Package ‘Rphylip’

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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://www.phylip.com for more information about installing PHYLIP.
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Rphylip-package

Description

Rphylip provides an R interface for programs in the PHYLIP phylogeny methods package (Felsenstein 1989, 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. The latest code for the development version of Rphylip can also be found on github at the following URL: http://github.com/liamrevell/Rphylip.

Author(s)

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References


as.proseq
Converts objects to protein sequences, phylip.data, or rest.data object

Description

Converts objects to class "proseq", "phylip.data", or "rest.data".

Usage

as.proseq(x, ...) 
as.phylip.data(x, ...) 
as.rest.data(x, ...)

Arguments

x an object containing amino sequences, a set of binary characters, an arbitrary user-defined multistate character, or presences ("+") and absences ("-")) of restriction sites. as.proseq and as.phylip.data also converts objects of class "phyDat" from the phangorn package.

... optional arguments.

Value

An object of class "proseq" containing protein sequences; an object of class "phylip.data"; or an object of class "rest.data".

Author(s)

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See Also

print.proseq, Rproml
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

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. 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 1989, 2013) should first be installed. Instructions for 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)

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References


See Also

Rdnaml

Examples

```r
## 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 datasets

**Description**

`primates` is an object of class "DNAbin" containing nucleotide sequence data of mysterious origin for 12 species of primates. `chloroplast` is an object of class "proseq" containing a chloroplast alignment from the phangorn package (Schliep 2011). `primates.bin` is an object of class "phylip.data" containing "0" and "1" character data for primates. `cotton` is a list with two parts: `cotton$tree` is an object of class "phylo", containing a phylogenetic tree for 37 species of cotton (*Gossypium*); `cotton$data` is an object of class "matrix" containing traits for each species. Most trait values are real, but a few values were not available and so random values were used so there were no missing values in the dataset. `restriction.data` is an object of class "rest.data" containing an example dataset of restriction site data.

**Usage**

- `data(primates)`
- `data(chloroplast)`
- `data(primates.bin)`
- `data(cotton)`
- `data(restriction.data)`
print.proseq

Format

The data are stored as an object of class "DNAbin", "proseq", "phylip.data", or "rest.data". cotton is a list containing an object "phylo" and a matrix of continuous trait data.

Author(s)

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Source


print.proseq

Print method protein sequences, phylip.data, or rest.data object

Description

Print method for an objects of class "proseq", "phylip.data", or "rest.data".

Usage

```r
## S3 method for class 'proseq'
print(x, printlen=6, digits=3, ...)
```

Arguments

- **x**: an object of class "proseq", an object of class "phylip.data", or an object of class "rest.data".
- **printlen**: number of sequence names to print.
- **digits**: number of digits to print.
- **...**: optional arguments.

Value

Prints to screen.

Author(s)

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See Also

as.proseq, print.DNAbin, Rproml
Description

This function is an R interface for clique in the PHYLIP package (Felsenstein 2013). clique can be used for phylogeny inference using the compatibility method (Le Quesne 1969; Estabrook et al. 1976).

Usage

Rclique(x, path=NULL, ...)

Arguments

x an object of class "phylip.data" with a set of binary characters; or a matrix.
path path to the executable containing clique. If path = NULL, the R will search several commonly used directories for the correct executable file.
... optional arguments to be passed to clique. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); ancestral vector of ancestral states; weights vector of weights of length equal to the number of columns in x (defaults to unweighted); minimum clique, if specified, will cause Rclique to print out all cliques (and corresponding trees) greater than minimum clique; 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 1989, 2013) should first be installed. Instructions for 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)

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References


See Also

`Rdnacomp`, `Rmix`

Examples

```r
## Not run:
data(primates.bin)
tree<-'Rclique(primates.bin)

## End(Not run)
```

---

**Rconsense**

*R interface for consense*

Description

This function is an R interface for consense in the PHYLIP package (Felsenstein 2013). consense can be used to compute the consensus tree from a set of phylogenies.

Usage

```r
Rconsense(trees, path=NULL, ...)
```

Arguments

- **trees**
  - an object of class "multiPhylo".

- **path**
  - path to the directory containing the executable consense. If path = NULL, the R will search several commonly used directories for the correct executable file.

- **...**
  - optional arguments to be passed to consense. See details for more information.
Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method which can be "extended" (extended majority rule consensus, the default), "strict" (strict consensus), or regular majority rule consensus ("majority"); "outgroup" single taxon label or vector of taxa that should be used to root all trees before analysis; rooted logical value indicated whether to treat the input trees as rooted (defaults to rooted = FALSE); 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 1989, 2013) should first be installed. Instructions for 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". For methods other than method = "strict", tree$node.label contains the proportion of phylogenies in trees containing that subtree.

Author(s)

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References


Examples

```r
## Not run:
trees<-rmmtree(n=10,N=10)
tree<-Rconsense(trees)

## End(Not run)
```
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 matrix 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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain

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References


See Also

`rclonaml`, `rproml`

---

**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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: [http://evolution.genetics.washington.edu/phylip.html](http://evolution.genetics.washington.edu/phylip.html).

**Usage**

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

**Arguments**

- `tree` object of class "phylo".
- `X` a matrix of continuous valued traits (in columns) with rownames containing species names. For one trait, `X` can be a matrix with one column or a vector with `names(X)` containing species names matching `tree$tip.label`. 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.
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).

If \( X \) contains one observation per species (say, the species mean), then Rcontrast returns a list with the following components: Contrasts, a matrix with all phylogenetically independent contrasts; Covariance_matrix, a matrix containing the evolutionary variances (on diagonals) and covariances; Regressions, a matrix containing the pair-wise bivariate regression coefficients (columns on rows); Correlations, a correlation matrix of contrasts.

If \( X \) contains more than one sample per species, then Rcontrast returns a list with the following elements: VarA, the estimated among-species variance-covariance matrix; VarE, the estimated within-species (i.e., 'environmental') variance-covariance matrix; VarA.Regression, a matrix containing the pair-wise bivariate among-species regression coefficients (columns on rows); VarA.Correlations, a matrix with the among-species evolutionary correlations; VarE.Regressions, the pair-wise bivariate within-species regression coefficients; VarE.Correlations, the within-species correlations; nonVa.VarE, nonVa.VarE.Regressions, and nonVa.VarA.Correlations, estimates obtained when VarA is not included in the model; logLik and nonVa.logLik, log-likelihood when VarA is included (or not) in the model; \( k \) and nonVa.k the number of parameters estimated in each model; and \( P \) the p-value of a likelihood-ratio test of VarA, in which \( df = k - nonVa.k \).

Author(s)
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References

See Also
pic, Rcontml, Rthreshml

Examples
```r
## Not run:
data(cotton)
contrasts<-Rcontrast(tree = cotton$tree, X = cotton$data)

## End(Not run)
```
Rdnacomp

R interface for dnacomp

Description

This function is an R interface for dnacomp in the PHYLIP package (Felsenstein 2013). dnacomp can be used for phylogeny inference from DNA sequences using the compatibility method (Le Quesne 1969; Fitch 1975).

Usage

Rdnacomp(X, path=NULL, ...)

Arguments

X an object of class "DNAbin".
path path to the executable containing dnacomp. If path = NULL, the R will search several commonly used directories for the correct executable file.
... optional arguments to be passed to dnacomp. 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 number of compatible sites will be computed on a fixed input topology; 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); 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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>
References


See Also

*rdnapars, rdnapenny*

Examples

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

## End(Not run)
```

Rdnadist

**R interfaces for dnadist**

Description

This function is an R interface for dnadist in the PHYLIP package (Felsenstein 2013). dnadist can be used to estimate the evolutionary distances between DNA sequences under various models.

Usage

`Rdnadist(X, method=c("F84","K80","JC","LogDet"), path=NULL, ...)`

Arguments

- **X**: an object of class "DNAbin".
- **method**: method for calculating the distances. Can be "F84" (Kishino & Hasegawa 1989; Felsenstein & Churchill 1996), "K80" (Kimura 1980), "JC" (Jukes & Cantor 1969), or "LogDet" (Barry & Hartigan 1987; Lake 1994; Steel 1994; Lockhart et. al. 1994). Also `method="similarity"` computes the sequence similarity among the rows of `X`.
- **path**: path to the executable containing dnadist. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
- **...**: optional arguments to be passed to dnadist. See details for more information.
Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); kappa transition:transversion ratio (defaults to kappa = 2.0); rates vector of rates (defaults to single rate); rate.categories vector of rate categories corresponding to the order of rates; weights vector of weights of length equal to the number of columns in X (defaults to unweighted); bf vector of base frequencies in alphabetical order (i.e., A, C, G, & T) - if not provided, then defaults to empirical frequencies; 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: http://evolution.genetics.washington.edu/phyllip.html.

Value

This function returns an object of class "dist".

Author(s)

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References


See Also

Rneighbor

Examples

```r
## Not run:
data(primates)
D<-Rnadinvar(primates,kappa=10)
tree<-Rnadinvar(D)

## End(Not run)
```

Rnadinvar

R interface for dnainvar

Description

This function is an R interface for dnainvar in the PHYLIP package (Felsenstein 2013). dnainvar reads DNA sequences and computes Lake’s invariants (Cavender & Felsenstein 1987; Lake 1987).

Usage

```r
Rnadinvar(X, path=NULL, ...)
```

Arguments

- `X` an object of class "DNAbin". `X` cannot contain more than four species.
- `path` path to the executable containing dnainvar. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
- `...` optional arguments to be passed to dnainvar. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `weights` vector of weights of length equal to the number of columns in `X` (defaults to unweighted); 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: [http://evolution.genetics.washington.edu/phylip.html](http://evolution.genetics.washington.edu/phylip.html).

Value

At present, this function merely prints the results of dnainvar to screen.
Author(s)

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References


See Also

Rdnapars

Examples

```r
## Not run:
data(primates)
primates<-primates[sample(nrow(primates),4),]
tree<-Rdnainvar(primates)

## End(Not run)
```

---

**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 (Felsenstein 1981; Felsenstein & Churchill 1996).

Usage

```r
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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain

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

References

Rdnapars

See Also

opt.Rdnaml, Rcontml, Rproml

Examples

```R
## 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 MP phylogeny estimation from DNA sequences (Eck & Dayhoff 1966; Kluge & Farris 1969; Fitch 1971).

Usage

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

Arguments

- `X` an object of class "DNAbin".
- `path` path to the executable containing dnapars. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
- `...` 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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain

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References


See Also

Rdnaml, Rdnapenny

Examples

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

## End(Not run)```
Rdnapenny

R interface for dnapenny

Description

This function is an R interface for dnapenny in the PHYLIP package (Felsenstein 2013). dnapenny performs branch & bound parsimony searching following Hendy & Penny (1982).

Usage

Rdnapenny(X, path=NULL, ...)

Arguments

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

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); groups number of groups of 1,000 trees (defaults to groups = 10000); report reporting frequency, in numbers of trees (defaults to report = 1000); simple simple branch & bound (defaults to simple = TRUE); threshold threshold value for threshold parsimony (defaults to ordinary parsimony); 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 1989, 2013) should first be installed. Instructions for 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" or "multiPhylo" that is the tree or trees with the best parsimony score. tree$score gives the parsimony score, for "phylo" object tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain
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References


See Also

Rdnapars

Examples

```r
## Not run:
data(primates)
tree<-Rdnapenny(primates)
## End(Not run)
```

Rdollop  

Description

This function is an R interface for dollop in the PHYLIP package (Felsenstein 2013). dollop can be used for Dollo (Le Quesne 1974; Farris 1977) and polymorphism (Inger 1967; Farris 1978; Felsenstein 1979) parsimony tree inference.

Usage

```r
Rdollop(X, path=NULL, ...)
```

Arguments

- **X**: an object of class "phylip.data" with a set of binary characters; or a matrix. Data should be "0" and "1". The states "P" (or "B"), for polymorphism, and "?" are also permitted.
- **path**: path to the executable containing dollop. If path = NULL, the R will search several commonly used directories for the correct executable file.
- **...**: optional arguments to be passed to dollop. 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 Dollo or polymorphism parsimony score will be computed on a fixed input topology; method indicating whether Dollo (method="dollo", the default) or polymorphism (method="polymorphism") should be used; 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); ancestral vector of ancestral states, which allows for the unordered Dollo parsimony method of Felsenstein (1984); weights vector of weights of length equal to the number of columns in X (defaults to unweighted); 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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

References

Rdolpenny

See Also

Rpars, Rdnapars

Examples

```r
## Not run:
data(primates.bin)
tree<-Rdollop(primates.bin)
## End(Not run)
```

Rdolpenny

R interface for dolpenny

Description

This function is an R interface for dolpenny in the PHYLIP package (Felsenstein 2013). dolpenny performs Dollo (Le Quesne 1974; Farris 1977) or polymorphism (Inger 1967; Farris 1978; Felsenstein 1979) parsimony using the branch and bound algorithm of Hendy & Penny (1982).

Usage

```r
Rdolpenny(X, path=NULL, ...)
```

Arguments

- `X` an object of class "phylip.data" with a binary character; or a matrix. Data should be "0" and "1". The states "P" (or "B"), for polymorphism, and "?" are also permitted.
- `path` path to the executable containing dolpenny. If path = NULL, the R will search several commonly used directories for the correct executable file.
- `...` optional arguments to be passed to dolpenny. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method indicating whether Dollo (method="dollo", the default) or polymorphism (method="polymorphism") should be used; groups number of groups of 1,000 trees (defaults to groups = 100); report reporting frequency, in numbers of trees (defaults to report = 1000); simple simple branch & bound (defaults to simple = TRUE); threshold threshold value for threshold parsimony (defaults to ordinary parsimony); ancestors vector of ancestral states, which allows for the unordered Dollo parsimony method of Felsenstein (1984); weights vector of weights of length equal to the number of columns in X (defaults to unweighted); outgroup outgroup if out-group 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 1989, 2013) should first be installed. Instructions for 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" or "multiPhylo" that is the tree or trees with the best parsimony score. tree$score gives the parsimony score, for "phylo" object tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

References


See Also

Rdnapars

Examples

```r
## Not run:
data(primates.bin)
tree<-Rdolpenny(primates.bin)

## End(Not run)
```
read.protein          \hspace{1cm} \textit{Reads protein sequences from file in multiple formats}

\textbf{Description}

Reads protein sequences from a file.

\textbf{Usage}

\begin{verbatim}
read.protein(file, format="fasta", ...)
\end{verbatim}

\textbf{Arguments}

- \texttt{file} \hspace{1cm} file name for file containing protein sequences.
- \texttt{format} \hspace{1cm} format of input file. Permitted formats are "fasta" and "sequential". See \texttt{read.dna} for more information.
- ... \hspace{1cm} optional arguments.

\textbf{Value}

An object of class "proseq" containing protein sequences.

\textbf{Author(s)}

Liam J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

\textbf{See Also}

\begin{verbatim}
as.proseq, print.proseq, Rproml
\end{verbatim}

Rfitch          \hspace{1cm} \textit{R interface for fitch}

\textbf{Description}

This function is an R interface for fitch in the PHYLIP package (Felsenstein 2013). fitch can be used for tree inference using the Fitch-Margoliash method (Fitch \& Margoliash 1967), the Cavalli-Sforza \& Edwards least-squares method (Cavalli-Sforza \& Edwards 1967), and the minimum evolution criterion (Kidd \& Sgaramella-Zonta 1971; Nei \& Rzhetsky 1993).

\textbf{Usage}

\begin{verbatim}
Rfitch(D, path=NULL, ...)
\end{verbatim}
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 `fitch`. If `path` is `NULL`, the R will search several commonly used directories for the correct executable file.
- ... Optional arguments to be passed to `fitch`. 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 "FM" or "fm" (for the Fitch-Margoliash criterion; Fitch & Margoliash 1967), "LS" or "ls" for the Cavalli-Sforza & Edwards (1967) least-squares criterion, or "ME" or "me" (for Minimum Evolution); **tree** object of class "phylo" - if supplied, then branch lengths are optimized & the optimality criterion is computed on the input tree; **negative** a logical value indicating whether negative branch lengths should be permitted (defaults to `negative = TRUE`); **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** 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 Fitch-Margoliash, LS, or ME tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References


Rgendist

See Also

Rdnadist

Examples

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

## End(Not run)
```

Rgendist

R interface for gendist

Description

This function is an R interface for gendist in the PHYLIP package (Felsenstein 2013). gendist can be used to estimate the evolutionary distances between populations based on gene frequency data. Three methods can be used for computing these distances. These are (1) Nei’s genetic distance (Nei 1972), (2) Cavalli-Sforza’s chord measure (Cavalli-Sforza & Edwards 1967), and (3) Reynolds et al.’s (1983) genetic distance.

Usage

```r
Rgendist(X, path=NULL, ...)
```

Arguments

- **X**
  - either: (a) A matrix of allele frequencies (in columns) with rownames containing species names. In this case it is assumed that \( m - 1 \) allele frequencies are reported for a locus with \( m \) segregating alleles. (The \( m \)th frequency is just one minus the sum of the other \( m-1 \).) Or (b) a list of matrices in which each row contains the relative frequency of alleles at a locus for a species. In this case, the rownames of each matrix in the list should contain the species names. Here the number of alleles at each locus can be inferred from the number of columns in the matrix, and no frequencies should be omitted. (I.e., rows should add to 1.0.)

- **path**
  - path to the executable containing gendist. If `path = NULL`, the R will search several paths for gendist. See details for more information.

- **...**
  - optional arguments to be passed to gendist. See details for more information.
Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method, the method for calculating the genetic distance - options are "Nei", "Cavalli-Sforza", and "Reynolds" (defaults to method="Nei"); nalleles a vector containing the number of alleles per locus in x (not used if x is a list, and assumed to be a vector of 2s if omitted); 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: http://evolution.genetics.washington.edu/phylip.html.

Value

This function returns an object of class "dist".

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References


See Also

Rdnadist, Rprotdist
Rkitch

R interface for kitsch

Description

This function is an R interface for kitsch in the PHYLIP package (Felsenstein 2013). kitsch can be used for tree inference using the Fitch-Margoliash method (Fitch & Margoliash 1967), the Cavalli-Sforza & Edwards least-squares method (Cavalli-Sforza & Edwards 1967), and the minimum evolution criterion (Kidd & Sgaramella-Zonta 1971; Nei & Rzhetsky 1993), but contraining the branch lengths of the tree to be clock-like (i.e., all paths from the root to any tip are equal in length).

Usage

Rkitch(D, path=NULL, ...)

Arguments

D a distance matrix as an object of class "matrix", "data.frame", or "dist". If a matrix, then D should be symmetrical with a diagonal of zeros.

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

... optional arguments to be passed to kitsch. 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 "FM" or "fm" (for the Fitch-Margoliash criterion; Fitch & Margoliash 1967), "LS" or "ls" for the Cavalli-Sforza & Edwards (1967) least-squares criterion, or "ME" or "me" (for Minimum Evolution); tree object of class "phylo" - if supplied, then branch lengths are optimized & the optimality criterion is computed on the input tree: negative a logical value indicating whether negative branch lengths should be permitted (defaults to negative = 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; subreplicate, a logical value indicating whether or not to perform the subreplication test of Felsenstein (1986); and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE). Note that for some reason subreplicate=TRUE does not appear to work in the current version of kitsch.


Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 1989, 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 J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

References


See Also

`Rfitch`

Examples

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

## End(Not run)
```

Rmix

\[ R \text{ interface for mix} \]

Description

This function is an R interface for mix in the PHYLIP package (Felsenstein 2013). mix performs branch & bound parsimony searching following Hendy & Penny (1982).

Usage

```
Rmix(X, path=NULL, ...)
```
Arguments

- **X**: an object of class "phylib.data" with a binary character; or a matrix. Data should be "0", "1", and "?".
- **path**: path to the executable containing mix. If path = NULL, the R will search several commonly used directories for the correct executable file.
- **...**: optional arguments to be passed to mix. 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; mixture, a vector containing "W" and "C" in upper or lower case indicating which characters should be evaluated using Wagner (Eck & Dayhoff 1966: Kluge & Farris 1969) or Camin-Sokal (Camin & Sokal 1965) parsimony methods, respectively - this argument takes precedence over method (see below); method either "Wagner" or "Camin-Sokal", in upper or lower case, indicating whether Wagner (Eck & Dayhoff 1966; Kluge & Farris 1969) or Camin-Sokal (Camin & Sokal 1965) parsimony should be used; 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); ancestral a vector of length equal to the number of columns in X containing the the ancestral state at the root of the tree for each character, these should be "0", "1", and "?"; 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 1989, 2013) should first be installed. Instructions for 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" or "multiPhylo" that is the tree or trees with the best parsimony score. tree$score gives the parsimony score, for "phylo" object tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References


**See Also**

`Rdnapars`

**Examples**

```r
# Not run:
data(primates.bin)
tree<-Rmix(primates.bin)
# 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 (Saitou & Nei 1987) and UPGMA (Sokal & Michener 1958) phylogeny inference.

**Usage**

```r
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.
- `...` 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 1989, 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 J. Revell, Scott A. Chamberlain

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

References


See Also

rdnadist

Examples

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

## End(Not run)
```
Rpars

R interface for pars

Description

This function is an R interface for pars in the PHYLIP package (Felsenstein 2013). pars can be used for MP phylogeny estimation from DNA sequences (Eck & Dayhoff 1966; Kluge & Farris 1969; Fitch 1971).

Usage

Rpars(x, path=NULL, ...)

Arguments

x an object of class "phylip.data" with a set of binary or multistate characters; or a matrix.

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

... optional arguments to be passed to pars. 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); 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 1989, 2013) should first be installed. Instructions for 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 J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

References


See Also

Rdnam1, Rdnapenny

Examples

```r
## Not run:
data(primates.bin)
tree<-Rpars(primates.bin)

## End(Not run)
```

Rpenny

*R interface for penny*

Description

This function is an R interface for penny in the PHYLIP package (Felsenstein 2013). penny performs branch & bound parsimony searching following Hendy & Penny (1982).

Usage

```r
Rpenny(X, path=NULL, ...)
```

Arguments

- **X**: an object of class "phylip.data" with a binary character; or a matrix. Data should be "0", "1", and "?".
- **path**: path to the executable containing penny. If path = NULL, the R will search several commonly used directories for the correct executable file.
- **...**: optional arguments to be passed to penny. See details for more information.
Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); mixture, a vector containing "w" and "c" in upper or lower case indicating which characters should be evaluated using Wagner (Eck & Dayhoff 1966; Kluge & Farris 1969) or Camin-Sokal (Camin & Sokal 1965) parsimony methods, respectively - this argument takes precedence over method (see below); method either "wagner" or "camin-sokal", in upper or lower case, indicating whether Wagner (Eck & Dayhoff 1966; Kluge & Farris 1969) or Camin-Sokal (Camin & Sokal 1965) parsimony should be used; groups number of groups of 1,000 trees (defaults to groups = 100); report reporting frequency, in numbers of trees (defaults to report = 1000); simple simple branch & bound (defaults to simple = TRUE); threshold threshold value for threshold parsimony (defaults to ordinary parsimony); ancestral a vector of length equal to the number of columns in X containing the the ancestral state at the root of the tree for each character, these should be "0", "1", and "?"; 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).

More information about the penny program in PHYLIP can be found here http://evolution.genetics.washington.edu/phylip/doc/penny.html.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 1989, 2013) should first be installed. Instructions for 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" or "multiPhylo" that is the tree or trees with the best parsimony score. tree$score gives the parsimony score, for "phylo" object tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References


See Also

Rdnapars

Examples

```r
## Not run:
data(primates.bin)
tree<-Rpenny(primates.bin)
## End(Not run)
```

Rproml

R interfaces for proml and promlk

Description

This function is an R interface for proml in the PHYLIP package (Felsenstein 1989, 2013). proml can be used for ML phylogeny estimation from amino acid sequences.

Usage

```r
Rproml(X, path=NULL, ...)  
Rpromlk(X, path=NULL, ...)
```

Arguments

- `X` an object of class "proseq".
- `path` path to the executable containing proml. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
- `...` optional arguments to be passed to proml or promlk. 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; `model` amino acid model - could be "JTT" (Jones et al. 1992), "PMB" (Veerassamy et al. 2003), or "PAM" (Dayhoff & Eck 1968; Dayhoff et al. 1979; Koisol & Goldman 2005); `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 \texttt{Rproml}. If clock=TRUE then promlk is used internally. For \texttt{Rpromlk} a molecular clock is assumed, thus \texttt{Rproml(...,clock=TRUE)} and \texttt{Rpromlk(...)} are equivalent. Note that in PHYLIP 3.695 my tests of promlk yielded peculiar results (all branch lengths zero length, random topology), so I’m not sure what to make of that.


Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: \url{http://evolution.genetics.washington.edu/phylip.html}.

\textbf{Value}

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

\textbf{Author(s)}

Liam J. Revell, Scott A. Chamberlain

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

\textbf{References}


\textbf{See Also}

\texttt{as.proseq,Rdnaml,read.protein}
Examples

```r
## Not run:
data(chloroplast)
tree<-rprotml(chloroplast)
## End(Not run)
```

Description

This function is an R interface for protdist in the PHYLIP package (Felsenstein 2013). protdist can be used to estimate the evolutionary distances between amino acid sequences under various models.

Usage

```r
rprotdist(x, path=NULL, ...)
```

Arguments

- `x`: an object of class "proseq" containing aligned amino acid sequences.
- `path`: path to the executable containing protdist. If `path = NULL`, the R will search for arguments to be passed to protdist. See details for more information.
- `...`: optional arguments to be passed to protdist. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `model` can be "JTT" (Jones et al. 1992), "PMB" (Veerassamy et al. 2003), "PAM" (Dayhoff & Eck 1968; Dayhoff et al. 1979; Koisol & Goldman 2005), "Kimura" (a simple model based on Kimura 1980), "similarity" which gives the similarity between sequences, and "categories" which is due to Felsenstein; `gamma` shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity) - note that gamma rate heterogeneity does not apply to `model = "Kimura"` or `model = "similarity"`; `kappa` transition:transversion ratio (defaults to `kappa = 2.0`), `genetic.code`, type of genetic code to assume (options are "universal", the default, "mitochondrial", "vertebrate.mitochondrial", "fly.mitochondrial", and "yeast.mitochondrial"), `categorization`, categorization scheme for amino acids (options are "GHB", the George et al. 1988 classification, "Hall", a classification scheme provided by Ben Hall, and "chemical", a scheme based on Conn & Stumpf 1963); and, finally, `ease`, a numerical parameter that indicates the facility of getting between amino acids of different categories in which 0 is nearly impossible, and 1 is no difficulty (defaults to `ease = 0.457`) - note that `kappa`, `bf`, `genetic.code`, `categorization`, and `ease` apply only to `model = "categories"`; `rates` vector of rates (defaults to single rate); `rate.categories` vector of rate categories corresponding to the order of rates; `weights` vector of weights of length equal to the number of columns in `x` (defaults to unweighted); and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).
More information about the protdist program in PHYLIP can be found here http://evolution.genetics.washington.edu/phylib/doc/protdist.html.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: http://evolution.genetics.washington.edu/phylib.html.

Value

This function returns an object of class "dist".

Author(s)

Liam J. Revell, Scott A. Chamberlain
Maintainer: Liam J. Revell <liam.revell@umb.edu>

References


See Also

Rneighbor
Examples

```r
## Not run:
data(chloroplast)
D<-Rprotdist(chloroplast,model="PAM")
tree<-Rneighbor(D)
## End(Not run)
```

Description

This function is an R interface for protpars in the PHYLIP package (Felsenstein 2013). protpars can be used for MP phylogeny estimation from protein sequences (Eck & Dayhoff 1966; Fitch 1971).

Usage

```r
Rprotpars(X, path=NULL, ...)
```

Arguments

- `X` an object of class "proseq" containing aligned amino acid sequences.
- `path` path to the executable containing protpars. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
- `...` optional arguments to be passed to protpars. 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; 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); genetic.code, type of genetic code to assume (options are "universal", the default, "mitochondrial", "vertebrate.mitochondrial", "fly.mitochondrial", and "yeast.mitochondrial"); 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: [http://evolution.genetics.washington.edu/phylip.html](http://evolution.genetics.washington.edu/phylip.html).
rrestdist

**Value**

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

**Author(s)**

Liam J. Revell, Scott A. Chamberlain

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**References**


**See Also**

`asproseq, Rdnapars, read.protein`

**Examples**

```r
## Not run:
data(chloroplast)
tree<-Rprotpars(chloroplast)

## End(Not run)
```

---

**Description**

This function is an R interface for restdist in the PHYLIP package (Felsenstein 2013). restdist can be used to estimate the evolutionary distances between populations based on restriction site or fragment data.

**Usage**

```r
rrestdist(X, path=NULL, ...)
```
Arguments

- **x**
  - an object of class "rest.data" containing data for restriction sites.

- **path**
  - path to the executable containing restdist. If path = NULL, the R will search several paths for restdist. See details for more information.

- **...**
  - optional arguments to be passed to restdist. See details for more information.

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method, the method for calculating the genetic distance - options are "Modified" (the default), and "Nei/Li" (Nei & Li 1979); data, the type of data - either "sites" or "fragments"; gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); kappa transition:transversion ratio (defaults to kappa = 2.0); site.length the restriction site length (defaults to site.length=0); 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: [http://evolution.genetics.washington.edu/phylip.html](http://evolution.genetics.washington.edu/phylip.html).

Value

This function returns an object of class "dist".

Author(s)

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References


See Also

- Rdnadist, Rgendist, Rprotdist
Description

This function is an R interface for restml in the PHYLIP package (Felsenstein 2013). restml can be used to conduct ML phylogeny inference from restriction site or fragment data (Nei & Li 1979; Smouse & Li 1987; Felsenstein 1992).

Usage

Rrestml(X, path=NULL, ...)

Arguments

X
an object of class "rest.data" containing data for restriction sites.

path
path to the executable containing restml. If path = NULL, the R will search several paths for restml. See details for more information.

...optional arguments to be passed to restml. 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; 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); site.length the restriction site length (defaults to site.length=6); 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 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: http://evolution.genetics.washington.edu/phylip.html.

Value

This function returns an object of class "dist".
Author(s)

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

References


See Also

*Restdist*

Examples

```r
## Not run:
data(restriction.data)
tree<-Rrestml(restriction.data)

## End(Not run)
```

Rseqboot                R interface for seqboot

Description

This function is an R interface for seqboot in the PHYLIP package (Felsenstein 2013). seqboot can be used to perform the non-parametric bootstrap following Felsenstein (1985).

Usage

```r
Rseqboot(X, path=NULL, ...)
```
Arguments

\(X\) either: (a) an object of class "DNAbin" containing DNA sequences or an object of class "proseq" containing amino acid sequences; (b) an object of class "phylip.data" containing data for a binary or multi-state discrete character; (c) an object of class "rest.data" containing restriction site data; or (d) a matrix with gene frequency data (this option does not presently work properly).

\(\text{path}\) path to the executable containing seqboot. If \(\text{path}\) = NULL, the R will search several paths for seqboot. See details for more information.

... optional arguments to be passed to seqboot. See details for more information.

Details

Optional arguments include the following: \(\text{quiet}\) suppress some output to R console (defaults to \(\text{quiet}\) = FALSE); \(\text{type}\) the data type (options are "sequence", "morph", "rest", or "gene.freq"); \(\text{method}\) analysis method (options are "bootstrap", "jackknife", and "permute"); \(\text{percentage}\) a bootstrap or jackknife percentage (can be >100); \(\text{block.size}\) block size in number of characters for the bootstrap, jackknife, or permutation (defaults to 1, the regular bootstrap); \(\text{replicates}\) number of replicates (defaults to 100); \(\text{weights}\) a vector of weights that must be \(0\) or \(1\)-characters with weight of \(0\) are excluded from the resampling procedure; \(\text{rate.categories}\) vector of integers between 1 and 9 indicating the rate category for each character - this is supplied so that resampled rate categories can be output by the method; \(\text{mixture}\) vector of "w" and "c" (see \texttt{Rmix}); and \(\text{cleanup}\) remove PHYLIP input & output files after the analysis is completed (defaults to \(\text{cleanup}\) = TRUE). More information about the seqboot program in PHYLIP can be found here http://evolution.genetics.washington.edu/phylip/doc/seqboot.html.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 1989, 2013) should first be installed. Instructions for installing PHYLIP can be found on the PHYLIP webpage: http://evolution.genetics.washington.edu/phylip.html.

Value

This function returns a list of objects of class "DNAbin", "proseq", "phylip.data", or "rest.data" depending on the input data type. If \(\text{ancestors}\), \(\text{mixture}\), or \(\text{rate.categories}\) are supplied, then each element of the list contains an object data (containing the data), and vectors \(\text{ancestors}\), \(\text{mixture}\), and/or \(\text{categories}\), containing the resampled input vectors.

Author(s)

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References

Rthreshml

R interface for threshml

Description

This function is an R interface for threshml in the PHYLIP package (Felsenstein 1989, 2013). threshml fits the threshold model of Felsenstein (2005; 2012). Note that threshml is new & not in the currently released version of PHYLIP (as of December 2013). It can be downloaded from its webpage here: http://evolution.gs.washington.edu/phylip/download/threshml/. If not specifying path, the executable file for threshml (e.g., threshml.exe in Windows) should be placed in the folder containing all other executable files for PHYLIP (e.g., C:/Program Files/phylip=3.695/exe in Windows).

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 data.frame of continuous valued or discrete character traits with rownames containing species names. Discrete & continuous characters can be supplied in any order. All discrete character traits must be two-state, but can be coded using any convention (i.e., \(\theta, 1, "A", "B", etc\.)

types

character vector containing the types (e.g., "discrete", "continuous"). If types are not supplied, Rthreshml will try to figure out which columns via is.numeric.

path

path to the executable containing threshml. 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)

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References


See Also

rcontrast

See Also

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 1989, 2013) should first be installed. Instructions for 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)

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References


Examples

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

Set path to the folder containing **PHYLIP** executables for the current R session.

Sets the path to the folder containing PHYLIP executables for the current R session. Once `setPath` has been used, Rphylib functions will no longer search for the path to the PHYLIP executable, using `path` instead.

`clearPath` clears the path.

**Usage**

```r
setPath(path)
clearPath()
```

**Arguments**

- `path` : path to the folder contains PHYLIP executables.

**Author(s)**

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**setupOSX**

Help set up PHYLIP in Mac OS X

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

**Usage**

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

**Arguments**

- `path` : path to the folder containing the PHYLIP package. If `path = NULL`, the R will search several commonly used directories.

**Details**

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

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

**References**


**Examples**

```r
## Not run:
setupOSX()

## End(Not run)
```
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