

Package ‘Rphylip’

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Title Rphylip: An R interface for PHYLIP

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Description Rphylip provides an R interface for the PHYLIP package. All users of Rphylip will thus first have to install the PHYLIP phylogeny methods program package (Felsenstein 2013). See <http://evolution.genetics.washington.edu/phylip.html> for more information about installing PHYLIP.

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URL <http://www.phytools.org/Rphylip>

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Rphylip-package	<i>Rphylip: An R interface for PHYLIP</i>
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Description

Rphylip provides an R interface for programs in the PHYLIP phylogeny methods package (Felsenstein 2013).

Details

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

Obviously, before any of the functions of this package can be used, users must first install PHYLIP (Felsenstein 2013). More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

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

Author(s)

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References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Revell, L. J. (2013) Rphylip: An R interface for PHYLIP. R package version x-y.z.

opt.Rdnaml	<i>Parameter optimizer for Rdnaml</i>
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Description

This function is an wrapper for `Rdnaml` that attempts to optimize `gamma` (the alpha shape parameter of the gamma model of rate heterogeneity among sites), `kappa` (the transition:transversion ratio), and `bf` (the base frequencies).

Usage

```
opt.Rdnaml(X, path=NULL, ...)
```

Arguments

<code>X</code>	an object of class "DNAbin".
<code>path</code>	path to the executable containing <code>dnaml</code> . If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file.
<code>...</code>	optional arguments. See details for more information.

Details

Optional arguments include the following: `tree` fixed tree to use in optimization - if not provided, it will be estimated using `Rdnaml` under the default conditions; `bounds` a list with bounds for optimization - for `kappa` and `gamma` this should be a two-element vector, whereas for `bf` this should be a 4 x 2 matrix with lower bounds in column 1 and upper bounds in column 2.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns a list with the following components: `kappa`, `gamma`, `bf` (see Details), and `logLik` (the log-likelihood of the fitted model).

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

`opt.Rdnaml`

Examples

```
## Not run:
data(primates)
fit<-opt.Rdnaml(primates,bounds=list(kappa=c(0.1,40))
tree<-Rdnaml(primates,kappa=fit$kappa,gamma=fit$gamma,bf=fit$bf)

## End(Not run)
```

primates

Example DNA dataset from primates

Description

An object of class "DNAbin" containing nucleotide sequence data of mysterious origin for 12 species of primates.

Usage

```
data(primates)
```

Format

The data are stored as a modified object "DNAbin".

Source

Unknown.

Rcontml

R interface for contml

Description

This function is an R interface for contml in the PHYLIP package (Felsenstein 2013). contml can be used for ML phylogeny estimation from gene frequency data or continuous characters. The continuous characters should be rotated so as to be uncorrelated before analysis.

Usage

```
Rcontml(X, path=NULL, ...)
```

Arguments

X	either (a) a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names; or (b) a list of matrices in which each row contains the relative frequency of alleles at a locus for a species. In the latter case the rownames of each matrix in the list should contain the species names.
path	path to the executable containing contml. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to contml. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); tree object of class "phylo" - if supplied, then the model will be optimized on a fixed input topology; global perform global search (defaults to global = TRUE); random.order add taxa to tree in random order (defaults to random.order = TRUE); random.addition number of random addition replicates for random.order = TRUE (defaults to random.addition = 10); outgroup outgroup if outgroup rooting of the estimated tree is desired; and cleanup remove PHYLIP input/output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns an object of class "phylo" that is the optimized tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

Rdnaml

Rcontrast

R interface for contrast

Description

This function is an R interface for contrast in the PHYLIP package (Felsenstein 2013). contrast can be used to perform the among species phylogenetically independent contrasts method of Felsenstein (1985) and the within & among species method of Felsenstein (2008).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Usage

```
Rcontrast(tree, X, path=NULL, ...)
```

Arguments

tree	object of class "phylo".
X	a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names. For within-species contrasts analysis, the matrix should contain repeating (identical) row names for conspecifics.
path	path to the executable containing contrast. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to contrast. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); and cleanup remove PHYLIP input/output files after the analysis is completed (defaults to cleanup = TRUE).

Value

This function returns an object of class "phylo" that is the optimized tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Felsenstein, J. (2008) Comparative methods with sampling error and within-species variation: Contrasts revisited and revised. *American Naturalist*, 171, 713-725.

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

pic

Rdnaml

R interfaces for dnaml and dnamlk

Description

This function is an R interface for dnaml in the PHYLIP package (Felsenstein 2013). dnaml can be used for ML phylogeny estimation from DNA sequences.

Usage

```
Rdnaml(X, path=NULL, ...)
Rdnamlk(X, path=NULL, ...)
```

Arguments

X	an object of class "DNABin".
path	path to the executable containing dnaml. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to dnaml or dnamlk. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); tree object of class "phylo" - if supplied, then the model will be optimized on a fixed input topology; kappa transition:transversion ratio (defaults to kappa = 2.0); bf vector of base frequencies in alphabetical order (i.e., A, C, G, & T) - if not provided, then defaults to empirical frequencies; rates vector of rates (defaults to single rate); rate.categories vector of rate categories corresponding to the order of rates; gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); ncat number of rate categories for the gamma model; inv proportion of invariant sites for the invariant sites model (defaults to inv = 0); weights vector of weights of length equal to the number of columns in X (defaults to unweighted); speedier speedier but rougher analysis (defaults to speedier = FALSE); global perform global search (defaults to global = TRUE); random.order add taxa to tree in random order (defaults to random.order = TRUE); random.addition number of random addition replicates for random.order = TRUE (defaults to random.addition = 10); outgroup outgroup if outgroup rooting of the estimated tree is desired; and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Finally clock=TRUE enforces a molecular clock. The argument clock is only available for Rdnaml. If clock=TRUE then dnamlk is used internally. For Rdnamlk a molecular clock is assumed, thus Rdnaml(..., clock=TRUE) and Rdnamlk(...) are equivalent.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns an object of class "phylo" that is the optimized tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

`opt.Rdnaml`, `Rcontml`

Examples

```
## Not run:
data(primates)
tree<-Rdnaml(primates,kappa=10)
clockTree<-Rdnamlk(primates,kappa=10)

## End(Not run)
```

Rdnapars

R interface for dnapars

Description

This function is an R interface for dnapars in the PHYLIP package (Felsenstein 2013). dnapars can be used for ML phylogeny estimation from DNA sequences.

Usage

```
Rdnapars(X, path=NULL, ...)
```

Arguments

<code>X</code>	an object of class "DNABin".
<code>path</code>	path to the executable containing dnapars. If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file.
<code>...</code>	optional arguments to be passed to dnapars. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `tree` object of class "phylo" - if supplied, then the parsimony score will be computed on a fixed input topology; `thorough` logical value indicating whether to conduct a more thorough search (defaults to `thorough=TRUE`); `nsave` number of trees to save if multiple equally parsimonious trees are found (defaults to `nsave=10000`); `random.order` add taxa to tree in random order (defaults to `random.order = TRUE`); `random.addition` number of random addition replicates for `random.order = TRUE` (defaults to `random.addition = 10`); `threshold` threshold value for threshold parsimony (defaults to ordinary parsimony); `transversion` logical value indicating whether to use transversion parsimony (defaults to `transversion=FALSE`); `weights` vector of weights of length equal to the number of columns in `X` (defaults to `unweighted`); `outgroup` outgroup if outgroup rooting of the estimated tree is desired; and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns an object of class "phylo" that is the optimized tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

`Rdnaml`

Examples

```
## Not run:
data(primates)
tree<-Rdnapars(primates)

## End(Not run)
```

Rneighbor

R interface for neighbor

Description

This function is an R interface for `neighbor` in the PHYLIP package (Felsenstein 2013). `neighbor` can be used for neighbor-joining and UPGMA phylogeny inference.

Usage

```
Rneighbor(D, path=NULL , ...)
```

Arguments

<code>D</code>	a distance matrix as an object of class "matrix" or "dist". If a matrix, then <code>D</code> should be symmetrical with a diagonal of zeros.
<code>path</code>	path to the executable containing neighbor. If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file.
<code>...</code>	optional arguments to be passed to neighbor. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `method` - can be "NJ" or "nj" (for neighbor-joining), or "UPGMA" or "UPGMA" (for UPGMA); `random.order` add taxa to tree in random order (defaults to `random.order = TRUE`); `outgroup` outgroup if outgroup rooting of the estimated tree is desired (only works for `method = "NJ"`, UPGMA trees are already rooted); and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns an object of class "phylo" that is the NJ or UPGMA tree.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

`Rdnaml`

Examples

```
## Not run:
data(primates)
D<-dist.dna(data(primates),model="JC")
tree<-Rneighbor(D)

## End(Not run)
```

Rthreshml

R interface for threshml

Description

This function is an R interface for threshml in the PHYLIP package (Felsenstein 2013). threshml fits the threshold model of Felsenstein (2005; 2012).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Usage

```
Rthreshml(tree, X, types=NULL, path=NULL, ...)
```

Arguments

tree	object of class "phylo".
X	a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names. For within-species contrasts analysis, the matrix should contain repeating (identical) row names for conspecifics.
types	character vector containing the types (e.g., "discrete", "continuous"). If types are not supplied, Rthreshml will try to figure them out.
path	path to the executable containing contrast. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to threshml. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `burnin` burnin generations for the MCMC; `nchain` number of chains of the MCMC; `ngen` number of generations in each chain; `proposal` variance on the proposal distribution for the MCMC; `lrtest` logical value indicating whether to conduct a likelihood-ratio test of the hypothesis that some correlations are zero (does not appear to work in the present version); and `cleanup` remove PHYLIP input/output files after the analysis is completed (defaults to `cleanup = TRUE`).

Value

This function returns a list containing the results from threshml.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

Rcontrast

Rtreedist

*R interface for treedist***Description**

This function is an R interface for treedist in the PHYLIP package (Felsenstein 2013). treedist can be used to compute the distance between trees by two different methods.

Usage

```
Rtreedist(trees, method=c("branch.score", "symmetric"), path=NULL, ...)
```

Arguments

trees	an object of class "multiPhylo". (Or, under rare circumstances, an object of class "phylo". See below.)
method	method to compute the distance between trees. method="branch.score" is the branch score method of Kuhner & Felsenstein (1994). method="symmetric" is the symmetric distance or Robinson-Foulds distance (Bourque 1978; Robinson & Foulds 1981).
path	path to the directory containing the executable treedist. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to treedist. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); trees2 object of class "multiPhylo" or "phylo" - if two sets of trees are to be compared; rooted logical value indicating whether trees should be treated as rooted (defaults to rooted = FALSE); distances argument telling treedist which distances to compute - could be "all" (all pairwise in trees), "all.1to2" (all in trees by all in trees2), "adjacent" (adjacent species in trees only), and "corresponding" (all corresponding trees in trees and trees2); and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

Value

This function returns a matrix of pairwise distances for distances = "all" and distances = "all.1to2", or a named vector for distances = "adjacent" and distances = "corresponding".

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Examples

```
## Not run:
trees<-rmtree(n=10,N=10)
D<-Rtreedist(trees,method="symmetric")

## End(Not run)
```

setupOSX

Help set up PHYLIP in Mac OS X

Description

This function attempts to help set up PHYLIP on a Mac OS X machine.

Usage

```
setupOSX(path=NULL)
```

Arguments

`path` path to the executable containing dnaml. If `path = NULL`, the R will search several commonly used directories for the correct executable file.

Details

This function can be used to help set up PHYLIP (<http://evolution.genetics.washington.edu/phylip.html>) following the special instructions found here: <http://evolution.genetics.washington.edu/phylip/install.html>. setupOSX should only be run once - when PHYLIP is first installed.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Examples

```
## Not run:
setupOSX()

## End(Not run)
```