

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.

License GPL (>= 2)

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

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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 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

- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- 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 0-1.09.

as.proseq	<i>Converts objects to protein sequences, phylip.data, or rest.data object</i>
-----------	--

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.

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

- Felsenstein, J. (1981) Evolutionary trees from DNA sequences: A Maximum Likelihood approach. *Journal of Molecular Evolution*, 17, 368-376.
- Felsenstein, J. (1989) PHYLIP-Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Felsenstein, J., Churchill, G. A. (1996) A Hidden Markov Model approach to variation among sites in rate of evolution. *Molecular Biology and Evolution*, 13, 93-104.

See Also[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 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 a 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)
```

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.

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Source

Chamberlain, S.A., & J.A. Rudgers. 2012. How do plants balance multiple mutualists? Correlations among traits for attracting protective bodyguards and pollinators in cotton (*Gossypium*). *Evolutionary Ecology* 26:65-77. DOI: 10.1007/s10682-011-9497-3.

<code>print.proseq</code>	<i>Print method protein sequences, phylip.data, or rest.data object</i>
---------------------------	---

Description

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

Usage

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

Arguments

<code>x</code>	an object of class "proseq", an object of class "phylip.data", or an object of class "rest.data".
<code>printlen</code>	number of sequence names to print.
<code>digits</code>	number of digits to print.
<code>...</code>	optional arguments.

Value

Prints to screen.

Author(s)

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See Also

[as.proseq](#), [print.DNAbin](#), [Rproml](#)

Rclique	<i>R interface for clique</i>
---------	-------------------------------

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).

More information about the clique program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/clique.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" that is the optimized tree.

Author(s)

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References

- Estabrook, G. F., Johnson, C. S. Jr., McMorris, F. R. (1976). A mathematical foundation for the analysis of character compatibility. *Mathematical Biosciences*, 23, 181-187.
- Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Le Quesne, W.J. (1969) A method of selection of characters in numerical taxonomy. *Systematic Zoology*, 18, 201-205.

See Also

[Rdnacomp](#), [Rmix](#)

Examples

```
## 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

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

Arguments

<code>trees</code>	an object of class "multiPhylo".
<code>path</code>	path to the directory containing the executable consense. If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file.
<code>...</code>	optional arguments to be passed to <code>consense</code> . 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`).

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

- Margush, T., McMorris, F.R. (1981) Consensus n-trees. *Bulletin of Mathematical Biology*, 43, 239-244.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Examples

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

## End(Not run)
```

Rcontml

R interface for contml

Description

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

Usage

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

Arguments

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

Details

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

More information about the contml program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/contml.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" that is the optimized tree.

Author(s)

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References

Felsenstein, J. (1981) Maximum likelihood estimation of evolutionary trees from continuous characters. *American Journal of Human Genetics*, 25, 471-492.

Felsenstein, J. (1981) Maximum likelihood estimation of evolutionary trees from continuous characters. *American Journal of Human Genetics*, 25, 471-492.

Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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](#), [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).

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

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 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.

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

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

- Felsenstein, J. (1985) Phylogenies and the comparative method. *American Naturalist*, 125, 1-15.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- 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](#), `Rcontml`, `Rthreshml`

Examples

```
## 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).

More information about the dnacomp program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dnacomp.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" that is the optimized tree.

Author(s)

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References

Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Fitch, W.M. (1975) Toward finding the tree of maximum parsimony. pp. 189-230 in *Proceedings of the Eighth International Conference on Numerical Taxonomy*, ed. G. F. Estabrook. W. H. Freeman, San Francisco.

Le Quesne, W.J. (1969) A method of selection of characters in numerical taxonomy. *Systematic Zoology*, 18, 201-205.

See Also

[Rdnapars](#), [Rdnapenny](#)

Examples

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

## End(Not run)
```

Rdnadist	<i>R interfaces for dnadist</i>
----------	---------------------------------

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`).

More information about the `dnadist` program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dnadist.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 "dist".

Author(s)

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References

- Barry, D., Hartigan, J.A. (1987) Statistical analysis of hominoid molecular evolution. *Statistical Science*, 2, 191-200.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Felsenstein, J., Churchill, G. A. (1996) A Hidden Markov Model approach to variation among sites in rate of evolution. *Molecular Biology and Evolution*, 13, 93-104.
- Jukes, T.H., Cantor, C.R. (1969) Evolution of protein molecules. pp. 21-132 in *Mammalian Protein Metabolism Vol. III*, ed. M.N. Munro. Academic Press, New York.
- Kimura, M. (1980) A simple model for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*, 16, 111-120.
- Kishino, H., Hasegawa, M. (1989) Evaluation of the maximum likelihood estimate of the evolutionary tree topology from DNA sequence data, and the branching order in Hominoidea. *Journal of Molecular Evolution*, 29, 170-179.
- Lake, J.A. (1994) Reconstructing evolutionary trees from DNA and protein sequences: Paralinear distances. *Proceedings of the National Academy of Sciences*, 91, 1455-1459.
- Lockhart, P.J., Steel, M.A., Hendy, M.D., Penny, D. (1994) Recovering evolutionary trees under a more realistic model of sequence evolution. *Molecular Biology and Evolution*, 11, 605-612.
- Steel, M.A. (1994) Recovering a tree from the Markov leaf colourations it generates under a Markov model. *Applied Mathematics Letters*, 7, 19-23.

See Also

[Rneighbor](#)

Examples

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

## End(Not run)
```

Rdnainvar

*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

```
Rdnainvar(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).

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

At present, this function merely prints the results of dnainvar to screen.

Author(s)

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References

- Cavender, J.A., Felsenstein, J. (1987) Invariants of phylogenies in a simple case with discrete states. *Journal of Classification*, 4, 57-71.
- Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Lake, J.A. (1987) A rate-independent technique for analysis of nucleic acid sequences: evolutionary parsimony. *Molecular Biology and Evolution*, 4, 167-191.

See Also

[Rdnapars](#)

Examples

```
## 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

```
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.

More information about the `dnaml` and `dnamlk` programs in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dnaml.html>, and here <http://evolution.genetics.washington.edu/phylip/doc/dnamlk.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Felsenstein, J. (1981) Evolutionary trees from DNA sequences: A Maximum Likelihood approach. *Journal of Molecular Evolution*, 17, 368-376.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Felsenstein, J., Churchill, G. A. (1996) A Hidden Markov Model approach to variation among sites in rate of evolution. *Molecular Biology and Evolution*, 13, 93-104.

See Also

[opt.Rdnaml](#), [Rcontml](#), [Rproml](#)

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

Usage

```
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).

More information about the dnapars program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dnapars.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

Eck, R.V., Dayhoff, M.O. (1966) *Atlas of Protein Sequence and Structure 1966*. National Biomedical Research Foundation, Silver Spring, Maryland.

Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Fitch, W.M. (1971) Toward defining the course of evolution: Minimum change for a specified tree topology. *Systematic Zoology*, 20, 406-416.

Kluge, A.G., Farris, J.S. (1969) Quantitative phyletics and the evolution of anurans. *Systematic Zoology*, 18, 1-32.

See Also

[Rdnaml](#), [Rdnapenny](#)

Examples

```
## 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`).

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

Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Hendy, M.D., Penny, D. (1982) Branch and bound algorithms to determine minimal evolutionary trees. *Mathematical Biosciences*, 60, 133-142.

See Also

[Rdnapars](#)

Examples

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

## End(Not run)
```

Rdollop

*R interface for dollop***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

```
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="dollop", 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).

More information about the dollop program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dollop.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Farris, J.S. (1977) Phylogenetic analysis under Dollo's Law. *Systematic Zoology*, 26, 77-88.
- Farris, J.S. (1978) Inferring phylogenetic trees from chromosome inversion data. *Systematic Zoology*, 27, 275-284.
- Felsenstein, J. (1979) Alternative methods of phylogenetic inference and their interrelationship. *Systematic Zoology*, 28, 49-62.
- Felsenstein, J. (1984) The statistical approach to inferring evolutionary trees and what it tells us about parsimony and compatibility. pp. 169-191 in: *Cladistics: Perspectives in the Reconstruction of Evolutionary History*, edited by T. Duncan and T. F. Stuessy. Columbia University Press, New York.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Inger, R.F. (1967) The development of a phylogeny of frogs. *Evolution*, 21, 369-384.
- Le Quesne, W.J. (1974) The uniquely evolved character concept and its cladistic application. *Systematic Zoology*, 23, 513-517.

See Also

[Rpars](#), [Rdnarpars](#)

Examples

```
## 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

```
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 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 `rdolpenny` program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/dolpenny.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

- Farris, J.S. (1977) Phylogenetic analysis under Dollo's Law. *Systematic Zoology*, 26, 77-88.
- Farris, J.S. (1978) Inferring phylogenetic trees from chromosome inversion data. *Systematic Zoology*, 27, 275-284.
- Felsenstein, J. (1979) Alternative methods of phylogenetic inference and their interrelationship. *Systematic Zoology*, 28, 49-62.
- Felsenstein, J. (1984) The statistical approach to inferring evolutionary trees and what it tells us about parsimony and compatibility. pp. 169-191 in: *Cladistics: Perspectives in the Reconstruction of Evolutionary History*, edited by T. Duncan and T. F. Stuessy. Columbia University Press, New York.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Hendy, M.D., Penny, D. (1982) Branch and bound algorithms to determine minimal evolutionary trees. *Mathematical Biosciences*, 60, 133-142.
- Inger, R.F. (1967) The development of a phylogeny of frogs. *Evolution*, 21, 369-384.
- Le Quesne, W.J. (1974) The uniquely evolved character concept and its cladistic application. *Systematic Zoology*, 23, 513-517.

See Also

[Rdnapars](#)

Examples

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

read.protein	<i>Reads protein sequences from file in multiple formats</i>
--------------	--

Description

Reads protein sequences from a file.

Usage

```
read.protein(file, format="fasta", ...)
```

Arguments

file	file name for file containing protein sequences.
format	format of input file. Permitted formats are "fasta" and "sequential". See read.dna for more information.
...	optional arguments.

Value

An object of class "proseq" containing protein sequences.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

See Also

[as.proseq](#), [print.proseq](#), [Rproml](#)

Rfitch

*R interface for fitch***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).

Usage

```
Rfitch(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 <code>fitch</code> . If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to <code>fitch</code> . 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` 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 `fitch` program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/fitch.html>.

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 Fitch-Margoliash, LS, or ME tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Cavalli-Sforza, L.L., Edwards, A.W.F. (1967) Phylogenetic analysis: models and estimation procedures. *Evolution*, 32, 550-570.
- Fitch, W.M., Margoliash, E. (1967) Construction of phylogenetic trees. *Science*, 155, 279-284.
- Kidd, K.K., Sgaramella-Zonta, L.A. (1971) Phylogenetic analysis: concepts and methods. *American Journal of Human Genetics*, 23, 235-252.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

[Rdnadist](#)

Examples

```
## 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

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

Arguments

- | | |
|------|--|
| X | either: (a) A <i>matrix</i> 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`).

More information about the `gendist` program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/gendist.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 "dist".

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Cavalli-Sforza, L.L., Edwards, A.W.F. (1967) Phylogenetic analysis: models and estimation procedures. *Evolution*, 32, 550-570.
- Felsenstein, J. (1989) PHYLIP-Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Nei, M. (1972) Genetic distance between populations. *American Naturalist*, 106, 283-292.
- Reynolds, J.B., Weir, B.S., Cockerham, C.C. (1983) Estimation of the coancestry coefficient: basis for a short-term genetic distance. *Genetics*, 105, 767-779.

See Also

[Rdnadist](#), [Rprotdist](#)

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 constraining 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

```
Rkitsch(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.

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

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

- Cavalli-Sforza, L.L., Edwards, A.W.F. (1967) Phylogenetic analysis: models and estimation procedures. *Evolution*, 32, 550-570.
- Felsenstein, J. (1986) Distance methods: a reply to Farris. *Cladistics*, 2, 130-144.
- Fitch, W.M., Margoliash, E. (1967) Construction of phylogenetic trees. *Science*, 155, 279-284.
- Kidd, K.K., Sgaramella-Zonta, L.A. (1971) Phylogenetic analysis: concepts and methods. *American Journal of Human Genetics*, 23, 235-252.
- Felsenstein, J. (1989) PHYLIP-Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

See Also

[Rfitch](#)

Examples

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

## End(Not run)
```

Rmix

R 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 "phylip.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).

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

- Camin, J.H., Sokal, R.R. (1965) A method for deducing branching sequences in phylogeny. *Evolution*, 19, 311-326.
- Eck, R.V., Dayhoff, M.O. (1966) *Atlas of Protein Sequence and Structure 1966*. National Biomedical Research Foundation, Silver Spring, Maryland.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Kluge, A.G., Farris, J.S. (1969) Quantitative phyletics and the evolution of anurans. *Systematic Zoology*, 18, 1-32.
- Hendy, M.D., Penny, D. (1982) Branch and bound algorithms to determine minimal evolutionary trees. *Mathematical Biosciences*, 60, 133-142.

See Also

[Rdnapars](#)

Examples

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

## End(Not run)
```

Rneighbor	<i>R interface for neighbor</i>
-----------	---------------------------------

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

```
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).

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

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

- Saitou, N., Nei, M. (1987) The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, 4, 406-425.
- Sokal, R., Michener, C. (1958) A statistical method for evaluating systematic relationships. *University of Kansas Science Bulletin*, 38, 1409-1438.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

See Also

[Rdnadist](#)

Examples

```
## 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`).

More information about the pars program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/pars.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Eck, R.V., Dayhoff, M.O. (1966) *Atlas of Protein Sequence and Structure 1966*. National Biomedical Research Foundation, Silver Spring, Maryland.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Fitch, W.M. (1971) Toward defining the course of evolution: Minimum change for a specified tree topology. *Systematic Zoology*, 20, 406-416.
- Kluge, A.G., Farris, J.S. (1969) Quantitative phyletics and the evolution of anurans. *Systematic Zoology*, 18, 1-32.

See Also

[Rdnaml](#), [Rdnapenny](#)

Examples

```
## 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

```
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

Camin, J.H., Sokal, R.R. (1965) A method for deducing branching sequences in phylogeny. *Evolution*, 19, 311-326.

Eck, R.V., Dayhoff, M.O. (1966) *Atlas of Protein Sequence and Structure 1966*. National Biomedical Research Foundation, Silver Spring, Maryland.

Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Kluge, A.G., Farris, J.S. (1969) Quantitative phyletics and the evolution of anurans. *Systematic Zoology*, 18, 1-32.

Hendy, M.D., Penny, D. (1982) Branch and bound algorithms to determine minimal evolutionary trees. *Mathematical Biosciences*, 60, 133-142.

See Also

[Rdnapars](#)

Examples

```
## 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

```
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 `Rproml`. If `clock=TRUE` then `promlk` is used internally. For `Rpromlk` a molecular clock is assumed, thus `Rproml(...,clock=TRUE)` and `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.

More information about the `proml` and `promlk` programs in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/proml.html>, and here <http://evolution.genetics.washington.edu/phylip/doc/promlk.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Dayhoff, M.O., Eck, R.V. (1968) *Atlas of Protein Sequence and Structure 1967-1968*. National Biomedical Research Foundation, Silver Spring, Maryland.
- Dayhoff, M.O., Schwartz, R.M., Orcutt, B.C. (1979) A model of evolutionary change in proteins. pp. 345-352 in *Atlas of Protein Sequence and Structure, Volume 5, Supplement 3, 1978*, ed. M.O. Dayhoff. National Biomedical Research Foundation, Silver Spring, Maryland.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- Jones, D.T., Taylor, W.R., Thornton, J.M. (1992) The rapid generation of mutation data matrices from protein sequences. *Computer Applications in the Biosciences (CABIOS)*, 8, 275-282.

Koisol, C., Goldman, N. (2005) Different versions of the Dayhoff rate matrix. *Molecular Biology and Evolution*, 22, 193-199.

Veerassamy, S., Smith, A., Tillier, E.R. (2003) A transition probability model for amino acid substitutions from blocks. *Journal of Computational Biology*, 10, 997-1010.

See Also

[as.proseq](#), [Rdnaml](#), [read.protein](#)

Examples

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

## End(Not run)
```

Rprotdist

R interfaces for protdist

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

```
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 sev 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 alpha 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/phylip/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/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

- Conn, E.E., Stumpf, P.K. (1963) *Outlines of Biochemistry*. John Wiley and Sons, New York.
- Dayhoff, M.O., Eck, R.V. (1968) *Atlas of Protein Sequence and Structure 1967-1968*. National Biomedical Research Foundation, Silver Spring, Maryland.
- Dayhoff, M.O., Schwartz, R.M., Orcutt, B.C. (1979) A model of evolutionary change in proteins. pp. 345-352 in *Atlas of Protein Sequence and Structure, Volume 5, Supplement 3, 1978*, ed. M.O. Dayhoff. National Biomedical Research Foundation, Silver Spring, Maryland.
- Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
- George, D.G., Hunt, L.T., Barker, W.C. (1988) *Current methods in sequence comparison and analysis*. pp. 127-149 in *Macromolecular Sequencing and Synthesis*, ed. D. H. Schlesinger. Alan R. Liss, New York.
- Jones, D.T., Taylor, W.R., Thornton, J.M. (1992) The rapid generation of mutation data matrices from protein sequences. *Computer Applications in the Biosciences (CABIOS)*, 8, 275-282.
- Kimura, M. (1980) A simple model for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*, 16, 111-120.
- Koisol, C., Goldman, N. (2005) Different versions of the Dayhoff rate matrix. *Molecular Biology and Evolution*, 22, 193-199.
- Veerassamy, S., Smith, A., Tillier, E.R. (2003) A transition probability model for amino acid substitutions from blocks. *Journal of Computational Biology*, 10, 997-1010.

See Also

[Rneighbor](#)

Examples

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

## End(Not run)
```

Rprotpars

*R interface for protpars***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

```
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).

More information about the protpars program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/protpars.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" that is the optimized tree.

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

Eck, R.V., Dayhoff, M.O. (1966) *Atlas of Protein Sequence and Structure 1966*. National Biomedical Research Foundation, Silver Spring, Maryland.

Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Fitch, W.M. (1971) Toward defining the course of evolution: Minimum change for a specified tree topology. *Systematic Zoology*, 20, 406-416.

See Also

[as.proseq](#), [Rdnapars](#), [read.protein](#)

Examples

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

## End(Not run)
```

Rrestdist

R interface for restdist

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

```
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=6`); and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

More information about the `restdist` program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/restdist.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 "dist".

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

Felsenstein, J. (1989) PHYLIP—Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.

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

Nei, M., Li, W.-H. (1979) Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences*, 76, 5269-5273.

See Also

[Rdnadist](#), [Rgendist](#), [Rprotodist](#)

Examples

```
## Not run:
data(restriction.data)
D<-Rrestdist(restriction.data)

## End(Not run)
```

Rrestml

*R interface for restml***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).

More information about the restml program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/restml.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 "dist".

Author(s)

Liam J. Revell, Scott A. Chamberlain

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

References

- Felsenstein, J. (1989) PHYLIP–Phylogeny Inference Package (Version 3.2). *Cladistics*, 5, 164-166.
- Felsenstein, J. (1992) Phylogenies from restriction sites, a maximum likelihood approach. *Evolution*, 46, 159-173.
- Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.
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See Also

[Rrestdist](#)

Examples

```
## 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 to perform the non-parametric bootstrap following Felsenstein (1985).

Usage

```
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). |
| path | path to the executable containing seqboot. If 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: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `type` the data type (options are "sequence", "morph", "rest", or "gene.freq"); `method` analysis method (options are "bootstrap", "jackknife", and "permute"); `percentage` a bootstrap or jackknife percentage (can be >100); `block.size` block size in number of characters for the bootstrap, jackknife, or permutation (defaults to 1, the regular bootstrap); `replicates` number of replicates (defaults to 100); `weights` a vector of weights that must be 0 or 1 - characters with weight of 0 are excluded from the resampling procedure; `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; `mixture` vector of "W" and "C" (see [Rmix](#)); and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `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 ancestors, mixture, or `rate.categories` are supplied, then each element of the list contains an object data (containing the data), and vectors ancestors, mixture, and/or categories, containing the resampled input vectors.

Author(s)

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

References

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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 <i>data.frame</i> 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., 0, 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 <code>is.numeric</code> .
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; `lrttest` 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

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

See Also[Rcontrast](#)

Rtreedist*R interface for treedist*

Description

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

Usage

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

Arguments

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

Details

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

More information about the treedist program in PHYLIP can be found here <http://evolution.genetics.washington.edu/phylip/doc/treedist.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 matrix of pairwise distances for distances = "all" and distances = "all.1to2", or a named vector for distances = "adjacent" and distances = "corresponding".

Author(s)

Liam J. Revell, Scott A. Chamberlain

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References

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Robinson, D.F., Foulds, L.R. (1981) Comparison of phylogenetic trees. *Mathematical Biosciences*, 53, 131-147.

Examples

```
## 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

Description

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

clearPath clears the path.

Usage

```
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*

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 folder containing the PHYLIP package. If <code>path = NULL</code> , 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>) 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 J. Revell, Scott A. Chamberlain

Maintainer: Liam J. 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)
```


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