

Package ‘TreeSearch’

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Title Phylogenetic Tree Search Using Custom Optimality Criteria

Version 0.2.2

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License GPL (>= 3)

Copyright Incorporates C/C++ code from: ape by Emmanuel Paradis;
phangorn by Klaus Scheip <doi:10.1093/bioinformatics/btq706>;
Morphy Phylogenetic Library by Martin Brazeau
<<https://github.com/mbrazeau/MorphLib>> (GPL3)

Description Searches for phylogenetic trees that are optimal using a user-defined criterion.
Implements Profile Parsimony (Faith and Trueman, 2001) <doi:10.1080/10635150118627>, and
Successive Approximations (Farris, 1969) <doi:10.2307/2412182>.
Handles inapplicable data using the algorithm of Brazeau, Guillerme and Smith
(2019) <doi:10.1093/sysbio/syy083>.

URL <https://github.com/ms609/TreeSearch>

BugReports <https://github.com/ms609/TreeSearch/issues>

Depends R (>= 3.4.0)

Imports ape (>= 5.0), colorspace, gmp, memoise, phangorn (>= 2.2.1),
R.cache, Rdpack, stats

Suggests knitr, Rcpp, rmarkdown, shiny, testthat, xlsx

RdMacros Rdpack

LazyData true

ByteCompile true

LinkingTo Rcpp

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VignetteBuilder knitr

RoxygenNote 6.1.1

NeedsCompilation yes

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R topics documented:

AddTip	3
AllAncestors	4
AllSPR	5
ApeTime	6
AsBinary	6
brewer	7
CollapseNode	8
congreveLamsdellMatrices	9
ConsensusWithout	10
DescendantEdges	11
DFact	11
DropSingleSplits	12
EdgeAncestry	13
EnforceOutgroup	13
Evaluate	14
Fitch	14
FitchSteps	15
ICSteps	16
inapplicable.citations	17
inapplicable.datasets	20
inapplicable.phyData	23
InfoAmounts	26
IWScore	26
IWScoreMorphy	27
LDFact	29
LDFactorial	29
Lobo.data	30
Lobo.phy	31
LogisticPoints	32
MatrixToList	32
MinimumSteps	33
MorphyBootstrap	33
MorphyWeights	34
N1Spr	35
NamedConstant	36
NewickTree	36

NJTree	37
NNI	37
NRooted	39
PhyDat2Morphy	40
PhyToString	41
PrepareDataProfile	41
RandomMorphyTree	42
RandomTree	43
RandomTreeScore	43
ReadCharacters	44
ReadTntTree	45
RearrangeEdges	47
referenceTree	48
ReNumber	49
ReNumberTips	49
RootTree	50
SetMorphyWeights	50
SingleCharMorphy	51
SingleTaxonTree	52
SortTree	52
SplitFrequency	53
SPR	54
StringToPhyDat	56
Subtree	57
SuccessiveApproximations	58
summary.morphyPtr	59
SupportColour	59
TBR	60
UniqueSplits	62
UnloadMorphy	62
UnloadTreeSearch	63
WithOneExtraStep	63
Index	64

AddTip

Add a tip to a phylogenetic tree

Description

AddTip adds a tip to a phylogenetic tree at a specified location.

Usage

AddTip(tree, where, label)

Arguments

tree	A tree of class phylo .
where	The node or tip that should form the sister taxon to the new node. To add a new tip at the root, use "where = 0";
label	A character string providing the label the new tip.

Details

AddTip extends [bind.tree](#), which cannot handle single-taxon trees.

Value

This function returns a tree of class `phylo` with an additional tip at the desired location.

Author(s)

Martin R. Smith

See Also

[bind.tree](#)
[nodelabels](#)

Examples

```
{
  library('ape')
  plot(tree <- rtree(10, br=NULL)); nodelabels(); nodelabels(15, 15, bg='green'); dev.new()
  plot(AddTip(tree, 15, 'NEW_TIP'))
}
```

AllAncestors

List all ancestral nodes

Description

AllAncestors lists ancestors of each parent node in a tree

Usage

```
AllAncestors(parent, child)
```

Arguments

parent	the first column of the edge matrix of a tree of class phylo , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class phylo , i.e. <code>tree\$edge[, 2]</code>

Details

Note that the tree's edges must be listed in an order whereby each entry in `tr$edge[, 1]` (with the exception of the root) has appeared already in `tr$edge[, 2]`

Value

This function returns a list. Entry `i` contains a vector containing, in order, the nodes encountered when traversing the tree from node `i` to the root node. The last entry of each member of the list will therefore be the root node, with the exception of the entry for the root node itself, which will be `NULL`.

Author(s)

Martin R. Smith

Examples

```
tr <- ape::rtree(20, br=NULL)
edge <- tr$edge
AllAncestors(edge[, 1], edge[, 2])
```

AllSPR

All SPR trees

Description

All SPR trees

Usage

```
AllSPR(parent, child, nEdge, notDuplicateRoot, edgeToBreak)
```

Arguments

<code>parent</code>	the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code>
<code>child</code>	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
<code>nEdge</code>	integer specifying the number of edges of a tree of class <code>phylo</code> , i.e. <code>dim(tree\$edge)[1]</code>
<code>notDuplicateRoot</code>	logical vector of length <code>nEdge</code> , specifying for each edge whether it is the second edge leading to the root (in which case its breaking will be equivalent to breaking the other root edge... except insofar as it moves the position of the root.)
<code>edgeToBreak</code>	(optional) integer specifying the index of an edge to <code>bisect/prune</code> , generated randomly if not specified. Alternatively, set to <code>-1</code> to return a complete list of all trees one step from the input tree.

Value

a list of edge matrices for all trees one SPR rearrangement from the starting tree

Author(s)

Martin R. Smith

ApeTime	<i>Ape Time</i>
---------	-----------------

Description

Reads the time that an ape tree was modified from the comment in the nexus file

Usage

```
ApeTime(filename, format = "double")
```

Arguments

filename	Character string specifying path to the file
format	Format in which to return the time: 'double' as a sortable numeric; any other value to return a string in the format YYYY-MM-DD hh:mm:ss

Value

The time that the specified file was created by ape.

Author(s)

Martin R. Smith

AsBinary	<i>Convert a number to binary</i>
----------	-----------------------------------

Description

Provides a (reversed) binary representation of a decimal integer

Usage

```
AsBinary(x)
```

Arguments

x	Decimal integer to be converted to binary bits
---	--

Details

Provides an array corresponding to binary digits 1, 2, 4, 8, 16, ...

Binary number 0100 (= decimal 4) will be represented as 0 0 1.

Value

An array corresponding to binary digits 1, 2, 4, 8, 16, ...

'Leading zeros' are not included.

Author(s)

Martin R. Smith, adapted from code posted to R mailing list by Spencer Graves

Examples

```
AsBinary(4) # 0 0 1
AsBinary(10) # 0 1 0 1
```

brewer

Brewer palettes

Description

A list of eleven Brewer palettes containing one to eleven colours that are readily distinguished by colourblind viewers, followed by a twelfth 12-colour palette adapted for colour blindness.

Usage

```
brewer
```

Format

An object of class `list` of length 12.

Source

[ColourBrewer2.org](<http://colorbrewer2.org/#type=diverging&scheme=RdYlBu&n=3>) [Martin Krzywinski](<http://mkweb.bcgsc.ca/colorblind/>)

CollapseNode

Collapse nodes on a phylogenetic tree

Description

Collapse nodes on a phylogenetic tree

Usage

```
CollapseNode(tree, nodes)
```

```
CollapseEdge(tree, edges)
```

Arguments

tree	A tree of class phylo .
nodes, edges	Integer vector specifying the nodes or edges in the tree to be dropped. (Use [ape:nodelabels] or [ape:edgelabels] to view numbers on a plotted tree.)

Value

'tree', with the specified nodes or edges collapsed. The length of each dropped edge will (naively) be added to each descendant edge.

Author(s)

Martin R. Smith

Examples

```
library(ape)
set.seed(1)

tree <- rtree(7)
par(mfrow=c(2, 1), mar=rep(0.5, 4))
plot(tree)
nodelabels()
edgelabels(round(tree$edge.length, 2), cex=0.6, frame='n', adj=c(1, -1))

newTree <- CollapseNode(tree, c(12, 13))
plot(newTree)
nodelabels()
edgelabels(round(newTree$edge.length, 2), cex=0.6, frame='n', adj=c(1, -1))
```

`congreveLamsdellMatrices`*100 simulated data matrices*

Description

Contains the 100 simulated matrices generated by Congreve & Lamsdell (2016) using a heterogeneous Markov-k model, generated from the [referenceTree](#) topology, with all branches sharing an equal length.

Usage`congreveLamsdellMatrices`**Format**

A list with 100 entries, each comprising a phyDat object of 55 characters for 22 taxa

Source

<https://datadryad.org/resource/doi:10.5061/dryad.7dq0j>

References

Congreve CR, Lamsdell JC (2016). “Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices.” *Palaeontology*, **59**, 447-465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).
Congreve CR, Lamsdell JC (2016). “Data from: Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices.” *Dryad Digital Repository*, doi:10.5061/dryad.7dq0j. doi: [10.5061/dryad.7dq0j](https://doi.org/10.5061/dryad.7dq0j).

Examples

```
data('referenceTree')
data('congreveLamsdellMatrices')
## Not run: ProfileScore(referenceTree,
  PrepareDataProfile(congreveLamsdellMatrices[[17]]))
## End(Not run)
```

ConsensusWithout

Consensus without taxa

Description

Displays a consensus plot with selected taxa excluded.

Usage

```
ConsensusWithout(trees, tip, ...)
```

```
MarkMissing(tip, position = "bottomleft", ...)
```

Arguments

trees	A list of phylogenetic trees, of class 'multiPhylo' or 'list'
tip	A character vector specifying the names (or numbers) of tips to drop (using <code>ape::drop.tip</code>)
...	Additional parameters to pass on to <code>ape::[consensus]</code> or <code>[legend]</code>
position	Where to plot the missing taxa. See <code>[legend]</code> for options.

Details

A useful way to gain resolution if a few wildcard taxa obscure a consistent set of relationship.

Value

A consensus tree without the excluded taxa

Functions

- `MarkMissing`: Adds missing taxa to a plotted consensus tree

Author(s)

Martin R. Smith

Martin R. Smith

DescendantEdges *Descendant Edges*

Description

Quickly identifies edges that are 'descended' from a particular edge in a tree

Usage

```
DescendantEdges(edge, parent, child, nEdge = length(parent))
```

```
AllDescendantEdges(parent, child, nEdge = length(parent))
```

Arguments

edge	number of the edge whose child edges are required
parent	the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
nEdge	number of edges (calculated from <code>length(parent)</code> if not supplied)

Value

'DescendantEdges' returns a logical vector stating whether each edge in turn is a descendant of the specified edge (or the edge itself)

'AllDescendantEdges' returns a matrix of class `logical`, with row N specifying whether each edge is a descendant of edge N (or the edge itself)

Functions

- AllDescendantEdges: Quickly identifies edges that are 'descended' from each edge in a tree

DFact *Double factorial*

Description

Double factorial

Usage

```
DFact(x)
```

```
DoubleFactorial(ints)
```

Arguments

x a positive integer
ints a vector of integers

Functions

- DoubleFactorial: Accepts a vector as input

DropSingleSplits *Drop Single Splits*

Description

Removes splits that pertain only to a single taxon from a splits object.

Usage

```
DropSingleSplits(split)
```

Arguments

split A matrix in which each column corresponds to a bipartition split

Details

Bipartition splits are divisions, implied by each edge or node of an unrooted tree topology, that divide the taxa into two groups (one of which is a clade).

By default, a list of splits will include those that separate a single taxon (a leaf) from all others. Such splits are, by definition, present in all trees that contain that taxon; they are not of interest when comparing trees. This function removes such splits from a list of bipartitions.

Value

The input matrix, with any columns that separate only a single pendant tip removed.

Author(s)

Martin R. Smith

EdgeAncestry	<i>EdgeAncestry</i>
--------------	---------------------

Description

Descendant Edges

Usage

```
EdgeAncestry(edge, parent, child, stopAt = (parent == min(parent)))
```

Arguments

edge	number of the edge whose child edges are required
parent	the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
stopAt	number of the edge at which the search should terminate; defaults to the root edges

Details

Quickly identifies edges that are 'ancestral' to a particular edge in a tree

Value

a logical vector stating whether each edge in turn is a descendant of the specified edge

Author(s)

Martin R. Smith

EnforceOutgroup	<i>Force taxa to form an outgroup</i>
-----------------	---------------------------------------

Description

Given a tree or a list of taxa, rearrange the ingroup and outgroup taxa such that the two are sister taxa across the root, without altering the relationships within the ingroup or within the outgroup.

Usage

```
EnforceOutgroup(tree, outgroup)
```

Arguments

tree	either a tree of class <code>phylo</code> , or a character vector listing the names of all the taxa in the tree, from which a random tree will be generated.
outgroup	a vector containing the names of taxa to include in the outgroup

Value

a tree where all outgroup taxa are sister to all remaining taxa, otherwise retaining the topology of the ingroup.

Author(s)

Martin R. Smith

Evaluate	<i>Evaluate tree</i>
----------	----------------------

Description

Evaluate tree

Usage

```
Evaluate(tree, dataset, warn = TRUE)
```

Arguments

tree	A tree of class <code>phylo</code> .
dataset	A phylogenetic data matrix of class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree.
warn	Boolean (TRUE/FALSE): display warnings when concavity functions are generated by approximation.

Fitch	<i>Calculate parsimony score with inapplicable data</i>
-------	---

Description

Uses code modified from the Morphy library to calculate a parsimony score in datasets that contain inapplicable data

Usage

```
Fitch(tree, dataset)
```

Arguments

tree	A tree of class phylo .
dataset	A phylogenetic data matrix of class phyDat , whose names correspond to the labels of any accompanying tree.

Value

This function returns the elements from a list containing:

- The total parsimony score
- The parsimony score associated with each character
- A matrix comprising character reconstructions for each node after the final pass

The elements to return are specified by the parameter `detail`. If a single element is requested (default) then just that element will be returned. If multiple elements are requested then these will be returned in a list.

Author(s)

Martin R. Smith (using Morphy C library, by Martin Brazeau)

See Also

[TreeSearch](#)

Examples

```
data('inapplicable.datasets')
tree <- RandomTree(inapplicable.phyData[[1]])
result <- Fitch(tree, inapplicable.phyData[[1]])
```

FitchSteps

Fitch score

Description

Fitch score

Usage

```
FitchSteps(tree, dataset)
```

Arguments

tree	A tree of class phylo .
dataset	A phylogenetic data matrix of class phyDat , whose names correspond to the labels of any accompanying tree.

Value

A vector listing the number of 'parsimony steps' calculated by the Fitch algorithm for each character. Inapplicable tokens are treated as per Brazeau, Guillerme and Smith (2017)

References

Brazeau MD, Guillerme T, Smith MR (2019). "An algorithm for morphological phylogenetic analysis with inapplicable data." *Systematic Biology*, in press. doi: [10.1093/sysbio/syy083](https://doi.org/10.1093/sysbio/syy083).

Examples

```
{
}
```

ICSteps

Information Content Steps

Description

This function estimates the information content of a character `char` when `e` extra steps are present, for all possible values of `e`.

Usage

```
ICSteps(char, ambiguousToken = 0, expectedMinima = 25,
        maxIter = 10000, warn = TRUE)
```

Arguments

<code>char</code>	The character in question.
<code>ambiguousToken</code>	Which token, if any, corresponds to the ambiguous token (?) (not yet fully implemented).
<code>expectedMinima</code>	sample enough trees that the rarest step counts is expected to be seen at least this many times.
<code>maxIter</code>	Maximum iterations to conduct.
<code>warn</code>	Boolean (TRUE/FALSE): display warnings when concavity functions are generated by approximation.

Details

Calculates the number of trees consistent with the character having e extra steps, where e ranges from its minimum possible value (i.e. number of different tokens minus one) to its maximum. The number of trees with no extra steps can be calculated exactly; the number of trees with more additional steps must be approximated. The function samples `n.iter` trees, or enough trees that the trees with the minimum number of steps will be recovered at least `expected.minima` times, in order to obtain precise results.

Author(s)

Martin R. Smith

References

Faith DP, Trueman JWH (2001). “Towards an inclusive philosophy for phylogenetic inference.” *Systematic Biology*, **50**(3), 331–350. doi: [10.1080/10635150118627](https://doi.org/10.1080/10635150118627).

Examples

```
{  
  # A character that is present in ten taxa and absent in five  
  character <- c(rep(1, 10), rep(2, 5))  
  ICSteps (character)  
}
```

inapplicable.citations

Thirty Datasets with Inapplicable data

Description

These are the datasets used to evaluate the behaviour of the inapplicable algorithm in Brazeau, Guillerme and Smith (2018).

Usage

```
inapplicable.citations
```

Format

An object of class character of length 30.

Details

The name of each item corresponds to the datasets listed below. The value gives its citation.

Source

Agnarsson2004 AGNARSSON, I. 2004. Morphological phylogeny of cobweb spiders and their relatives (Araneae, Araneoidea, Theridiidae). *Zoological Journal of the Linnean Society*, 141, 447–626.

Capa2011 CAPA, M., HUTCHINGS, P., AGUADO, M. T. and BOTT, N. J. 2011. Phylogeny of Sabellidae (Annelida) and relationships with other taxa inferred from morphology and multiple genes. *Cladistics*, 27, 449–469.

DeAssis2011 DE ASSIS, J. E. and CHRISTOFFERSEN, M. L. 2011. Phylogenetic relationships within Maldanidae (Capitellida, Annelida), based on morphological characters. *Systematics and Biodiversity*, 9, 233–245.

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Zhu2013 ZHU, M., YU, X., AHLBERG, P. E., CHOO, B., LU, J., QIAO, T., QU, Q., ZHAO, W., JIA, L., BLOM, H. and ZHU, Y. 2013. A Silurian placoderm with osteichthyan-like marginal jaw bones. *Nature*, 502, 188–193.

References

Brazeau MD, Guillaume T, Smith MR (2019). “An algorithm for morphological phylogenetic analysis with inapplicable data.” *Systematic Biology*, in press. doi: [10.1093/sysbio/syy083](https://doi.org/10.1093/sysbio/syy083).

inapplicable.datasets *Thirty Datasets with Inapplicable data*

Description

These are the datasets used to evaluate the behaviour of the inapplicable algorithm in Brazeau, Guillaume and Smith (2017).

Usage

inapplicable.datasets

Format

An object of class `list` of length 30.

Details

The name of each item corresponds to the datasets listed below. Datasets are sorted into two subsets, each sorted alphabetically; the first subset comprise simpler datasets with faster processing times. The value is the dataset in the format generated by [read.nexus.data](#).

Source

Agnarsson2004 AGNARSSON, I. 2004. Morphological phylogeny of cobweb spiders and their relatives (Araneae, Araneoidea, Theridiidae). *Zoological Journal of the Linnean Society*, 141, 447–626.

Capa2011 CAPA, M., HUTCHINGS, P., AGUADO, M. T. and BOTT, N. J. 2011. Phylogeny of Sabellidae (Annelida) and relationships with other taxa inferred from morphology and multiple genes. *Cladistics*, 27, 449–469.

DeAssis2011 DE ASSIS, J. E. and CHRISTOFFERSEN, M. L. 2011. Phylogenetic relationships within Maldanidae (Capitellida, Annelida), based on morphological characters. *Systematics and Biodiversity*, 9, 233–245.

O’Leary1999 O’LEARY, M. A. and GEISLER, J. H. 1999. The position of Cetacea within Mammalia: phylogenetic analysis of morphological data from extinct and extant taxa. *Systematic Biology*, 48, 455–490.

- Rousset2004** ROUSSET, V., ROUSE, G. W., SIDDALL, M. E., TILLIER, A. and PLEIJEL, F. 2004. The phylogenetic position of Siboglinidae (Annelida) inferred from 18S rRNA, 28S rRNA and morphological data. *Cladistics*, 20, 518–533.
- Sano2011** SANO, M. and AKIMOTO, S.-I. 2011. Morphological phylogeny of gall-forming aphids of the tribe Eriosomatini (Aphididae: Eriosomatinae). *Systematic Entomology*, 36, 607–627.
- Sansom2010** SANSOM, R. S., FREEDMAN, K., GABBOTT, S. E., ALDRIDGE, R. J. and PURNELL, M. A. 2010. Taphonomy and affinity of an enigmatic Silurian vertebrate, *Jamoytius kerwoodi* White. *Palaeontology*, 53, 1393–1409.
- Schulze2007** SCHULZE, A., CUTLER, E. B. and GIRIBET, G. 2007. Phylogeny of sipunculan worms: A combined analysis of four gene regions and morphology. *Molecular Phylogenetics and Evolution*, 42, 171–92.
- Shultz2007** SHULTZ, J. W. 2007. A phylogenetic analysis of the arachnid orders based on morphological characters. *Zoological Journal of the Linnean Society*, 150, 221–265.
- Wetterer2000** WETTERER, A. L., ROCKKMAN, M. V. and SIMMONS, N. B. 2000. Phylogeny of phyllostomid bats (Mammalia: Chiroptera): data from diverse morphological systems, sex chromosomes, and restriction sites. *Bulletin of the American Museum of Natural History*, 248, 1–200.
- Wills2012** WILLS, M. A., GERBER, S., RUTA, M. and HUGHES, M. 2012. The disparity of priapulid, archaeopriapulid and palaeoscolecid worms in the light of new data. *Journal of Evolutionary Biology*, 25, 2056–2076.
- Aguado2009** AGUADO, M. T. and SAN MARTIN, G. 2009. Phylogeny of Syllidae (Polychaeta) based on morphological data. *Zoologica Scripta*, 38, 379–402.
- Aria2015** ARIA, C., CARON, J. B. and GAINES, R. 2015. A large new leanchoiliid from the Burgess Shale and the influence of inapplicable states on stem arthropod phylogeny. *Palaeontology*, 58, 629–660.
- Asher2005** ASHER, R. J. and HOFREITER, M. 2006. Tenrec phylogeny and the noninvasive extraction of nuclear DNA. *Systematic biology*, 55, 181–94.
- Baker2009** BAKER, W. J., SAVOLAINEN, V., ASMUSSEN-LANGE, C. B., CHASE, M. W., DRANSFIELD, J., FOREST, F., HARLEY, M. M., UHL, N. W. and WILKINSON, M. 2009. Complete generic-level phylogenetic analyses of palms (Arecaceae) with comparisons of supertree and supermatrix approaches. *Systematic Biology*, 58, 240–256.
- Bouchenak2010** BOUCHENAK-KHELLADI, Y., VERBOOM, G. A., SAVOLAINEN, V. and HODKINSON, T. R. 2010. Biogeography of the grasses (Poaceae): a phylogenetic approach to reveal evolutionary history in geographical space and geological time. *Botanical Journal of the Linnean Society*, 162, 543–557.
- Conrad2008** CONRAD, J. L. 2008. Phylogeny And Systematics Of Squamata (Reptilia) Based On Morphology. *Bulletin of the American Museum of Natural History*, 310, 1–182.
- Dikow2009** DIKOW, T. 2009. A phylogenetic hypothesis for Asilidae based on a total evidence analysis of morphological and DNA sequence data (Insecta: Diptera: Brachycera: Asiloidea). *Organisms Diversity and Evolution*, 9, 165–188.
- Eklund2004** EKLUND, H., DOYLE, J. A. and HERENDEEN, P. S. 2004. Morphological phylogenetic analysis of living and fossil Chloranthaceae. *International Journal of Plant Sciences*, 165, 107–151.
- Geisler2001** GEISLER, J. H. 2001. New morphological evidence for the phylogeny of Artiodactyla, Cetacea, and Mesonychidae. *American Museum Novitates*, 3344, 53.

- Giles2015** GILES, S., FRIEDMAN, M. and BRAZEAU, M. D. 2015. Osteichthyan-like cranial conditions in an Early Devonian stem gnathostome. *Nature*, 520, 82–85.
- Griswold1999** GRISWOLD, C. E., CODDINGTON, J. A., PLATNICK, N. I. and FORSTER, R. R. 1999. Towards a phylogeny of entelegyne spiders (Araneae, Araneomorphae, Entelegynae). *Journal of Arachnology*, 27, 53–63.
- Liljeblad2008** LILJEBLAD, J., RONQUIST, F., NIEVES-ALDREY, J. L., FONTAL-CAZALLA, F., ROS-FARRE, P., GAITROS, D. and PUJADE-VILLAR, J. 2008. A fully web-illustrated morphological phylogenetic study of relationships among oak gall wasps and their closest relatives (Hymenoptera: Cynipidae).
- Loconte1991** LOCONTE, H. and STEVENSON, D. W. 1991. Cladistics of the Magnoliidae. *Cladistics*, 7, 267–296.
- Longrich2010** LONGRICH, N. R., SANKEY, J. and TANKE, D. 2010. *Texacephale langstoni*, a new genus of pachycephalosaurid (Dinosauria: Ornithischia) from the upper Campanian Aguja Formation, southern Texas, USA. *Cretaceous Research*, 31, 274–284.
- OMeara2014** O’MEARA, R. N. and THOMPSON, R. S. 2014. Were There Miocene Meridiolestidans? Assessing the phylogenetic placement of *Necrolestes patagonensis* and the presence of a 40 million year Meridiolestidan ghost lineage. *Journal of Mammalian Evolution*, 21, 271–284.
- Rougier2012** ROUGIER, G. W., WIBLE, J. R., BECK, R. M. D. and APESTEGUIA, S. 2012. The Miocene mammal *Necrolestes* demonstrates the survival of a Mesozoic nontherian lineage into the late Cenozoic of South America. *Proceedings of the National Academy of Sciences*, 109, 20053–8.
- Sharkey2011** SHARKEY, M. J., CARPENTER, J. M., VILHELMSSEN, L., HERATY, J., LILJEBLAD, J., DOWLING, A. P. G., SCHULMEISTER, S., MURRAY, D., DEANS, A. R., RONQUIST, F., KROGMANN, L. and WHEELER, W. C. 2012. Phylogenetic relationships among superfamilies of Hymenoptera. *Cladistics*, 28, 80–112.
- Sundue2010** SUNDUE, M. A., ISLAM, M. B. and RANKER, T. A. 2010. Systematics of Grammitid Ferns (Polypodiaceae): Using Morphology and Plastid Sequence Data to Resolve the Circumscriptions of *Melpomene* and the Polyphyletic Genera *Lellingeria* and *Terpsichore*. *Systematic Botany*, 35, 701–715.
- Vinther2008** VINTHER, J., VAN ROY, P. and BRIGGS, D. E. G. 2008. Machaeridians are Palaeozoic armoured annelids. *Nature*, 451, 185–188.
- Wilson2003** WILSON, G. D. F. and EDGECOMBE, G. D. 2003. The Triassic isopod *Protamphisopus wianamattensis* (Chilton) and comparison by extant taxa (Crustacea, Phreatoicoidea). *Journal of Paleontology*, 77, 454–470.
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References

Brazeau MD, Guillaume T, Smith MR (2019). “An algorithm for morphological phylogenetic analysis with inapplicable data.” *Systematic Biology*, in press. doi: [10.1093/sysbio/syy083](https://doi.org/10.1093/sysbio/syy083).

inapplicable.phyData *Thirty Datasets with Inapplicable data*

Description

These are the datasets used to evaluate the behaviour of the inapplicable algorithm in Brazeau, Guillaume and Smith (2017).

Usage

```
inapplicable.phyData
```

Format

An object of class `list` of length 30.

Details

The name of each item corresponds to the datasets listed below. Datasets are sorted into two subsets, each sorted alphabetically; the first subset comprise simpler datasets with faster processing times. The value is the dataset in `phyDat` format.

Source

- Agnarsson2004** AGNARSSON, I. 2004. Morphological phylogeny of cobweb spiders and their relatives (Araneae, Araneoidea, Theridiidae). *Zoological Journal of the Linnean Society*, 141, 447–626.
- Capa2011** CAPA, M., HUTCHINGS, P., AGUADO, M. T. and BOTT, N. J. 2011. Phylogeny of Sabellidae (Annelida) and relationships with other taxa inferred from morphology and multiple genes. *Cladistics*, 27, 449–469.
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- OLeary1999** O’LEARY, M. A. and GEISLER, J. H. 1999. The position of Cetacea within Mammalia: phylogenetic analysis of morphological data from extinct and extant taxa. *Systematic Biology*, 48, 455–490.
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- Wilson2003** WILSON, G. D. F. and EDGECOMBE, G. D. 2003. The Triassic isopod *Protamphisopus wianamattensis* (Chilton) and comparison by extant taxa (Crustacea, Phreatoicoidea). *Journal of Paleontology*, 77, 454–470.
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References

- Brazeau MD, Guillerme T, Smith MR (2019). “An algorithm for morphological phylogenetic analysis with inapplicable data.” *Systematic Biology*, in press. doi: [10.1093/sysbio/syy083](https://doi.org/10.1093/sysbio/syy083).

InfoAmounts	<i>Amount of information in each character</i>
-------------	--

Description

As presently implemented, this function requires that there be no ambiguous tokens and two applicable tokens, '1' and '2'.

Usage

```
InfoAmounts(tokenTable, precision = 1e+06, warn = TRUE)
```

Arguments

tokenTable	A matrix, where each row corresponds to a character, each column to a tip, and each entry to the value (1 or 2) of the character at that tip.
precision	number of random trees to generate when calculating Profile curves
warn	Boolean (TRUE/FALSE): display warnings when concavity functions are generated by approximation.

Value

information content of each extra step, in bits

Author(s)

Martin R. Smith

IWScore	<i>Implied weights parsimony Score</i>
---------	--

Description

Calculate a tree's Parsimony score with a given dataset using implied weights (Goloboff 1997)

Usage

```
IWScore(tree, dataset, concavity = 4, ...)
```

```
IWInitMorphy(dataset)
```

```
IWDestroyMorphy(dataset)
```

Arguments

tree	A tree of class <code>phylo</code> .
dataset	Dataset of class <code>phyDat</code> . The dataset should have been prepared using <code>dataset <- PrepareDataIW(dataset)</code> if this step has not been completed, the dataset will be (time-consumingly) prepared within the function. In subsidiary functions, the dataset will have been initialized using <code>IWInitMorphy</code> , and must be destroyed using <code>IWDestroyMorphy</code> .
concavity	A numeric value to use as the concavity constant ('k') in implied weighting.
...	unused; allows additional parameters specified within ... to be received by the function without throwing an error.

Value

The 'fit', $h / h + k$, where 'h' is the amount of homoplasy ('extra steps') and 'k' is a constant (the 'concavity constant')

Functions

- `IWInitMorphy`: Initialize dataset by adding `morphyObjs` and `min.steps`.
- `IWDestroyMorphy`: Free memory from `morphyObjs` initialized by `IWScoreMorphy`.

Author(s)

Martin R. Smith

References

Goloboff PA (1997). "Self-weighted optimization: tree searches and character state reconstructions under implied transformation costs." *Cladistics*, **13**(3), 225–245. <http://dx.doi.org/10.1111/j.1096-0031.1997.tb00317.x>.

Examples

```
data(referenceTree)
data(congreveLamsdellMatrices)
dataset <- PrepareDataIW(congreveLamsdellMatrices[[42]])
IWScore(referenceTree, dataset)
```

IWScoreMorphy

Profile Parsimony Score

Description

Calculate a tree's Profile Parsimony score with a given dataset, after Faith and Trueman (2001)

Usage

```
IWScoreMorphy(parent, child, dataset, concavity = 4,
  minSteps = attr(dataset, "min.steps"), ...)
```

```
ProfileScore(tree, dataset)
```

```
ProfileScoreMorphy(parent, child, dataset, ...)
```

```
ProfileInitMorphy(dataset)
```

```
ProfileDestroyMorphy(dataset)
```

Arguments

parent	the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
dataset	Dataset of class <code>phyDat</code> . The dataset should have been prepared using <code>dataset <- PrepareDataProfile</code> if this step has not been completed, the dataset will be (time-consumingly) prepared within the function. In subsidiary functions, the dataset will have been initialized using <code>ProfileInitMorphy</code> , must be destroyed using <code>ProfileDestroyMorphy</code> .
concavity	A numeric value to use as the concavity constant ('k') in implied weighting.
minSteps	Integer vector specifying the minimum number of steps possible for each character in 'dataset', perhaps calculated using <code>MinimumSteps</code> .
...	unused; allows additional parameters specified within ... to be received by the function without throwing an error.
tree	A tree of class <code>phylo</code> .

Value

Zero minus the profile score (because the optimization algorithm treats smaller numbers as better)

Functions

- `IWScoreMorphy`: Scorer for initialized dataset.
- `ProfileScoreMorphy`: Scorer for initialized dataset.
- `ProfileInitMorphy`: Initialize dataset by adding `morphObj`s.
- `ProfileDestroyMorphy`: Free memory from `morphObj`s initialized by `ProfileScoreMorphy`.

Author(s)

Martin R. Smith

References

Faith DP, Trueman JWH (2001). "Towards an inclusive philosophy for phylogenetic inference." *Systematic Biology*, **50**(3), 331–350. doi: [10.1080/10635150118627](https://doi.org/10.1080/10635150118627).

Examples

```

data(referenceTree)
data(congreveLamsdellMatrices)
# In actual use, the dataset should be prepared with a much higher
# precision: try 1e+06?
# Of course, gaining higher precision takes substantially longer.
dataset <- PrepareDataProfile(congreveLamsdellMatrices[[42]], precision=1e+03)
ProfileScore(referenceTree, dataset)

```

LDFact

Log double factorial Handles odd and even inout numbers

Description

Log double factorial Handles odd and even inout numbers

Usage

```
LDFact(x)
```

Arguments

x a positive integer

LDFactorial

Log double factorial

Description

Memoised version of phangorn's [ldfactorial](#)

Usage

```
LDFactorial(x)
```

Arguments

x (integer) number to crunch.

Lobo.data

Raw data from Zhang et al. 2016

Description

Raw data from Zhang et al. 2016

Modified so that absences are treated appropriately:

Character 7 inapplicable to absent where cephalic shield (char 3) is absent

Character 40 inapplicable to absent where paired appendages absent

Character 46 inapplicable to absent

Character 64 76: stet; trunk annulations / limbs may primitively have been papillate or non-papillate

Character 69 a good case that the fusion of flaps with endopods is secondary; thus inapplicable to absent where 67 is applicable

Character 72 inapplicable to absent where appendages are present

Character 77 inapplicable to absent where papillae applicable, as spine is a secondary elaboration of papillae

Character 78 inapplicable to absent

Character 79 stet, as possible that limbs evolved by extension of plate-like exoskeletal element

Character 80 inapplicable to absent, on assumption that ancestral claws were simple

Characters 83, 84, 86, 87, 92 inapplicable to absent; an obvious elaboration

Character 93 inapplicable to absent; ancestrally undifferentiated by definition?

Character 96 inapplicable to absent; ancestrally undifferentiated by definition. Ambiguous in taxa that lack claws as rotation would not be observed.]

Usage

Lobo.data

Format

An object of class list of length 48.

Source

Zhang X, Smith MR, Yang J, Hou J (2016). “Onychophoran-like musculature in a phosphatized Cambrian lobopodian.” *Biology Letters*, **12**(9), 20160492. doi: [10.1098/rsbl.2016.0492](https://doi.org/10.1098/rsbl.2016.0492), <http://rsbl.royalsocietypublishing.org/content/12/9/20160492>.

Lobo.phy

Data from Zhang et al. 2016 in phyDat format

Description

Data from Zhang et al. 2016 in phyDat format

Modified so that absences are treated appropriately:

Character 7 inapplicable to absent where cephalic shield (char 3) is absent

Character 40 inapplicable to absent where paired appendages absent

Character 46 inapplicable to absent

Character 64 76: stet; trunk annulations / limbs may primitively have been papillate or non-papillate

Character 69 a good case that the fusion of flaps with endopods is secondary; thus inapplicable to absent where 67 is applicable

Character 72 inapplicable to absent where appendages are present

Character 77 inapplicable to absent where papillae applicable, as spine is a secondary elaboration of papillae

Character 78 inapplicable to absent

Character 79 stet, as possible that limbs evolved by extension of plate-like exoskeletal element

Character 80 inapplicable to absent, on assumption that ancestral claws were simple

Characters 83, 84, 86, 87, 92 inapplicable to absent; an obvious elaboration

Character 93 inapplicable to absent; ancestrally undifferentiated by definition?

Character 96 inapplicable to absent; ancestrally undifferentiated by definition. Ambiguous in taxa that lack claws as rotation would not be observed.]

Usage

Lobo.phy

Format

An object of class phyDat of length 48.

Source

Zhang X, Smith MR, Yang J, Hou J (2016). "Onychophoran-like musculature in a phosphatized Cambrian lobopodian." *Biology Letters*, **12**(9), 20160492. doi: [10.1098/rsbl.2016.0492](https://doi.org/10.1098/rsbl.2016.0492), <http://rsbl.royalsocietypublishing.org/content/12/9/20160492>.

LogisticPoints *Logistic Points Extract points from a fitted model*

Description

Logistic Points Extract points from a fitted model

Usage

```
LogisticPoints(x, fittedModel)
```

Arguments

`x` an integer vector giving x co-ordinates.
`fittedModel` a fitted model, perhaps generated using `nls(cumP ~ SSlogis(nSteps, Asym, xmid, scal))`.

Value

values of y co-ordinates corresponding to the x co-ordinates provided

Author(s)

Martin R. Smith

MatrixToList *Edge matrix to edge list*

Description

Edge matrix to edge list

Usage

```
MatrixToList(edge)
```

Arguments

`edge` edges in the matrix format used by `tree$edge`, where `tree` is a tree of class `phylo`

Value

tree edges in the format `list(parent, child)`.

MinimumSteps	<i>Minimum steps</i>
--------------	----------------------

Description

Smallest number of steps that a character can take on any tree

Usage

MinimumSteps(states)

Arguments

states	Integer vector listing the tokens that may be present at each tip along a single character, with each token represented as a binary digit; e.g. a value of 11 means that the tip may have tokens 0, 1 or 3 (as $11 = 2^0 + 2^1 + 2^3$). As the minimum steps can be found when inapplicables occur together, inapplicable tokens can be denoted as ?s or with the integer 0 (not 2^0).
--------	--

Value

An integer specifying the minimum number of steps that the character must contain

MorphyBootstrap	<i>Ratchet bootstrapper</i>
-----------------	-----------------------------

Description

Ratchet bootstrapper

Usage

MorphyBootstrap(edgeList, morphyObj, EdgeSwapper = NNISwap, maxIter, maxHits, verbosity = 1L, stopAtPeak = FALSE, stopAtPlateau = 0L, ...)

ProfileBootstrap(edgeList, dataset, EdgeSwapper = NNISwap, maxIter, maxHits, verbosity = 1L, ...)

IWBootstrap(edgeList, dataset, concavity = 4L, EdgeSwapper = NNISwap, maxIter, maxHits, verbosity = 1L, ...)

Arguments

edgeList	a list containing the following: - vector of integers corresponding to the parent of each edge in turn - vector of integers corresponding to the child of each edge in turn - (optionally) score of the tree - (optionally, if score provided) number of times this score has been hit
morphObj	A morphy object, perhaps created with PhyDat2Morphy .
EdgeSwapper	a function that rearranges a parent and child vector, and returns a list with modified vectors; for example SPRSwap .
maxIter	maximum number of iterations to perform in tree search
maxHits	maximum number of hits to accomplish in tree search
verbosity	Level of detail to display in console: larger numbers provide more verbose feedback to the user.
stopAtPeak	Logical specifying whether to terminate search once a subsequent iteration recovers a sub-optimal score. Useful with methods that return all trees one rearrangement from the current tree, such as AllTBR . Will be overridden if a passed function has an attribute 'stopAtPeak' set by 'attr(FunctionName, 'stopAtPeak') <- TRUE'.
stopAtPlateau	Integer. If > 0, tree search will terminate if the score has not improved after 'stopAtPlateau' iterations. Useful with methods that return all trees one rearrangement from the current tree, such as AllTBR . Will be overridden if a passed function has an attribute 'stopAtPlateau' set by 'attr(FunctionName, 'stopAtPlateau') <- TRUE'.
...	further parameters to send to TreeScorer
dataset	A phylogenetic data matrix of class phyDat , whose names correspond to the labels of any accompanying tree.
concavity	A numeric value to use as the concavity constant ('k') in implied weighting.

Value

A tree that is optimal under a random sampling of the original characters

Functions

- [ProfileBootstrap](#): Bootstrapper for Profile Parsimony
- [IWBootstrap](#): Bootstrapper for Implied weighting

MorphyWeights

Report the character weightings associated with a Morphy object

Description

Report the character weightings associated with a Morphy object

Usage

MorphyWeights(morphyObj)

Arguments

morphyObj A morphy object, perhaps created with [PhyDat2Morphy](#).

Value

a matrix of dimensions (2, number of characters); row 1 lists the exact rates specified by the user; row 2 the approximate (integral) weights used by MorphyLib

Author(s)

Martin R. Smith

N1Spr	<i>Number of trees on SPR step away Formula given by Given by Allen and Steel 2001.</i>
-------	---

Description

Number of trees on SPR step away Formula given by Given by Allen and Steel 2001.

Usage

N1Spr(n)

IC1Spr(n)

Arguments

n Number of tips in tree.

Functions

- IC1Spr: Information content of trees 0 or 1 SPR step from tree with n tips.

References

Allen BL, Steel MA (2001). "Subtree transfer operations and their induced metrics on evolutionary trees." *Annals of Combinatorics*, **5**(1), 1–15. ISSN 0218-0006, doi: [10.1007/s0002600180068](https://doi.org/10.1007/s0002600180068).

NamedConstant *Named constant*

Description

Named constant

Usage

NamedConstant(X, name)

Arguments

X a vector.
name name to apply to the vector.

Value

the vector, named as requested

Author(s)

Martin R. Smith

NewickTree *Newick Tree*

Description

Writes a tree in Newick format

Usage

NewickTree(tree)

Arguments

tree A tree of class [phylo](#).

Value

A character string describing 'tree' in Newick format

NJTree	<i>Neighbour Joining Tree</i>
--------	-------------------------------

Description

Generates a rooted neighbour joining tree, with no edge lengths

Usage

```
NJTree(dataset)
```

Arguments

dataset A phylogenetic data matrix of class [phyDat](#), whose names correspond to the labels of any accompanying tree.

Value

an object of class phylo

Author(s)

Martin R. Smith

NNI	<i>NNI</i>
-----	------------

Description

Nearest Neighbour Interchange

Usage

```
NNI(tree, edgeToBreak = NULL)
```

```
NNISwap(parent, child, nTips = (length(parent)/2L) + 1L,  
edgeToBreak = NULL)
```

```
RootedNNI(tree, edgeToBreak = NULL)
```

```
RootedNNISwap(parent, child, nTips = (length(parent)/2L) + 1L,  
edgeToBreak = NULL)
```

Arguments

tree	A tree of class <code>phylo</code> .
edgeToBreak	(optional) integer specifying the index of an edge to bisect/prune, generated randomly if not specified. Alternatively, set to -1 to return a complete list of all trees one step from the input tree.
parent	the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
nTips	(optional) Number of tips.

Details

Performs a single iteration of the nearest-neighbour interchange algorithm. Based on the corresponding phangorn function, but re-coded to improve speed.

Branch lengths are not supported.

Value

Returns a tree with class `phylo` (if `returnAll = FALSE`) or a set of trees, with class `multiPhylo` (if `returnAll = TRUE`).

a list containing two elements, corresponding in turn to the rearranged parent and child parameters

a list containing two elements, corresponding in turn to the rearranged parent and child parameters

Functions

- `NNISwap`: faster version that takes and returns parent and child parameters
- `RootedNNI`: Perform NNI rearrangement, retaining position of root
- `RootedNNISwap`: faster version that takes and returns parent and child parameters

Author(s)

Martin R. Smith

References

The algorithm is summarized in Felsenstein J (2004). *Inferring phylogenies*. Sinauer Associates, Sunderland, Massachusetts.

Examples

```
tree <- ape::rtree(20, br=NULL)
NNI(tree)
NNI(tree, edgeToBreak = -1)
```

NRooted	<i>Number of rooted/unrooted trees These functions return the number of rooted or unrooted trees consistent with a given pattern of splits.</i>
---------	---

Description

Functions starting N return the number of rooted or unrooted trees, functions starting Ln provide the log of this number. Calculations follow Carter et al. 1990, Theorem 2.

Usage

```
NRooted(tips, extra = 0)
NUnrooted1(tips, extra = 0)
LnUnrooted1(tips, extra = 0)
LnRooted(tips, extra = 0)
LnUnrooted(splits)
NUnrooted(splits)
LnUnrootedMult(splits)
NUnrootedMult(splits)
```

Arguments

tips	The number of tips.
extra	the number of points at which another branch cannot be added.
splits	vector listing the number of taxa in each tree bipartition.

Functions

- NUnrooted1: Number of unrooted trees
- LnUnrooted1: Log Number of unrooted trees
- LnRooted: Log Number of rooted trees
- LnUnrooted: Log number of unrooted trees
- NUnrooted: Number of unrooted trees
- LnUnrootedMult: Log unrooted mult
- NUnrootedMult: Number of unrooted trees (mult)

Author(s)

Martin R. Smith

References

Carter M, Hendy M, Penny D, Székely LA, Wormald NC (1990). “On the distribution of lengths of evolutionary trees.” *SIAM Journal on Discrete Mathematics*, **3**(1), 38–47. doi: [10.1137/0403005](https://doi.org/10.1137/0403005), <http://epubs.siam.org/doi/abs/10.1137/0403005>.

Carter M, Hendy M, Penny D, Székely LA, Wormald NC (1990). “On the distribution of lengths of evolutionary trees.” *SIAM Journal on Discrete Mathematics*, **3**(1), 38–47. doi: [10.1137/0403005](https://doi.org/10.1137/0403005), <http://epubs.siam.org/doi/abs/10.1137/0403005>.

Examples

```
NRooted(10)
NUnrooted(10)
LnRooted(10)
LnUnrooted(10)
# Number of trees consistent with a character whose states are 00000 11111 222
NUnrootedMult(c(5,5,3))
```

PhyDat2Morphy

Initialize a Morphy Object from a phyDat object

Description

Creates a new Morphy object with the same size and characters as the phyDat object

Usage

```
PhyDat2Morphy(phy)
```

Arguments

phy An object of class `phyDat`.

Value

A pointer to an initialized Morphy object.

Author(s)

Martin R. Smith

PhyToString	<i>Extract character data from a phyDat object as a string</i>
-------------	--

Description

Extract character data from a phyDat object as a string

Usage

```
PhyToString(phy, ps = "", useIndex = TRUE, byTaxon = TRUE,
            concatenate = TRUE)
```

Arguments

phy	An object of class phyDat
ps	Character specifying text, perhaps ';', to append to the end of the string
useIndex	(default: TRUE) Print duplicate characters multiple times, as they appeared in the original matrix
byTaxon	If TRUE, write one taxon followed by the next. If FALSE, write one character followed by the next.
concatenate	Logical specifying whether to concatenate all characters/taxa into a single string, or to return a separate string for each entry.

Author(s)

Martin R. Smith

PrepareDataProfile	<i>Prepare data for Profile Parsimony</i>
--------------------	---

Description

Prepare data for Profile Parsimony

Usage

```
PrepareDataProfile(dataset, precision = 1e+06, warn = TRUE)
```

```
PrepareDataIW(dataset)
```

Arguments

dataset	dataset of class phyDat
precision	number of random trees to generate when calculating Profile curves. With 22 tokens (taxa): - Increasing precision from 4e+05 to 4e+06 reduces error by a mean of 0.005 bits for each step after the first (max = 0.11 bits, sd=0.017 bits) - Increasing precision from 1e+06 to 4e+06 reduces error by a mean of 0.0003 bits for each step after the first (max = 0.046 bits, sd=0.01 bits)
warn	Boolean (TRUE/FALSE): display warnings when concavity functions are generated by approximation.

Value

An object of class phyDat with additional attributes: `info.amounts`: details the information represented by each character when subject to N additional steps. `split.sizes`: The size of the splits implied by each character `bootstrap`: The character vector `c('info.amounts', 'split.sizes')`, indicating attributes to sample when bootstrapping the dataset 9e.g. in Ratchet searches).

Functions

- `PrepareDataIW`: Prepare data for implied weighting

Author(s)

Martin R. Smith; written with reference to `phangorn::prepareDataFitch`

RandomMorphyTree

Random postorder tree

Description

Random postorder tree

Usage

`RandomMorphyTree(nTip)`

Arguments

nTip number of tips (minimum 3)

Value

A list with three elements, each a vector of integers, respectively containing: - The parent of each tip and node, in order - The left child of each node - The right child of each node.

RandomTree	<i>Generate random tree topology from dataset</i>
------------	---

Description

Generate random tree topology from dataset

Usage

```
RandomTree(dataset, root = FALSE)
```

Arguments

dataset	A dataset in phyDat format
root	Taxon to use as root (if desired; FALSE otherwise)

Author(s)

Martin R. Smith

RandomTreeScore	<i>Parsimony score of random postorder tree</i>
-----------------	---

Description

Parsimony score of random postorder tree

Usage

```
RandomTreeScore(nTip, morphyObj)
```

Arguments

nTip	number of tips (minimum 3)
morphyObj	A morphy object, perhaps created with PhyDat2Morphy .

Value

the parsimony score of a random tree, for the given Morphy object.

ReadCharacters *Read characters from Nexus file*

Description

Parses Nexus file, reading character states and names

Usage

```
ReadCharacters(filepath, character_num = NULL, session = NULL)
```

```
ReadTntCharacters(filepath, character_num = NULL, session = NULL)
```

```
ReadAsPhyDat(filepath)
```

```
ReadTntAsPhyDat(filepath)
```

```
PhyDat(dataset)
```

Arguments

filepath	character string specifying location of file
character_num	Index of character(s) to return. 'NULL', the default, returns all characters.
session	(optionally) a Shiny session with a numericInput named character_num whose maximum should be updated.
dataset	list of taxa and characters, in the format produced by [read.nexus.data]: a list of sequences each made of a single vector of mode character, and named with the taxon name.

Details

Tested with nexus files downloaded from MorphoBank with the "no notes" option, but should also work more generally.

Do [report](<https://github.org/ms609/TreeSearch/issues> "New GitHub Issue") incorrectly parsed files.

Value

A matrix whose row names correspond to tip labels, and column names correspond to character labels, with the attribute 'state.labels' listing the state labels for each character; or a character string explaining why the character cannot be returned.

Functions

- ReadTntCharacters: Read characters from TNT file
- ReadAsPhyDat: Read nexus characters as phyDat object
- ReadTntAsPhyDat: Read TNT characters as phyDat object
- PhyDat: A convenient wrapper for **phangorn**'s phyDat, which converts a *list* of morphological characters into a phyDat object. If your morphological characters are in the form of a *matrix*, perhaps because they have been read using 'read.table', try [MatrixToPhyDat] instead.

Author(s)

Martin R. Smith

Martin R. Smith

Martin R. Smith

References

Maddison, D. R., Swofford, D. L. and Maddison, W. P. (1997) NEXUS: an extensible file format for systematic information. *Systematic Biology*, 46, 590-621.

ReadTntTree

Parse TNT Tree

Description

Reads a tree from TNT's paranthetical output.

Usage

```
ReadTntTree(filename, relativePath = NULL, keepEnd = 1L,
            tipLabels = NULL)
```

```
TNTText2Tree(treeText)
```

Arguments

filename	character string specifying path to TNT '.tre' file.
relativePath	(optional) character string specifying location of the matrix file used to generate the TNT results, relative to the current working directory, for portability. Taxon names will be read from this file if they are not specified by 'tipLabels'.
keepEnd	(optional, default 1) integer specifying how many elements of the file path to conserve when creating relative path (see examples).
tipLabels	(optional) character vector specifying the names of the taxa, in the sequence that they appear in the TNT file. If not specified, taxon names will be loaded from the data file linked in the first line of the '.tre' file specified in 'filename'.
treeText	Character string describing a tree, in the parenthetical format output by TNT.

Value

a tree of class phylo.

Functions

- TNTText2Tree: Converts text representation of a tree in TNT to an object of class ‘phylo’

Author(s)

Martin R. Smith

Martin R. Smith

Examples

```
{
  ## Not run:
  # TNT read a matrix from c:/myproject/tnt/coding1/dataset.nex
  # The results of an analysis were written to c:/myproject/tnt/output/results1.tnt
  # results1.tnt will contain a hard-coded reference to
  # "c:/myproject/tnt/coding1/dataset.nex"

  getwd() # Gives the current working directory

  # Say that working directory is c:/myproject, which perhaps corresponds to a
  # Git repository.
  # This directory may be saved into another location by collaborators, or on a
  # different filesystem by a continuous integration platform.

  # Works on local machine but not elsewhere:
  ReadTntTree('tnt/output/results1.tnt')

  # Takes only the filename from the results
  ReadTntTree('tnt/output.results1.tnt', 'tnt/coding1')

  # Uses the last three elements of c:/myproject/tnt/coding1/dataset.nex
  #           3       2       1
  # '.' means "relative to the current directory", which is c:/myproject
  ReadTntTree('tnt/output/results1.tnt', '.', 3)

  # If the current working directory was c:/myproject/rscripts/testing,
  # you could navigate up the directory path with '..':
  ReadTntTree('../tnt/output/results1.tnt', '..', 3)

  ## End(Not run)
}
```

RearrangeEdges *Rearrange edges of a phylogenetic tree*

Description

Rearranges a matrix that corresponds to the edges of a phylogenetic tree, returning the score of the new tree. Will generally be called from within a tree search function.

Usage

```
RearrangeEdges(parent, child, dataset, TreeScorer = MorphyLength,
  EdgeSwapper, scoreToBeat = TreeScorer(parent, child, dataset, ...),
  iter = "?", hits = 0L, verbosity = 0L, ...)
```

Arguments

parent	the first column of the edge matrix of a tree of class phylo , i.e. <code>tree\$edge[, 1]</code>
child	the second column of the edge matrix of a tree of class phylo , i.e. <code>tree\$edge[, 2]</code>
dataset	Third argument to pass to <code>TreeScorer</code> .
TreeScorer	function to score a given tree. The function will be passed three parameters, corresponding to the ‘parent’ and ‘child’ entries of a tree’s edge list, and a dataset.
EdgeSwapper	a function that rearranges a parent and child vector, and returns a list with modified vectors; for example SPRSwap .
scoreToBeat	Double giving score of input tree.
iter	iteration number of calling function, for reporting to user only.
hits	Integer giving number of times the input tree has already been hit.
verbosity	Level of detail to display in console: larger numbers provide more verbose feedback to the user.
...	further arguments to pass to <code>TreeScorer</code> function (e.g. TipsAreColumns , <code>dataset</code>)

Details

`RearrangeTree` performs one tree rearrangement of a specified type, and returns the score of the tree (with the given dataset). It also reports the number of times that this score was hit in the current function call.

Value

This function returns a list with two to four elements, corresponding to a binary tree: - 1. Integer vector listing the parent node of each edge; - 2. Integer vector listing the child node of each edge; - 3. Score of the tree; - 4. Number of times that score has been hit.

Author(s)

Martin R. Smith

Examples

```
data('Lobo')
random.tree <- RandomTree(Lobo.phy)
edge <- random.tree$edge
parent <- edge[, 1]
child <- edge[, 2]
dataset <- PhyDat2Morph(Lobo.phy)
RearrangeEdges(parent, child, dataset, EdgeSwapper=RootedNNISwap)
```

referenceTree

Tree topology for matrix simulation

Description

The tree topology used to generate the matrices in [congreveLamsdellMatrices](#) Congreve & Lamsdell (2016)

Usage

```
referenceTree
```

Format

A single phylogenetic tree saved as an object of class phylo

Source

<https://dx.doi.org/10.1111/pala.12236>

References

Congreve CR, Lamsdell JC (2016). “Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices.” *Palaeontology*, **59**, 447-465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).
Congreve CR, Lamsdell JC (2016). “Data from: Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices.” *Dryad Digital Repository*, doi:10.5061/dryad.7dq0j. doi: [10.5061/dryad.7dq0j](https://doi.org/10.5061/dryad.7dq0j).

Examples

```
data(referenceTree)
plot(referenceTree)
```

Renumber	<i>Renumber a tree's nodes and tips</i>
----------	---

Description

Renumber numbers the nodes and tips in a tree to conform with the phylo standards.

Usage

```
Renumber(tree)
```

Arguments

tree A tree of class [phylo](#).

Value

This function returns a tree of class phylo

Author(s)

Martin R. Smith

Examples

```
library('ape')
tree <- rtree(10)
Renumber (tree)
```

RenumberTips	<i>Reorder tips</i>
--------------	---------------------

Description

RenumberTips(tree, tipOrder) sorts the tips of a phylogenetic tree such that the indices in tree\$edge[, 2] correspond to the order of tips given in tipOrder

Usage

```
RenumberTips(tree, tipOrder)
```

Arguments

tree A tree of class [phylo](#).
tipOrder A character vector containing the values of tree\$tip.label in the desired sort order

Author(s)

Martin R. Smith

Examples

```
data(Lobo) # Loads the phyDat object Lobo.phy
tree <- RandomTree(Lobo.phy)
tree <- Renumertips(tree, names(Lobo.phy))
```

RootTree

Root Tree on specified tips

Description

Roots a tree on the smallest clade containing the specified tips.

Usage

```
RootTree(tree, outgroupTips)
```

Arguments

`tree` A tree of class `phylo`.
`outgroupTips` Character vector specifying the names of the tips to include in the outgroup.

Value

A tree of class `phylo`, rooted on the smallest clade that contains the specified tips

Author(s)

Martin R. Smith

SetMorphWeights

Set the character weightings associated with a Morphy object

Description

Set the character weightings associated with a Morphy object

Usage

```
SetMorphWeights(weight, morphyObj, checkInput = TRUE)
```

Arguments

weight	A vector listing the new weights to be applied to each character
morphyObj	A morphy object, perhaps created with PhyDat2Morphy .
checkInput	Whether to sanity-check input data before applying. Defaults to TRUE to protect the user from crashes.

Value

The Morphy error code generated when applying tipData

Author(s)

Martin R. Smith

SingleCharMorphy *Morphy object from single character*

Description

Morphy object from single character

Usage

```
SingleCharMorphy(char)
```

Arguments

char	State of each character at each tip in turn, in a format that will be converted to a character string by paste0 (char, ';', collapse='').
------	---

Value

A pointer to a morphyObj. Don't forget to unload it when you've finished with it: `morphyObj <- UnloadMorphy(morphyObj)`

Author(s)

Martin R. Smith

SingleTaxonTree	<i>SingleTaxonTree</i>
-----------------	------------------------

Description

Single taxon tree

Usage

```
SingleTaxonTree(label)
```

Arguments

label a character vector specifying the label of the tip.

Details

Create a phylogenetic 'tree' that comprises a single taxon.

Value

This function returns a phylo object containing a single tip with the specified label.

Examples

```
SingleTaxonTree('Homo_sapiens')
```

SortTree	<i>Sort tree</i>
----------	------------------

Description

Sorts each node into a consistent order, so similar trees look visually similar.

Usage

```
SortTree(tree)
```

Arguments

tree A tree of class [phylo](#).

Value

A tree of class phylo, with each node sorted such that the larger clade is first.

Author(s)

Martin R. Smith

SplitFrequency	<i>Frequency of splits</i>
----------------	----------------------------

Description

‘SplitFrequency’ provides a simple way to count the number of times that bipartition splits, as defined by a reference tree, occur in a forest of trees.

Usage

```
SplitFrequency(reference, forest)

SplitNumber(tips, tree, tipIndex, powersOf2)

ForestSplits(forest, powersOf2)

TreeSplits(tree)
```

Arguments

reference	A tree of class <code>phylo</code> , or a character vector specifying its splits (as obtained through <code>[Quartet::Tree2Splits]</code>)
forest	a list of trees of class <code>phylo</code> , or a <code>multiPhylo</code> object; or a list of their constituent splits (as obtained through <code>[Quartet::Tree2Splits]</code>)
tips	Integer vector specifying the tips of the tree within the chosen split
tree	A tree of class <code>phylo</code> .
tipIndex	Character vector of tip names, in a fixed order
powersOf2	Integer vector of same length as <code>tipIndex</code> , specifying a power of 2 to be associated with each tip in turn

Details

If multiple calculations are required, some time can be saved by using the constituent functions (see examples)

Value

Number of trees in ‘forest’ that contain each split in ‘reference’. if ‘reference’ is a tree of class `phylo`, then the sequence will correspond to the order of nodes (use ‘ape::nodelabels to view). Note that the three nodes at the root of the tree correspond to a single split; see the example for how these might be plotted on a tree.

Functions

- `SplitNumber`: Assign a unique integer to each split
- `ForestSplits`: Frequency of splits in a given forest of trees
- `TreeSplits`: Lists the splits in a given tree

Author(s)

Martin R. Smith

Examples

```
{
  library(ape) # for functions rtree & nodelabels
  set.seed(0) # Set seed so random trees are reproducible
  tree1 <- rtree(7)
  tree2 <- rtree(7)
  tree3 <- rtree(7)
  forest <- list(tree1, tree2, tree2, tree3, rtree(7))

  # Simple, but means counting each split in the forest twice:
  tree1Freqs <- SplitFrequency(tree1, forest)
  SplitFrequency(tree2, forest)

  plot(tree1)
  nodelabels(tree1Freqs, node=as.integer(names(tree1Freqs)))
}
```

 SPR

Subtree Pruning and Rearrangement

Description

Perform one SPR rearrangement on a tree

Usage

```
SPR(tree, edgeToBreak = NULL, mergeEdge = NULL)
```

```
SPRSwap(parent, child, nEdge = length(parent), nNode = nEdge/2L,
  edgeToBreak = NULL, mergeEdge = NULL)
```

```
RootedSPR(tree, edgeToBreak = NULL, mergeEdge = NULL)
```

```
RootedSPRSwap(parent, child, nEdge = length(parent), nNode = nEdge/2L,
  edgeToBreak = NULL, mergeEdge = NULL)
```

Arguments

tree	A tree of class phylo .
edgeToBreak	the index of an edge to bisect, generated randomly if not specified.
mergeEdge	the index of an edge on which to merge the broken edge.
parent	the first column of the edge matrix of a tree of class phylo , i.e. <code>tree\$edge[, 1]</code>

child	the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code>
nEdge	(optional) integer specifying the number of edges of a tree of class <code>phylo</code> , i.e. <code>dim(tree\$edge)[1]</code>
nNode	(optional) Number of nodes.

Details

Equivalent to phangorn's kSPR, but faster. Note that rearrangements that only change the position of the root WILL be returned by SPR. If the position of the root is irrelevant (as in Fitch parsimony, for example) then this function will occasionally return a functionally equivalent topology. `RootIrrelevantSPR` will search tree space more efficiently in these cases. Branch lengths are not (yet) supported.

Value

This function returns a tree in `phyDat` format that has undergone one SPR iteration.

a list containing two elements, corresponding in turn to the rearranged parent and child parameters

a list containing two elements, corresponding in turn to the rearranged parent and child parameters

Functions

- `SPRswap`: faster version that takes and returns parent and child parameters
- `RootedSPR`: Perform SPR rearrangement, retaining position of root
- `RootedSPRswap`: faster version that takes and returns parent and child parameters

Author(s)

Martin R. Smith

References

The SPR algorithm is summarized in Felsenstein J (2004). *Inferring phylogenies*. Sinauer Associates, Sunderland, Massachusetts.

See Also

`RootedSPR` useful when the position of the root node should be retained.

TBR

NNI

Examples

```
{
tree <- ape::rtree(20, br=FALSE)
SPR(tree)
}
```

StringToPhyDat *String to phyDat*

Description

Converts a PhyDat object to allow processing by MorphyDat

Usage

```
StringToPhyDat(string, tips, byTaxon = TRUE)
```

Arguments

string	a string of tokens, optionally containing whitespace, with no terminating semi-colon. Polytomies not (yet) supported; each character must correspond to a unique state, ?, or the inapplicable token (-)
tips,	a character vector corresponding to the names (in order) of each taxon in the matrix
byTaxon	= TRUE, string is one TAXON's coding at a time; FALSE: one CHARACTER's coding at a time

Value

This function returns a data matrix in [phyDat](#) format.

Author(s)

Martin R. Smith

See Also

[phyDat](#)

Examples

```
morphy <- StringToPhyDat("-?01231230?-", c('Lion', 'Gazelle'), byTaxon=TRUE)
# encodes the following matrix:
# Lion      -?0123
# Gazelle  1230?-
```

Subtree	<i>Extract subtree</i>
---------	------------------------

Description

Safely extracts a clade from a phylogenetic tree.

Usage

```
Subtree(tree, node)
```

Arguments

tree	A tree of class <code>phylo</code> , with internal numbering in cladewise order (use <code>Preorder</code> (tree) or (slower) <code>Cladewise</code> (tree))
node	The number of the node at the base of the clade to be extracted.

Details

Modified from the `ape` function `extract.clade`, which sometimes behaves erratically. Unlike `extract.clade`, this function supports the extraction of 'clades' that constitute a single tip.

Value

This function returns a tree of class `phylo` that represents a clade extracted from the original tree.

Author(s)

Martin R. Smith

Examples

```
{
tree <- Preorder(ape::rtree(20, br=NULL))
plot(tree); ape::nodelabels(); ape::nodelabels(33, 33, bg='yellow'); dev.new()
plot(Subtree(tree, 33))
}
```

 SuccessiveApproximations

Tree Search using Successive Approximations

Description

Searches for a tree that is optimal under the Successive Approximations criterion

Usage

```
SuccessiveApproximations(tree, dataset, outgroup = NULL, k = 3,
  maxSuccIter = 20, ratchetHits = 100, searchHits = 50,
  searchIter = 500, ratchetIter = 5000, verbosity = 0,
  suboptimal = 0.1)
```

Arguments

tree	A tree of class phylo .
dataset	A phylogenetic data matrix of class phyDat , whose names correspond to the labels of any accompanying tree.
outgroup	if not NULL, taxa on which the tree should be rooted
k	Constant for successive approximations, see Farris 1969 p. 379
maxSuccIter	maximum iterations of successive approximation
ratchetHits	maximum hits for parsimony ratchet
searchHits	maximum hits in tree search
searchIter	maximum iterations in tree search
ratchetIter	maximum iterations of parsimony ratchet
verbosity	integer (default 0) specifying how much detail to print to stdout
suboptimal	retain trees that are this proportion less optimal than the optimal tree

Value

list of optimal (and slightly suboptimal, if suboptimal > 0) trees

summary.morphyPtr *Details the attributes of a morphy object*

Description

Details the attributes of a morphy object

Usage

```
## S3 method for class 'morphyPtr'
summary(object, ...)
```

Arguments

object	A Morphy object
...	any other parameters...

Value

A list detailing the number of taxa, internal nodes, and characters and their weights.

Author(s)

Martin R. Smith

SupportColour *Support colour*

Description

Support colour

Usage

```
SupportColour(support, show1 = TRUE)
```

```
SupportColor(support, show1 = TRUE)
```

Arguments

support	A vector of doubles in the range 0-1
show1	Logical specifying whether to display values of 1. A transparent white will be returned if 'FALSE'.

Value

A string containing the hexadecimal code for a colour picked from a diverging scale, or 'red' if a value is invalid.

Functions

- SupportColor: alternative spelling

TBR

TBR

Description

Tree bisection and reconnection

Usage

TBR(tree, edgeToBreak = NULL, mergeEdges = NULL)

TBRSwap(parent, child, nEdge = length(parent), edgeToBreak = NULL, mergeEdges = NULL)

TBRMoves(parent, child, nEdge = length(parent), avoid = NULL, retainRoot = FALSE)

AllTBR(parent, child, nEdge = length(parent), avoid = NULL, retainRoot = FALSE)

RootedTBR(tree, edgeToBreak = NULL, mergeEdges = NULL)

RootedTBRSwap(parent, child, nEdge = length(parent), edgeToBreak = NULL, mergeEdges = NULL)

Arguments

tree	A bifurcating tree of class phylo , with all nodes resolved;
edgeToBreak	(optional) integer specifying the index of an edge to bisect/prune, generated randomly if not specified. Alternatively, set to -1 to return a complete list of all trees one step from the input tree.
mergeEdges	(optional) vector of length 1 or 2, listing edge(s) to be joined: In SPR, this is where the pruned subtree will be reconnected. In TBR, these edges will be reconnected (so must be on opposite sides of edgeToBreak); if only a single edge is specified, the second will be chosen at random
parent	the first column of the edge matrix of a tree of class phylo , i.e. tree\$edge[, 1]
child	the second column of the edge matrix of a tree of class phylo , i.e. tree\$edge[, 2]

nEdge	(optional) Number of edges.
avoid	Integer vector specifying which edges should not be broken
retainRoot	logical specifying whether taxa may be swapped across the root

Details

TBR performs a single random TBR iteration.

Branch lengths are not (yet) supported.

Value

This function returns a tree in phyDat format that has undergone one TBR iteration.

a list containing two elements, corresponding in turn to the rearranged parent and child parameters

a matrix with two columns, each row listing an edge that can be broken and an edge into which it can be merged

a list of trees, in parent-child format

Functions

- TBRSwap: faster version that takes and returns parent and child parameters
- TBRMoves: Possible TBR moves
- AllTBR: All unique trees one TBR move away
- RootedTBR: Perform TBR rearrangement, retaining position of root
- RootedTBRSwap: faster version that takes and returns parent and child parameters

Author(s)

Martin R. Smith

References

The TBR algorithm is summarized in Felsenstein J (2004). *Inferring phylogenies*. Sinauer Associates, Sunderland, Massachusetts.

See Also

RootedTBR useful when the position of the root node should be retained.

Examples

```
{
library('ape')
tree <- rtree(20, br=NULL)
TBR(tree)
}
```

 UniqueSplits

Unique Splits

Description

Removes equivalent duplicates from a matrix of bipartitions.

Usage

```
UniqueSplits(splits, preserveParity = FALSE)
```

Arguments

splits A vector of integers listing the number of tips in each of a number of tree splits (e.g. bipartitions). For example, `c(3, 5)` states that a character divides a set of eight tips into a group of three and a group of five.

preserveParity Logical specifying whether to preserve the 'TRUE' and 'FALSE' status within each split (which takes marginally longer). If 'FALSE', each split will be defined such that taxa in the same partition as the first element are marked 'FALSE', and other taxa marked 'TRUE'.

Value

The splits element, with all duplicate splits removed.

Author(s)

Martin R. Smith

Examples

```
set.seed(1)
splits <- Tree2Splits(ape::rtree(6, br=NULL))
UniqueSplits(splits, preserveParity=TRUE)
```

 UnloadMorphy

Destroy a Morphy Object

Description

Best practice is to call `morphyObj <- UnloadMorphy(morphyObj)` Failure to do so will cause a crash if `UnloadMorphy` is called on an object that has already been destroyed

Usage

```
UnloadMorphy(morphyObj)
```

Arguments

morphyObj A morphy object, perhaps created with [PhyDat2Morphy](#).

Value

Morphy error code, decipherable using [mpl_translate_error](#)

Author(s)

Martin R. Smith

UnloadTreeSearch *Unload this library*

Description

Unload this library

Usage

UnloadTreeSearch()

WithOneExtraStep *Number of trees with one extra step*

Description

Number of trees with one extra step

Usage

WithOneExtraStep(splits)

Arguments

splits A vector of integers listing the number of tips in each of a number of tree splits (e.g. bipartitions). For example, c(3, 5) states that a character divides a set of eight tips into a group of three and a group of five.

Index

*Topic **datasets**

- brewer, 7
- congreveLamsdellMatrices, 9
- inapplicable.citations, 17
- inapplicable.datasets, 20
- inapplicable.phyData, 23
- Lobo.data, 30
- Lobo.phy, 31
- referenceTree, 48

*Topic **tree**

- AddTip, 3
- ICSteps, 16
- IWScore, 26
- IWScoreMorphy, 27
- SingleTaxonTree, 52

- AddTip, 3
- AllAncestors, 4
- AllDescendantEdges (DescendantEdges), 11
- AllSPR, 5
- AllTBR, 34
- AllTBR (TBR), 60
- ApeTime, 6
- AsBinary, 6

- bind.tree, 4
- brewer, 7

- Cladewise, 57
- CollapseEdge (CollapseNode), 8
- CollapseNode, 8
- congreveLamsdellMatrices, 9, 48
- ConsensusWithout, 10

- DescendantEdges, 11
- DFact, 11
- DoubleFactorial (DFact), 11
- DropSingleSplits, 12

- EdgeAncestry, 13
- EnforceOutgroup, 13

- Evaluate, 14
- extract.clade, 57
- Fitch, 14
- FitchSteps, 15
- ForestSplits (SplitFrequency), 53

- IC1Spr (N1Spr), 35
- ICSteps, 16
- inapplicable.citations, 17
- inapplicable.datasets, 20
- inapplicable.phyData, 23
- InfoAmounts, 26
- IWBootstrap (MorphyBootstrap), 33
- IWDestroyMorphy (IWScore), 26
- IWInitMorphy (IWScore), 26
- IWScore, 26
- IWScoreMorphy, 27

- LDFact, 29
- LDFactorial, 29
- ldfactorial, 29
- LnRooted (NRooted), 39
- LnUnrooted (NRooted), 39
- LnUnrooted1 (NRooted), 39
- LnUnrootedMult (NRooted), 39
- Lobo.data, 30
- Lobo.phy, 31
- LogisticPoints, 32

- MarkMissing (ConsensusWithout), 10
- MatrixToList, 32
- MinimumSteps, 28, 33
- MorphyBootstrap, 33
- MorphyWeights, 34
- mpl_translate_error, 63

- N1Spr, 35
- NamedConstant, 36
- NewickTree, 36
- NJTree, 37

- NNI, 37
- NNISwap (NNI), 37
- nodeLabels, 4
- NRooted, 39
- NUnrooted (NRooted), 39
- NUnrooted1 (NRooted), 39
- NUnrootedMult (NRooted), 39

- paste0, 51
- PhyDat (ReadCharacters), 44
- phyDat, 14, 15, 34, 37, 40, 41, 43, 56, 58
- PhyDat2Morph, 34, 35, 40, 43, 51, 63
- phylo, 4, 5, 8, 11, 13–15, 27, 28, 36, 38, 47, 49, 50, 52–55, 57, 58, 60
- PhyToString, 41
- Preorder, 57
- PrepareDataIW, 27
- PrepareDataIW (PrepareDataProfile), 41
- PrepareDataProfile, 28, 41
- ProfileBootstrap (MorphyBootstrap), 33
- ProfileDestroyMorph (IWScoreMorph), 27
- ProfileInitMorph (IWScoreMorph), 27
- ProfileScore (IWScoreMorph), 27
- ProfileScoreMorph (IWScoreMorph), 27

- RandomMorphyTree, 42
- RandomTree, 43
- RandomTreeScore, 43
- read.nexus.data, 20
- ReadAsPhyDat (ReadCharacters), 44
- ReadCharacters, 44
- ReadTntAsPhyDat (ReadCharacters), 44
- ReadTntCharacters (ReadCharacters), 44
- ReadTntTree, 45
- RearrangeEdges, 47
- referenceTree, 9, 48
- Renumber, 49
- RenumberTips, 49
- RootedNNI (NNI), 37
- RootedNNISwap (NNI), 37
- RootedSPR (SPR), 54
- RootedSPRSwap (SPR), 54
- RootedTBR (TBR), 60
- RootedTBRSwap (TBR), 60
- RootTree, 50

- SetMorphyWeights, 50
- SingleCharMorph, 51
- SingleTaxonTree, 52

- SortTree, 52
- SplitFrequency, 53
- SplitNumber (SplitFrequency), 53
- SPR, 54
- SPRSwap, 34, 47
- SPRSwap (SPR), 54
- StringToPhyDat, 56
- StringToPhydat (StringToPhyDat), 56
- Subtree, 57
- SuccessiveApproximations, 58
- summary.morphyPtr, 59
- SupportColor (SupportColour), 59
- SupportColour, 59

- TBR, 60
- TBRMoves (TBR), 60
- TBRSwap (TBR), 60
- TipsAreColumns, 47
- TNTText2Tree (ReadTntTree), 45
- TreeSearch, 15
- TreeSplits (SplitFrequency), 53

- UniqueSplits, 62
- UnloadMorphy, 51, 62
- UnloadTreeSearch, 63

- WithOneExtraStep, 63