

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>

Repository

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Rphylip-package

Rphylip: An R interface for PHYLIP

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

Parameter optimizer for Rdnaml

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. (Currently works only for <code>.Platform\$OS.type = "windows"</code> .)
<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. (Currently works only for .Platform\$OS.type = "windows".)
...	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. (Currently works only for .Platform\$OS.type = "windows".)
...	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

<code>X</code>	an object of class "DNABin".
<code>path</code>	path to the executable containing dnaml. If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file. (Currently works only for <code>.Platform\$OS.type = "windows"</code> .)
<code>...</code>	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 <code>dnapars</code> . If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file. (Currently works only for <code>.Platform\$OS.type = "windows"</code> .)
<code>...</code>	optional arguments to be passed to <code>dnapars</code> . 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

D	a distance matrix as an object of class "matrix" or "dist". If a matrix, then D should be symmetrical with a diagonal of zeros.
path	path to the executable containing neighbor. If path = NULL, the R will search several commonly used directories for the correct executable file. (Currently works only for <code>.Platform\$OS.type = "windows"</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)
```

`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

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