number of generations for the simulation: will rescale the tree to this total length.
<code>...</code>	arguments to be passed to different methods.

Value

This function conducts and plots discrete time Brownian simulation and returns a vector containing the simulated states at internal nodes and tips of the tree. It also returns, by default (although this can be turned off) a tree with the branch lengths in discrete time and with a mapped discrete character (for `type="threshold"`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. 2012. A comparative method for both discrete and continuous characters using the threshold model. *American Naturalist*, **179**, 145-156.

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

Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[fastBM](#), [pbtree](#), [phenogram](#), [threshBayes](#)

Examples

```
# plot BM simulation on 20 taxon tree
tree<-pbtree(n=20)
x<-bmPlot(tree)

# plot simulation of a threshold character
tree<-pbtree(n=20)
x<-bmPlot(tree,type="threshold",thresholds=c(0,1,2))
```

branching.diffusion *Animation of branching random diffusion*

Description

This function creates an animation of branching random diffusion (i.e., BM with speciation).

Usage

```
branching.diffusion(sig2=1, b=0.0023, time.stop=1000, ylim=NULL,
smooth=TRUE, pause=0.02, record=NULL, path=NULL)
```

Arguments

sig2	variance of BM process.
b	birthrate for branching process.
time.stop	number of generations to run.
ylim	y limits (for plotting).
smooth	no longer used.

pause	pause (in s) between generations.
record	filename for video file output (no video if NULL).
path	full path to file for video rendering (by default is C:/Program Files/ffmpeg/bin/ffmpeg.exe).

Value

An animated plot and (optionally) a recorded video file. For animation to be recorded to file, the function requires the package "animation" as well as a video renderer.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[bmPlot](#), [fastBM](#)

brownie.lite

Likelihood test for rate variation in a continuous trait

Description

This function takes a modified "phylo" object with a mapped binary or multistate trait (see [read.simmap](#)) and data for a single continuously valued character. It then fits the Brownian rate variation ("non-censored") model of O'Meara et al. (2006; *Evolution*). This is also the basic model implemented in Brian O'Meara's "Brownie" program.

Usage

```
brownie.lite(tree, x, maxit=2000, test="chisq", nsim=100, se=NULL, ...)
```

Arguments

tree	a phylogenetic tree in modified "phylo" format (see read.simmap , make.simmap , or paintSubTree).
x	a vector of tip values for species; names(x) should be the species names.
maxit	an optional integer value indicating the maximum number of iterations for optimization - may need to be increased for large trees.
test	an optional string indicating the method for hypothesis testing - options are "chisq" or "simulation".
nsim	number of simulations (only used if test="simulation").
se	a vector containing the standard errors for each estimated mean in x.
...	optional arguments.

Details

Sampling error in the estimation of species means can also be accounted for by assigning the vector `se` with the species specific sampling errors for `x`.

Value

A list with the following components:

<code>sig2.single</code>	is the rate for a single rate model - this is usually the "null" model.
<code>a.single</code>	is the estimated state at the root node for the single rate model.
<code>var.single</code>	variance on the single rate estimator - obtained from the Hessian.
<code>logL1</code>	log-likelihood of the single-rate model.
<code>k1</code>	number of parameters in the single rate model (always 2).
<code>sig2.multiple</code>	is a length p (for p rates) vector of BM rates from the multi-rate model.
<code>a.multiple</code>	is the estimated state at the root node for the multi-rate model.
<code>var.multiple</code>	$p \times p$ variance-covariance matrix for the p rates - the square-roots of the diagonals should give the standard error for each rate.
<code>logL.multiple</code>	log-likelihood of the multi-rate model.
<code>k2</code>	number of parameters in the multi-rate model ($p+1$).
<code>P.chisq</code>	P-value for a likelihood ratio test against the χ^2 distribution; or
<code>P.sim</code>	P-value for a likelihood ratio test against a simulated null distribution.
<code>convergence</code>	logical value indicating if the likelihood optimization converged.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- O'Meara, B. C., C. Ane, M. J. Sanderson, and P. C. Wainwright. (2006) Testing for different rates of continuous trait evolution using likelihood. *Evolution*, **60**, 922–933.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[brownieREML](#), [evol.vcv](#)

brownieREML

REML version of brownie.lite

Description

This function takes a modified "phylo" object with a mapped binary or multistate trait (see [read.simmap](#)) and data for a single continuously valued character. It then uses restricted maximum likelihood (REML) to fit the Brownian rate variation ("noncensored") model of O'Meara et al. (2006; *Evolution*). This function is similar to [brownie.lite](#) but uses REML (which is faster and unbiased) instead of ML. REML optimization takes advantage of Felsenstein's (1985) contrasts algorithm.

Usage

```
brownieREML(tree, x, maxit=2000, ...)
```

Arguments

tree	a phylogenetic tree in modified "phylo" format (see read.simmap and make.simmap).
x	a vector of tip values for species; names(x) should be the species names.
maxit	an optional integer value indicating the maximum number of iterations for optimization - may need to be increased for large trees.
...	optional arguments.

Value

A list with the following components:

sig2.single	is the rate for a single rate model - this is usually the "null" model.
logL1	log-likelihood of the single-rate model.
sig2.multiple	is a length p (for p rates) vector of BM rates from the multi-rate model.
logL2	log-likelihood of the multi-rate model.
convergence	numerical value from optim .

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

O'Meara, B. C., C. Ane, M. J. Sanderson, and P. C. Wainwright. 2006. Testing for different rates of continuous trait evolution using likelihood. *Evolution*, **60**, 922-933.

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

See Also

[brownie.lite](#), [evol.vcv](#), [evol.rate.mcmc](#)

cladelabels	<i>Add labels to subtrees of a plotted phylogeny</i>
-------------	--

Description

This function adds clade labels to a plotted tree.

Usage

```
cladelabels(tree=NULL, text, node, offset=NULL, wing.length=NULL, cex=1,
orientation="vertical")
```

Arguments

tree	an object of class "phylo". If not supplied, the function will obtain the last plotted phylogeny from the environmental variable <code>last_plot.phylo</code> .
text	desired clade label text.
node	node number for the most recent common ancestor of members of the clade.
offset	offset (as a multiplier of character width) for the label. Defaults to <code>offset=1</code> if tree is supplied or <code>offset=8</code> otherwise.
wing.length	length of the wings to add to the top & bottom of the label bar (in character widths).
cex	character expansion factor.
orientation	orientation of the text. Can be <code>orientation = "vertical"</code> (the default) or <code>"horizontal"</code> .

Details

This function presently works only for rightward facing plotted phylogenies - but no warning will be returned if your tree does not conform to this requirement!

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.

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

See Also[nodelabels](#)

collapse.to.star	<i>Collapse a subtree to a star phylogeny</i>
------------------	---

Description

This function collapses a subtree to a star. If the tree has edge lengths, the function will keep the tips at the same height above the root as in the original tree.

Usage

```
collapse.to.star(tree, node)
```

Arguments

tree	an object of class "phylo".
node	node for the clade to be collapsed.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also[splitTree](#), [starTree](#)

`collapseTree`*Interactive tree visualizer*

Description

Function creates an interactive visualization of collapsing & expanding clades on the tree.

Usage

```
collapseTree(tree, ...)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>...</code>	optional arguments. These <i>mostly</i> match the arguments of <code>plotSimmap</code> , but also include the argument <code>drop.extinct</code> which will (if the input tree is ultrametric) drop any 'extinct' lineages from the tree that is returned by the function.

Details

Function first plots a fan style tree, and then the user collapses node on the tree by clicking on them. Collapsed nodes are collapsed to the common ancestor of the clade. Nodes that have been collapsed can also be expanded by clicking.

Value

Returns the final plotted tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotTree](#), [plotSimmap](#)

consensus.edges	<i>Compute consensus edges for a tree under some criterion</i>
-----------------	--

Description

This function computes consensus edge lengths by different methods.

Usage

```
consensus.edges(trees, method=c("mean.edge", "least.squares"), ...)
```

Arguments

trees	object of class "multiPhylo" in which the trees must have edge lengths. This could be, for instance, a sample from the posterior distribution of trees in a Bayesian analysis.
method	method for computing the edge lengths. Could be the mean of all trees in which the edge is present, or it could be the least-squares edge lengths computed on the mean patristic distance matrices from the input phylogenies in trees. Note that in the latter case the phangorn function <code>npls.tree</code> is used and the option <code>rooted</code> will be set to <code>is.rooted(tree)</code> for the consensus tree.
...	optional arguments, the most popular of which is <code>consensus.tree</code> - a user supplied consensus tree. Another optional argument for <code>method="mean.edge"</code> is <code>if.absent</code> which tells the function how to include absent edges in the computation of average edge lengths. Possible values are "zero" (the default) or "ignore".

Value

An object of class "phylo" with edge lengths.

Author(s)

Liam Revell <liam.revell@umb.edu>

contMap	<i>Map continuous trait evolution on the tree</i>
---------	---

Description

Function plots a tree with a mapped continuous character. The mapping is accomplished by estimating states at internal nodes using ML with [fastAnc](#), and the interpolating the states along each edge using equation [2] of Felsenstein (1985).

Usage

```
contMap(tree, x, res=100, fsize=NULL, ftype=NULL, lwd=4, legend=NULL,
        lims=NULL, outline=TRUE, sig=3, type="phylogram", direction="rightwards",
        plot=TRUE, ...)
## S3 method for class 'contMap'
plot(x, ...)
```

Arguments

tree	object of class "phylo".
x	vector of phenotypic trait values for species. names(x) should contain the species names and match tree\$tip.label. Or, for plot.contMap, an object of class "contMap".
res	resolution for gradient plotting. Larger numbers indicate a finer (smoother) gradient.
fsize	relative font size - can be a vector with the second element giving the font size for the legend.
ftype	font type - see options in plotSimmap . As with fsize, this can be a vector with the second element giving font type for the legend.
lwd	line width for branches. Can be a single integer number or a vector. In the latter case, the second number will be taken to be the desired legend width.
legend	if FALSE no legend is plotted; if a numeric value, it gives the length of the legend in units of branch length. Default is 0.5 times the total tree length.
lims	range for the color map. By default, this will be c(min(x), max(x)), and should always include this range.
outline	logical value indicating whether or not to outline the branches of the tree in black.
sig	the number of decimal places to show on the legend limits.
type	type of plot desired. Options are "phylogram" for a rightward square phylogram; and "fan" for a circular phylogram.
direction	plotting direction for type="phylogram".
plot	logical value indicating whether or not to plot the tree. If plot=FALSE then an object of class "contMap" will be returned without plotting.
...	optional arguments for plot.contMap which include all the arguments of contMap except for tree, x, res, and lims. Also method, "fastAnc", "anc.ML", or "user" (for user-supplied states) specifying which function to use for ancestral state estimation; hold specifies whether or not to hold output to graphical device before plotting (defaults to hold=TRUE); and anc.states a vector containing some or multiple ancestral user-supplied ancestral states at nodes. Some other plotting arguments, such as xlim and ylim, may also work.

Value

Plots a tree. An object of class "contMap" is returned invisibly.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

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

Revell, L. J. 2013. Two new graphical methods for mapping trait evolution on phylogenies. *Methods in Ecology and Evolution*, **4**, 754-759.

See Also

[anc.ML](#), [densityMap](#), [fastAnc](#), [plotSimmap](#)

cophylo	<i>Creates a co-phylogenetic plot</i>
---------	---------------------------------------

Description

This function creates an object of class "cophylo" or, in the case of `plot.cophylo`, plots that object. The function can (optionally) first attempt to rotate the nodes of both trees to optimize vertical matching of tips.

Usage

```
cophylo(tr1, tr2, assoc=NULL, rotate=TRUE, ...)
## S3 method for class 'cophylo'
plot(x, ...)
```

Arguments

tr1	object of class "phylo".
tr2	object of class "phylo".
assoc	matrix containing the tip labels in tr1 to match to the tip labels in tr2. Note that not all labels in either tree need to be included; and, furthermore, one label in tr1 can be matched with more than one label in tr2, or vice versa.
rotate	logical argument indicating whether nodes on both trees should be rotated to attempt to match in vertical position.
x	in the case of <code>plot.cophylo</code> , an object of class "cophylo" to be plotted.
...	optional arguments to be passed to <code>tipRotate</code> , or, in the case of <code>plot.cophylo</code> , to the internally used tree plotting function, <code>phylogram</code> . <code>phylogram</code> takes similar arguments to <code>plotSimmap</code> , such as <code>fsize</code> , <code>ftype</code> , <code>lwd</code> , and <code>pts</code> , though not all options from <code>plotSimmap</code> and <code>plotTree</code> are available. If <code>fsize</code> is supplied as a vector, different size fonts for the left & right facing trees may be used. In

addition, the optional argument `scale.bar`, which should be a vector containing the lengths of the scale bars desired for the right & left trees, will add scale bars to the plot when supplied to `plot.cophylo`. If either tree contains polytomies, the `cophylo` argument `rotate.multi` should be set to `TRUE`. If curved linking lines are desired, the `plot.cophylo` argument `link.type` should be set to `"curved"`. Other arguments for the plot method include `link.col`, `link.lty`, and `link.lty`, which can be supplied as a scalar or a vector in which the order of the elements corresponds to the order of the associations in `assoc`.

Details

If no matrix of associations, `assoc`, is provided, then `cophylo` will look for exact matches of tip labels between trees.

Value

An object of class `"cophylo"` which includes the following components or a pair of plotted facing phylogenies with links between tips as specified in `assoc`.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[cophyloplot](#), [plotSimmap](#)

Examples

```
tr1<-pbtree(n=26,tip.label=LETTERS)
tr2<-pbtree(n=26,tip.label=sample(LETTERS))
obj<-cophylo(tr1,tr2)
plot(obj)
```

cospeciation

Conducts a statistical test of cospeciation between two trees

Description

This function conducts a test for cospeciation based on tree distance, applying a distance metric selected by the user. Note that this method should be prone to be quite liberal as the null hypothesis is no similarity between trees!

Usage

```
cospeciation(t1, t2, distance=c("RF", "SPR"),
method=c("simulation", "permutation"), assoc=NULL,
nsim=100, ...)
## S3 method for class 'cospeciation'
plot(x, ...)
## S3 method for class 'cospeciation'
print(x, ...)
```

Arguments

t1	object of class "phylo".
t2	object of class "phylo".
distance	distance method to compare trees.
method	method to use (simulation of pure-birth trees, or permutation of tip labels on a fixed tree) to obtain a null distribution of tree distances via <code>distance</code> .
assoc	matrix containing the tip labels in t1 to match to the tip labels in t2. Note that not all labels in either tree need to be included; however, unlike <code>cophylo</code> , one label in t1 cannot be matched with more than one label in t2, nor vice versa. If NULL then an exact match of tip labels will be sought.
nsim	number of simulations or permutations.
x	for plot and print methods, an object of class "cospeciation".
...	optional arguments.

Value

An object of class "cospeciation", which includes the test-statistic, the null distribution, and a p-value for the test of the null hypothesis of no topological similarity between the two trees.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[cophylo](#)

countSimmap	<i>Counts the number of character changes on a SIMMAP style tree or set of trees</i>
-------------	--

Description

This function takes a tree or a set of trees with a mapped discrete character (SIMMAP style, e.g., see [make.simmap](#) or [read.simmap](#)), and computes the total number of character changes as well as the number of character changes between all states.

Usage

```
countSimmap(tree, states=NULL, message=TRUE)
```

Arguments

tree	a single tree or a set of trees with a mapped discrete character (e.g. see make.simmap or read.simmap).
states	optional argument with the states for the mapped character. If not provided, these will be computed from the tree. This is useful if averaging across many trees, some of which may lack certain states.
message	optional logical argument indicating whether or not to return an informative message about the function output.

Value

A list with up to three elements: N is an integer value giving the total number of character changes on the tree; Tr gives the number of transitions between row and column states (or a matrix containing both N and the transitions between states, in rows, for an object of class "multiPhylo"); and (optionally) message contains an explanatory message about the function output.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Examples

```
tree<-pbtree(n=100,scale=1)
Q<-matrix(c(-2,1,1,1,-2,1,1,1,-2),3,3)
colnames(Q)<-rownames(Q)<-c("A","B","C")
mtree<-sim.history(tree,Q)
countSimmap(mtree,states=rownames(Q))
```

densityMap

*Plot posterior density of stochastic mapping on a tree***Description**

Function plots a tree with the posterior density for a mapped character from stochastic character mapping on the tree. Since the mapped value is the probability of being in state "1", only binary [0,1] characters are allowed.

Usage

```
densityMap(trees, res=100, fsize=NULL, ftype=NULL, lwd=3, check=FALSE,
legend=NULL, outline=FALSE, type="phylogram", direction="rightwards",
plot=TRUE, ...)
## S3 method for class 'densityMap'
plot(x, ...)
```

Arguments

trees	set of phylogenetic trees in a modified "multiPhylo" object. Values for a two-state discrete character are mapped on the tree. See make.simmap and read.simmap for details.
res	resolution for gradient plotting. Larger numbers indicate a finer (smoother) gradient.
fsize	relative font size - can be a vector with the second element giving the font size for the legend.
ftype	font type - see options in plotSimmap . As with fsize, can be a vector with the second element giving font type for the legend.
lwd	line width for branches. If a vector of two elements is supplied, the second element will be taken to be the desired width of the legend bar.
check	check to make sure that the topology and branch lengths of all phylogenies in trees are equal.
legend	if FALSE no legend is plotted; if a numeric value, it gives the length of the legend in units of branch length. Default is 0.5 times the total tree length.
outline	logical value indicating whether or not to outline the branches of the tree in black.
type	type of plot desired. Options are "phylogram" for a rightward square phylogram; and "fan" for a circular phylogram.
plot	logical value indicating whether or not to plot the tree. If plot=FALSE then an object of class "densityMap" will be returned without plotting.
direction	plotting direction for type="phylogram".
x	for plot.densityMap, an object of class "densityMap".

... optional arguments for `plot.densityMap`. These include all the arguments of `densityMap` except `trees` and `res`. Additional optional arguments include `mar` (margins), `offset` (tip label offset), and `hold` (whether or not to use `dev.hold` to hold output to graphical device before plotting; defaults to `hold=TRUE`). Also, the argument `states` can be used to 'order' the states on the probability axis (that is, which state should correspond to a posterior probability of 0 or 1). Some other plotting arguments, such as `xlim` and `ylim`, may also work.

Value

Plots a tree and returns an object of class "densityMap" invisibly.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Bollback, J. P. 2006. Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.
- Huelsenbeck, J. P., R. Nielsen, and J. P. Bollback. 2003. Stochastic mapping of morphological characters. *Systematic Biology*, **52**, 131-138.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Revell, L. J. 2013. Two new graphical methods for mapping trait evolution on phylogenies. *Methods in Ecology and Evolution*, **4**, 754-759.

See Also

[make.simmap](#), [plotSimmap](#), [read.simmap](#)

densityTree

Plots a posterior sample of trees

Description

Functions plots a posterior sample of trees, including with mapped discrete characters.

`make.transparent` is used internally and converts a color to transparent with a certain user-specified alpha level.

Usage

```
densityTree(trees, colors="blue", alpha=NULL, method="plotTree", fix.depth=FALSE,
use.edge.length=TRUE, compute.consensus=FALSE, ...)
make.transparent(color, alpha)
```


Arguments

trees	an object of class "multiPhylo" or "multiSimmap".
colors	a color or a named vector of colors in which names correspond to mapped states in an object of class "multiSimmap".
alpha	transparency level for plotted trees which is passed to internally used function, <code>make.transparent</code> . (0 is fully transparent, which 1 is fully opaque.) By default will be one divided by the number of trees.
method	plotting method to be used internally. Can be "plotTree" or "plotSimmap".
fix.depth	logical value indicating whether or not to plot trees with a fixed depth or to permit plotted trees to have different depths.
use.edge.length	logical value indicating whether to use the edge lengths of the input tree. Defaults to <code>use.edge.length=TRUE</code> unless any input tree edge lengths are NULL.
compute.consensus	logical value indicating whether or not to use the tip order from a consensus tree. (Defaults to <code>compute.consensus=FALSE</code> .)
...	arguments to be passed to <code>plotTree</code> or <code>plotSimmap</code> .
color	in <code>make.transparent</code> , the color to render transparent.

Value

Function creates a plot.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

describe.simmap	<i>Summarizes a stochastic mapped tree or set of trees</i>
-----------------	--

Description

This function summarizes the result of one or more stochastic maps.

Usage

```
describe.simap(tree, ...)
## S3 method for class 'simmap'
summary(object, ...)
## S3 method for class 'multiSimmap'
summary(object, ...)
## S3 method for class 'describe.simap'
plot(x, ...)
```

Arguments

tree	a single tree or a set of trees as an object of class "simmap" or "multiSimmap", respectively.
object	object of class "simmap" or "multiSimmap".
x	for S3 plot method, an object of class "describe.simap".
...	optional arguments which include: plot, a logical value indicating whether or not to plot the posterior probabilities at nodes (default is plot=FALSE); check.equal, a logical value indicating whether or not to check if all trees are equal using all.equal.phylo (default is check.equal=FALSE); and message, a logical indicating whether or not to print an informative message to the screen (default is message=TRUE).

Value

An object of class "describe.simap" with the following elements:

count	a matrix containing the number and types of transitions for each tree, if tree is an object of class "multiSimmap".
times	a matrix containing the times spent in each state on each tree.
ace	the posterior probabilities of each node being in each state, if tree is an object of class "multiSimmap".
legend	a vector containing the plot legend, if plot=TRUE.

if class(tree)="simmap" then the function simply returns the results of [countSimmap](#) combined with the states at each node of the tree and a matrix containing the total and relative times spent in each state on the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

di2multi.simapmap	<i>Collapse branches of zero length to polytomy in stochastic map style tree</i>
-------------------	--

Description

This function collapses branches of zero length (or, more specifically, branches with length shorter than `tol`) to create a polytomy in a stochastic-map style tree.

Usage

```
## S3 method for class 'simmap'  
di2multi(phy, ...)
```

Arguments

<code>phy</code>	object of class "simmap" containing a stochastically mapped discrete character.
<code>...</code>	optional argument <code>tol</code> , length below which edges should be treated as having zero length.

Details

This function should theoretically perform similarly to `di2multi` in `ape`.

Value

A tree with a stochastically mapped discrete character

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[di2multi](#), [make.simapmap](#), [read.simapmap](#)

dotTree *Creates a phylogenetic dot plot*

Description

Creates a plot in which different sized dots/circles represent different tip values for a quantitative trait.

Usage

```
dotTree(tree, x, legend=TRUE, method="plotTree", standardize=FALSE, ...)
dot.legend(x, y, min, max, Ntip, length=5, prompt=FALSE, method="plotTree", ...)
```

Arguments

tree	an object of class "phylo".
x	vector of trait values; or a matrix. In the case of dot.legend, the x coordinate of the legend.
legend	logical value indicating whether or not a legend should be plotted.
method	tree plotting method to be used internally. Will switch to method="phylogram" if the number of traits is greater than one. For dot.legend, it should be the method that was used for the plot.
standardize	a logical value indicating whether or not to standardize x, or each column of x, to have a mean of zero & variance of one prior to analysis.
y	y coordinate of the legend.
min	minimum value for dot.legend.
max	maximum value for dot.legend.
Ntip	number of tips in the plotted tree for dot.legend.
length	length of legend.
prompt	logical value indicating whether or not to prompt for legend position.
...	optional arguments. In the case of dotTree, these will be passed to plotTree or a different internally used plotting function for method="phylogram". See phylo.heatmap for more detail on these arguments. Other options for dotTree also include data.type ("continuous" or "discrete"), colors, length, for data type "continuous" the length of the legend in terms of plotted circles, x.space, the spacing of the columns in the plotted data matrix, and leg.space, the spacing of the legend dots (again, for data.type="continuous" only).

Value

Function creates a plot.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

drop.clade	<i>Drop a clade from a tree</i>
------------	---------------------------------

Description

Mostly internal function for `posterior.evolrate`; function drops the clade containing the species in tip.

Usage

```
drop.clade(tree, tip)
```

Arguments

tree	object of class "phylo".
tip	set of tips in a clade.

Details

Probably should not use unless you know what you're doing.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

drop.leaves	<i>Drop all the leaves (tips) from a tree</i>
-------------	---

Description

Drops all the leaves from a tree, leaving behind only the structure leading to internal nodes.

Usage

```
drop.leaves(tree, ...)
```

Arguments

tree	object of class "phylo".
...	optional arguments. Presently includes only the logical value <code>keep.tip.labels</code> which tells the function how to labels the tips on the reduced tree.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

drop.tip.contMap	<i>Drop tip or tips from an object of class "contMap" or "densityMap"</i>
------------------	---

Description

This function drops one or multiple tips from an object of class "contMap" or "densityMap". This function is equivalent to [drop.tip](#) but for an object of this class.

Usage

```
drop.tip.contMap(x, tip)  
drop.tip.densityMap(x, tip)
```

Arguments

x an object of class "contMap" or "densityMap".
 tip name or names of species to be dropped.

Details

For more information about objects of class "contMap" or "densityMap", please refer to the documentation pages for [contMap](#) or [densityMap](#), respectively.

Value

An object of class "contMap" or "densityMap".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[contMap](#), [densityMap](#), [drop.tip](#), [drop.tip.simapmap](#)

drop.tip.simapmap	<i>Drop tips or extract clade from tree with mapped discrete character</i>
-------------------	--

Description

This function drops one or multiple tips from the modified "phylo" object with a mapped binary or multistate trait (see [read.simapmap](#)) while maintaining the matrix \$mapped.edge and list of mappings by branch maps. This function is equivalent to [drop.tip](#) but for a tree with a mapped discrete character.

`extract.clade.simapmap` is functionally equivalent to [extract.clade](#) but preserves discrete character mappings on the tree.

Usage

```
drop.tip.simapmap(tree, tip)
extract.clade.simapmap(tree, node)
```

Arguments

tree a modified object of class "phylo" (see [read.simapmap](#)).
 tip name or names of species to be dropped.
 node node number for the root node of the clade to be extracted.

Value

A modified object of class "phylo" containing the elements maps and \$mapped.edge with the time spent in each state along each edge of the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[brownie.lite](#), [drop.tip](#), [extract.clade](#), [make.simmap](#), [read.simmap](#), [sim.history](#)

edgeProbs

Compute the relative frequencies of state changes along edges

Description

This function computes the relative frequencies of character state changes along edges from a sample of stochastically mapped character histories. This function assumes that all trees in the sample differ only in their mapped histories & not at all in topology or branch lengths. Note that it only asks whether the starting and ending states of the edge differ in a particular way, and thus ignores multiple-hits along a single edge.

Usage

```
edgeProbs(trees)
```

Arguments

trees an object of class "multiSimmap" containing a sample of trees that are identical in topology & branch lengths with different stochastically mapped character histories.

Value

The object that is returned is a matrix with the state changes & the relative frequency of each state change. Rows are in the order of the matrix edge for any of the mapped trees.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotSimmap](#)

estDiversity	<i>Estimate diversity at each node of the tree</i>
--------------	--

Description

This function estimates the lineage density at each node in the tree based on a biogeographic model (based on Mahler et al. 2010).

Usage

```
estDiversity(tree, x, method=c("asr", "simulation"), model="ER", ...)
```

Arguments

tree	is a phylogenetic tree in "phylo" format.
x	a vector containing the biogeographic area for each of the tip taxa.
method	method for reconstructing ancestral biogeography.
model	model for ancestral character estimation. In theory, any model from ace ; however only symmetric models permitted for method="asr".
...	optional arguments. So far, this includes only nsim, the number of stochastic mappings to conduct using make.simmap for method="simulation".

Details

Two different methods are implemented in the current version. For method="asr" the state at the current node, and at each position along each co-extant internal edge, is computed as the marginal (empirical Bayesian) ancestral state reconstruction using the re-rooting method of Yang (2006). The lineage density is then computed as the sum of the marginal reconstructions (posterior probabilities) times the summed marginal ancestral reconstructions across co-extant edges. In method="simulation", stochastic character mapping is used to generate optional argument nsim stochastic maps of ancestral biogeography. Then the lineage density at each node is computed as the number of co-existing lineages with the same biogeography as the focal node, averaged across stochastic maps. The importance of this distinction may depend on the degree to which reconstructions at internal nodes are independent, which relates to the distinction between marginal and joint reconstruction (e.g., see Yang 2006).

Value

A vector containing the estimated lineage density at each node

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Mahler, D. L., L. J. Revell, R. E. Glor, and J. B. Losos. (2010) Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean anoles. *Evolution*, **64**, 2731-2745.

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

Yang, Z. (2006) *Computational Molecular Evolution*. Oxford University Press.

See Also

[fitDiversityModel](#)

evol.rate.mcmc

Bayesian MCMC method for identifying exceptional phenotypic diversification in a phylogeny

Description

This function takes a phylogenetic tree and data for a single continuously valued character and uses a Bayesian MCMC approach to identify the phylogenetic location of a shift in the evolutionary rate through time.

Usage

```
evol.rate.mcmc(tree, x, ngen=10000, control=list())
```

Arguments

tree	a phylogenetic tree in "phylo" format.
x	a vector of tip values for species; names(x) should be the species names.
ngen	an optional integer value indicating the number of generations for the MCMC.
control	a list of control parameters containing the following elements: sig1: starting value for $\sigma(1)^2$; sig2: starting value for $\sigma(2)^2$; a: starting value for a; sd1: standard deviation for the normal proposal distribution for $\sigma(1)^2$; sd2: standard deviation for the normal proposal distribution for $\sigma(2)^2$; kloc: scaling parameter for tree move proposals - $1/\lambda$ for the reflected exponential distribution; sdlnr: standard deviation on the log-normal prior on $\sigma(1)^2/\sigma(2)^2$; rand.shift: probability of proposing a random shift in the tree (improves mixing); print: print frequency for the MCMC; sample: sample frequency.

Details

Default values of control are given in Revell et al. (2012).

Value

A list with the following components:

mcmc	results from the MCMC run.
tips	list of stips in rate $\sigma(1)^2$ for each sampled generation of MCMC (to polarize the rate shift).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Revell, L. J., D. L. Mahler, P. Peres-Neto, and B. D. Redelings. (2012) A new method for identifying exceptional phenotypic diversification. *Evolution*, **66**, 135-146.

See Also

[anc.Bayes](#), [brownie.lite](#), [evol.vcv](#), [minSplit](#), [posterior.evolrate](#)

evol.vcv

Likelihood test for variation in the evolutionary VCV matrix

Description

This function takes a modified "phylo" object with a mapped binary or multistate trait and data for an arbitrary number of continuously valued character. It then fits the multiple evolutionary variance-covariance matrix (rate matrix) model of Revell & Collar (2009; *Evolution*).

Usage

```
evol.vcv(tree, X, maxit=2000, vars=FALSE, ...)
```

Arguments

tree	a phylogenetic tree in modified "phylo" format (see read.simmap).
X	an n x m matrix of tip values for m continuously valued traits in n species - row names should be species names.
maxit	an optional integer value indicating the maximum number of iterations for optimization - may need to be increased for large trees.

`vars` an optional logical value indicating whether or not to estimate the variances of the parameter estimates from the Hessian matrix.

`...` optional arguments.

Details

This function performs optimization by first optimizing the likelihood with respect to the Cholesky matrices using `optim`. Optimization is by `method="Nelder-Mead"`. Using box constraints does not make sense here as they would be applied to the Cholesky matrix rather than the target parameters. May have to increase `maxit` for large trees and more than 2 traits.

Value

A list with the following components:

`R.single` vcv matrix for the single rate matrix model.

`vars.single` optionally, a matrix containing the variances of the elements of `R.single`.

`logL1` log-likelihood for single matrix model.

`k1` number of parameters in the single matrix model.

`R.multiple` $m \times m \times p$ array containing the p estimated vcv matrices for the p regimes painted on the tree.

`vars.multiple` optionally, an array containing the variances of the parameter estimates in `R.multiple`.

`logL.multiple` log-likelihood of the multi-matrix model.

`k2` number of parameters estimated in this model.

`P.chisq` P-value of the χ^2 test on the likelihood ratio.

`convergence` logical value indicating whether or not the optimization has converged.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J., and D. C. Collar (2009) Phylogenetic analysis of the evolutionary correlation using likelihood. *Evolution*, **63**, 1090-1100.

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

See Also

[evol.rate.mcmc](#), [brownie.lite](#)

`evolvcv.lite`*Likelihood test for a shift in the evolutionary correlation between traits*

Description

This function takes a modified "phylo" object with a mapped binary or multistate trait and data for two and only two continuously valued character. It then fits four different evolutionary models: common rates and correlation; different rates, common correlation; different correlations, common rates; no common structure.

Usage

```
evolvcv.lite(tree, X, maxit=2000, tol=1e-10)
```

Arguments

<code>tree</code>	a phylogenetic tree in modified "phylo" format (see read.simap).
<code>X</code>	an $n \times m$ matrix of tip values for m continuously valued traits in n species - row names should be species names.
<code>maxit</code>	an optional integer value indicating the maximum number of iterations for optimization - may need to be increased for large trees.
<code>tol</code>	tolerance value for "L-BFGS-B" optimization.

Value

A list with the results summarized for each model.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J., and D. C. Collar (2009) Phylogenetic analysis of the evolutionary correlation using likelihood. *Evolution*, **63**, 1090-1100.

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

See Also

[brownie.lite](#), [evol.vcv](#)

`exhaustiveMP`*Exhaustive and branch & bound MP optimization*

Description

This function does exhaustive and branch & bound MP searches.

Usage

```
exhaustiveMP(data, tree=NULL, method="branch.and.bound")
```

Arguments

<code>data</code>	is a phyDat (Schliep 2011) object containing DNA or other data.
<code>tree</code>	an optional input tree (used only with <code>method="branch.and.bound"</code>).
<code>method</code>	an optional string indicating method to use: <code>"branch.and.bound"</code> or <code>"exhaustive"</code> .

Details

Should probably not be used for more than about 8 species (and definitely not more than 10 species). Performs parsimony calculations using [parsimony](#) in the "phangorn" package (Schliep 2011).

Value

A "phylo" or "multiPhylo" object that is the MP tree or set of MP trees. It also returns the parsimony scores in `attr("trees","pscore")` or `attr(trees[[i]], "pscore")` for the *i*th tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Felsenstein, J. (2004) *Inferring Phylogenies*. Sinauer.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Schliep, K. P. (2011) phangorn: phylogenetic analysis in R. *Bioinformatics*, **27**, 592-593.

See Also

[mrp.supertree](#), [optim.parsimony](#), [pratchet](#)

expm	<i>Matrix exponential</i>
------	---------------------------

Description

Wrapper for [MatrixExp](#) that retains row/column names.

Usage

```
expm(Y)
```

Arguments

Y a matrix.

Value

A matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

export.as.xml	<i>Export trees & data in XML format</i>
---------------	--

Description

This function exports trees & character data in XML format.

Usage

```
export.as.xml(file, trees, X)
```

Arguments

file filename for export.
trees a phylogenetic tree or trees in "phylo" or "multiPhylo" format.
X a matrix of class "DNAbin" or a matrix with discretely valued non-DNA character data.

Details

Can be used to create input file for the program SIMMAP v1.5 (Bollback 2006), also see: <http://www.simmap.com>.

Value

A file.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Bollback, J. P. (2006) Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.

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

See Also

[make.simmap](#), [read.nexus](#), [read.simmap](#), [write.simmap](#)

fancyTree

Plots special types of phylogenetic trees

Description

This function plots different types of phylogenetic trees. If `type="extinction"` (or any unambiguous abbreviation) the function will plot a tree in which branches preceding the MRCA of all extant taxa and branches leading only to extinct lineages are plotted with dashed red lines. If `type="traitgram3d"` the function will plot a three dimensional traitgram (that is, a projection of the tree into three dimensional morphospace where two dimensions are the phenotypic trait and the third axis is time since the root). In this case, the additional argument `X`, a matrix containing the tip values of all species (with species IDs as row names) should be supplied. Optionally, the user can also supply the matrix `A`, which contains the ancestral states in the tree with rows labeled by node number. If `type="droptip"` the function will create a two panel figure in which the first panel is the tree with lineages to be pruned highlighted; and the second panel is the pruned tree. In this case, the additional argument `tip`, the tip name or vector of tip names to be dropped, must be supplied. If `type="densitymap"`, a posterior probability density "heat-map" is created based on a set of trees in a "multiPhylo" object containing a binary [0,1] mapped character. (See [densityMap](#) for additional optional arguments if `type="densitymap"`.) If `type="contmap"`, reconstructed continuous trait evolution is mapped on the tree. Again, see [contMap](#) for additional arguments if `type="contmap"`. If `type="phenogram95"` a 95-percent phenogram is plotted using transparency to visualize uncertainty at ancestral nodes and along branches. Most of the options of [phenogram](#) are available. Finally, if `type="scattergram"` a phylogenetic scatter plot matrix

containing [contMap](#) style trees on the diagonal and [phyloMorphospace](#) plots in non-diagonal panels is produced. For `type="scattergram"` a trait matrix `X` must be supplied. The only additional arguments available for this type are `fsize`, `colors`, and `label`. (See [phyloMorphospace](#) for details.) Presently only `type="traitgram3d"` uses the list control which can be supplied the same set of control parameters as [phyloMorphospace3d](#), as well as the control parameter `maxit` which will be passed to `anc.ML`. Finally, the optional argument `hold` will be passed to multiple methods if supplied. It is a logical value that indicates whether or not the output to the graphical device should be held using `dev.hold` before plotting (defaults to `hold=TRUE`).

Usage

```
fancyTree(tree, type=c("extinction", "traitgram3d", "droptip", "densitymap",
"contmap", "phenogram95", "scattergram"), ..., control=list())
```

Arguments

<code>tree</code>	a phylogenetic tree in "phylo" format.
<code>type</code>	the type of special plot to create. See Description.
<code>...</code>	arguments to be passed to different methods.
<code>control</code>	a list of control parameters, depending on type.

Value

This function plots different types of phylogenetic trees. For `type="droptip"` the function also returns the pruned tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[contMap](#), [densityMap](#), [drop.tip](#), [phenogram](#), [phyloMorphospace3d](#), [plot.phylo](#), [plotSimmap](#)

Examples

```
# plot tree with extinction
set.seed(10)
tree<-pbtree(b=1,d=0.4,t=4)
fancyTree(tree,type="extinction")

## Not run:
# plot 3D traitgram
tree<-pbtree(n=50,scale=10)
Y<-sim.corrstree(tree,vcv=matrix(c(1,0.75,0.75,1),2,2))
```

```
fancyTree(tree,type="traitgram3d",X=Y,control=list(spin=FALSE))

# plot with internal nodes from simulation
Y<-sim.corr(matrix(c(1,0.75,0.75,1),2,2),internal=TRUE)
B<-Y[length(tree$tip)+1:tree$Nnode,]; Y<-Y[1:length(tree$tip),]
fancyTree(tree,type="traitgram3d",X=Y,A=B,control=list(simple.axes=TRUE,spin=FALSE))

## End(Not run)

# plot with dropped tips
tree<-pbtree(n=30)
tips<-sample(tree$tip.label)[1:10]
pruned<-fancyTree(tree,type="droptip",tip=tips)

## Not run:
# plot 95-percent CI phenogram
tree<-pbtree(n=30)
x<-fastBM(tree)
fancyTree(tree,type="phenogram95",x=x)

## End(Not run)
```

fastAnc

Fast estimation of ML ancestral states

Description

This function performs fast estimation of the ML ancestral states for a continuous trait by taking advantage of the fact that the state computed for the root node of the tree during Felsenstein's (1985) contrasts algorithm is also the MLE of the root node. Thus, the function reroots the tree at all internal nodes and computes the contrasts state at the root each time. The function can also (optionally) compute variances or 95-percent confidence intervals on the estimates.

Usage

```
fastAnc(tree, x, vars=FALSE, CI=FALSE, ...)
```

Arguments

tree	an object of class "phylo".
x	a vector of tip values for species; names(x) should be the species names.
vars	a logical value indicating whether or not to compute variances on the ancestral state estimates. Variances are based on Equation (6) of Rohlf (2001).
CI	a logical value indicating whether or not to compute 95-percent confidence intervals on state estimates.
...	optional arguments. Presently this consists of anc.states, a named vector containing ancestral states to fix. Names should correspond to node numbers in the input tree.

Value

A named vector containing the states at internal nodes - names are node numbers; or a list containing ancestral state estimates (`ace`), variances on the estimates (`var`), and/or 95-percent confidence intervals (`CI95`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ace](#), [anc.Bayes](#), [anc.ML](#), [pic](#)

Examples

```
tree<-pbtree(n=50)
x<-fastBM(tree) # simulate using fastBM
fastAnc(tree,x) # estimate states
```

fastBM

Fast Brownian simulation

Description

This function conducts fast quantitative trait simulation on a phylogeny under several different models: Brownian motion (default), BM with a trend (for $\mu \neq 0$), bounds (for $\text{bounds} = c(-\text{Inf}, \text{Inf})$), and OU.

Usage

```
fastBM(tree, a=0, mu=0, sig2=1, bounds=c(-Inf,Inf), internal=FALSE, nsim=1, ...)
```

Arguments

<code>tree</code>	is a phylogenetic tree in "phylo" format.
<code>a</code>	a value for ancestral state at the root node.
<code>mu</code>	an optional value for the mean of random normal changes along branches of the tree - can be used to simulate a trend if $\mu \neq 0$.
<code>sig2</code>	instantaneous variance of the BM process.
<code>bounds</code>	a vector with the lower and upper bounds (respectively) for bounded Brownian simulation - by default simulation is unbounded.

internal logical value indicating whether or not to return states for internal nodes.
 nsim number of simulations.
 ... optional arguments alpha and theta used for OU simulation. If alpha is set
 then mu and bounds are ignored with a warning.

Value

A vector (for nsim=1) or matrix containing the tip states for the n species in the tree, and (optionally) the ancestral states for internal nodes.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[sim.corr](#)s

Examples

```
tree<-pbtree(n=1000)
x<-fastBM(tree,sig2=0.1) # Brownian motion
y<-fastBM(tree,mu=1) # with a trend
```

fastMRCA	<i>Get the MRCA (or height above the root of the MRCA) of a pair of tip taxa</i>
----------	--

Description

This function returns the most recent common ancestor (node number) for a pair of taxa; or, in the case of fastHeight, the height above the root of the MRCA of a pair of taxa; or, in the case of fastDist, the patristic distance between a pair of taxa.

Usage

```
fastMRCA(tree, sp1, sp2)
fastHeight(tree, sp1, sp2)
fastDist(tree, sp1, sp2)
```

Arguments

tree	a phylogenetic tree as an object of class "phylo".
sp1	species name.
sp2	species name.

Details

This function is mostly redundant with [findMRCA](#) (or `findMRCA(..., type="height")` in the case of `fastHeight`) but for very large trees will be considerably faster.

Value

The node number of the MRCA or the height above the root (for `fastHeight`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[findMRCA](#), [mrca](#)

Examples

```
tree<-pbtrees(n=2000)
anc<-fastMRCA(tree,"t1","t15")
```

findMRCA	<i>Get the MRCA of a set of taxa</i>
----------	--------------------------------------

Description

This function returns the most recent common ancestor (node number) for a set of taxa. If `tips=NULL` will be redundant with [mrca](#) (for `type="node"`) or [vcv.phylo](#), but much slower (for `type="height"`).

Usage

```
findMRCA(tree, tips=NULL, type=c("node","height"))
```

Arguments

tree	a phylogenetic tree as an object of class "phylo".
tips	a vector containing a set of tip labels.
type	either "node" to return the node of the MRCA; or "height" to return the height above the root of the MRCA of tips.

Details

If tips==NULL will return the result of a normal function call to [mrca](#). If tips=NULL will return a matrix equal to [vcv.phylo](#).

Value

The node number of the MRCA, or a matrix of node numbers (if tips==NULL) - for type="node"; or the height of the MRCA, or a matrix of heights (if tips==NULL) - for type="height".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[findMRCA](#), [mrca](#)

Examples

```
tree<-pbtree(n=20)
anc<-findMRCA(tree,c("t1","t10","t15"))
```

fitBayes

Evolutionary model fitting with intraspecific variability using Bayesian MCMC

Description

This function uses Bayesian MCMC to sample terminal states (species means) as well as evolutionary parameters.

Usage

```
fitBayes(tree, x, ngen=10000, model="BM", method="reduced", control=list())
```

Arguments

tree	an object of class "phylo".
x	a vector of phenotypic values for individuals; names(x) should contain the species names (not individual IDs).
ngen	a integer indicating the number of generations for the MCMC.
model	an evolutionary model: either "BM" or "lambda".
method	a method: either "reduced" or "full".
control	a list of control parameters containing the following elements: sig2: starting value for σ^2 (BM rate); lambda: starting value for the λ parameter; a: starting for the state at the root node; xbar: starting values for the states at the tips; intV: starting value for the intraspecific variance (reduced method); or v: starting value for the vector of intraspecific variances for all species (full method); pr.mean: means for the prior distributions in the following order - sig2, lambda (if applicable), a, xbar, intV or v (if applicable), note that the prior probability distribution is exponential for sig2 and normal for a and y; pr.var: variances on the prior distributions, same order as pr.mean.

Value

A matrix with number of rows ngen/control\$sample+1 containing the posterior sample and likelihoods. Matrix columns are labeled by species (for species means and variances), or by the corresponding evolutionary parameter.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Revell, L. J. and R. G. Reynolds. (2012) A new Bayesian method for fitting evolutionary models to comparative data with intraspecific variation. *Evolution*, **66**, 2697-2707.

See Also

[anc.Bayes](#), [brownie.lite](#), [evol.rate.mcmc](#)

fitDiversityModel *Fit diversity-dependent phenotypic evolution model*

Description

This function fits a diversity-dependent phenotypic evolution model (based on Mahler et al. 2010).

Usage

```
fitDiversityModel(tree, x, d=NULL, showTree=TRUE, tol=1e-6)
```

Arguments

tree	an object of class "phylo".
x	a vector with tip values for a continuously distributed trait.
d	a vector containing the inferred historical diversity at each node in the tree - if d=NULL (the default) function will treat the diversification as if it occurred in a single geographic area.
showTree	optional logical value indicating whether to plot the tree transformation implied by the model.
tol	some small value by which d is incremented during rescaling of psi for optimization. If R thinks your matrices are singular during optimization, try increasing tol slightly.

Value

A list with the following components:

logL	log-likelihood of the fitted model.
sig0	estimated starting value for the rate at the root of the tree.
psi	the estimated rate of change in the rate associated with the addition of a lineage.
vcv	a matrix with the variances and covariance of the estimated parameters (from the Hessian).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Mahler, D. L., L. J. Revell, R. E. Glor, and J. B. Losos. 2010. Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean anoles. *Evolution*, **64**, 2731-2745.

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

See Also

[brownie.lite](#), [estDiversity](#), [evol.rate.mcmc](#)

fitMk

Fits Mk model

Description

This function fits a so-called Mk model for discrete character evolution. It is primarily designed to be used inside of `make.simmap`.

Two plot methods are available. `plot.fitMk` plots an object of class "fitMk" returned by `fitMk`. `plot.gfit` plots an object of class "gfit" from geiger's `fitDiscrete` function. Both plots portray the fitted model using a graph of arrows connecting states.

Usage

```
fitMk(tree, x, model="SYM", fixedQ=NULL, ...)
## S3 method for class 'fitMk'
plot(x, ...)
## S3 method for class 'gfit'
plot(x, ...)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>x</code>	a vector of tip values for species; <code>names(x)</code> should be the species names. In the case of <code>plot.fitMk</code> , an object of class "fitMk".
<code>model</code>	model. See <code>make.simmap</code> or <code>ace</code> for details.
<code>fixedQ</code>	fixed value of transition matrix Q, if one is desired.
<code>...</code>	optional arguments, including <code>pi</code> , the prior distribution at the root node (defaults to <code>pi="equal"</code>). For plot method optional arguments include (but may not be limited to): <code>signif</code> , the number of digits for the rates to be plotted; <code>main</code> , a character vector of length two with the headings for each subplot; <code>cex.main</code> , <code>cex.traits</code> , and <code>cex.rates</code> , font sizes for the various text elements of the plot; and <code>show.zeros</code> , a logical argument specifying whether or not to plot arrows with the ML estimated transition rate is not different from zero (with tolerance specified by the optional argument <code>tol</code>).

Value

An object of class "fitMk". In the case of `plot.fitMk`, a plotted Mk model.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ace](#), [make.simap](#)

fitPagel

Function to test for correlated evolution of binary traits

Description

This function fits Pagel's (1994) model for the correlated evolution of two binary characters. `plot.fitPagel` plots the fitted models using arrows.

Usage

```
fitPagel(tree, x, y, method="fitMk", model="ARD", dep.var="xy", ...)
## S3 method for class 'fitPagel'
plot(x, ...)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>x</code>	a vector of phenotypic values for a binary trait for the species in tree. For S3 plot method, an object of class "fitPagel".
<code>y</code>	a second binary character for the species in tree.
<code>method</code>	function to use for optimization (defaults to <code>method="fitMk"</code>). Other options are "ace" to use the ace function in <code>ape</code> for optimization, or to "fitDiscrete" (if the <code>geiger</code> package is installed) to use <code>geiger</code> 's <code>fitDiscrete</code> for optimization.
<code>model</code>	model of evolution for the individual characters. Can be <code>model="ER"</code> , "SYM" (equivalent to "ER" in this case), and "ARD".
<code>dep.var</code>	dependent variable. If <code>dep.var="xy"</code> then the rate of substitution in x depends on y & vice versa. If <code>dep.var="x"</code> then the substitution rate in x depends on y, but not the converse. Finally, if <code>dep.var="y"</code> then the rate of substitution in y depends on x, but not the converse.
<code>...</code>	optional arguments to be passed to fitMk , ace , or <code>fitDiscrete</code> . For plot method optional arguments include (but may not be limited to): <code>signif</code> , the number of digits for the rates to be plotted; <code>main</code> , a character vector of length two with the headings for each subplot; <code>cex.main</code> , <code>cex.sub</code> , <code>cex.traits</code> , and <code>cex.rates</code> , font sizes for the various text elements of the plot; and <code>lwd.by.rate</code> , a logical argument specifying whether or not to scale arrow line widths in proportion to the estimated rates.

Value

An object of class "fitPagel" which contains the optimized matrices under an independence & a dependence model, log-likelihoods, a likelihood ratio, and a P-value for the independence model based on a chi-squared test.

plot.fitPagel creates a plot showing the different fitted models with arrows.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Pagel, M. (1994) Detecting correlated evolution on phylogenies: A general method for the comparative analysis fo discrete characters. *Proceedings of the Royal Society B*, **255**, 37-45.

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

See Also

[ace](#), [fitMk](#), [make.simmap](#)

 gammatest

Gamma test of Pybus & Harvey (2000)

Description

Conducts γ -test of Pybus & Harvey (2000).

Usage

```
gammatest(x)
```

Arguments

x list from function call of `ltt` in which `ltt(..., gamma=F)`.

Details

Do not use for object returned by `ltt(..., gamma=T)`.

Value

A list containing:

gamma optionally, a value for the γ -statistic.

p two-tailed P-value for the γ -test.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Pybus, O. G., and P. H. Harvey (2000) Testing macro-evolutionary models using incomplete molecular phylogenies. *Proc. R. Soc. Lond. B*, **267**, 2267-2272.

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

See Also

[ltt](#)

Examples

```
tree<-pbtree(n=200)
z<-ltt(tree,gamma=FALSE)
g<-gammatest(z)
```

genSeq

Simulate a DNA alignment on the tree under a model

Description

Simulates DNA sequence on tree under the specified model. Uses [sim.history](#) internally.

Usage

```
genSeq(tree, l=1000, Q=NULL, rate=1, format="DNABin", ...)
```

Arguments

tree	object of class "phylo".
l	length of desired sequences.
Q	transition matrix for the simulation. Row and column names c("a", "c", "g", "t") (although not necessarily in that order, should be provided. If NULL, a single rate is assumed.
rate	multiplier for Q, or a vector for Gamma rate heterogeneity.
format	format of the output object. Can be "DNABin", "phyDat", or "matrix".
...	optional arguments.

Value

An object of class "DNABin" or "phyDat", or a matrix of nucleotides.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Examples

```
## simulate gamma rate heterogeneity
tree<-pbtree(n=26,tip.label=LETTERS)
gg<-rgamma(n=100,shape=0.25,rate=0.25)
X<-genSeq(tree,l=100,rate=gg)
```

getCladesofSize *Get all subtrees larger than or equal to a specified size*

Description

This function gets all subtrees that cannot be further subdivided into two reciprocally monophyletic subtrees of size \geq clade.size.

Usage

```
getCladesofSize(tree, clade.size=2)
```

Arguments

tree is an object of class "phylo".
clade.size subtree size.

Value

An object of class "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[extract.clade](#), [getDescendants](#)

getDescendants	<i>Get descendant node numbers</i>
----------------	------------------------------------

Description

This function returns the set of node & tip numbers descended from node.

Usage

```
getDescendants(tree, node, curr=NULL)
```

Arguments

tree	a phylogenetic tree as an object of class "phylo".
node	an integer specifying a node number in the tree.
curr	the set of previously stored node numbers - used in recursive function calls.

Value

The set of node and tip numbers for the nodes and tips descended from node in a vector.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[paintSubTree](#)

getExtant	<i>Returns a list of the extant or extinct lineages in a tree containing non-contemporaneous tips</i>
-----------	---

Description

The function getExtant takes a tree as input and returns a vector containing the names of all the tips that have a height above the root that is equal (to a degree of numerical precision determined by tol) to the height of the highest tip. getExtinct returns the complement.

Usage

```
getExtant(tree, tol=1e-8)  
getExtinct(tree, tol=1e-8)
```

Arguments

tree	a phylogeny stored as an object of class "phylo" with some tips that are non-contemporaneous (i.e., end before the present).
tol	a tolerance value to account for numerical imprecision.

Value

A vector with the tip names of extant or extinct species in the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[nodeHeights](#)

getSisters

Get the sister node number, label, or set of nodes for a node or tip

Description

This function takes a tree and node or tip number of label and returns the number or label of the sister or sisters to that node or tip.

Usage

```
getSisters(tree, node, mode=c("number","label"))
```

Arguments

tree	object of class "phylo".
node	a node number, tip number, node label, or tip label.
mode	an optional string indicating whether to return the node or tip number(s) or the node or tip label(s), if available.

Value

If mode="number" this function returns an integer or vector containing the node number of numbers of the sister node or tip. If mode="label" that this function returns a list containing up to two vectors: one for the node numbers of labels of sister nodes (if available); and the other containing the tip labels of the sister tips.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

getStates

Get the states at nodes or tips from a mapped tree

Description

This function gets the states from the nodes or tips of a mapped tree (e.g., [make.simmap](#)).

Usage

```
getStates(tree, type=c("nodes", "tips"))
```

Arguments

tree is a modified object of class "phylo" or "multiPhylo".
type mode indicating whether to get states at the nodes (type="nodes") or the tips (type="tips") of the tree.

Value

A named vector (for "phylo") or matrix (for "multiPhylo").

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[describe.simmap](#), [make.simmap](#), [read.simmap](#), [sim.history](#)

ladderize.simap	<i>Ladderize a tree with a mapped discrete character</i>
-----------------	--

Description

This function "ladderizes" an object of class "phylo" with a mapped discrete character. For more information, please see [ladderize](#).

Usage

```
ladderize.simap(tree, right=TRUE)
```

Arguments

tree	an object of class "phylo" with a mapped discrete character.
right	a logical specifying how the tree should be ladderized.

Value

An object of class "phylo" with a mapped discrete character.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simap](#), [ladderize](#)

lambda.transform	<i>Lambda transformation of matrix</i>
------------------	--

Description

Function multiplies the off-diagonals of a square matrix by lambda. Used internally in [phyl.pca](#) and other functions.

Usage

```
lambda.transform(lambda, C)
```

Arguments

lambda scalar, usually (but not necessarily) on the interval 0,1.
C matrix probably returned by [vcv.phylo](#).

Details

Do not use unless you know what you're doing.

Value

A matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

likMlambda

Likelihood for joint lambda

Description

Computes the likelihood.

Usage

```
likMlambda(lambda, X, C)
```

Arguments

lambda scalar, usually on the interval 0,1.
X data, in a matrix.
C matrix probably returned by [vcv.phylo](#).

Details

Do not use unless you know what you're doing.

Value

A scalar.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

locate.fossil

Locate a fossil lineage in a tree using continuous characters

Description

This function uses ML to place a fossil lineage into a tree using continuous traits.

Usage

```
locate.fossil(tree, X, ...)
```

Arguments

tree	an object of class "phylo".
X	a matrix with continuous character data.
...	optional arguments including time.constraint which can be a scalar (positive height above the root of the fossil or negative time before present) or a vector (age range of fossil, either positive or negative); edge.constraint, which is equivalent to constraint in locate.yeti ; plot, rotate, and quiet, which have the same interpretation (and defaults) as the equivalent arguments in locate.yeti .

Value

Optimized tree as an object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (1981) Maximum likelihood estimation of evolutionary trees from continuous characters. *American Journal of Human Genetics*, **25**, 471-492.

Felsenstein, J. (2002) Quantitative characters, phylogenies, and morphometrics. In: MacLeod, N. and P. Forey (Eds.) *Morphology, Shape and Phylogeny* (pp. 27-44). Taylor and Francis, London.

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

Revell, L. J., D. L. Mahler, R. G. Reynolds, and G. J. Slater. (In press) Placing cryptic, recently extinct, or hypothesized taxa into an ultrametric phylogeny using continuous character data: A case study with the lizard *Anolis roosevelti*. *Evolution*.

locate.yeti

Locate a cryptic, recently extinct, or missing taxon on a tree

Description

This function uses ML (or REML) to place a recently extinct, cryptic, or missing taxon on an ultrametric (i.e., time-calibrated) phylogeny.

Usage

```
locate.yeti(tree, X, ...)
```

Arguments

tree	an object of class "phylo".
X	a matrix with continuous character data.
...	optional arguments including: method ("ML" or "REML", defaults to "ML"); search ("heuristic" or "exhaustive", defaults to "heuristic"); constraint, a vector containing the daughter node numbers from tree\$edge for each edge to try; plot a logical argument specifying whether or not to plot the likelihood profile on edges (defaults to FALSE); rotate a logical indicating whether or not to rotate the data based on the input tree; and quiet, which is logical and has an obvious interpretation.

Value

Optimized tree as an object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (1981) Maximum likelihood estimation of evolutionary trees from continuous characters. *American Journal of Human Genetics*, 25, 471-492.

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

Revell, L. J., D. L. Mahler, R. G. Reynolds, and G. J. Slater. (In press) Placing cryptic, recently extinct, or hypothesized taxa into an ultrametric phylogeny using continuous character data: A case study with the lizard *Anolis roosevelti*. *Evolution*.

ls.tree	<i>Least squares branch lengths for a given tree</i>
---------	--

Description

Computes the least squares branch lengths conditioned on a topology and distance matrix. Internal function for [optim.phylo.ls](#).

Usage

```
ls.tree(tree, D)
```

Arguments

tree	phylogeny.
D	distance matrix.

Details

Do not use unless you know what you're doing.

Value

A tree with branch lengths.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

ltt	<i>Creates lineage-through-time plot (including extinct lineages)</i>
-----	---

Description

This function computes LTT plot with extant and extinct lineages, and optionally conducts γ -test of Pybus & Harvey (2000). The object returned by `ltt` can be plotted or re-plotted using [plot](#).

Usage

```
ltt(tree, plot=TRUE, drop.extinct=FALSE, log.lineages=TRUE, gamma=TRUE, ...)
```

Arguments

tree	is a phylogenetic tree in "phylo" format, or an object of class "multiPhylo" containing a list of phylogenetic trees.
plot	a logical value indicating whether or not to create LTT plot.
drop.extinct	logical value indicating whether or not to drop extinct tips from the tree.
log.lineages	logical value indicating whether LTT plot should be on log-linear (default) or linear-linear scale.
gamma	logical value indicating whether or not to compute eqngamma from Pybus & Harvey (2000; <i>Proc. Roy. Soc. B</i>).
...	other arguments to be passed to plotting methods. See plot.default .

Details

Although it is calculated here, it's unclear how to interpret the γ -statistic if not all the tips in the tree are contemporaneous.

Value

An object of class "ltt" which includes the following components:

times	a vector of branching times.
ltt	a vector of linages.
gamma	optionally, a value for the gamma-statistic.
p	two-tailed P-value for the gamma-test.

If tree is an object of class "multiPhylo", then an object of class "multiLtt" is returned consisting of a list of object of class "ltt".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Pybus, O. G., and P. H. Harvey (2000) Testing macro-evolutionary models using incomplete molecular phylogenies. *Proc. R. Soc. Lond. B*, **267**, 2267-2272.

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

See Also

[gammatest](#), [ltt95](#)

Examples

```
trees<-pbtree(n=100,scale=100,nsim=10)
obj<-ltt(trees,plot=FALSE)
plot(obj,log="y",log.lineages=FALSE,main="lineage through time plots")
tree<-pbtree(b=1,d=0.25,t=4)
obj<-ltt(tree,gamma=FALSE)
obj
```

ltt95

*Creates a (1- α)-percent CI for a set of LTTs***Description**

This function computes LTT plots for a set of trees & plots a (1- α)-percent CI by various methods.

Usage

```
ltt95(trees, alpha=0.05, log=FALSE, method=c("lineages","times"),
mode=c("median","mean"), ...)
## S3 method for class 'ltt95'
plot(x, ...)
```

Arguments

trees	is an object of class "multiPhylo" containing a list of phylogenetic trees.
alpha	confidence level.
log	logical value indicating whether or not to plot on the log-scale.
method	plot the CI on the number of lineages given time ("lineages"); or on times given a number of lineages ("times").
mode	plot the median or mean LTT.
x	object of class "ltt95" for plotting method.
...	optional arguments to be used by ltt95 or the plotting method. So far, res gives the number of time-steps (defaults to res=100. xaxis("standard", "negative", or "flipped") determines the scale (time from the root, time back from the present, or time from the present) of the x-axis of the plot.

Details

This function creates a plot and invisibly returns an object of class "ltt95".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ltt](#)

make.era.map

Create "era" map on a phylogenetic tree

Description

This function creates a temporal map on the tree based on limits provided by the user.

Usage

```
make.era.map(tree, limits, ...)
```

Arguments

tree	a phylogenetic tree as an object of class "phylo".
limits	a vector containing the temporal limits, in time since the root node of the tree, for the mappings.
...	optional arguments.

Value

A modified phylogenetic tree of class "phylo" with the following additional elements:

maps	a list of named vectors containing the times spent in each state on each branch, in the order in which they occur.
mapped.edge	a matrix containing the total time spent in each state along each edge of the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#), [plotSimmap](#)

Examples

```
tree<-pbtree(n=1000,scale=100)
tree<-make.era.map(tree,c(0,25,50,75))
plotSimmap(tree,pts=FALSE,ftype="off")
```

make.simmap

Simulate stochastic character maps on a phylogenetic tree or trees

Description

This function performs stochastic mapping using several methods.

For $Q = \text{"empirical"}$, it first fits a continuous-time reversible Markov model for the evolution of x and then simulates stochastic character histories using that model and the tip states on the tree. This is the same procedure that is described in Bollback (2006), except that simulation is performed using a fixed value of the transition matrix, Q , instead of by sampling Q from its posterior distribution.

For $Q = \text{"mcmc"}$, it first samples Q $nsim$ times from the posterior probability distribution of Q using MCMC, then it simulates $nsim$ stochastic maps conditioned on each sampled value of Q .

For Q set to a matrix, it samples stochastic mappings conditioned on the fixed input matrix.

Usage

```
make.simmap(tree, x, model="SYM", nsim=1, ...)
```

Arguments

tree	a phylogenetic tree as an object of class "phylo", or a list of trees as an object of class "multiPhylo".
x	a vector containing the tip states for a discretely valued character, or a matrix containing the prior probabilities of tip states in rows.
model	a character string containing the model - options as in ace .
nsim	number of simulations. If tree is an object of class "multiPhylo", then nsim simulations will be conducted per tree.
...	optional arguments. So far, pi gives the prior distribution on the root node of the tree - options are "equal", "estimated", or a vector with the frequencies. If pi="estimated" then the stationary distribution is estimated by numerically solving $\pi * Q = 0$ for pi, and this is used as a prior on the root. Defaults to pi="equal" which results in the root node being sampled from the conditional scaled likelihood distribution at the root. message tells whether or not to print a message containing the rate matrix, Q and state frequencies. Defaults to message=TRUE. For optional argument $Q = \text{"mcmc"}$ the mean value of Q from the posterior sample is printed. tol gives the tolerance for zero elements in Q . (Elements less than tol will be reset to tol). Q can be a string ("empirical" or "mcmc"), or a fixed value of the transition matrix, Q . If "empirical" than a single value of Q , the most likely value, is used for all simulations. If "mcmc",

then `nsim` values of `Q` are first obtained from the posterior distribution for `Q` using Bayesian MCMC, then a simulated stochastic character map is generated for each value of `Q`. `vQ` a single numeric value or a vector containing the (normal) sampling variances for the MCMC. The order of `vQ` is assumed to be in the order of the `index.matrix` in `ace` for the chosen model. `prior` a list containing `alpha` and `beta` parameters for the gamma prior distribution on the transition rates in `Q`. Note that `alpha` and `beta` can be single values or vectors, if different priors are desired for each value in `Q`. As for `vQ`, the order of `prior` is assumed to be the order of `index.matrix` in `ace`. `prior` can also be given the optional logical value `use.empirical` which tells the function whether or not to give the prior distribution the empirical mean for `Q`. If `TRUE` then only `prior$beta` is used and `prior$alpha` is set equal to `prior$beta` times the empirical mean of `Q`. `burnin` and `samplefreq` are burn-in and sample frequency for the MCMC, respectively.

Details

Uses code modified from `ace` (by Paradis et al.) to perform Felsenstein's pruning algorithm & compute the likelihood.

As of phytools >= 0.2-33 `x` can be a vector of states or a matrix containing the prior probabilities of tip states in rows. In this case the column names of `x` should contain the states, and the row names should contain the tip names.

Note that there was a small (but potentially significant) bug in how node states were simulated by `make.simmap` in versions of phytools <= 0.2-26. Between phytools 0.2-26 and 0.2-36 there was also a bug for asymmetric models of character change (e.g., `model="ARD"`). Finally, between phytools 0.2-33 and phytools 0.2-47 there was an error in use of the conditional likelihoods for the root node, which caused the root node of the tree to be sampled incorrectly. All of these issues should be fixed in the present version.

`Q="mcmc"` and `Q` set to a fixed value were introduced to phytools >= 0.2-53. As of the present version of phytools, this method is still somewhat experimental & should be used with caution.

If `tree` is an object of class `"multiPhylo"` then `nsim` stochastic maps are generated for each input tree.

Value

A modified phylogenetic tree of class `"phylo"` (or a modified `"multiPhylo"` object, for `nsim > 1`) with the following additional elements:

<code>maps</code>	a list of named vectors containing the times spent in each state on each branch, in the order in which they occur.
<code>mapped.edge</code>	a matrix containing the total time spent in each state along each edge of the tree.
<code>Q</code>	the assumed or sampled value of <code>Q</code> .
<code>logL</code>	the log-likelihood of the assumed or sampled <code>Q</code> .

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Bollback, J. P. (2006) Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.
- Huelsenbeck, J. P., R. Neilsen, and J. P. Bollback (2003) Stochastic mapping of morphological characters. *Systematic Biology*, **52**, 131-138.
- Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[brownie.lite](#), [brownieREML](#), [countSimmap](#), [describe.simmap](#), [evol.vcv](#), [plotSimmap](#), [read.simmap](#), [write.simmap](#)

map.overlap	<i>Proportional overlap between two mapped character histories on a tree</i>
-------------	--

Description

This function computes the fraction of a stochastic character mapping that is shared between two differently mapped trees. In `map.overlap` it will compute a single quantity giving the overall similarity of the maps, consequently this measure only makes sense if some or all of the states are shared between the two mapped trees. In `Map.Overlap` is computed in which the rows are states observed in `tree1` and columns give the states for `tree2`.

Usage

```
map.overlap(tree1, tree2, tol=1e-6, ...)
Map.Overlap(tree1, tree2, tol=1e-06, standardize=TRUE, ...)
```

Arguments

<code>tree1</code>	an object of class "simmap".
<code>tree2</code>	an object of class "simmap".
<code>tol</code>	an optional tolerance value.
<code>standardize</code>	for <code>Map.Overlap</code> , a logical value indicating whether or not to standardize overlap by dividing by the summed branch length of the tree.
<code>...</code>	optional arguments, such as <code>check.equal</code> , a logical value indicating whether or not to check if <code>tree1</code> and <code>tree2</code> match in underlying topology and branch lengths (they should). This value is TRUE by default, but can be set to FALSE if <code>tree1</code> and <code>tree2</code> are known to be equal to speed up calculation.

Value

A numerical value on the interval 0-1, for `map.overlap`; or a matrix (`Map.Overlap`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#)

map.to.singleton	<i>Converts a mapped tree to a tree with singleton nodes</i>
------------------	--

Description

The function `map.to.singleton` takes an object of class "phylo" with a mapped discrete character and converts it to a tree with singleton nodes, in which edge has only one state. The states for each edge are stored in `names(tree$edge.length)`. `plotTree.singletons` plots a tree with singleton nodes. Finally, `drop.tip.singleton` drops tips from the tree leaving ancestral nodes for all remaining tips as singletons. `rootedge.to.singleton` converts a tree with a root edge to a tree with a singleton node instead.

Usage

```
map.to.singleton(tree)
plotTree.singletons(tree)
drop.tip.singleton(tree, tip)
rootedge.to.singleton(tree)
```

Arguments

tree	a modified object of class "phylo" with a mapped discrete character or (for <code>plotTree.singletons</code>) a tree with singleton nodes.
tip	a tip label or vector of tip labels.

Value

An object of class "phylo" with singleton nodes. `plotTree.singletons` plots a tree. If `names(tree$edge.length) != NULL` it will use a different color from `palette` for each mapped state.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[collapse.singles](#), [drop.tip](#), [make.simmap](#)

mapped.states	Returns a vector, matrix, or list of the mapped states on a tree or set of trees
---------------	--

Description

Computes and orders a vector, matrix, or list of the unique mapped states on a tree or state of trees of class "simmap" or "multiSimmap".

Usage

```
mapped.states(tree, ...)
```

Arguments

tree	a single tree or a set of trees as an object of class "simmap" or "multiSimmap", respectively.
...	optional arguments.

Value

A vector, matrix, or list.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

markChanges	<i>Add marked changes to a plotted tree with mapped discrete character</i>
-------------	--

Description

This function adds the reconstructed changes to a plotted tree with a stochastically mapped discrete character.

Usage

```
markChanges(tree, colors=NULL, cex=1, lwd=2, plot=TRUE)
```

Arguments

tree	an object of class "simmap".
colors	a named vector of colors used to plot the stochastically mapped character on the tree.
cex	expansion factor for line height.
lwd	line width.
plot	logical value indicating whether the changes should be plotted or not.

Value

This function returns (invisibly) a matrix containing the x & y coordinates of the marked changes.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotSimmap](#)

matchNodes	<i>Matches nodes between two trees</i>
------------	--

Description

This function returns a matrix in which the first column contains all the internal nodes for `tr1` and the second column contains the matching nodes from `tr2`, inasmuch as they can be identified. For `method="descendants"`, pairs of matching nodes are defined by sharing all descendant leaves in common. for `method="distances"`, nodes are considered to be matched if they share the same set of distances (or proportional distances, for optional argument `corr=TRUE`) to all tips. `matchLabels` is functionally equivalent but matches node (tip) numbers based on the labels only.

Usage

```
matchNodes(tr1, tr2, method=c("descendants", "distances"), ...)  
matchLabels(tr1, tr2)
```

Arguments

<code>tr1</code>	first tree.
<code>tr2</code>	second tree.
<code>method</code>	method to use to match nodes between trees. "descendants" uses the tip species descended from each node; "distances" uses the distances from the nodes to the tips. Any unambiguous shortening of "descendants" or "distances" is allowed.
<code>...</code>	optional arguments which may or may not be used depending on method. <code>tol</code> is a tolerance value for the difference from exact matching that is allowed for <code>method="distances"</code> . <code>corr</code> , which is <code>FALSE</code> by default, indicates whether to match nodes under <code>method="distances"</code> using the correlation (<code>corr=TRUE</code>) or the absolute similarity of distances.

Details

Primarily designed to be used internally by [fastAnc](#).

Value

A matrix in which the first column contains the nodes of `tr1` with the second column containing matching nodes in `tr2`, with the criterion for matching defined by `method`.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

mergeMappedStates	<i>Merge two or more mapped states into one state</i>
-------------------	---

Description

This function merges two or mapped states on the tree to get one new state. For instance, one could merge the states "C", "G", and "T" to get the state "not-A".

Usage

```
mergeMappedStates(tree, old.states, new.state)
```

Arguments

tree	a modified object of class "phylo" or "multiPhylo" with a mapped discrete character.
old.states	states to merge.
new.state	name for new state.

Value

A modified object of class "phylo" or "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#)

midpoint.root	<i>Midpoint root a phylogeny</i>
---------------	----------------------------------

Description

This function midpoint roots a rooted or unrooted tree (Farris 1972).

Usage

```
midpoint.root(tree)
```

Arguments

tree an object of class "phylo".

Details

Midpoint rooting involves locating the midpoint of the longest path between any two tips and putting the root in that location. This function performs the same operation as `midpoint` in the `phangorn` package, but uses no `phangorn` code internally.

Value

A phylogenetic tree in "phylo" format.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Farris, J. (1972) Estimating phylogenetic trees from distance matrices. *American Naturalist*, **106**, 645-667.
- Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[reroot](#), [root](#)

minRotate	<i>Rotates all nodes of the tree to minimize the difference in order with a vector</i>
-----------	--

Description

This function rotates all the nodes of the tree to try and minimize the different between the order of the tips and the rank-order of a numeric vector `x` or (in the case of `tipRotate` the actual integer vector, `x`).

Usage

```
minRotate(tree, x, ...)  
tipRotate(tree, x, ...)
```

Arguments

<code>tree</code>	tree.
<code>x</code>	numeric vector.
<code>...</code>	optional arguments to be used by <code>tipRotate</code> . Presently optional arguments can be <code>fn</code> , function to be used to compute the distance between the order of the tip labels in <code>tree</code> and the numeric vector <code>x</code> (presently <code>fn=function(x) x^2</code> by default); <code>methods</code> , the methods of tree traversal (can be "pre", "post", or <code>c("pre", "post")</code> , for pre-, post-, or both pre- and post-order tree traversal); <code>rotate.multi</code> , whether to rotate multifurcations in all possible ways using <code>rotate.multi</code> (defaults to FALSE); and <code>print</code> , a logical argument specifying whether to print the search progress or to behave quietly. Only the option <code>print</code> is available for <code>minRotate</code> .

Details

Primarily designed to be used internally by `phylo.to.map`, in the case of `minRotate`, or `cophylo`, in the case of `tipRotate`.

Value

A object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

`minSplit`*Finding the minimum (median) split in the posterior sample*

Description

This function takes a phylogenetic tree and a list of splits and identifies the split with the smallest summed or summed squared distances to all the other splits. Used to be called `min.split()` but was changed to avoid conflict with the generic `min`.

Usage

```
minSplit(tree, split.list, method="sum", printD=FALSE)
```

Arguments

<code>tree</code>	a phylogeny stored as an object of class "phylo".
<code>split.list</code>	either a matrix with two named columns, "node" and "bp"; a <code>\$mcmc</code> matrix from <code>evol.rate.mcmc()</code> ; or the entire raw output from <code>evol.rate.mcmc()</code> .
<code>method</code>	an optional string indicating the criterion to minimize: options are "sum" and "sumsq".
<code>printD</code>	logical specifying whether to print distances to screen (FALSE by default).

Value

A list with the following components:

<code>node</code>	node for the minimum split.
<code>bp</code>	location on the branch leading to node of the minimum split.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Revell, L. J., D. L. Mahler, P. Peres-Neto, and B. D. Redelings (2012) A new method for identifying exceptional phenotypic diversification. *Evolution*, **66**, 135-146.

See Also

[evol.rate.mcmc](#), [posterior.evolrate](#)

modified.Grafen	<i>Computes modified Grafen edge lengths</i>
-----------------	--

Description

This function computes modified Grafen edge lengths in which the length of the edge is determined not by the number of descendant leaves, but instead by the maximum number of node lengths in the path from the node to any leaf.

node.paths is used internally by modified.Grafen and computes the set of paths from a node to all tips descended from that node.

Usage

```
modified.Grafen(tree, power=2)
node.paths(tree, node)
```

Arguments

tree	object of class "phylo".
power	power to raise the depths of each node (in nodes).
node	node number for node.paths.

Value

An object of class "phylo" with edge lengths.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

mrp.supertree	<i>Matrix representation parsimony supertree estimation</i>
---------------	---

Description

This function estimates the MRP (matrix representation parsimony) supertree from a set of trees (Baum 1992; Ragan 1992).

Usage

```
mrp.supertree(trees, method=c("pratchet","optim.parsimony"), ...)
compute.mr(trees, type=c("phyDat","matrix"))
```

Arguments

trees	an object of class "multiPhylo" (i.e., a list of trees).
method	an argument specifying whether to optimize the tree using <code>pratchet</code> or <code>optim.parsimony</code> .
type	for <code>compute.mr</code> , the type of object to return.
...	optional arguments - mostly to be passed to <code>pratchet</code> or <code>optim.parsimony</code> .

Details

Function uses `pratchet` or `optim.parsimony` from the "phangorn" package (Schliep 2011) and `prop.part` from the "ape" package (Paradis et al. 2004). See `pratchet` or `optim.parsimony` for optional arguments, which vary slightly depending on the method. All optional arguments of these methods are available to the user with one exception. The argument `tree` in `optim.parsimony` is supplied instead as `start`. In addition to being an object of class "phylo", `start` can also be assigned the string values of "NJ" or "random", in which case either a neighbor-joining or random tree will be used as the starting tree for optimization.

The function `compute.mr` computes the matrix-representation matrix of the input trees. It is used internally by `mrp.supertree`, but can also be used to export an object that can be written to file if desired.

Value

A "phylo" or "multiPhylo" object that is the MP or set of MP MRP trees.

In the case of `compute.mr`, an object of class "phyDat" or a matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Baum, B. R., (1992) Combining trees as a way of combining data sets for phylogenetic inference, and the desirability of combining gene trees. *Taxon*, **41**, 3-10.
- Felsenstein, J. (2004) *Inferring Phylogenies*. Sinauer.
- Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.
- Ragan, M. A. (1992) Phylogenetic inference based on matrix representation of trees. *Molecular Phylogenetics and Evolution*, **1**, 53-58.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Schliep, K. P. (2011) phangorn: phylogenetic analysis in R. *Bioinformatics*, **27**, 592-593.

See Also

[exhaustiveMP](#), [optim.parsimony](#), [pratchet](#)

multi.mantel

Multiple matrix regression (partial Mantel test)

Description

This function conducting a multiple matrix regression (partial Mantel test) and uses Mantel (1967) permutations to test the significance of the model and individual coefficients. It also returns the residual and predicted matrices.

Usage

```
multi.mantel(Y, X, nperm=1000)
```

Arguments

Y	single "dependent" square matrix. Can be either a symmetric matrix of class "matrix" or a distance matrix of class "dist".
X	a single independent matrix or multiple independent matrices in a list. As with Y can be a object of class "matrix" or class "dist".
nperm	number of Mantel permutations.

Value

A list with the following components:

r.squared	multiple R-squared.
coefficients	model coefficients, including intercept.
tstatistic	t-statistics for model coefficients.
fstatistic	F-statistic for the overall model.
probt	vector of probabilities, based on permutations, for tstatistic.
probF	probability of F, based on Mantel permutations.
residuals	matrix of residuals.
predicted	matrix of predicted values.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Mantel, N. (1967) The detection of disease clustering and a generalized regression approach. *Cancer Research*, **27**, 209–220.

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

multiC	Returns a list with phylogenetic VCV matrix for each mapped state
--------	---

Description

This function takes a modified "phylo" object as input and returns a set of so-called phylogenetic covariance matrices as a list: one for each mapped state.

Usage

```
multiC(tree,internal=FALSE)
```

Arguments

tree	a phylogeny with mapped discrete state in a modified object of class "phylo" (e.g., see read.simap).
internal	logical value indicating whether or not internal nodes should be returned.

Value

A list of matrices.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[evolvcv.lite](#), [read.simap](#), [vcvPhylo](#), [vcv.phylo](#)

multiRF	Computes Robinson-Foulds distance between a set of trees
---------	--

Description

Computes the Robinson-Foulds (Robinson & Foulds 1981) distance between a set of trees in an object of class "multiPhylo". If trees contains a large number of phylogenies (say 100 or 1,000) this will be much faster than calling `RF.dist` in the `phangorn` package for all pairwise comparisons because it avoids repeating some internal calculations. Nonetheless for large numbers `multiRF` is slow, and will use lots of memory.

Usage

```
multiRF(trees)
```

Arguments

`trees` object of class "multiPhylo" consisting of two or more fully bifurcating, unrooted trees. If trees are rooted, they will be unrooted.

Details

Computes the Robinson-Foulds distance between all phylogenies in an object of class "multiPhylo". Uses `prop.part` internally for most of the heavy lifting.

Value

A distance matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Robinson, D. R., Foulds, L. R. (1981) Comparison of phylogenetic trees. *Mathematical Biosciences*, **53**, 131-147.

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

nodeHeights

Compute the heights above the root of each node

Description

`nodeHeights` computes the height above the root for all nodes in the tree. `nodeheight` computes the height above the root for a single node.

Usage

```
nodeHeights(tree, ...)
nodeheight(tree, node, ...)
```

Arguments

`tree` a phylogeny as an object of class "phylo".

`node` for `nodeheight`, the node for which we want to compute a height above the root (or including the root edge, for `root.edge=TRUE`).

`...` optional arguments - presently only `root.edge`, a logical value indicating whether or not to include the root edge length in the calculation of node heights.

Details

The function `nodeHeights` also gives a handy way to get the total length of the tree from the root to the highest tip which will be given by `max(nodeHeights(tree))`. Generally speaking, `nodeHeights` will be faster if the heights of all or a large proportion of nodes is needed, whereas `nodeheight` will be faster if the height of one or a small number of nodes are needed.

Value

Either a matrix of the same dimensions as `tree$edge` containing the height above the root of each node in edge (for `nodeHeights`); or a single positive number (for `nodeheight`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[vcvPhylo](#)

Examples

```
tree<-rtree(10)
X<-nodeHeights(tree)
```

`nodelabels.cophylo` *Add labels to a plotted "cophylo" object*

Description

This function adds node, edge, or tip labels to the plotted trees of a "cophylo" object.

Usage

```
nodelabels.cophylo(..., which=c("left","right"))
edgelabels.cophylo(..., which=c("left","right"))
tiplabels.cophylo(..., which=c("left","right"))
```

Arguments

... arguments to be passed to `nodelabels`, `edgelabels`, or `tiplabels`.
which argument indicated which of the two plotted trees (the "left" or "right" tree) to be used.

Details

Note that the order of tips, edges, and nodes may be different in the object of class "cophylo" than they are in the original input trees, particularly if `cophylo(..., rotate=TRUE)` was used.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.

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

See Also

[cophylo](#), [edgelabels](#), [nodelabels](#), [tiplabels](#)

optim.phylo.ls

Phylogeny inference using the least squares method

Description

This function performs phylogeny inference using least-squares.

Usage

```
optim.phylo.ls(D, stree=NULL, set.neg.to.zero=TRUE, fixed=FALSE,  
tol=1e-10, collapse=TRUE)
```

Arguments

D	a distance matrix.
stree	an optional starting tree for the optimization.
set.neg.to.zero	a logical value indicating whether to set negative branch lengths to zero (default TRUE).
fixed	a logical value indicating whether to estimate the topology - if TRUE only the branch lengths will be computed.
tol	a tolerance value used to assess whether the optimization has converged.
collapse	a logical indicating whether to collapse branches with zero length.

Details

Function uses `nni` from the "phangorn" package (Schliep 2011) to conduct NNIs for topology estimation. Since topology optimization is performed using NNIs, converge to the true least-squares topology is not guaranteed. It is consequently probably wise to start with a very good tree - such as a NJ tree.

Value

An object of class "phylo" that (may be) the least-squares tree with branch lengths; also returns the sum of squares in `attr("Q-score")`.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Cavalli-Sforza, L. L., and A. W. F. Edwards. (1967) Phylogenetic analysis: Models and estimation procedures. *American Journal of Human Genetics*, **19**, 233-257.

Felsenstein, J. (2004) *Inferring Phylogenies*. Sinauer.

Paradis, E., J. Claude, and K. Strimmer. (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.

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

Schliep, K. P. (2011) phangorn: phylogenetic analysis in R. *Bioinformatics*, **27**, 592-593.

See Also

[exhaustiveMP](#), [nni](#)

orderMappedEdge

Order the columns of mapped.edge to match across trees

Description

This function takes a modified object of class "multiPhylo" with a mapped discrete character (e.g., see [read.simmmap](#) and sorts the columns of each `tree$mapped.edge` to have the same state ordering. This is handy if we want to, for instance, run `brownie.lite` on a set of mapped trees, and then average the fitted parameter values across trees. The function also works for a single tree.

Usage

```
orderMappedEdge(trees, ordering=NULL)
```

Arguments

trees	object of class "phylo" or "multiPhylo".
ordering	ordering for the columns of \$mapped.edge. If NULL, then an alphabetical order is assumed. Options are "alphabetical", "numerical", or any specific ordering of the mapped traits (e.g., c("A", "B", "C")).

Value

A modified object of class "phylo" or "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

paintSubTree	<i>Paint sub-trees with a discrete character</i>
--------------	--

Description

This function maps or "paints" an arbitrary, i.e., user-specified, discrete character history on the tree. paintSubTree paints the clade downstream of node with a particular state; whereas paintBranches paints only a specified branch.

Usage

```
paintSubTree(tree, node, state, anc.state="1", stem=FALSE)
paintBranches(tree, edge, state, anc.state="1")
```

Arguments

tree	a phylogenetic tree as an object of class "phylo" or a modified object with mapped character traits.
node	an integer specifying the node number tipward of which the function should paint the derived state.
edge	an integer or vector of integers specifying the node or tip numbers of the edges that should be painted in paintBranches.
state	a string (or numeric value) specifying the state to paint on the tree tipward of node.
anc.state	the ancestral state to use; will only be applied if there are presently no character values mapped on the tree.

stem logical or numeric value indicating whether to use the derived state on the stem leading to node (or not, if stem=FALSE), or, alternatively, what fraction of the stem should be assigned to the derived clade. Note that for tip clades stem=FALSE is not allowed.

Value

A modified phylogenetic tree of class "phylo" with the following additional elements:

maps a list of named vectors containing the times spent in each state on each branch, in the order in which they occur.

mapped.edge a matrix containing the total time spent in each state along each edge of the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#), [plotSimmap](#), [sim.history](#)

paste.tree *Paste two trees together*

Description

Primarily internal function for [posterior.evolrate](#); can be used to graft a clade into a receptor tree, at the "sticky tip" labeled with "NA".

Usage

```
paste.tree(tr1, tr2)
```

Arguments

tr1 receptor tree.

tr2 donor clade.

Details

The donor clade needs to have a root edge, even if it is zero length.

Value

A tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Examples

```
tr1<-rtree(10)
tr2<-rtree(10)
tr1$tip.label[1]<-"NA"
tr2$root.edge<-0
tr3<-paste.tree(tr1, tr2)
```

pbtree

Simulate pure-birth or birth-death stochastic tree or trees

Description

This function simulates stochastic birth-death trees. Simulation can be performed conditioning on n , on t , or on both simultaneously. If the both, then (for optional argument `method="rejection"`) rejection sampling is performed whereby trees are simulated given b and t until a tree containing n taxa is found. The giving-up point can be set using the optional argument `max.count`. Simulations can also be performed in continuous time (the default) or discrete time; the difference being that wait times in the continuous-time simulation come from the exponential distribution; whereas waiting times in discrete-time simulations come from the geometric distribution. In addition, discrete-time simulations allow for the possibility that multiple speciation events can occur at (exactly) the same time, so long as they are on separate branches. Finally, sometimes for stopping criterion n in discrete-time there will be a number of tips different from n . This indicates that the last event contained more than one speciation event, and a warning is printed.

`method="direct"` is presently experimental. It does not really perform direct sampling; however waiting times & birth or death events are sampled first - with only wait-times consistent with n and t being retained. This rejection sampling occurs one layer earlier than for `method="rejection"`. This results in a significant (several-fold) speed-up of the code and enables sampling conditioned on n and t simultaneously for much higher b and d . At the present time, `extant.only=TRUE` does not work for this mode, nor does `type="discrete"`.

Note that if `ape=FALSE`, then the function will run faster, and the tree is theoretically compatible with the `ape` "phylo" standard; however some downstream errors with functions such as `bind.tree` have been observed.

Usage

```
pbtree(b=1, d=0, n=NULL, t=NULL, scale=NULL, nsim=1,
type=c("continuous", "discrete"), ...)
```

Arguments

b	birth rate or speciation rate for type="continuous"; the probability of speciating per time-step for type="discrete".
d	death rate or extinction rate for type="continuous"; the probability of going extinct per time-step for type="discrete".
n	desired number of species (i.e., taxa-stop criterion).
t	total time for simulation (i.e., time-stop criterion).
scale	if set, rescales tree to have total length scale.
nsim	number of simulated trees to return.
type	string to indicate whether to simulate trees in continuous or discrete time. If the former, then wait times between speciation events are drawn from an exponential distribution; whereas if the latter then wait times comes from a geometric distribution.
...	optional arguments including ape, a logical value indicating whether to return nodes in a 'ape' compatible ordering (default is TRUE); extant.only a logical value indicating whether or not to return only extant species (defaults to FALSE); max.count a numeric value indicating the maximum number of iterations to run is sampling conditioned on both n and t (defaults to 1e5); method gives the method used for simultaneously conditioning on n and t - options are "rejection" and "direct"; tip.label, a vector of tip labels (only works for n!=NULL); and, finally, quiet, a logical value indicating whether or not to suppress certain message (defaults to FALSE).

Value

A tree or list of trees as an object of class "phylo" or "multiPhylo", respectively.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Examples

```
# simulate a pure-birth tree with 400 tips, scaled to a length of 1.0
tree<-pbtree(n=400,scale=1)
# simulate a pure-birth tree conditioning on n & t
tt<-log(50)-log(2)
tree<-pbtree(n=50,t=tt)
```

 pgls.Ives

Phylogenetic regression with intraspecific sampling error

Description

This function fits the phylogenetic regression model with within-species sampling error following Ives et al. (2007).

Usage

```
pgls.Ives(tree, X, y, Vx=NULL, Vy=NULL, Cxy=NULL, lower=c(1e-8,1e-8))
```

Arguments

tree	a phylogeny as an object of class "phylo".
X	a named vector containing a <i>single</i> independent variable (multiple independent variables to be added in future). X can contain the species means, or a single long vector containing the sample of values for each species. In the latter case the names(X) will be repeating - all samples from the same species should have the same name.
y	vector the dependent variable. Can be species means or individual values, as for X.
Vx	sampling variances for X. If NULL, then the within-species variance is computed from the data assuming that individual samples, not species means, have been provided in X.
Vy	sampling variances for y. If NULL, then the within-species variance is computed from the data assuming that individual samples, not species means, have been provided in y.
Cxy	sampling covariances between X and y. This will also be computed from the data if Cxy==NULL. Note than in this case - but not for the calculation of Vx and Vy, the same number of observations and the same ordering must be provided for X and y. If this is not the case, then it is assumed that different individuals have been sampled for X and y and thus Cxy is assumed to be zero for all species.
lower	vector specifying the lower bounds for estimation for sig2x and sig2y, respectively. (Must be >0.)

Details

Presently only the bivariate regression model is implemented. Uses `optim(..., method="L-BFGS-B")` for optimization. Note that some problems have been reported with the optimization algorithm for this model, which is simple and thus may fail to find the ML solution.

Value

A list with the following components:

beta	a vector or matrix of regression coefficients.
sig2x	fitted BM rate for X.
sig2y	fitted BM rate for y.
a	fitted ancestral states for X and y.
logL	log-likelihood.
convergence	a value for convergence. convergence=0 is good; see optim for more details.
message	a message for convergence.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Ives, A. R., P. E. Midford, and T. Garland Jr. (2007) Within-species measurement error in phylogenetic comparative methods. *Systematic Biology*, **56**, 252-270.

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

See Also

[brownie.lite](#), [phylosig](#), [phyl.resid](#)

phenogram	<i>Plot phenogram (traitgram)</i>
-----------	-----------------------------------

Description

Function plots a traitgram (Evans et al. 2009), that is, a projection of the phylogenetic tree in a space defined by phenotype (on the y axis) and time (on the x). If a discrete character is mapped on the tree this will also be plotted.

Usage

```
phenogram(tree, x, fsize=1.0, ftype="reg", colors=NULL, axes=list(),  
add=FALSE, ...)
```

Arguments

tree	an object of class "phylo", with or without a mapped discrete character.
x	a vector containing the states at the tips <i>or</i> the states at all the tips and the internal nodes of the tree.
fsize	relative font size for tip labels.
ftype	font type - options are "reg", "i" (italics), "b" (bold), or "bi" (bold-italics).
colors	colors for plotting the mapped character (if available) in tree. If no character is mapped on the tree, then a single color for all the branches of the tree can be provided.
axes	list of axis dimensions. Items are time and trait.
add	optional logical value indicating whether to add to an open plot. If TRUE, then new axes will not be plotted.
...	optional arguments including xlim, ylim, log, main, sub, xlab, ylab, asp, type, lty, lwd, offset, and digits are as in <code>plot.default</code> or <code>par</code> . Note that axes overrides xlim and ylim. spread.labels is a logical value indicating whether or not to minimize tip label overlap (default is TRUE); spread.cost is a numeric vector indicating the relative penalty to be used for label overlap and deviance, respectively (if spread.labels=TRUE); spread.range is the range over which to (potentially) spread the labels - note that if labels do not overlap, not all of that range will be used; finally, link is a numeric value by which to offset the tip labels, linking them to the tips with a dashed line (default is 0, if spread.labels=FALSE, or 10-percent of the total tree length otherwise). The optional argument offsetFudge "fudges" the computation of label offset in scaling xlim. It is 1.37, which is the correct fudge in the Windows R GUI, but this may need to be changed in other systems. hold indicates whether (or not) the output to the graphical device should be held using <code>dev.hold</code> before plotting (defaults to hold=TRUE). quiet suppresses some system messages if set to quiet=TRUE.

Details

For `spread.labels=TRUE` numerical optimization is performed to optimize the distribution of the labels vertically, where the solution depends on the vector `spread.cost` containing the cost of overlap (first) and the cost of deviation from the vertical position of the tip. Note that because this is done via numerical optimization, plotting may hang briefly while the best solution is found (especially for large trees).

Value

Plots a traitgram, optionally with a mapped discrete character, and (invisibly) returns a matrix containing the coordinates of the plotted tip labels.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Evans, M. E. K., Smith, S. A., Flynn, R. S., Donoghue, M. J. (2009) Climate, niche evolution, and diversification of the "bird-cage" evening primroses (*Oenothera*, sections *Anogra* and *Kleinia*). *American Naturalist*, **173**, 225-240.

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

Examples

```
## Not run:
tree<-pbtree(n=20,scale=2)
x<-fastBM(tree)
phenogram(tree,x)
# or, simulate a discrete character history
tree<-sim.history(tree,Q=matrix(c(-1,1,1,-1),2,2),anc="1")
# simulate in which the rate depends on the state
x<-sim.rates(tree,c(1,10))
phenogram(tree,x)
# now use spread.labels
tree<-pbtree(n=40)
x<-fastBM(tree)
phenogram(tree,x,spread.labels=TRUE,spread.cost=c(1,0))

## End(Not run)
```

phyl.cca

Phylogenetic canonical correlation analysis

Description

This function performs phylogenetic canonical correlation analysis (e.g., Revell & Harrison 2008; *Bioinformatics*).

Usage

```
phyl.cca(tree, X, Y, lambda=1.0, fixed=TRUE)
```

Arguments

tree	a phylogenetic tree in "phylo" format.
X	a data matrix with traits in columns.
Y	data matrix with traits in columns, to be correlated with X.
lambda	optionally, a (fixed) value for lambda.
fixed	optionally, a logical value indicating whether or not to estimate lambda using likelihood.

Details

(Optional) joint optimization of λ is performed using `optimize` on the interval (0,1).

Value

A list with the following components:

<code>cor</code>	canonical correlations.
<code>xcoef</code>	coefficients for the canonical variables for X.
<code>ycoef</code>	coefficients for the canonical variables for Y.
<code>xscores</code>	matrix with the canonical scores for X.
<code>yscores</code>	matrix with the canonical scores for Y.
<code>chisq</code>	vector of χ^2 values.
<code>p</code>	P-values for the hypothesis test that the <i>i</i> th and all subsequent correlations are zero.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J., Harrison, A. S. (2008) PCCA: A program for phylogenetic canonical correlation analysis. *Bioinformatics*, **24**, 1018-1020.

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

See Also

[phyl.pca](#)

phyl.pairedttest *Phylogenetic paired t-test*

Description

This function conducts a phylogenetic paired t-test, roughly following Lindenfors et al. (2010; *J. Evol. Biol.*). This is not a phylogenetic ANOVA, in which we want to compare the means of different sets of species on the tree. Instead, we are interested in the difference between two characters, or two measures of a character within a species, and we want to know if this difference is significantly different from zero controlling for the phylogenetic non-independence of species.

Usage

```
phyl.pairedttest(tree, x1, x2=NULL, se1=NULL, se2=NULL, lambda=1.0, h0=0.0,  
fixed=FALSE)
```

Arguments

tree	a phylogeny as an object of class "phylo".
x1	data vector for first trait, or matrix with two traits in columns.
x2	data vector for second trait (or null if x1 is a matrix).
se1	standard errors for x1.
se2	standard errors for x2.
lambda	starting value for Pagel's lambda (or fixed value, if fixed=TRUE).
h0	null hypothesis (to be tested) for the mean difference between x1 and x2.
fixed	logical value specifying whether or not to optimize lambda.

Details

Likelihood optimization is performed using `optim` with `method="L-BFGS-B"` with box constraints on lambda (0,1).

Value

A list with the following components:

dbar	phylogenetic mean difference.
se	standard error of dbar.
sig2	estimated evolutionary variance (of the difference).
lambda	fitted (or fixed) value of lambda.
logL	log-likelihood of the fitted model.
t.dbar	t-value $((\text{dbar}-h_0)/\text{se})$ where se is computed from the Hessian).
P.dbar	P-value.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Lindenfors, P., L. J. Revell, and C. L. Nunn (2010) Sexual dimorphism in primate aerobic capacity: A phylogenetic test. *J. Evol. Biol.*, **23**, 1183-1194.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

 phyl.pca

Phylogenetic principal components analysis

Description

This function performs phylogenetic PCA (e.g., Revell 2009; *Evolution*).

Usage

```
phyl.pca(tree, Y, method="BM", mode="cov", ...)
## S3 method for class 'phyl.pca'
biplot(x, ...)
```

Arguments

tree	phylogeny as an object of class "phylo".
Y	data matrix with traits in columns.
method	method to obtain the correlation structure: can be "BM" or "lambda".
mode	is the mode for the PCA: can be "cov" or "corr".
x	object of class "phyl.pca" for biplot.phyl.pca.
...	for S3 plotting method biplot.phyl.pca, other arguments to be passed to biplot .

Details

If method="lambda" λ is optimized on the interval (0,1) using [optimize](#). S3 methods (print, summary, and biplot) are modified from code provided by Joan Maspons and are based on the same methods for objects of class "prcomp". Function biplot now permits the argument choices to be supplied, which should be a vector of length two indicated the two PC axes to be plotted.

Value

An object of class phyl.pca which is a list with some or all of the following components:

Eval	diagonal matrix of eigenvalues.
Evec	matrix with eigenvectors in columns.
S	matrix with scores.
L	matrix with loadings.
lambda	fitted value of lambda (method="lambda" only).
logL	log-likelihood for lambda model (method="logL" only).

Author(s)

Liam Revell <liam.revell@umb.edu>, Joan Maspons

References

- Revell, L. J. (2009) Size-correction and principal components for interspecific comparative studies. *Evolution*, **63**, 3258-3268.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[phyl.cca](#), [phyl.resid](#)

phyl.resid

Phylogenetic size-correction via GLS regression

Description

This function fits one or multiple phylogenetic regressions (depending on the number of columns in Y) and computes the residuals. Designed for phylogenetic size correction using GLS regression (e.g., Revell 2009; *Evolution*).

Usage

```
phyl.resid(tree, x, Y, method="BM")
```

Arguments

tree	a phylogenetic tree in "phylo" format.
x	vector containing the single independent variable (e.g., size), or matrix with multiple independent variables in columns.
Y	vector or matrix with one or multiple dependent variables in columns.
method	method to obtain the correlation structure: can be "BM" or "lambda".

Details

Optionally fits λ for each regression model. Likelihood optimization of λ is performed for method="lambda" using `optimize` on the interval (0,1). This function is redundant with `residuals(gls(..., correlation=corPagel(...)))` but some users may find this method simpler, and it provides a good way to cross-check your results & make sure that you are using `gls` correctly.

Value

A list with the following components:

beta	a vector or matrix of regression coefficients.
resid	a vector or matrix of residuals for species.
lambda	a vector of lambda values (method="lambda" only).
logL	a vector of log-likelihoods (method="lambda" only).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Revell, L. J. (2009) Size-correction and principal components for interspecific comparative studies. *Evolution*, **63**, 3258-3268.
- Revell, L. J. (2010) Phylogenetic signal and linear regression on species data. *Methods in Ecology and Evolution*, **1**, 319-329.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[phyl.pca](#), [gls](#)

phyl.RMA

Phylogenetic reduced major axis (RMA) regression

Description

This function performs phylogenetic RMA regression.

Usage

```
phyl.RMA(x, y, tree, method="BM", lambda=NULL, fixed=FALSE, h0=1.0)
```

Arguments

x	vector with names.
y	vector with names.
tree	a phylogenetic tree in "phylo" format.
method	method to obtain the correlation structure: can be "BM" or "lambda".
lambda	value of lambda for fixed λ .
fixed	logical value indicating whether or not λ should be optimized using likelihood.
h0	null hypothesis for beta. Defaults to 1.0. Note that a null hypothesis of 0.0 is not allowed.

Details

Optionally jointly estimates lambda if method="lambda". Likelihood optimization of lambda is performed using [optimize](#) on the interval (0,1). Note that some statistician think there is *never* a condition in which a reduced-major-axis regression should be used.

Value

A list with the following components:

RMA.beta	a vector of RMA regression coefficients.
V	a VCV matrix for the traits.
lambda	fitted value of lambda (method="lambda" only).
logL	log-likelihood (method="lambda" only).
test	a vector containing results for hypothesis tests on beta.
resid	a vector of residuals for y given x.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[phyl.cca](#), [phyl.pca](#), [phyl.resid](#)

phyl.vcv

Compute evolutionary VCV matrix for a tree & dataset

Description

Primarily an internal function for [phyl.pca](#); this can be used to compute the phylogenetic trait variance-covariance matrix given a phylogenetic VCV, lambda, and a data matrix. Should not be confused with [vcv.phylo](#) in the "ape" package (although one of the objects returned is the output of [vcv.phylo](#)).

Usage

```
phyl.vcv(X, C, lambda)
```

Arguments

lambda	value for λ transformation.
X	data matrix.
C	matrix containing the height above the root of each pair of species in the tree. Typically this will have been produced by calling vcv.phylo .

Details

Do not use unless you know what you're doing.

Value

A list containing three elements, as follows: C, the matrix `vcv.phylo` transformed by `lambda`; R, the among trait variance-covariance matrix for the data in X; and `alpha`, a vector of ancestral states at the root node of the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

 phylANOVA

Phylogenetic ANOVA and post-hoc tests

Description

This function performs the simulation-based phylogenetic ANOVA of Garland et al. (1993) and (optionally) conducts all posthoc comparisons of means among groups (also obtaining the P-values by phylogenetic simulation).

Usage

```
phylANOVA(tree, x, y, nsim=1000, posthoc=TRUE, p.adj="holm")
```

Arguments

<code>tree</code>	a phylogenetic tree in "phylo" format.
<code>x</code>	a vector containing the groups.
<code>y</code>	a vector containing the response variable (continuously valued).
<code>nsim</code>	an integer specifying the number of simulations (including the observed data).
<code>posthoc</code>	a logical value indicating whether or not to conduct posthoc tests to compare the mean among groups.
<code>p.adj</code>	method to adjust P-values for the posthoc tests to account for multiple testing. Options same as p.adjust .

Details

Uses a little bit of code from `phy.anova` in the "geiger" package as well as [pairwise.t.test](#).

Value

A list containing the following elements:

F	F from observed data.
Pf	P-value for F from simulation.
T	matrix of t-values.
Pt	matrix of multiple test corrected P-values from posthoc t-tests.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Garland, T., Jr., A. W. Dickerman, C. M. Janis, & J. A. Jones. (1993) Phylogenetic analysis of covariance by computer simulation. *Systematic Biology*, **42**, 265-292.
- Harmon, L. J., J. T. Weir, C. D. Brock, R. E. Glor, W. Challenger. (2008) GEIGER: investigating evolutionary radiations. *Bioinformatics*, *24*, 129-131.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[anova](#), [pairwise.t.test](#)

phylo.heatmap	<i>Creates a phylogenetic heat map</i>
---------------	--

Description

Functions creates a multivariate phylogenetic [heatmap](#).

Usage

```
phylo.heatmap(tree, X, fsize=1, colors=NULL, standardize=FALSE, ...)
```

Arguments

tree	an object of class "phylo".
X	a matrix containing data for multiple continuous characters in which rownames correspond to the tip labels of the tree.
fsize	an integer or vector of length 3 containing the font size for the tip labels, the trait labels, and the legend text. (If a single integer is supplied, then the value will be recycled.)
colors	a vector of colors to be passed to image . Can be a function call (e.g., <code>heat.colors(n=200)[200:1]</code>).

`standardize` a logical value indicating whether or not to standardize each column of X to have the same variance & mean prior to analysis.

... optional arguments. So far these include: `legend`, a logical value indicating whether or not to plot a figure legend (defaults to `legend=TRUE`); `labels`, a logical value indicating whether or not to plot trait labels (defaults to `labels=TRUE`); `split`, a numeric vector indicating the fraction of the horizontal dimension to use for the tree & heatmap, respectively (defaults to `split=c(0.5,0.5)`); `xlim`, `ylim`, & `mar`, defined as in [par](#); and `ftype`, `lwd`, and `pts` as defined in [plotSimmap](#).

Value

Function creates a plot.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

phylo.to.map

Plot tree with tips linked to geographic coordinates

Description

Function plots a tree and tips pointing to coordinates on a global map.

Usage

```
phylo.to.map(tree, coords, rotate=TRUE, ...)
## S3 method for class 'phylo.to.map'
plot(x, type=c("phylogram","direct"), ...)
```

Arguments

`tree` an object of class "phylo".

`coords` a matrix containing the latitude (in column 1) and the longitude of all tip species in the tree. The row names should be the same as `tree$tip.label`.

`rotate` a logical value indicating whether or not to rotate nodes of the tree to better match longitudinal positions.

`x` for `plot.phylo.to.map`, an object of class "phylo.to.map".

`type` a string indicating whether to map the tips of the tree onto a geographic map from a square phylogram (`type="phylogram"`) or to project the tree directly onto the map (`type="direct"`).

... optional arguments. For `phylo.to.map`, which creates an object of class "phylo.to.map" and (optionally) plots that object, arguments include: `database` and `regions` (see [map](#)), as well as any arguments that should be passed to `plot.phylo.to.map` internally. For `phylo.to.map`, optional arguments `xlim` and `ylim`, which control the plot area for the map; `fsize` for the font size of plot labels and `ftype` for the font type (following [plotSimmap](#); `split` which controls the proportion of vertical (or horizontal) space for the tree (first) and map, in a vector; `psize` the size of the plotted points on the map - or `cex.points`, a vector contain the size of the tip points and geographic coordinate points, respectively; `from.tip` a logical value indicating whether to plot the linking lines from the tips (if TRUE) or from the end of the tip label, the default; `colors`, a single value or a vector of colors for the points and the linking lines; `pch` a single value or a vector of point types; `lwd` and `lty` for the linking lines; and `pts` a logical value indicating whether or not to plot points at the tips of the tree. `mar` and `asp` are as in [par](#).

Value

`phylo.to.map` creates an object of class "phylo.to.map" and (if `plot=TRUE`) plots a phylogeny projected onto a geographic map.

`plot.phylo.to.map` plots on object of class "phylo.to.map".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

`phylo.toBackbone` *Converts tree to backbone or vice versa*

Description

Converts between "phylo" and "backbonePhylo".

Usage

```
phylo.toBackbone(x, trans, ...)
backbone.toPhylo(x)
```

Arguments

x	an object of class "phylo" (for phylo.toBackbone); or an object of class backbone.toPhylo (for backbone.toPhylo).
trans	data frame containing the attributes necessary to translate a backbone tree to an object of class "backbonePhylo". The data frame should contain the following variables: tip.label: the tip labels in the input tree (not all need be included); clade.label: labels for the unobserved subtrees; N: number of species in each subtree; and depth: desired depth of each subtree. depth for each terminal taxon in x cannot be greater than the terminal edge length for that taxon.
...	optional arguments.

Value

Either an object of class "phylo" or an object of class "backbonePhylo", depending on the method.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plot.backbonePhylo](#)

phyloDesign

Compute design matrix for least squares analyses

Description

Primarily an internal function for [optim.phylo.ls](#), this function creates a design matrix for least squares phylogenetic analysis.

Usage

```
phyloDesign(tree)
```

Arguments

tree phylogenetic tree.

Details

This function returns a matrix containing the edges in the tree (in columns) and pairs of tip node numbers (in rows). Values in the matrix are either 1 if the edge is on the shortest path between the two tips; and 0 otherwise. Probably do not use unless you know what you're doing.

Value

A matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

phylomorphospace *Creates phylomorphospace plot*

Description

This function creates a phylomorphospace plot (a projection of the tree into morphospace) for two characters following Sidlauskas (2008; *Evolution*). It will also plot a discrete character mapped on tree.

Usage

```
phylomorphospace(tree, X, A=NULL, label=c("radial","horizontal","off"),
control=list(), ...)
```

Arguments

- tree a phylogenetic tree in "phylo" format, or a modified "phylo" object with a mapped discrete character.
- X an n x 2 matrix of tip values for two characters in n species.
- A an optional m x 2 matrix (for m nodes) of values for two traits at internal nodes in the tree - if not supplied, these values will be estimated using [fastAnc](#).
- label string indicating whether to plot the tip labels in the same direction as the terminal edge (label="radial"), horizontally label="horizontal", or not at all "off". label=TRUE and label=FALSE are also acceptable, for compatibility with phytools <= 0.3-03.
- control a list containing the following optional control parameters: col.edge: a vector of edge colors; and col.node: a vector of node colors.

... optional arguments for plotting, including `xlim`, `ylim`, `xlab`, `ylab`, `lwd`, `colors`, `fsize`, and `node.by.map`. `colors` is only used when there is a mapped discrete character on the tree, in which case `control$col.edge` is ignored. `fsize` is relative to the default, which is `textxy(..., cx=0.75)`. `node.by.map` is a logical value (defaults to `FALSE` which tells the function whether or not to plot the node colors using the colors of the mapped discrete character. Setting this option to `TRUE` will cause `control$col.node` to be ignored. `node.size` is a vector containing the point size relative to the default (see `par` for plotted internal nodes and tips, respectively. Defaults to `node.size=c(1, 1.3)`. If only one number is provided it will be recycled. `axes` is a logical value indicating whether or not axes should be plotted (see `plot.default`). Finally, `add` indicates whether to add the phylmorphospace to the current plot.

Value

This function creates a phylomorphospace plot

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-90.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Sidlauskas, B. (2008) Continuous and arrested morphological diversification in sister clades of characiform fishes: A phylomorphospace approach. *Evolution*, **62**, 3135-3156.

Examples

```
tree<-pbtree(n=25)
X<-fastBM(tree,nsim=2)
phylomorphospace(tree,X,xlab="trait 1",ylab="trait 2")
```

phylomorphospace3d *Creates tree-dimensional phylomorphospace plot*

Description

This function creates a phylomorphospace plot for three characters using the 3D visualization package, 'rgl'.

Usage

```
phylomorphospace3d(tree, X, A=NULL, label=TRUE, control=list(),
method=c("dynamic","static"), ...)
```


Arguments

tree	a phylogenetic tree in "phylo" format.
X	an n x 3 matrix of tip values for two characters in n species.
A	an optional m x 3 matrix (for m nodes) of values for two traits at internal nodes in the tree - if not supplied, these values will be estimated using anc.ML .
label	logical value indicating whether to print tip labels next to terminal nodes in the plot (presently doesn't do anything, but labels can be dropped using <code>control</code>). <code>spin=TRUE,axes=TRUE,box=TRUE,simple.axes=FALSE,lwd=1,ftype="reg"</code>
control	a list containing the following optional control parameters: <code>spin</code> : a logical value indicating whether to animate the plot when created; <code>axes</code> : a logical indicating whether to plot the axes; <code>box</code> : a logical value indicating whether to plot in box; <code>simple.axes</code> : logical value indicating whether to replace box and axes with simpler axes; <code>lwd</code> : line widths; <code>ftype</code> : font type ("off" turns off labels altogether); <code>col.edge</code> a vector of colors of length <code>nrow(tree\$edge)</code> .
method	a string either "dynamic" for a dynamic (animated) plot created using <code>rgl</code> ; or "static" for a flat 3D plot created using <code>scatterplot3d</code> and base graphics. The latter has the advantage of being very easy to export in standard format.
...	optional arguments to be passed to <code>scatterplot3d</code> . Most options not available. <code>angle</code> is an important option that does work here.

Value

This function creates a three dimensional phylomorphospace plot. The function returns a function from `spin3d` (for `method="dynamic"`); or a series of functions from `scatterplot3d` (for `method="static"`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Sidlauskas, B. (2008) Continuous and arrested morphological diversification in sister clades of characiform fishes: A phylomorphospace approach. *Evolution*, **62**, 3135-3156.

See Also

[fancyTree](#), [phenogram](#), [phylomorphospace](#)

Examples

```
tree<-pbtree(n=26,tip.label=LETTERS)
X<-fastBM(tree,nsim=3)
## Not run:
phylomorphospace3d(tree,X,control=list(spin=FALSE))
```

```
## End(Not run)
phylomorphospace3d(tree,X,method="static")
```

phylosig

Compute phylogenetic signal with two methods

Description

This function computes phylogenetic signal using two different methods. It can also conduct the hypothesis tests for significant phylogenetic signal, and estimate phylogenetic signal incorporating sampling error following Ives et al. (2007).

Usage

```
phylosig(tree, x, method="K", test=FALSE, nsim=1000, se=NULL, start=NULL,
control=list())
```

Arguments

tree	a phylogenetic tree in "phylo" format.
x	vector containing values for a single continuously distributed trait.
method	method to compute signal: can be "K" or "lambda".
test	logical indicating whether or not to conduct a hypothesis test of "K" or "lambda".
nsim	for method="K", number of simulations in randomization test.
se	named vector containing the standard errors for each species.
start	vector of starting values for optimization of (respectively) σ^2 and lambda. Only used in method="lambda" and se!=NULL.
control	list of control parameters for multidimensional optimization, implemented in optim . Only used in method="lambda" and se!=NULL.

Details

λ optimization is performed using [optimize](#) with the range of lambda set between 0 and the theoretical upper limit of lambda (determined by the relative height of the most recent internal node on the tree).

Value

If (method="K"), a list with the following components:

K	value of the K-statistic.
sig2	rate of evolution, σ^2 , for estimation with sampling error.
logL	log-likelihood, for estimation with sampling error.
P	optionally, the P-value from the randomization test.

If (method="lambda"), a list with the following components:

lambda	fitted value of lambda.
sig2	rate of evolution, for estimation with sampling error.
logL	log-likelihood.
logL0	log-likelihood for lambda=0.0.
P	P-value of the likelihood ratio test.
convergence	value for convergence, for estimation with sampling error only. (See optim).
message	message from optim , for estimation with sampling error only.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Blomberg, S. P., T. Garland Jr., A. R. Ives (2003) Testing for phylogenetic signal in comparative data: Behavioral traits are more labile. *Evolution*, **57**, 717-745.
- Ives, A. R., P. E. Midford, T. Garland Jr. (2007) Within-species variation and measurement error in phylogenetic comparative biology. *Systematic Biology*, **56**, 252-270.
- Pagel, M. (1999) Inferring the historical patterns of biological evolution. *Nature*, **401**, 877-884.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

Examples

```
tree<-pbtree(n=100)
x<-fastBM(tree)
phylosig(tree,x,method="lambda",test=TRUE)
```

plot.backbonePhylo *Plots backbone tree with triangles as clades*

Description

Function plots a backbone tree (stored as an object of class "backbonePhylo") with triangles as subtrees.

Usage

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

Arguments

`x` an object of class "backbonePhylo".

`...` optional arguments. Includes `vscale` (to rescale the vertical dimension in plotting), `fixed.height` (logical value to fix the plotted height of subtree triangles), `print.clade.size` (logical), `fixed.n1` (logical value indicating whether or not to use the fixed triangle height for subtrees containing only one taxon, or to plot as a leaf - defaults to FALSE), and `col` (a single value, or a vector with names, giving the clade colors), as well as `xlim`, `ylim`, and `lwd` (as well as perhaps other standard plotting arguments).

Value

Plots a tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[phylo.toBackbone](#)

Examples

```
## first create our backbone tree with
## random subtree diversities
tree<-phytools::lambdaTree(pbtrees(n=10),lambda=0.5)
## create a translation table
## leaving a couple of single-taxon clades for fun
tip.label<-sample(tree$tip.label,8)
clade.label<-LETTERS[1:8]
N<-ceiling(runif(n=8,min=1,max=20))
## set crown node depth to 1/2 the maximum depth
depth<-sapply(tip.label,function(x,y)
0.5*y$edge.length[which(tree$edge[,2]==
which(y$tip.label==x))],y=tree)
trans<-data.frame(tip.label,clade.label,N,depth)
rownames(trans)<-NULL
rm(tip.label,clade.label,N,depth)
## here's what trans looks like
trans
## convert
obj<-phylo.toBackbone(tree,trans)
## plot
plot(obj)
```

plotBranchbyTrait *Plot branch colors by a quantitative trait or value*

Description

Function plots a tree with branches colored by the value for a quantitative trait or probability, by various methods. Unlike most other tree plotting functions in phytools, this function calls `plot.phylo` (not `plotSimmap`) internally.

Usage

```
plotBranchbyTrait(tree, x, mode=c("edges","tips","nodes"), palette="rainbow",
  legend=TRUE, xlims=NULL, ...)
```

Arguments

tree	an object of class "phylo".
x	either a vector of states for the edges, tips, or nodes of the tree (for mode="edges", "tips", and "nodes", respectively).
mode	string indicating plotting mode. mode="edges", the default, requires that the mapping state of each edge in the tree should be provided. mode="tips" takes the tip values and estimates the state at each internal node. The mapped character value along each branch is the average of the nodes subtending that branch. mode="nodes" similar to "tips", except that the node values are provided instead of estimated.
palette	color palette to translate character values to color. Options are presently "rainbow" (the default), "heat.colors", and "gray".
legend	can be a logical value (TRUE or FALSE) or a numeric value greater than 0. In the latter case the numeric value gives the length of the plotted legend, which also acts as a scale bar for the branch lengths of the tree.
xlims	range for the translation map between trait values and the color map. Should be inclusive of all the values in x.
...	other optional arguments to be passed to <code>plot.phylo</code> - pretty much all arguments are available. In addition, there <code>plotBranchbyTrait</code> has the following additional optional arguments: <code>tol</code> a small tolerance value to be added to the range of x; <code>prompt</code> for <code>legend=TRUE</code> , a logical value indicating whether to prompt for the position of the legend (or not) - the default is to put the legend in the lower left hand size of the plot; <code>title</code> for <code>legend=TRUE</code> , the title of the legend; and <code>digits</code> for <code>legend=TRUE</code> , the number of digits in the quantitative scale of the legend.

Details

Note that if `prompt=TRUE`, the function will prompt for the position of the legend.

Value

Plots a phylogeny.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

plotSimmap

Plot stochastic character mapped tree

Description

Function plots one or multiple stochastic character mapped trees.

Usage

```
plotSimmap(tree, colors=NULL, fsize=1.0, ftype="reg", lwd=2, pts=FALSE,
node.numbers=FALSE, mar=NULL, add=FALSE, offset=NULL, direction="rightwards",
type="phylogram", setEnv=TRUE, part=1.0, xlim=NULL, ylim=NULL,
nodes="intermediate", tips=NULL, maxY=NULL, hold=TRUE, split.vertical=FALSE,
lend=2)
## S3 method for class 'simmap'
plot(x, ...)
## S3 method for class 'multiSimmap'
plot(x, ...)
```

Arguments

tree	a modified object of class "phylo" or "multiPhylo" containing a stochastic mapping or set of mappings (e.g., see read.simmap & make.simmap).
colors	a vector with names translating the mapped states to colors - see Examples.
fsize	relative font size for tip labels.
ftype	font type - options are "reg", "i" (italics), "b" (bold), or "bi" (bold-italics).
lwd	line width for plotting.
pts	logical value indicating whether or not to plot filled circles at each vertex of the tree, as well as at transition points between mapped states. Default is FALSE.
node.numbers	a logical value indicating whether or not node numbers should be plotted.
mar	vector containing the margins for the plot to be passed to par . If not specified, the default margins are [0.1,0.1,0.1,0.1].

add	a logical value indicating whether or not to add the plotted tree to the current plot (TRUE) or create a new plot (FALSE, the default).
offset	offset for the tip labels. Primarily to be used internally by densityMap .
direction	plotting direction. Options are "rightwards" (the default) and "leftwards". Note that for some reason that is not totally clear, <code>node.numbers=TRUE</code> does not work for <code>direction="leftwards"</code> .
type	plot type. Can be "phylogram" or "fan". Only a subset of options are presently available for <code>type="fan"</code> .
setEnv	logical value indicating whether or not to set the environment <code>.PlotPhyloEnv</code> . Setting this to TRUE (the default) will allow compatibility with ape labeling functions such as nodelabels .
part	value between 0 and 1 for <code>type="fan"</code> indicating what fraction of the full circular tree to use as plotting area. For instance, <code>part=0.5</code> will plot a half fan phylogeny. It also affects the axis scaling used.
xlim	x-limits for the plot.
ylim	y-limits for the plot.
nodes	node placement following Felsenstein (2004; pp. 574-576). Can be "intermediate", "centered", "weighted", or "inner". So far only works for <code>type="phylogram"</code> .
tips	labeled vector containing the vertical position of tips. Normally this will be 1:N for N tips in the tree.
maxY	maximum value of y to use before rotating a tree into fan configuration. This will only make a difference if different from <code>Ntip(tree)</code> .
hold	logical argument indicating whether or not to hold the output to the graphical device before plotting. Defaults to <code>hold=TRUE</code> .
split.vertical	split the color of the vertically plotted edges by the state of the daughter edges. Only applies if the edge state changes exactly at a node.
lend	line end style. See par .
x	for S3 plotting method, object of class "simmap" or "multiSimmap".
...	for S3 plotting method, other arguments to be passed to plotSimmap .

Details

The underscore character "_" is automatically swapped for a space in tip labels, as in [plot.phylo](#).

Value

Plots a tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Bollback, J. P. (2006) Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.
- Felsenstein, J. (2004) *Inferring Phylogenies*. Sinauer.
- Huelsenbeck, J. P., R. Nielsen, and J. P. Bollback. (2003) Stochastic mapping of morphological characters. *Systematic Biology*, **52**, 131-138.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[densityMap](#), [make.simap](#), [read.simap](#)

Examples

```
# simulate a mapped tree
Q<-matrix(c(-2,1,1,1,-2,1,1,1,-2),3,3)
rownames(Q)<-colnames(Q)<-letters[1:3]
tree<-sim.history(pbtree(n=100,scale=1),Q)
cols<-setNames(c("blue","red","green"),letters[1:3])
# plot the mapping
plot(tree,cols,ftype="i",fsize=0.7)
```

plotThresh	<i>Tree plotting with posterior probabilities of ancestral states from the threshold model</i>
------------	--

Description

This function uses the object returned by [ancThresh](#) to plot the posterior probabilities of ancestral states under the threshold model. It is also called internally by [ancThresh](#).

Usage

```
plotThresh(tree, x, mcmc, burnin=NULL, piecol, tipcol="input", legend=TRUE, ...)
```

Arguments

tree	phylogenetic tree.
x	a named vector containing discrete character states; or a matrix containing the tip species, in rows, and probabilities of being in each state, in columns.
mcmc	list object returned by ancThresh .
burnin	number of generations (not samples) to exclude as burn in; if NULL then 20 percent of generations are excluded as burn-in.
piecol	a named vector containing the colors for the posterior probabilities plotted as pie charts at internal nodes.

tipcol	a string indicating whether the tip colors should be based on the input data ("input") or sampled tip liabilities ("estimated"). These will only differ if there is uncertainty in the tip states.
legend	logical value or text to be plotted in the legend.
...	other arguments to be passed to <code>plot.phylo</code> - <code>label.offset</code> should be >0 so that tip labels and species names do not overlap.

Value

Plots a tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[ancThresh](#), [plot.phylo](#)

plotTree	<i>Plots rooted phylogenetic tree</i>
----------	---------------------------------------

Description

This function plots a rooted phylogram. Arguments in ... are passed to `plotSimmap`, with the exception of optional argument `color` which is used to determine the plotted color of the branch lengths of the tree.

Usage

```
plotTree(tree, ...)
```

Arguments

tree	a phylogenetic tree in "phylo" format; or multiple trees as an object of class "multiPhylo".
...	optional arguments.

Value

This function plots a rooted phylogram.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plot.phylo](#), [plotSimmap](#)

Examples

```
tree<-pbtrees(n=25)
plotTree(tree,color="blue",ftype="i")
```

plotTree.wBars

Plot a tree with bars at the tips

Description

plotTree.wbars plots a phylogeny in phylogram or fan style with bars at the tips representing the values for a phenotypic trait.

plotTree.barplot creates a split plot in which a right-facing phylogram is on the left, and a bar plot is shown on the right.

plotTree.boxplot creates a split plot in which a right-facing phylogram is on the left, and a box plot is shown on the right.

Usage

```
plotTree.wBars(tree, x, scale=1, width=NULL, type="phylogram", method="plotTree",
tip.labels=FALSE, col="grey", border=NULL, ...)
plotTree.barplot(tree,x,args.plotTree=list(),args.barplot=list())
plotTree.boxplot(tree,x,args.plotTree=list(),args.boxplot=list())
```

Arguments

tree	an object of class "phylo".
x	a named vector of trait values. For plotTree.boxplot, the names should repeat for multiple observations per species. For plotTree.boxplot x can also be supplied as a formula, though in that case the factor levels need to be provided in a valid cladewise order of the tips in tree. This order doesn't need to correspond with the current order of the tip labels.
scale	scaling factor for the tip bars (relative to the total tree height).
width	width of the tip bars.
type	plot type. Can be "phylogram" or "fan".
method	plotting method to use. Can be "plotTree" (for plotTree) or "plotSimmap" (for plotSimmap).
tip.labels	argument indicating whether or not tip labels should be plotted. Defaults to tip.labels=FALSE.
col	colors of the plotted bars. Can be a single value or a vector with length equal to the number of tips in the tree.
border	single value specifying the color of the border for the plotted bars. Defaults to border=NULL, which means that black borders will be plotted.
args.plotTree	in plotTree.barplot, arguments to be passed to plotTree .
args.barplot	in plotTree.barplot, arguments to be passed to barplot .
args.boxplot	in plotTree.boxplot, arguments to be passed to boxplot .
...	optional arguments to be passed to plotTree or plotSimmap .

Value

Plots a tree with an associated bar plot for a continuously valued character at the tips.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[barplot](#), [dotTree](#), [plotSimmap](#), [plotTree](#)

posterior.evolrate *Analysis of the posterior sample from evol.rate.mcmc*

Description

This function takes a phylogenetic tree, an average split position, and a raw MCMC output from `evol.rate.mcmc` and returns a posterior sample of evolutionary rates rootward ($\sigma(1)^2$) and tipward ($\sigma(2)^2$) from the average split.

Usage

```
posterior.evolrate(tree, ave.shift, mcmc, tips, showTree=FALSE)
```

Arguments

<code>tree</code>	a phylogenetic tree in "phylo" format.
<code>ave.shift</code>	mean or median shift-point from the posterior sample (see minSplit).
<code>mcmc</code>	matrix <code>\$mcmc</code> from <code>evol.rate.mcmc</code> (probably with burnin excluded).
<code>tips</code>	list of tips in state $\sigma(1)^2$ for each sampled generation of MCMC.
<code>showTree</code>	optional logical value indicating whether or not to plot the stretched and shrunken tree generated by the pre-processing algorithm implemented in this function (default is FALSE).

Value

A matrix containing the posterior sample of evolutionary rates and shift-points between rates.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J., D. L. Mahler, P. Peres-Neto, and B. D. Redelings (2012) A new method for identifying exceptional phenotypic diversification. *Evolution*, **66**, 135-146.

See Also

[evol.rate.mcmc](#), [minSplit](#)

print.backbonePhylo *Print method for backbone phylogeny*

Description

Print method for an object of class "backbonePhylo".

Usage

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

Arguments

x an object of class "backbonePhylo".
... optional arguments.

Value

Prints to screen.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[phylo.toBackbone](#)

rateystate *Method for investigating the rate of one trait as a function of the state of another*

Description

This function attempts to ask if the rate of a continuous character, y, depends on the state of a separate continuous trait, x. This is accomplished by regressing the squared contrasts in y on the branch or node ancestral estimates of x.

Usage

```
ratebystate(tree, x, y, nsim=100, corr=c("pearson","spearman"), ...)
```

Arguments

tree	phylogenetic tree.
x	a continuous character - the dependent variable in the model.
y	a second continuous trait - the response variable.
nsim	number of simulations for hypothesis testing.
corr	correlation method to use. Same as in cor .
...	optional arguments which include <code>sim.method</code> ("fastBM" or "sim.corr"); see fastBM and sim.corr); <code>method</code> ("by.node" or "by.branch" indicating whether to assume the rate varies as a function of the node state or the mean branch state); <code>message</code> - a logical value indicating whether or not to return <code>corr</code> and <code>method</code> ; finally <code>logarithm</code> - indicating whether or not to fit a model in which the variance of Brownian evolution in <code>y</code> changes as a multiplicative function of <code>x</code> . The default is <code>logarithm=FALSE</code> .

Value

This function returns a list with up to the following four elements:

beta	value of the regression coefficient for square of the contrasts in <code>y</code> regressed on the ancestral or branch-wise estimated states for <code>x</code> .
r	correlation coefficient for <code>corr=corr</code> .
corr	string giving the value of <code>corr</code> .
method	string giving the value of <code>method</code> .

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

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

 rateshift

Find the temporal position of one or more rate shifts

Description

Function finds the location of one or more rate shifts. `likSurface.rateshift` plots the likelihood surface (which is sometimes quite rugged).

Usage

```
rateshift(tree, x, nrates=1, niter=10, method="ML", ...)
## S3 method for class 'rateshift'
plot(x, ...)
likSurface.rateshift(tree, x, nrates=2, shift.range=NULL,
density=20, plot=TRUE, ...)
```

Arguments

<code>tree</code>	object of class "phylo".
<code>x</code>	vector of phenotypic trait values for species. <code>names(x)</code> should contain the species names and match <code>tree\$tip.label</code> . For plot method, <code>x</code> is an object of class "rateshift".
<code>nrates</code>	number of rates.
<code>niter</code>	number of iterations of optimization routine to ensure convergence.
<code>method</code>	optimization method. Can be "ML" (maximum likelihood) or "REML" (restricted maximum likelihood).
<code>...</code>	optional arguments. In the case of the plot method, these will be passed to plotSimmap . For <code>rateshift</code> , optional arguments include: <code>tol</code> , tolerance; <code>plot & print</code> , logical values indicating whether to plot or print the progress of the optimization (default to FALSE); <code>quiet</code> , logical argument indicating whether to suppress all notifications (defaults to FALSE); <code>minL</code> , numeric value; and <code>fixed.shift</code> , either a vector of fixed shift points, or a logical value.
<code>shift.range</code>	for <code>likSurface.rateshift</code> .
<code>density</code>	for <code>likSurface.rateshift</code> .
<code>plot</code>	logical argument for <code>likSurface.rateshift</code> . If <code>plot=FALSE</code> then the surface is returned.

Value

A fitted object of class "rateshift", or, in the case of `likSurface.rateshift`, a likelihood surface for the shift points.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[brownie.lite](#)

read.newick

Robust Newick style tree reader

Description

This function reads a Newick style tree from file.

Usage

```
read.newick(file="", text, ...)
```

Arguments

file	name of text file with single Newick style tree or multiple trees, one per line.
text	character string containing tree.
...	optional arguments to be passed to scan . Note that if the arguments sep or what are supplied this could generate an error. Useful optional arguments might include skip (number of lines to skip) and nlines (number of lines to read).

Details

This function is almost completely redundant with [read.tree](#); however it is 'robust' in that it does not fail if the tree contains so-called 'singles' (nodes with only one descendant).

Value

An object of class "phylo", possibly containing singles (see [collapse.singles](#)).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[read.tree](#), [read.nexus](#)

Examples

```
tree<-"((Human,Chimp),Gorilla),Monkey);"
phy<-read.newick(text=tree)
```

read.simmap

Read SIMMAP style trees from file

Description

This reads one or multiple SIMMAP style trees from file.

Usage

```
read.simmap(file="", text, format="nexus", rev.order=TRUE, version=1)
```

Arguments

file	name of text file with one or multiple SIMMAP v1.0 or v1.5 style trees.
text	character string containing the tree. If version=1.5 this argument is ignored. (This format tree can only be read from file in the present version.)
format	format of the trees: either "phylip" or "nexus" - the latter is the default output from SIMMAP. If version=1.5 this argument is ignored.
rev.order	a logical value indicating whether the states and times along each branch is given (from root to tip) in right-to-left order (if TRUE) or in left-to-right order. If version=1.5 this argument is ignored.
version	version of SIMMAP for input tree. If the tree(s) was/were simulated in SIMMAP v1.0 or written to file by link{make.simmap} then version=1.0; if the tree(s) was/were simulated using SIMMAP v1.5 then version=1.5.

Details

This function now accepts trees in both SIMMAP v1.0 and SIMMAP v1.5 format. In addition, it can read a more flexible format than is produced by SIMMAP (for instance, multi-character mapped states and more than 7 mapped states). Uses some modified code from [read.nexus](#) from the "ape" package to read the NEXUS block created by SIMMAP. Also creates the attribute "map.order" which indicates whether the stochastic map was read in from left to right or right to left. This attribute is used by default by [write.simmap](#) to write the tree in the same order.

Value

A modified object of class "phylo" (or list of class "multiPhylo") with the following additional elements:

maps	a list of named vectors containing the times spent in each state on each branch, in the order in which they occur.
mapped.edge	a matrix containing the total time spent in each state along each edge of the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Bollback, J. P. (2006) Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.

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

See Also

[brownie.lite](#), [evol.vcv](#), [read.tree](#), [read.nexus](#)

reorder.backbonePhylo *Reorders a backbone phylogeny*

Description

Function reorders an object of class "backbonePhylo".

Usage

```
## S3 method for class 'backbonePhylo'  
reorder(x, order="cladewise", ...)
```

Arguments

x	an object of class "backbonePhylo".
order	order. See reorder.phylo for possible orderings.
...	optional arguments.

Value

An object of class "backbonePhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also[phylo.toBackbone](#)

reorderSimmap	<i>Reorder edges of a simmap tree</i>
---------------	---------------------------------------

Description

Function returns a reordered modified "phylo" object by using `reorder.phylo` but then sorting the additional elements `$mapped.edge` and `$maps` to have the same order as `$edge`.

Usage

```
reorderSimmap(tree, order="cladewise", index.only=FALSE, ...)
```

Arguments

<code>tree</code>	a modified object of class "phylo".
<code>order</code>	either "cladewise" or "pruningwise" (see reorder.phylo).
<code>index.only</code>	logical value indicating whether only an index should be returned.
<code>...</code>	other arguments.

Value

A modified object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also[reorder.phylo](#), [plotSimmap](#)

`rep.phylo`*Replicate a tree or set of trees*

Description

S3 method `rep` for object of class "phylo" or "multiPhylo". `repPhylo` is just an alias for `rep.phylo` and `rep.multiPhylo`.

Usage

```
## S3 method for class 'phylo'  
rep(x, ...)  
## S3 method for class 'multiPhylo'  
rep(x, ...)  
repPhylo(tree, times)
```

Arguments

<code>tree</code>	object of class "phylo".
<code>times</code>	number of times to replicate tree.
<code>x</code>	for S3 method an object of class "phylo" or "multiPhylo".
<code>...</code>	other arguments for <code>rep</code> (specifically, <code>times</code>).

Value

An object of class "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[c.phylo](#), [rep](#)

Examples

```
tree<-pbtree(n=100)  
trees<-rep(tree,100)
```

reroot *Re-root a tree along an edge*

Description

This function re-roots a phylogenetic tree at an arbitrary position along an edge.

Usage

```
reroot(tree, node.number, position=NULL, interactive=FALSE, ...)
```

Arguments

tree	a phylogenetic tree in "phylo" format.
node.number	number of the node descending from the target branch in tree\$edge - this can also be a tip in which case the node number is the index number of the tip in tree\$tip.label.
position	position along the target edge at which to re-root the tree. If not supplied, then the tree will be re-rooted <i>at</i> the node or tip.
interactive	logical value indicating whether to use interactive mode (defaults to interactive=FALSE).
...	arguments to be passed to plotTree for interactive=TRUE only.

Details

This function had an error for rootings along edges descended from the root node for phytools<=0.2-47. This should be fixed in the present version. Now uses [paste.tree](#), [root](#), and [splitTree](#) internally. Earlier versions also had an error related to node labels. This should be fixed in phytools>=0.4-47.

Value

A phylogenetic tree in "phylo" format.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.

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

See Also

[splitTree](#), [paste.tree](#), [root](#)

`rerootingMethod` *Get marginal ancestral state reconstructions by re-rooting*

Description

This function uses the re-rooting method of Yang et al. (1995) to get the marginal ancestral state estimates for each internal node of the tree using likelihood. This method get the conditional scaled likelihoods for the root node (which is the same as the marginal ancestral state reconstruction for that node) and successively moves the root to each node in the tree. The function can also return the posterior probabilities for the tip nodes of the tree.

Usage

```
rerootingMethod(tree, x, model=c("ER", "SYM"), ...)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>x</code>	a vector of tip values for species, or a matrix containing the prior probability that the tip is in each state. If <code>x</code> is a vector, then <code>names(x)</code> should be the species names. If <code>x</code> is a matrix of prior probabilities, then <code>rownames</code> should be species names, column names should be states for the discrete character, and rows of the matrix should sum to 1.0.
<code>model</code>	any reversible model. <code>model=c("ER", "SYM")</code> recommended.
<code>...</code>	optional arguments. Presently the logical argument <code>tips</code> . If <code>tips=TRUE</code> , then the function will also compute the empirical Bayes posterior probabilities of the tips following Yang (2006).

Details

This function calls `fitMk` internally. `fitMk` uses some code adapted from `ace` in the `ape` package.

Value

A list containing the following elements:

<code>loglik</code>	the log-likelihood.
<code>Q</code>	the fitted transition matrix between states.
<code>marginal.anc</code>	the marginal ancestral state reconstructions for each node (and, optionally, each tip).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, **20**, 289-290.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Yang, Z., Kumar, S., Nei, M. (1995) A new method of inference of ancestral nucleotide and amino acid sequences. *Genetics*, **141**, 1641-1650.

See Also

[ace](#), [fitMk](#), [make.simmap](#)

rescaleSimmap

Rescale SIMMAP style tree

Description

This function scales a tree with a mapped discrete character to an arbitrary total height, preserving the relative time spent in each state along each edge.

Usage

```
rescaleSimmap(tree, ...)
```

Arguments

tree	a phylogenetic tree in modified "phylo" format with a discrete character mapping (e.g., see read.simmap or make.simmap).
...	other arguments, such as depth.

Details

Replaces `rescaleTree` (now `rescale.phylo`) in the 'geiger' package for SIMMAP style trees.

Value

A phylogenetic tree in modified "phylo" format.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#)

resolveNode	<i>Compute all possible resolutions of a node or all nodes in a multifurcating tree</i>
-------------	---

Description

This functions resolves a single multifurcation or all multifurcations in a tree in all possible ways. If the input tree has edge lengths, then the resolutions will use internal edges of zero length.

Usage

```
resolveNode(tree, node)
resolveAllNodes(tree)
```

Arguments

tree	an object of class "phylo".
node	for resolveNode, the node with a polytomy to resolve.

Details

For resolveNode applied to a multifurcation with n descendants, the number of resolved trees will be equal to the number of possible rooted trees of n taxa. (For instance, three for a trifurcation, 15 for a quadrifurcation, and so on.)

For resolveAllNodes the number of fully resolved trees will be equal to the product of numbers for resolveNode applied to each multifurcation separately. (For instance, 45 for a tree containing one trifurcation and one quadrifurcation.)

Value

An object of class "multiPhylo" - or, if the input tree is already fully resolved, an object of class "phylo" identical to tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[multi2di](#)

`rotateNodes`*Rotates a node or set of nodes in a phylogenetic tree*

Description

The function `rotateNodes` is a simple wrapper for `rotate` which rotates a set of nodes or all nodes.

The function `rotate.multi` finds all possible rotations around a multifurcating node, given by node. This will be an object of class "multiPhylo", assuming that the node specified is indeed a multifurcation.

The function `allRotations` computes all possible rotated trees for a given input phylogeny. For a binary tree, this is generally two raised to the power of the number of internal nodes (so a very large number, if N is even modest in size).

Usage

```
rotateNodes(tree, nodes, polytom=c(1,2), ...)  
rotate.multi(tree, node)  
allRotations(tree)
```

Arguments

<code>tree</code>	object of class "phylo".
<code>nodes</code>	either a single node number to rotate, a vector of node numbers, or the string "all".
<code>polytom</code>	a vector of mode numeric and length two specifying the two clades that should be exchanged in a polytomy (see <code>rotate</code>).
<code>node</code>	a single node to rotate (in the case of <code>rotate.multi</code>).
<code>...</code>	optional arguments.

Details

All three functions also address the problem that the product of multiple rotations from `rotate` can be non-compliant with the implicit "phylo" standard because the tip numbers in `tree$edge` are not in numerical order 1:n for n tips.

Value

An object of class "phylo" (i.e., a phylogenetic tree), in the case of `rotateNodes`, or an object of class "multiPhylo" for `rotate.multi` or `allRotations`.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

roundBranches	<i>Rounds the branch lengths of a tree</i>
---------------	--

Description

This function rounds the branch lengths of a tree or trees and reconciles any mappings (as in [read.simap](#)) with the rounded branch lengths.

Usage

```
roundBranches(tree, digits)
```

Arguments

tree	an object of class "phylo" or "multiPhylo".
digits	number of digits for rounding. Passed to round .

Value

A tree with branch lengths, or modified "phylo" or "multiPhylo" object with a mapped discrete character.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

roundPhylogram *Plot a round phylogram*

Description

Function plots one or multiple round phylograms.

Usage

```
roundPhylogram(tree, fsize=1.0, ftype="reg", lwd=2, mar=NULL, offset=NULL,
direction="rightwards", type="phylogram", xlim=NULL, ylim=NULL, ...)
```

Arguments

tree	an object of class "phylo" or "multiPhylo" containing one or multiple phylogenies.
fsize	relative font size for tip labels.
ftype	font type - options are "reg", "i" (italics), "b" (bold), or "bi" (bold-italics).
lwd	line width for plotting.
mar	vector containing the margins for the plot to be passed to par . If not specified, the default margins are [0.1,0.1,0.1,0.1].
offset	offset for the tip labels.
direction	plotting direction. Only the option <code>direction="rightwards"</code> is presently supported.
type	plot type. Can be "phylogram" or "cladogram". If <code>type="cladogram"</code> then the branch lengths are not necessary (and, indeed, are not used).
xlim	x-limits for the plot.
ylim	y-limits for the plot.
...	optional arguments.

Details

The underscore character "_" is automatically swapped for a space in tip labels, as in [plotSimmmap](#).

Value

Plots a tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotSimmap](#), [plotTree](#)

rstate

Pick a random state according to a vector of probabilities

Description

Primarily an internal function for [make.simmap](#).

Usage

```
rstate(y)
```

Arguments

`y` vector of probabilities. Must have names & should probably add to 1.0.

Details

This function picks a random element in a vector according to the probability assigned that element. It returns the name. Uses [rmultinom](#).

Value

A character or string.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

sampleFrom	<i>Sample from a set of distributions</i>
------------	---

Description

Function samples from a set of normal distributions with parameters given in xbar and xvar.

Usage

```
sampleFrom(xbar=0, xvar=1, n=1, randn=NULL, type="norm")
```

Arguments

xbar	a named vector of means.
xvar	a named vector of variances.
n	a vector containing the sample sizes of each species.
randn	a range of sample sizes are to be random.
type	"norm" is the only distribution implemented so far.

Value

A vector, with labels.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

setMap	<i>Set color map for objects of class "contMap" or "densityMap"</i>
--------	---

Description

Function to change the color map (ramp) in an object of class "contMap" or "densityMap".

Usage

```
setMap(x, ...)
```

Arguments

`x` an object of class "contMap" or "densityMap".

`...` arguments to be passed to [colorRampPalette](#). Also, the argument `invert` which (if `invert=TRUE`) will just flip the current color ramp.

Value

An object of class "contMap" or "densityMap".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Revell, L. J. 2013. Two new graphical methods for mapping trait evolution on phylogenies. *Methods in Ecology and Evolution*, **4**, 754-759.

See Also

[contMap](#), [densityMap](#)

sim.corr

Multivariate Brownian simulation with multiple correlations and rates

Description

This function conducts BM simulation on a tree with multiple rates and/or multiple evolutionary correlations between characters. If `vcv` is a single matrix, instead of a list of matrices, `sim.corr` will simulate multivariate BM with a single rate matrix.

Usage

```
sim.corr(tree, vcv, anc=NULL, internal=FALSE)
```

Arguments

`tree` is a phylogenetic tree in 'phylo' format; or a modified 'phylo' tree with a mapped discrete character.

`vcv` is a square covariance matrix or named list of matrices (one for each mapped state on the tree).

`anc` optional vector of values for the root state.

`internal` logical value indicating whether to return states at internal nodes.

Value

A matrix containing the multivariate tip states for the n species in the tree (and nodes if `internal=TRUE`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Revell, L. J., and D. C. Collar (2009) Phylogenetic analysis of the evolutionary correlation using likelihood. *Evolution*, **63**, 1090-1100.

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

See Also

[fastBM](#), [make.simmmap](#), [read.simmmap](#), [sim.history](#), [sim.rates](#)

sim.history

Simulate stochastic character history under some model

Description

This function simulates a stochastic character history for a discretely valued character trait on the tree. The resultant tree is stored as a modified "phylo" object in stochastic character map (e.g., [make.simmmap](#)) format.

Usage

```
sim.history(tree, Q, anc=NULL, nsim=1, ...)
```

Arguments

tree	a phylogenetic tree as an object of class "phylo".
Q	a matrix containing the instantaneous transition rates between states. Note that normally this is the <i>transpose</i> of the matrix produced by <code>fitDiscrete</code> in the <code>geiger</code> package or make.simmmap in <code>phytools</code> ; that is to say the transition rate from $i \rightarrow j$ should be given by $Q[j, i]$. However, if your matrix is properly conformed (i.e., rows <i>or</i> columns sum to 0), then <code>sim.history</code> will attempt to transpose your matrix correctly & will return an informative message (if <code>message=TRUE</code> , see below).
anc	an optional value for the state at the root node; if <code>NULL</code> , a random state will be assigned. <code>anc</code> can be a vector of states, in which one of the states will be chosen randomly for each simulation. <code>anc</code> can be a vector of probabilities with names, in which case a state will be chosen in proportion to the given probabilities.
nsim	number of simulations.
...	other optional arguments. Currently only <code>message</code> , a logical value indicating whether or not to turn on informational messages (defaults to <code>message=TRUE</code>).

Value

A modified phylogenetic tree of class "phylo" (or a modified "multiPhylo" object, for `nsim > 1`) with the following additional elements:

<code>maps</code>	a list of named vectors containing the times spent in each state on each branch, in the order in which they occur.
<code>mapped.edge</code>	a matrix containing the total time spent in each state along each edge of the tree.
<code>states</code>	a vector containing the tip states.
<code>node.states</code>	a matrix containing the states at internal & terminal nodes (according to the dimensions of edge).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[make.simmap](#), [read.simmap](#), [plotSimmap](#), [sim.rates](#)

sim.ratebystate	<i>Conduct simulation of state dependent rate variation</i>
-----------------	---

Description

This function attempts to simulate two characters under a model in which the rate of evolution for the second (y) depends on the states for the first x. See [ratebystate](#) for more details.

Usage

```
sim.ratebystate(tree, sig2x=1, sig2y=1, beta=c(0,1), ...)
```

Arguments

<code>tree</code>	phylogenetic tree.
<code>sig2x</code>	variance of the Brownian process of evolution for x.
<code>sig2y</code>	variance of the Brownian process of evolution for y when <code>x-min(x)==1</code> (for <code>logarithm=FALSE</code>) or <code>x==0</code> (for <code>logarithm=TRUE</code>).
<code>beta</code>	intercept and slope of the relationship between the value of x and the Brownian rate in y.

... optional arguments which include `method` ("by.node" or "by.branch" indicating whether to assume the rate varies as a function of the node state or the mean branch state); `plot`, a logical value indicating whether or not to plot a phenogram with the branches used for simulation of `y` after rescaling by the state of `x`; and `logarithm`, a logical value indicating whether or not simulate changes in the variance of Brownian evolution for `y` as an additive `logarithm=FALSE` or multiplicative function of `x`. The default is `logarithm=FALSE`.

Value

This function returns a matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[fastBM](#), [ratebystate](#)

sim.rates

Brownian simulation with multiple evolutionary rates

Description

This function conducts BM simulation on a tree with multiple rates.

Usage

```
sim.rates(tree, sig2, anc=0, nsim=1, internal=F, plot=F)
```

Arguments

<code>tree</code>	is a stochastic map format phylogenetic tree in modified "phylo" format (e.g., see make.simmap).
<code>sig2</code>	a named vector containing the rates for each state; names should be states in <code>mtree</code> .
<code>anc</code>	optional value for the root state.
<code>nsim</code>	number of simulations.
<code>internal</code>	logical value indicating whether to return states at internal nodes.
<code>plot</code>	logical value indicating whether or not to visual the rate heterogeneity (default value is FALSE).

Value

A vector (for `nsim=1`) or matrix containing the tip states for the `n` species in the tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[fastBM](#), [make.simmap](#), [read.simmap](#), [sim.history](#)

skewers

Matrix comparison using the method of random skewers

Description

This function performs the random skewers matrix comparison method of Cheverud (1996; also see Cheverud & Marroig 2007 for more details). In addition, it includes a more robust hypothesis test in which random covariance matrices are simulated under a variety of models, and then the mean correlation between response vectors to random skewers are computed.

Usage

```
skewers(X, Y, nsim=100, method=NULL)
```

Arguments

<code>X</code>	covariance matrix.
<code>Y</code>	covariance matrix.
<code>nsim</code>	number of random vectors.
<code>method</code>	method to generate a null distribution of the random skewers correlation between matrices. If <code>method=NULL</code> then the correlation will be compared to the correlation between random vectors; however this test has type I error substantially above the nominal level for ostensibly random matrices. Other values of <code>method</code> will be passed as <code>covMethod</code> to <code>genPositiveDefMat</code> for a more robust hypothesis test (see below). Recommended values include "unifcorrmat".

Value

A list with the following components:

<code>r</code>	mean random skewers correlation.
<code>p</code>	p-value from simulation.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Cheverud, J. M. (1996) Quantitative genetic analysis of cranial morphology in the cotton-top (*Saguinus oedipus*) and saddle-back (*S. fuscicollis*) tamarins. *J. Evol. Biol.*, **9**, 5–42.
- Cheverud, J. M. & Marroig, G. (2007) Comparing covariance matrices: Random skewers method compared to the common principal components model. *Genetics & Molecular Biology*, **30**, 461–469.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217–223.

splitEdgeColor

Split edge colors when descendant edges have different mapped states

Description

This function splits the vertical line colors to match the daughter edges when the daughters have different states. Mostly to be used with trees generated using [paintBranches](#) or [paintSubTree](#). Also used internally by [plotSimmap](#).

Usage

```
splitEdgeColor(tree, colors, lwd=2)
```

Arguments

tree	object of class "simmap".
colors	named vector of colors to be used for plotting.
lwd	width of the plotted lines.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotSimmap](#)

splitplotTree *Plots a phylogeny in two columns*

Description

Function plots a tree in two columns or windows.

Usage

```
splitplotTree(tree, fsize=1.0, ftype="reg", lwd=2, split=NULL, new.window=FALSE)
plotTree.splits(tree, splits=NULL, file=NULL, fn=NULL, ...)
```

Arguments

tree	an object of class "phylo".
fsize	relative font size for tip labels.
ftype	font type - options are "reg", "i" (italics), "b" (bold), or "bi" (bold-italics).
lwd	line width for plotting.
split	relative vertical position for splitting the tree (between 0 & 1).
new.window	whether or not to plot the split tree in a new window. If FALSE then the tree will be plotted in two columns within the same plotting window.
splits	for plotTree.splits relative positions (from 0 to 1) to split the tree across pages or devices.
file	filename if saving to a PDF file is desired. Otherwise will plot to the default plotting device.
fn	function to be executed on each plotted page. For instance, might be: function() cladelabels() if clade labels are desired.
...	other arguments to be passed to plotTree .

Value

Plots a tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[plotTree](#), [plotSimmap](#)

splitTree	<i>Split tree at a point</i>
-----------	------------------------------

Description

Primarily an internal function for `posterior.evolrate`, this function splits the tree at a given point, and returns the two subtrees as an object of class "multiPhylo".

Usage

```
splitTree(tree, split)
```

Arguments

tree	phylogenetic tree.
split	split encoded as a list with two elements: node: the node number tipward of the split; and bp: the position along the branch to break the tree, measured from the rootward end of the edge.

Details

Probably do not use this unless you can figure out what you are doing.

Value

Two trees in a list.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

starTree	<i>Create star phylogeny</i>
----------	------------------------------

Description

This function creates a star phylogeny.

Usage

```
starTree(species, branch.lengths=NULL)
```

Arguments

`species` a list of species.

`branch.lengths` an optional list of branch lengths in the same order as `species`.

Details

Creates a star phylogeny with (optionally) user specified branch lengths.

Value

An object of class "phylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[stree](#)

strahlerNumber	<i>Computes Strahler number for trees and nodes</i>
----------------	---

Description

The function `strahlerNumber` computes the Strahler number of all nodes and tips in the tree. For more information about Strahler numbers see http://en.wikipedia.org/wiki/Strahler_number. The function `extract.strahlerNumber` extracts all of the most inclusive clades of Strahler number `i`.

Usage

```
strahlerNumber(tree, plot=TRUE)
extract.strahlerNumber(tree, i, plot=TRUE)
```

Arguments

<code>tree</code>	an object of class "phylo".
<code>i</code>	order of Strahler number to extract for <code>extract.strahlerNumber</code> .
<code>plot</code>	logical value indicating whether to plot the tree with Strahler numbers for node labels.

Value

Either a vector with the Strahler number for each tip and internal node; or (for `extract.strahlerNumber`) the set of (most inclusive) subtrees with Strahler number `i` as an object of class "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

 threshBayes

Threshold model using Bayesian MCMC

Description

This function uses Bayesian MCMC to fit the quantitative genetics threshold model (Felsenstein 2012) to data for two discrete characters or one discrete and one continuous character.

Usage

```
threshBayes(tree, X, types=NULL, ngen=1000, control=list())
```

Arguments

tree	an object of class "phylo".
X	a numeric matrix containing values for a numerically coded discrete character and a continuous character; or two discrete characters. The row names of X should be species names.
types	a vector of length ncol(X) containing the data types for each column of X, for instance c("discrete", "continuous").
ngen	a integer indicating the number of generations for the MCMC.
control	a list of control parameters for the MCMC. Control parameters include: <code>sample</code> , the sampling interval for the MCMC; <code>propvar</code> , a vector containing (in this order) proposal variances for the two rates (if the type is "discrete" this will be ignored), the two ancestral states, and the correlation; <code>propliab</code> , a single proposal variance for the liabilities; <code>pr.mean</code> , a vector for the mean of the prior probability distributions for each parameter, in the same order as <code>propvar</code> ; <code>pr.liab</code> , currently ignored; <code>pr.var</code> , a vector with variances for the prior densities for each parameter, in the same order as <code>pr.mean</code> - note that for the rates we use an exponential distribution so the first two means are currently ignored; and <code>pr.vliab</code> currently ignored.

Value

This function returns a list with two elements: `par` a matrix containing the posterior sample for the model parameters (evolutionary rates, ancestral states, and correlation); `liab` a matrix containing the posterior sample of the liabilities. For continuous characters, the liabilities are treated as known and so the posterior samples are just the observed values.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Felsenstein, J. (2012) A comparative method for both discrete and continuous characters using the threshold model. *American Naturalist*, **179**, 145-156.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.
- Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[anc.Bayes](#), [bmPlot](#), [evol.rate.mcmc](#)

threshDIC

Deviance Information Criterion from the threshold model

Description

This function computes the Deviance Information Criterion from the MCMC object returned by [ancThresh](#).

Usage

```
threshDIC(tree, x, mcmc, burnin=NULL, sequence=NULL, method="pD")
```

Arguments

tree	phylogenetic tree.
x	a named vector containing discrete character states; or a matrix containing the tip species, in rows, and probabilities of being in each state, in columns.
mcmc	list object returned by ancThresh .
burnin	number of generations (not samples) to exclude as burn in; if not supplied then 20 percent of generations are excluded.
sequence	assumed ordering of the discrete character state. If not supplied and x is a vector then numerical-alphabetical order is assumed; if not supplied and x is a matrix, then the column order of x is used.
method	method for computing the effective number of parameters (options are "pD" and "pV").

Value

A vector containing the mean deviance and deviance for the parameter means, the effective number of parameters, and the DIC.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[ancThresh](#)

threshState	<i>Computes value for a threshold character from a liability and thresholds</i>
-------------	---

Description

Primarily to be used internally by [ancThresh](#); can also be used to simulate threshold traits.

Usage

```
threshState(x, thresholds)
```

Arguments

x	liability.
thresholds	a named vector containing the thresholds.

Value

A discrete character value.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Revell, L. J. (2014) Ancestral character estimation under the threshold model from quantitative genetics. *Evolution*, bold68, 743-759.

See Also

[ancThresh](#), [threshDIC](#)

to.matrix	<i>Convert a character vector to a binary matrix</i>
-----------	--

Description

This function takes a vector of characters and computes a binary matrix. Primarily to be used internally by [make.simmap](#) and [rerootingMethod](#).

Usage

```
to.matrix(x, seq)
```

Arguments

x	a vector of characters.
seq	the sequence for the columns in the output matrix.

Value

A binary matrix of dimensions `length(x)` by `length(seq)`.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

treeSlice	<i>Slices the tree at a particular point and returns all subtrees</i>
-----------	---

Description

This function slices a tree at a particular height above the root and returns all subtrees or all non-trivial subtrees (i.e., subtrees with more than 1 taxon). Uses [extract.clade](#) in the "ape" package.

Usage

```
treeSlice(tree, slice, trivial=FALSE, prompt=FALSE, ...)
```

Arguments

tree	is a phylogenetic tree in "phylo" format.
slice	a real number indicating the height above the root at which to slice the tree.
trivial	a logical value indicating whether or not to return subtrees with a number of tips less than two (default is FALSE).
prompt	logical value indicating whether or not the height of the slice should be given interactively.
...	for prompt=TRUE, other arguments to be passed to plotTree .

Value

An object of class "phylo" or "multiPhylo".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[extract.clade](#)

untangle

Attempts to untangle crossing branches for plotting

Description

This function attempts to untangle the branches of a tree that are tangled in plotting with [plot.phylo](#), [plotTree](#), or [plotSimmap](#). Note that method="read.tree" does not presently work for SIMMAP style trees

Usage

```
untangle(tree, method=c("reorder", "read.tree"))
```

Arguments

tree	tree as an object of class "phylo". Can be a SIMMAP style tree (e.g., read.simmap).
method	method to use to attempt to untangle branches. method="reorder" uses two calls of reorder.phylo or reorderSimmap ; method="read.tree" writes the tree to a text string and then reads it back into memory using read.tree .

Value

A tree with branch lengths, or modified "phylo" object with a mapped discrete character.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

vcvPhylo

Calculates cophenetic (i.e., phylogenetic VCV) matrix

Description

This function returns a so-called *phylogenetic variance covariance matrix* (e.g., see [vcv.phylo](#)), but (optionally) including ancestral nodes and under different evolutionary models.

Usage

```
vcvPhylo(tree, anc.nodes=TRUE, ...)
```

Arguments

tree	object of class "phylo".
anc.nodes	logical value indicating whether or not to include ancestral nodes.
...	optional arguments including internal (synonym of anc.nodes) and model (can be "BM", "OU", or "lambda").

Value

A matrix.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

write.simmap	<i>Write a stochastic character mapped tree to file</i>
--------------	---

Description

This function writes stochastic character mapped trees to file using the Newick style format of SIMMAP v1.0 (Bollback 2006). Note, can only write one tree at a time to file (hence the append option).

Usage

```
write.simmap(tree, file=NULL, append=FALSE, map.order=NULL, quiet=FALSE)
```

Arguments

tree	a phylogenetic tree as a modified object of class "phylo". See make.simmap and read.simmap .
file	an optional filename.
append	a logical value indicating whether to append to file.
map.order	a optional value specifying whether to write the map in left-to-right or right-to-left order. Acceptable values are "left-to-right" or "right-to-left" or some abbreviation of either. If not provided, <code>write.simmap</code> will use <code>attr("map.order")</code> if available.
quiet	logical value indicating whether or not to print a warning message when <code>map.order</code> is neither specified by a function argument or as an attribute of <code>tree</code> .

Value

A file or string (if `file=NULL`).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

- Bollback, J. P. (2006) Stochastic character mapping of discrete traits on phylogenies. *BMC Bioinformatics*, **7**, 88.
- Huelsenbeck, J. P., R. Neilsen, and J. P. Bollback (2003) Stochastic mapping of morphological characters. *Systematic Biology*, **52**, 131-138.
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). *Methods Ecol. Evol.*, **3**, 217-223.

See Also

[make.simmap](#), [read.simmap](#), [plotSimmap](#)

writeAncestors	<i>Write a tree to file with ancestral states and (optionally) CIs at nodes</i>
----------------	---

Description

This function writes a tree to file with ancestral character states and (optionally) 95-percent confidence intervals stored as node value..

Usage

```
writeAncestors(tree, Anc=NULL, file="", digits=6, format=c("phylip","nexus"), ...)
```

Arguments

tree	a phylogenetic tree or set of trees as an object of class "phylo" or "multiPhylo".
Anc	a vector of ancestral states, a list containing the ancestral states and 95-percent confidence intervals (as from fastAnc or ace , or a list of such results.
file	an optional string with the filename for output.
digits	an integer indicating the number of digits to print for branch lengths and ancestral character values.
format	a string indicating whether to output the result in simple Newick (i.e., "phylip") or Nexus format.
...	additional arguments including x: a vector of character values, in which case ancestral states are estimated internally using fastAnc ; and CI: a logical value indicating whether or not to estimate 95-percent confidence intervals.

Value

A file, string, or vector of strings.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[ace](#), [fastAnc](#), [write.tree](#)

`writeNexus`*Write a tree to file in Nexus format*

Description

This function writes one or multiple phylogenetic trees to file in NEXUS format. Redundant with `ape::write.nexus`.

Usage

```
writeNexus(tree, file="")
```

Arguments

<code>tree</code>	object of class "phylo" or "multiPhylo".
<code>file</code>	file name for output.

Value

Trees written to file.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

See Also

[write.simap](#), [write.nexus](#)

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