

Package ‘conevol’

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Title Analysis of Convergent Evolution

Version 1.3

Description Quantifies and assesses the significance of convergent evolution using two different methods (and 5 different measures) as described in Stayton (2015) <DOI: 10.1111/evo.12729>. Also displays results in a phylomorphospace framework.

Depends R (>= 3.5.0), phytools, MASS, ape, cluster, geiger

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allmaxdist *Calculates maxdist for all pairs of taxa in a phylogeny.*

Description

allmaxdist Uses maxdist to calculate the maximum phenotypic distance between the ancestors of all pairs of taxa in a phylogeny. By default outputs these as a matrix, but can also output a list. Can take some time to run for large trees.

Usage

```
allmaxdist(phy1, phendata, mat = TRUE)
```

Arguments

phy1	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
mat	Whether or not to export the values in a matrix (default) or a list

Details

Regarding the output: the matrix is better organized, but the list avoids all the zeroes and is probably better for making histograms.

Value

A matrix or list of all maxdist values for all pairs of taxa in the phylogeny.

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.

Examples

```
phy1<-rtree(10)
phendata<-fastBM(phy1,nsim=2)
answer<-allmaxdist(phy1,phendata,mat=TRUE)
```

ancestrallineages	<i>Extracts lineages leading to two tips, t1 and t2, from their most recent common ancestor.</i>
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Description

Extracts lineages leading to two tips, t1 and t2, from their most recent common ancestor.

Usage

```
ancestrallineages(phy1, phendata, t1, t2)
```

Arguments

phy1	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
t1	The first tip of interest
t2	The second tip of interest

Details

None

Value

A list containing two matrices. Each matrix corresponds to a tip. The matrix consists of reconstructed ancestral values for all nodes leading from the mrca of both tips to the tip.

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.

Stayton, C.T. (2015). The definition, recognition, and interpretation of convergent evolution, and two new measure for quantifying and assessing the significance of convergence. *Evolution* 69:2140-2153.

Examples

```
phy1<-rtree(10)
phendata<-fastBM(phy1,nsim=2)
answer<-ancestrallineages(phy1,phendata,"t1","t2")
```

calcchanges	<i>Calculates all phenotypic changes that occur on all branches of a phylogeny.</i>
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Description

Calculates the Euclidean distance between all ancestors and descendants on a phylogeny to reconstruct the phenotypic changes that occur along all edges of a phylogeny.

Usage

```
calcchanges(phy1, phendata)
```

Arguments

phy1	The phylogeny of interest in phylo format
phendata	A matrix of phenotypic data for all tips, with taxa in rows and characters in columns.

Details

Calculates the Euclidean distance between all ancestors and descendants on a phylogeny to reconstruct the phenotypic changes that occur along all edges of a phylogeny.

Value

A vector in which each element represents an edge of the phylogeny, and the values are the magnitudes of evolutionary change that occur along those edges.

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.

Examples

```
phy1<-rtree(10)
phendata<-fastBM(phy1,nsim=5)
changes<-calcchanges(phy1,phendata)
```

convnum

*Quantify convergence by the number of convergent events***Description**

This program takes in a set of taxa that are already suspected to be convergent in a particular area of morphospace. It then counts the number of times that a lineage has invaded that region of morphospace.

Usage

```
convnum(phy1, phendata, convtips, plot = TRUE, ellipse = NULL,
        plotellipse = NULL)
```

Arguments

phy1	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
convtips	A list consisting of the names of all convergent taxa
plot	Whether or not to plot a phylomorphospace with lineages that cross into the region of interest highlighted as red arrows. Default=TRUE
ellipse	Optional. An ellipse defining the region of interest, into which groups may or may not converge.
plotellipse	Optional. The ellipse defining the region of interest in the first two dimensions.

Details

This function will construct an ellipse around all convergent taxa. Then it will reconstruct ancestral states throughout the phylogeny, and use those to determine how many lineages have crossed into this ellipse from the outside.

Value

The number of lineages that have crossed into the region of trait space occupied by the convergent taxa.

References

- Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M., Hornik, K.(2013). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.4.
- 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.

Examples

```

phyl<-rtree(10)
phendata<-fastBM(phyl,nsim=2)
convtips<-c("t1","t2","t3")
answer<-convnum(phyl,phendata,convtips,plot=TRUE,ellipse=NULL,plotellipse=NULL)

```

convnumsig	<i>Assess the significance of convergent evolution using simulations and the convnum metric</i>
------------	---

Description

Simulates evolution along a given phylogeny, using parameters derived from observed data, and calculates the convnum metric for each simulation for a set of user-defined taxa. Then compares the observed convnum value to the simulated values to assess the significance of the observed levels of convergent evolution.

Usage

```

convnumsig(phyl, phendata, convtips, nsim, ellipse = NULL,
plot = FALSE, plotellipse = NULL)

```

Arguments

phyl	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
convtips	A list consisting of the names of all convergent taxa
nsim	The number of simulatons to conduct
ellipse	Optional. An ellipse defining the region of interest, into which groups may or may not converge.
plot	Optional. Describes whether or not to show phylomorphospaces for all of the simulations.
plotellipse	Optional. The ellipse defining the region of interest in the first two dimensions.

Details

None

Value

A list, consisting first of the p-value for the observed convnum, and second of a vector containing all of the simulated convnum values. Also displays a histogram of all of the simulated convnum values.

References

- Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M., Hornik, K.(2013). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.4.
- 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.

Examples

```
phyl<-rtree(10)
phendata<-fastBM(phyl,nsim=2)
convtips<-c("t1","t2","t3")
answer<-convnumsig(phyl,phendata,convtips,10,plot=FALSE,ellipse=NULL,plotellipse=NULL)
```

convrat	<i>Quantifies convergent evolution using the C1, C2, C3, and C4 measures as described by Stayton (2015).</i>
---------	--

Description

Calculates the current phenotypic distance (Euclidean) between two taxa. Then uses ancestral state reconstruction under a BM model to calculate the maximum phenotypic distance at any time between lineages leading from the most recent common ancestor of those two taxa to the tips. Also calculate the total amount of phenotypic evolution in the clade defined by the most recent common ancestor of those lineages, and the total amount of phenotypic evolution in the input tree. These quantities are used to calculate C1-C4: C1 = 1-(current distance / maximum ancestral distance); C2 = maximum ancestral distance - current distance; C3=C2/(total phenotypic evolution in the clade defined by the two taxa); C4 = C2/(total amount of phenotypic evolution in the entire tree). If more than two convergent taxa are input, then C1-C4 are calculated for all possible pairs of taxa, and averaged.

Usage

```
convrat(phyl, phendata, convtips)
```

Arguments

phyl	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
convtips	A list consisting of the names of all convergent taxa

Details

None

Value

Four numbers - C1, C2, C3, C4.

References

Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M., Hornik, K.(2013). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.4.

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.

Stayton, C.T. (2015). The definition, recognition, and interpretation of convergent evolution, and two new measures for quantifying and assessing the significance of convergence. Evolution 69:2140-2153.

Examples

```
phyl<-rtree(10)
phendata<-fastBM(phyl,nsim=2)
convtips<-c("t1","t2","t3")
answer<-convrat(phyl,phendata,convtips)
```

convratsig

Tests the significance of convergent evolution by the ratio of the current to maximum past phenotypic distance

Description

convratsig tests the significance of convergence (as quantified by convrat) using evolutionary simulations.

Usage

```
convratsig(phyl, phendata, convtips, nsim)
```

Arguments

phyl	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
convtips	A list consisting of the names of all convergent taxa
nsim	The number of simulations to conduct

Details

The function simulates evolution via Brownian motion using the input tree and parameters derived from the observed data. It calculates a convergence metric for each simulation and calculates statistics from the number of times the simulated value exceeds the observed value.

Value

The convergence metric of interest (C1, C2, etc...), a cutoff value (the value that the observed measure would have to exceed in order to be considered significant), a P-value for the statistic, and all simulated values.

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.

Examples

```
phyl<-rtree(10)
phendata<-fastBM(phyl,nsim=2)
convtips<-c("t1","t2","t3")
answer<-convratsig(phyl,phendata,convtips,10)
```

findanc

Find the ancestor of a given node in a phylogeny

Description

This function will find the ancestor of a given node in a phylogeny. It will return a two-element vector, which will contain both the node of the ancestor and the number of the edge that connects the node and ancestor.

Usage

```
findanc(phyl, node)
```

Arguments

phyl	The phylogeny of interest in phylo format
node	The number of the node that you want the ancestor for

Details

Returns a two-element vector. The node of the ancestor is first; the edge that connects that node with its ancestor is second.

Value

A two-element vector, where the first element is the node of the ancestor and the second element is the number of the edge that connects the node and ancestor (i.e., the row number in `phyl$edge`).

References

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20, 289-290. Paradis, E. (2012) *Analysis of Phylogenetics and Evolution with R* (Second Edition). New York: Springer.

Examples

```
phyl<-rtree(10)
ancestor<-findanc(phyl,1)
```

labelstonumbers	<i>Converts taxon names to tip/edge numbers</i>
-----------------	---

Description

Converts taxon names to corresponding tip/edge numbers in the phylogeny.

Usage

```
labelstonumbers(phyl, tips)
```

Arguments

phyl	The phylogeny of interest in phylo format
tips	The names of the tips in question

Details

Simply reads in taxon names, determines which tip or edge number they correspond to, and returns those values

Value

The numbers of all of the tips of interest.

References

Paradis, E., J. Claude, and K. Strimmer (2004) APE: Analyses of phylogenetics and evolution in R language. *Bioinformatics*, 20, 289-290. Paradis, E. (2012) *Analysis of Phylogenetics and Evolution with R* (Second Edition). New York: Springer.

Examples

```
phyl<-rtree(10)
nums<-labelstonumbers(phyl,c("t1","t2","t3"))
```

maxdist	<i>Calculates the maximum phenotypic distance between the lineages leading to a pair of taxa.</i>
---------	---

Description

maxdist uses ancestral state reconstruction to determine the maximum distance between any ancestors of those two taxa.

Usage

```
maxdist(phyl, phendata, t1, t2)
```

Arguments

phyl	The phylogeny of interest in phylo format
phendata	Phenotypic data for all tips
t1	The first taxon of interest
t2	The second taxon of interest

Details

Returns the maximum Euclidean distance between any pair of ancestors of the two taxa, whether or not those two ancestors are contemporaries.

Value

The maximum phenotypic distance between the two taxa

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.

Examples

```
phyl<-rtree(10)
phendata<-fastBM(phyl,nsim=2)
answer<-maxdist(phyl,phendata,1,10)
```

`multianc`*Reconstructs ancestral states for multiple characters*

Description

Uses fastAnc to reconstruct ancestral states for multiple phenotypic characters

Usage

```
multianc(phy1, phendata)
```

Arguments

<code>phy1</code>	The phylogeny of interest in phylo format
<code>phendata</code>	Phenotypic data for all tips

Details

None

Value

A matrix with the tips data in the first n rows and the ancestral data in the remaining n-1 rows.

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.

Examples

```
phy1<-rtree(10)
phendata<-fastBM(phy1,nsim=2)
ancs<-multianc(phy1,phendata)
```

plotellipse	<i>Plots an ellipse</i>
-------------	-------------------------

Description

Plots a minimum ellipse around a set of data

Usage

```
plotellipse(ellipse)
```

Arguments

ellipse	Gives the parameters of the ellipse - output from the ellipsoidhull function in cluster.
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Details

Routine adapted from a suggestion made on CrossValidated: <http://stats.stackexchange.com/questions/9898/how-to-plot-an-ellipse-from-eigenvalues-and-eigenvectors-in-r>

Value

Nothing - just plots the ellipse.

References

Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M., Hornik, K.(2013). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.4.

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