Package 'Rphylip'

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Title Rphylip: An R interface for PHYLIP

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Depends R (>= 2.10), ape (>= 3.0-10)

ZipData no

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

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

Repository

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R topics documented:

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)

Liam J. Revell

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.

Revell, L. J. (2013) Rphylip: An R interface for PHYLIP. R package version 0-1.09.

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

Description

Converts objects to class ″proseq″ or ″phylip.data″.

Usage

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

Arguments

x   an object containing amino sequences, a set of binary characters, or an arbitrary
            user-defined multistate character. (Presently only objects of class ″phyDat″ are
            permitted.)

...   optional arguments.

Value

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

Author(s)

Liam Revell <liam.revell@umb.edu>

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)

Liam 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

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.

Usage

```
data(primates)
data(chloroplast)
data(primates.bin)
```

Format

The data are stored as an object of class ″DNAbin″, ″proseq″, or ″phylip.data″.

Source

Unknown.

---

print.proseq	*Print method protein sequences or phylip.data object*

Description

Print method for an objects of class ″proseq″ or class ″phylip.data″.

Usage

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

Arguments

x	an object of class ″proseq″ or an object of class ″phylip.data″.
printlen	number of sequence names to print.
digits	number of digits to print.
...	optional arguments.

Value

Prints to screen.

Author(s)

Liam Revell <liam.revell@umb.edu>

See Also

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

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

trees   an object of class "multiPhylo".

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

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

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method which can be "extended" (extended majority rule consensus, the default), "strict" (strict consensus), or regular majority rule consensus ("majority"); "outgroup" single taxon label or vector of taxa that should be used to root all trees before analysis; rooted logical value indicated whether to treat the input trees as rooted (defaults to rooted = FALSE); and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

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)

Liam Revell <liam.revell@umb.edu>

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

Details

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

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)

Liam Revell <liam.revell@umb.edu>

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 *matrix* of continuous valued traits (in columns) with rownames containing species names. For one trait, X can be a matrix with one column or a vector with `names(X)` containing species names matching `tree$tip.label`. For within-species contrasts analysis, the matrix should contain repeating (identical) row names for conspecifics.
path	path to the executable containing contrast. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to contrast. See details for more information.

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 contrats; `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)

Liam Revell <liam.revell@umb.edu>

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

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)

Liam 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.

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   *R interfaces for dnadist*

Description

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

Usage

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

Arguments

X   an object of class "DNAbin".

method   method for calculating the distances. Can be "F84" (Kishino & Hasegawa 1989; Felsenstein & Churchill 1996), "K80" (Kimura 1980), "JC" (Jukes & Cantor 1969), or "LogDet" (Barry & Hartigan 1987; Lake 1994; Steel 1994; Lockhart et. al. 1994). Also method="similarity" computes the sequence similarity among the rows of X.

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

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

Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); kappa transition:transversion ratio (defaults to kappa = 2.0); rates vector of rates (defaults to single rate); rate.categories vector of rate categories corresponding to the order of rates; weights vector of weights of length equal to the number of columns in X (defaults to unweighted); bf vector of base frequencies in alphabetical

order (i.e., A, C, G, & T) - if not provided, then defaults to empirical frequencies; and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

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)

Liam Revell <liam.revell@umb.edu>

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 teh evolutionary tree topology from DNA sequence data, and the branching order in Hominoidea. *Journal of Molecular Evolutioon*, 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 computest 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)

Liam Revell <liam.revell@umb.edu>

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 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 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: Minimu 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 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 binary character; or a matrix.
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; `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); `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); 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 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](), [Rdnapars]()

Examples

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

## End(Not run)
```

---

read.protein	*Reads protein sequences from file in multiple formats*

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 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 leasts-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 fitch. If `path = NULL`, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to fitch. See details for more information.

Details

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `method` - can be `"FM"` or `"fm"` (for the Fitch-Margoliash criterion; Fitch & Margoliash 1967), `"LS"` or `"ls"` for the Cavalli-Sforza & Edwards (1967) least-squares criterion, or `"ME"` or `"me"` (for Minimum Evolution); `tree` object of class `"phylo"` - if supplied, then branch lengths are optimized & the optimality criterion is computed on the input tree; `negative` a logical value indicating whether negative branch lengths should be permitted (defaults to `negative = TRUE`; `global` perform global search (defaults to `global = TRUE`); `random.order` add taxa to tree in random order (defaults to `random.order = TRUE`); `random.addition` number of random addition replicates for `random.order = TRUE` (defaults to `random.addition = 10`); `outgroup` 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 NJ or UPGMA tree.

Author(s)

Liam 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)
```

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 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   *R interface for neighbor*

Description

This function is an R interface for neighbor in the PHYLIP package (Felsenstein 2013). neighbor can be used for neighbor-joining (Saitou & Nei 1987) and UPGMA (Sokal & Michener 1958) phylogeny inference.

Usage

```
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 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 binary character or multistate character; 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 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: Minimu 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 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 infor-
                   mation.

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 or-der (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 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 Foundataion, 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 Revell <liam.revell@umb.edu>

References

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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.

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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 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.

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See Also

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

Examples

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

## End(Not run)
```

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 web-page here: <http://evolution.gs.washington.edu/phylip/download/threshml/>. If not specifying path, the executable file for threshml (e.g., threshml.exe in Windows) should be placed in the folder containing all other executable files for PHYLIP (e.g., C:/Program Files/phylip=3.695/exe in Windows).

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

Usage

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

Arguments

tree	object of class "phylo".
X	a *data.frame* of continuous valued or discrete character traits with rownames containing species names. Discrete & continuous characters can be supplied in any order. All discrete character traits must be two-state, but can be coded using any convention (i.e., 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 is.numeric.
path	path to the executable containing threshml. If path = NULL, the R will search several commonly used directories for the correct executable file.
...	optional arguments to be passed to threshml. See details for more information.

Details

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

Value

This function returns a list containing the results from threshml.

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Felsenstein, J. (2005) Using the quantitative genetic threshold model for inferences between and within species *Philosophical Transactions of the Royal Society London B*, 360, 1427-1434.

Felsenstein, J. (2012) A comparative method for both discrete and continuous characters using the threshold model. *American Naturalist*, 179, 145-156.

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)

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References

Bourque, M. (1978) *Arbres de Steiner et reseaux dont certains sommets sont a localisation variable*. Ph.D. Dissertation, Universite de Montreal, Montreal, Quebec.

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

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Kuhner, M.K., Felsenstein, J. (1994) A simulation comparison of phylogeny algorithms under equal and unequal evolutionary rates. *Molecular Biology and Evolution*, 11, 459-468.

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)

Liam Revell <liam.revell@umb.edu>

---

setupOSX   *Help set up PHYLIP in Mac OS X*

Description

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

Usage

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

Arguments

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

Details

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

Author(s)

Liam Revell <liam.revell@umb.edu>

References

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

Examples

```
## Not run:
setupOSX()

## End(Not run)
```

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