

Package ‘Rphylip’

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Title Rphylip: An R interface for PHYLIP

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ZipData no

Description Rphylip provides an R interface for the PHYLIP package

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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.

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`

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`).

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).

Usage

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

Arguments

<code>tree</code>	object of class "phylo".
<code>X</code>	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.
<code>path</code>	path to the executable containing contrast. 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 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 interface for dnaml

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, ...)
```

Arguments

- | | |
|------|--|
| X | an object of class "DNAbin". |
| path | 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> .) |
| ... | optional arguments to be passed to dnaml. 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`).

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`

Rdnapars	<i>R interface for dnapars</i>
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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. (Currently works only for <code>.Platform\$OS.type = "windows"</code> .) |
| <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`).

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