

# Package ‘TreeSearch’

April 27, 2023

**Title** Phylogenetic Analysis with Discrete Character Data

**Version** 1.3.2

**License** GPL (>= 3)

**Copyright** Incorporates C/C++ code from Morphy Phylogenetic Library by Martin Brazeau <<https://github.com/mbrazeau/MorphyLib>> (GPL3)

**Description** Reconstruct phylogenetic trees from discrete data. Inapplicable character states are handled using the algorithm of Brazeau, Guillaume and Smith (2019) <[doi:10.1093/sysbio/syy083](https://doi.org/10.1093/sysbio/syy083)> with the “Morphy” library, under equal or implied step weights. Contains a “shiny” user interface for interactive tree search and exploration of results, including character visualization, rogue taxon detection, tree space mapping, and cluster consensus trees (Smith 2022a, b) <[doi:10.1093/sysbio/syab099](https://doi.org/10.1093/sysbio/syab099)>, <[doi:10.1093/sysbio/syab100](https://doi.org/10.1093/sysbio/syab100)>. Profile Parsimony (Faith and Trueman, 2001) <[doi:10.1080/10635150118627](https://doi.org/10.1080/10635150118627)>, Successive Approximations (Farris, 1969) <[doi:10.2307/2412182](https://doi.org/10.2307/2412182)> and custom optimality criteria are implemented.

**URL** <https://ms609.github.io/TreeSearch/>,  
<https://github.com/ms609/TreeSearch/>

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

**Depends** R (>= 3.5.0)

**Imports** ape (>= 5.6), cli (>= 3.0), cluster, fastmatch (>= 1.1.3), future, PlotTools, promises, protoclust, Rcpp, Rdpack (>= 0.7), Rogue (> 2.0.0), shiny (>= 1.6.0), shinyjs, stats, TreeDist (>= 2.5.0), TreeTools (>= 1.9.0),

**Suggests** knitr, phangorn (>= 2.2.1), Quartet, readxl, rmarkdown, shinytest, spelling, testthat, vdiff (>= 1.0.0),

**Config/Needs/check** callr, pkgbuild, rcmdcheck,

**Config/Needs/coverage** covr, spelling

**Config/Needs/memcheck** devtools

**Config/Needs/metadata** codemeta

**Config/Needs/revdeps** revdepcheck

**Config/Needs/website** curl, igraph, pkgdown,  
**RdMacros** Rdpack  
**LinkingTo** Rcpp, TreeTools,  
**SystemRequirements** C++17  
**LazyData** true  
**ByteCompile** true  
**Encoding** UTF-8  
**Language** en-GB  
**VignetteBuilder** knitr  
**RoxygenNote** 7.2.3  
**NeedsCompilation** yes  
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**Repository** CRAN  
**Date/Publication** 2023-04-27 12:52:38 UTC

## R topics documented:

|                          |    |
|--------------------------|----|
| AdditionTree             | 3  |
| AllSPR                   | 4  |
| Carter1                  | 5  |
| CharacterLength          | 6  |
| ClusterStrings           | 7  |
| ConcordantInformation    | 8  |
| congreveLamsdellMatrices | 9  |
| Consistency              | 10 |
| cSPR                     | 11 |
| GapHandler               | 11 |
| inapplicable.datasets    | 12 |
| is.morphyPtr             | 16 |
| IWScore                  | 16 |
| Jackknife                | 18 |
| JackLabels               | 20 |
| LengthAdded              | 21 |
| MaximizeParsimony        | 23 |
| MinimumLength            | 28 |
| MorphyBootstrap          | 30 |
| MorphyWeights            | 33 |
| NNI                      | 35 |
| PhyDat2Morphy            | 37 |
| PlotCharacter            | 38 |

|                              |           |
|------------------------------|-----------|
| PrepareDataProfile . . . . . | 39        |
| profiles . . . . .           | 41        |
| QuartetResolution . . . . .  | 41        |
| RandomMorphyTree . . . . .   | 42        |
| RandomTreeScore . . . . .    | 43        |
| RearrangeEdges . . . . .     | 43        |
| referenceTree . . . . .      | 45        |
| SingleCharMorphy . . . . .   | 46        |
| SiteConcordance . . . . .    | 47        |
| SPR . . . . .                | 48        |
| StepInformation . . . . .    | 50        |
| summary.morphyPtr . . . . .  | 51        |
| TBR . . . . .                | 52        |
| UnloadMorphy . . . . .       | 54        |
| WhenFirstHit . . . . .       | 55        |
| WithOneExtraStep . . . . .   | 56        |
| <b>Index</b>                 | <b>57</b> |

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|              |                      |
|--------------|----------------------|
| AdditionTree | <i>Addition tree</i> |
|--------------|----------------------|

---

## Description

Generates a starting tree by adding each taxon in turn to the most parsimonious location.

## Usage

```
AdditionTree(dataset, concavity = Inf, constraint, sequence)
```

## Arguments

|            |   |
|------------|---|
| dataset    | A phylogenetic data matrix of <b>phangorn</b> class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree.  |
| concavity  | Numeric specifying concavity constant for implied step weighting. The most appropriate value will depend on the dataset, but values around 10–15 often perform well (Goloboff et al. 2018; Smith 2019). The character string "profile" employs an approximation of profile parsimony (Faith and Trueman 2001). Set as <code>Inf</code> for equal step weights, which underperforms step weighting approaches (Goloboff et al. 2008; Goloboff et al. 2018; Goloboff and Arias 2019; Smith 2019). |
| constraint | Either an object of class <code>phyDat</code> , in which case returned trees will be perfectly compatible with each character in <code>constraint</code> ; or a tree of class <code>phylo</code> , all of whose nodes will occur in any output tree. See <code>ImposeConstraint()</code> and <a href="#">vignette</a> for further examples.   |
| sequence   | Character or numeric vector listing sequence in which to add taxa. Randomized if not provided.  |

**Value**

AdditionTree() returns a tree of class `phylo`, rooted on `sequence[1]`.

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Impose a constraint: `TreeTools::ImposeConstraint()`

Neighbour-joining trees: `TreeTools::NJTree()`; `TreeTools::ConstrainedNJ()`

Other tree generation functions: `RandomMorphyTree()`

**Examples**

```
data("inapplicable.phyData", package = "TreeSearch")
AdditionTree(inapplicable.phyData[["Longrich2010"]], concavity = 10)
```

---

AllSPR

*All SPR trees*


---

**Description**

All SPR trees

**Usage**

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

**Arguments**

|                  |  |
|------------------|--|
| parent           | Integer vector corresponding to the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code> .  |
| child            | Integer vector corresponding to the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code> .   |
| nEdge            | integer specifying the number of edges of a tree of class <code>phylo</code> , i.e. <code>dim(tree\$edge)[1]</code>  |
| notDuplicateRoot | 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.) |
| edgeToBreak      | (optional) integer specifying the index of an edge to bisect/prune, 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**

AllSPR() returns a list of edge matrices for all trees one SPR rearrangement from the starting tree

**Author(s)**

Martin R. Smith

Carter1

*Number of trees with m steps***Description**

Calculate the number of trees in which Fitch parsimony will reconstruct  $m$  steps, where  $a$  leaves are labelled with one state, and  $b$  leaves are labelled with a second state.

**Usage**

Carter1(m, a, b)

Log2Carter1(m, a, b)

LogCarter1(m, a, b)

**Arguments**

|      |                                    |
|------|------------------------------------|
| m    | Number of steps.                   |
| a, b | Number of leaves labelled 0 and 1. |

**Details**

Implementation of theorem 1 from Carter et al. (1990)

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**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.

See also:

Steel MA (1993). "Distributions on bicoloured binary trees arising from the principle of parsimony." *Discrete Applied Mathematics*, **41**(3), 245–261. doi:10.1016/0166218X(90)90058K.

Steel M, Charleston M (1995). "Five surprising properties of parsimoniously colored trees." *Bulletin of Mathematical Biology*, **57**(2), 367–375. doi:10.1016/00928240(94)00051D.

(Steel M, Goldstein L, Waterman MS (1996). "A central limit theorem for the parsimony length of trees." *Advances in Applied Probability*, **28**(4), 1051–1071. doi:10.2307/1428164.)

**See Also**

Other profile parsimony functions: [PrepareDataProfile\(\)](#), [StepInformation\(\)](#), [WithOneExtraStep\(\)](#), [profiles](#)

**Examples**

```
# The character `0 0 0 1 1 1`
Carter1(1, 3, 3) # Exactly one step
Carter1(2, 3, 3) # Two steps (one extra step)

# Number of trees that the character can map onto with exactly _m_ steps
# if non-parsimonious reconstructions are permitted:
cumsum(sapply(1:3, Carter1, 3, 3))

# Three steps allow the character to map onto any of the 105 six-leaf trees.
```

---

|                 |                         |
|-----------------|-------------------------|
| CharacterLength | <i>Character length</i> |
|-----------------|-------------------------|

---

**Description**

Homoplasy length of each character in a dataset on a specified tree.

**Usage**

```
CharacterLength(tree, dataset, compress = FALSE)
```

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

```
FastCharacterLength(tree, dataset)
```

**Arguments**

|          |  |
|----------|--|
| tree     | A tree of class <a href="#">phylo</a> .  |
| dataset  | A phylogenetic data matrix of <b>phangorn</b> class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree.   |
| compress | Logical specifying whether to retain the compression of a <code>phyDat</code> object or to return a vector specifying to each individual character, decompressed using the dataset's <code>index</code> attribute. |

**Value**

`CharacterLength()` returns a vector listing the contribution of each character to tree score, according to the algorithm of Brazeau et al. (2019).

**Functions**

- `FastCharacterLength()`: Do not perform checks. Use with care: may cause erroneous results or software crash if variables are in the incorrect format.

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**References**

Brazeau MD, Guillaume T, Smith MR (2019). “An algorithm for morphological phylogenetic analysis with inapplicable data.” *Systematic Biology*, **68**(4), 619–631. doi:10.1093/sysbio/syy083.

**See Also**

Other tree scoring: `IWScore()`, `LengthAdded()`, `MinimumLength()`, `MorphyTreeLength()`

**Examples**

```
data("inapplicable.datasets")
dataset <- inapplicable.phyData[[12]]
tree <- TreeTools::NJTree(dataset)
CharacterLength(tree, dataset)
CharacterLength(tree, dataset, compress = TRUE)
```

---

ClusterStrings      *Cluster similar strings*

---

**Description**

Calculate string similarity using the Levenshtein distance and return clusters of similar strings.

**Usage**

```
ClusterStrings(x, maxCluster = 12)
```

**Arguments**

|                         |  |
|-------------------------|--|
| <code>x</code>          | Character vector.  |
| <code>maxCluster</code> | Integer specifying maximum number of clusters to consider. |

**Value**

`NameClusters()` returns an integer assigning each element of `x` to a cluster, with an attribute `med` specifying the median string in each cluster, and `silhouette` reporting the silhouette coefficient of the optimal clustering. Coefficients  $< 0.5$  indicate weak structure, and no clusters are returned. If the number of unique elements of `x` is less than `maxCluster`, all occurrences of each entry are assigned to an individual cluster.

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other utility functions: [QuartetResolution\(\)](#), [WhenFirstHit\(\)](#)

**Examples**

```
ClusterStrings(c(paste0("FirstCluster ", 1:5),
                 paste0("SecondCluster.", 8:12),
                 paste0("AnotherCluster_", letters[1:6])))
```

---

ConcordantInformation *Evaluate the concordance of information between a tree and a dataset*

---

**Description**

Details the amount of information in a phylogenetic dataset that is consistent with a specified phylogenetic tree, and the signal:noise ratio of the character matrix implied if the tree is true.

**Usage**

```
ConcordantInformation(tree, dataset)
```

```
Evaluate(tree, dataset)
```

```
ConcordantInfo(tree, dataset)
```

**Arguments**

|         |  |
|---------|--|
| tree    | A tree of class <a href="#">phylo</a> .  |
| dataset | A phylogenetic data matrix of <b>phangorn</b> class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree. |

**Details**

Presently restricted to datasets whose characters contain a maximum of two parsimony-informative states.

**Value**

`ConcordantInformation()` returns a named vector with elements:

- `informationContent`: cladistic information content of dataset
- `signal, noise`: amount of cladistic information that represents phylogenetic signal and noise, according to tree



- `signalToNoise`: the implied signal:noise ratio of dataset
- `treeInformation`: the cladistic information content of a bifurcating tree on dataset; this is the minimum amount of information necessary to resolve a bifurcating tree, assuming no duplicate information or noise
- `matrixToTree`: the ratio of the cladistic information content of the matrix to the cladistic information content of the tree, a measure of the redundancy of the matrix
- `ignored`: information content of characters whose signal and noise could not be calculated (too many states) and so are not included in the totals above.

### Author(s)

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### Examples

```
data(congreveLamsdellMatrices)
myMatrix <- congreveLamsdellMatrices[[10]]
ConcordantInformation(TreeTools::NJTree(myMatrix), myMatrix)
```

---

congreveLamsdellMatrices  
*100 simulated data matrices*

---

### Description

Contains the 100 simulated matrices generated by (Congreve and 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

[doi:10.5061/dryad.7dq0j](https://doi.org/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**(3), 447–465. [doi:10.1111/pala.12236](https://doi.org/10.1111/pala.12236).

**Examples**

```
data("referenceTree")
data("congreveLamsdellMatrices")
TreeLength(referenceTree, congreveLamsdellMatrices[[17]], "profile")
```

---

Consistency

*Consistency / retention "indices"*


---

**Description**

Consistency() calculates the so-called consistency and retention "indices" for each character in a dataset, given a bifurcating tree. Although there is not a straightforward interpretation of these indices, they are sometimes taken as an indicator of the fit of a character to a tree. Values correlate with the number of species sampled and the distribution of taxa between character states, so are not strictly comparable between characters in which these factors differ.

**Usage**

```
Consistency(dataset, tree, compress = FALSE)
```

**Arguments**

|          |  |
|----------|--|
| dataset  | A phylogenetic data matrix of <b>phangorn</b> class phyDat, whose names correspond to the labels of any accompanying tree.   |
| tree     | A tree of class <a href="#">phylo</a> .  |
| compress | Logical specifying whether to retain the compression of a phyDat object or to return a vector specifying to each individual character, decompressed using the dataset's index attribute. |

**Details**

#TODO: Retention index not yet implemented.

**Value**

Consistency() returns a named vector specifying the consistency index (ci), retention index (ri), and rescaled consistency index (rc).

**Author(s)**

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**Examples**

```
data(inapplicable.datasets)
dataset <- inapplicable.phyData[[4]]
Consistency(dataset, TreeTools::NJTree(dataset))
```

---

|      |  |
|------|--|
| cSPR | <i>cSPR()</i> expects a tree rooted on a single tip. |
|------|--|

---

### Description

`cSPR()` expects a tree rooted on a single tip.

### Usage

```
cSPR(tree, whichMove = NULL)
```

### Arguments

|           |   |
|-----------|---|
| tree      | A tree of class <code>phylo</code> .                |
| whichMove | Integer specifying which SPR move index to perform. |

### Author(s)

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### Examples

```
tree <- TreeTools::BalancedTree(8)

# Tree must be rooted on leaf
tree <- TreeTools::RootTree(tree, 1)

# Random rearrangement
cSPR(tree)

# Specific rearrangement
cSPR(tree, 9)
```

---

|            |  |
|------------|--|
| GapHandler | <i>Read how a Morphy Object handles the inapplicable token</i> |
|------------|--|

---

### Description

Gaps represented by the inapplicable token can be treated as "missing data", i.e. as equivalent to the ambiguous token `?`; as an extra state, equivalent to other states such as `0` or `1`; or as "inapplicable data" using the algorithm of Brazeau, Guillaume and Smith (2019).

### Usage

```
GapHandler(morphyObj)
```

**Arguments**

morphyObj      Object of class morphy, perhaps created with [PhyDat2Morphy\(\)](#).

**Value**

GapHandler() returns a character string stating how gaps are handled by morphyObj.

**Author(s)**

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other Morphy API functions: [MorphyErrorCheck\(\)](#), [MorphyWeights\(\)](#), [PhyDat2Morphy\(\)](#), [SingleCharMorphy\(\)](#), [UnloadMorphy\(\)](#), [is.morphyPtr\(\)](#), [mpl\\_apply\\_tipdata\(\)](#), [mpl\\_attach\\_rawdata\(\)](#), [mpl\\_attach\\_symbols\(\)](#), [mpl\\_delete\\_Morphy\(\)](#), [mpl\\_delete\\_rawdata\(\)](#), [mpl\\_first\\_down\\_recon\(\)](#), [mpl\\_first\\_up\\_recon\(\)](#), [mpl\\_get\\_charac\\_weight\(\)](#), [mpl\\_get\\_gaphandl\(\)](#), [mpl\\_get\\_num\\_charac\(\)](#), [mpl\\_get\\_num\\_internal\\_nodes\(\)](#), [mpl\\_get\\_numtaxa\(\)](#), [mpl\\_get\\_symbols\(\)](#), [mpl\\_init\\_Morphy\(\)](#), [mpl\\_new\\_Morphy\(\)](#), [mpl\\_second\\_down\\_recon\(\)](#), [mpl\\_second\\_up\\_recon\(\)](#), [mpl\\_set\\_charac\\_weight\(\)](#), [mpl\\_set\\_num\\_internal\\_nodes\(\)](#), [mpl\\_set\\_parsim\\_t\(\)](#), [mpl\\_translate\\_error\(\)](#), [mpl\\_update\\_lower\\_root\(\)](#), [mpl\\_update\\_tip\(\)](#), [summary.morphyPtr\(\)](#)

**Examples**

```
morphyObj <- SingleCharMorphy("-0-0", "Extra")
GapHandler(morphyObj)
morphyObj <- UnloadMorphy(morphyObj)
```

---

inapplicable.datasets *Thirty datasets with inapplicable data*

---

**Description**

These are the datasets used to evaluate the behaviour of the inapplicable algorithm in Brazeau et al. (2019). 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. `inapplicable.datasets` provide the data in the matrix format generated by [read.nexus.data\(\)](#); `inapplicable.phyData` are in phyDat format. `inapplicable.trees` lists for each dataset a sample of up to 50 trees obtained by tree search under each inapplicable treatment, named accordingly. `inapplicable.citations` is a named character vector specifying the source of each dataset.

**Usage**

`inapplicable.datasets`

`inapplicable.phyData`

inapplicable.trees

inapplicable.citations

### Format

An object of class `list` of length 30.

An object of class `list` of length 30.

An object of class `list` of length 31.

An object of class `character` of length 30.

### Source

Subset one (faster processing):

**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.

Subset two (longer processing times):

**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 leaenochilid 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.

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## Examples

```
data("inapplicable.datasets", package = "TreeSearch")
names(inapplicable.datasets)
```

---

|                           |  |
|---------------------------|--|
| <code>is.morphyPtr</code> | <i>Is an object a valid Morphy object?</i> |
|---------------------------|--|

---

**Description**

Is an object a valid Morphy object?

**Usage**

```
is.morphyPtr(morphyObj)
```

**Arguments**

`morphyObj`      Object of class `morphy`, perhaps created with `PhyDat2Morphy()`.

**Value**

`is.morphyPtr()` returns TRUE if `morphyObj` is a valid `morphy` pointer, FALSE otherwise.

**Author(s)**

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other Morphy API functions: `GapHandler()`, `MorphyErrorCheck()`, `MorphyWeights()`, `PhyDat2Morphy()`, `SingleCharMorphy()`, `UnloadMorphy()`, `mpl_apply_tipdata()`, `mpl_attach_rawdata()`, `mpl_attach_symbols()`, `mpl_delete_Morphy()`, `mpl_delete_rawdata()`, `mpl_first_down_recon()`, `mpl_first_up_recon()`, `mpl_get_charac_weight()`, `mpl_get_gaphandl()`, `mpl_get_num_charac()`, `mpl_get_num_internal_nodes()`, `mpl_get_numtaxa()`, `mpl_get_symbols()`, `mpl_init_Morphy()`, `mpl_new_Morphy()`, `mpl_second_down_recon()`, `mpl_second_up_recon()`, `mpl_set_charac_weight()`, `mpl_set_num_internal_nodes()`, `mpl_set_parsim_t()`, `mpl_translate_error()`, `mpl_update_lower_root()`, `mpl_update_tip()`, `summary.morphyPtr()`

---

|                      |  |
|----------------------|--|
| <code>IWScore</code> | <i>Calculate the parsimony score of a tree given a dataset</i> |
|----------------------|--|

---

**Description**

`TreeLength()` uses the Morphy library (Brazeau et al. 2017) to calculate a parsimony score for a tree, handling inapplicable data according to the algorithm of Brazeau et al. (2019). Trees may be scored using equal weights, implied weights (Goloboff 1993), or profile parsimony (Faith and Trueman 2001).



**Usage**

```

IWScore(tree, dataset, concavity = 10L, ...)

TreeLength(tree, dataset, concavity = Inf)

## S3 method for class 'phylo'
TreeLength(tree, dataset, concavity = Inf)

## S3 method for class 'numeric'
TreeLength(tree, dataset, concavity = Inf)

## S3 method for class 'list'
TreeLength(tree, dataset, concavity = Inf)

## S3 method for class 'multiPhylo'
TreeLength(tree, dataset, concavity = Inf)

Fitch(tree, dataset)

```

**Arguments**

|           |  |
|-----------|--|
| tree      | A tree of class phylo, a list thereof (optionally of class multiPhylo), or an integer – in which case tree random trees will be uniformly sampled.   |
| dataset   | A phylogenetic data matrix of <b>phangorn</b> class phyDat, whose names correspond to the labels of any accompanying tree.   |
| concavity | Determines the degree to which extra steps beyond the first are penalized. Specify a numeric value to use implied weighting (Goloboff 1993); concavity specifies $k$ in $k / e + k$ . A value of 10 is recommended; TNT sets a default of 3, but this is too low in some circumstances (Goloboff et al. 2018; Smith 2019). Better still explore the sensitivity of results under a range of concavity values, e.g. $k = 2^{(1:7)}$ . Specify Inf to weight each additional step equally. Specify "profile" to employ profile parsimony (Faith and Trueman 2001). |
| ...       | unused; allows additional parameters specified within ... to be received by the function without throwing an error.  |

**Value**

TreeLength() returns a numeric vector containing the score for each tree in tree.

**Author(s)**

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

**References**

Brazeau MD, Guillaume T, Smith MR (2019). "An algorithm for morphological phylogenetic analysis with inapplicable data." *Systematic Biology*, **68**(4), 619–631. doi:10.1093/sysbio/syy083.

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Smith MR (2019). “Bayesian and parsimony approaches reconstruct informative trees from simulated morphological datasets.” *Biology Letters*, **15**(2), 20180632. doi:10.1098/rsbl.2018.0632.

### See Also

- Conduct tree search using `MaximizeParsimony()` (command line), `EasyTrees()` (graphical user interface), or `TreeSearch()` (custom optimality criteria).
- See score for each character: `CharacterLength()`.

Other tree scoring: `CharacterLength()`, `LengthAdded()`, `MinimumLength()`, `MorphyTreeLength()`

### Examples

```
data("inapplicable.datasets")
tree <- TreeTools::BalancedTree(inapplicable.phyData[[1]])
TreeLength(tree, inapplicable.phyData[[1]])
TreeLength(tree, inapplicable.phyData[[1]], concavity = 10)
TreeLength(tree, inapplicable.phyData[[1]], concavity = "profile")
TreeLength(5, inapplicable.phyData[[1]])
```

---

Jackknife

*Jackknife resampling*

---

### Description

Resample trees using Jackknife resampling, i.e. removing a subset of characters.

### Usage

```
Jackknife(
  tree,
  dataset,
  resampleFreq = 2/3,
  InitializeData = PhyDat2Morph,
  CleanUpData = UnloadMorph,
```

```

    TreeScorer = MorphyLength,
    EdgeSwapper = TBRSwap,
    jackIter = 5000L,
    searchIter = 4000L,
    searchHits = 42L,
    verbosity = 1L,
    ...
)

```

### Arguments

|                |  |
|----------------|--|
| tree           | A tree of class <code>phylo</code> .   |
| dataset        | a dataset in the format required by <code>TreeScorer()</code> .  |
| resampleFreq   | Double between 0 and 1 stating proportion of characters to resample.   |
| InitializeData | Function that sets up data object to prepare for tree search. The function will be passed the <code>dataset</code> parameter. Its return value will be passed to <code>TreeScorer()</code> and <code>CleanUpData()</code> .              |
| CleanUpData    | Function to destroy data object on function exit. The function will be passed the value returned by <code>InitializeData()</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 <code>SPRSwap()</code> .   |
| jackIter       | Integer specifying number of jackknife iterations to conduct.  |
| searchIter     | Integer specifying maximum rearrangements to perform on each bootstrap or ratchet iteration. To override this value for a single swapper function, set e.g. <code>attr(SwapperFunction, "searchIter") &lt;- 99</code>                    |
| searchHits     | Integer specifying maximum times to hit best score before terminating a tree search within a ratchet iteration. To override this value for a single swapper function, set e.g. <code>attr(SwapperFunction, "searchHits") &lt;- 99</code> |
| verbosity      | Numeric specifying level of detail to display in console: larger numbers provide more verbose feedback to the user.  |
| ...            | further arguments to pass to <code>TreeScorer()</code> , e.g. <code>dataset = .</code>   |

### Details

The function assumes that `InitializeData()` will return a `morphy` object; if this doesn't hold for you, post a [GitHub issue](#) or e-mail the maintainer.

### Value

`Jackknife()` returns a list of trees recovered after jackknife iterations.

### Author(s)

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

- [JackLabels\(\)](#): Label nodes of a tree with jackknife supports.

Other split support functions: [JackLabels\(\)](#), [MaximizeParsimony\(\)](#), [SiteConcordance](#)

Other custom search functions: [EdgeListSearch\(\)](#), [MorphyBootstrap\(\)](#), [SuccessiveApproximations\(\)](#)

---

JackLabels

*Label nodes with jackknife support values*

---

**Description**

Label nodes with jackknife support values

**Usage**

```
JackLabels(
  tree,
  jackTrees,
  plot = TRUE,
  add = FALSE,
  adj = 0,
  col = NULL,
  frame = "none",
  pos = 2L,
  ...
)
```

**Arguments**

|                           |  |
|---------------------------|--|
| tree                      | A tree of class <a href="#">phylo</a> .  |
| jackTrees                 | A list or <code>multiPhylo</code> object containing trees generated by <a href="#">Jackknife()</a> .   |
| plot                      | Logical specifying whether to plot results; if FALSE, returns blank labels for nodes near the root that do not correspond to a unique split. |
| add                       | Logical specifying whether to add the labels to an existing plot.  |
| adj, col, frame, pos, ... | Parameters to pass to <code>nodeLabels()</code> .  |

**Value**

A named vector specifying the proportion of jackknife trees consistent with each node in `tree`, as plotted. If `plot = FALSE`, blank entries are included corresponding to nodes that do not require labelling; the return value is in the value required by `phylo$node.label`.

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

[Jackknife\(\)](#): Generate trees by jackknife resampling

Other split support functions: [Jackknife\(\)](#), [MaximizeParsimony\(\)](#), [SiteConcordance](#)

**Examples**

```
library("TreeTools", quietly = TRUE) # for as.phylo

# jackTrees will usually be generated with Jackknife(), but for simplicity:
jackTrees <- as.phylo(1:100, 8)

tree <- as.phylo(0, 8)
JackLabels(tree, jackTrees)

tree$node.label <- JackLabels(tree, jackTrees, plot = FALSE)
```

---

LengthAdded

*Contribution of character to leaf instability*

---

**Description**

Would tree lengths change if a character was coded as ambiguous for each leaf (Pol and Escapa 2009)?

**Usage**

```
LengthAdded(trees, char, concavity = Inf)
```

```
PolEscapa(trees, char, concavity = Inf)
```

**Arguments**

|           |  |
|-----------|--|
| trees     | List of trees of class phylo, or multiPhylo object.  |
| char      | phyDat object containing a single character.   |
| concavity | Determines the degree to which extra steps beyond the first are penalized. Specify a numeric value to use implied weighting (Goloboff 1993); concavity specifies $k$ in $k / e + k$ . A value of 10 is recommended; TNT sets a default of 3, but this is too low in some circumstances (Goloboff et al. 2018; Smith 2019). Better still explore the sensitivity of results under a range of concavity values, e.g. $k = 2^{(1:7)}$ . Specify Inf to weight each additional step equally. Specify "profile" to employ profile parsimony (Faith and Trueman 2001). |

## Details

High values for a leaf indicate that its coding contributes to instability ("wildcard" or "roguish" behaviour; see **Rogue** for further details). The coding is in tension with other data, which may indicate that the assumptions of homology that underlie the character's construction and scoring require careful scrutiny – or that the taxon in question has been subject to convergent evolution.

When inapplicable tokens are present in a character, the applicability of each coding is maintained: i.e. a leaf coded with an applicable token is never allowed to take an inapplicable value; and an inapplicable token remains inapplicable.

## Value

LengthAdded() returns a named numeric vector listing the mean absolute change to tree length resulting if the character were coded ambiguous for each leaf in turn, under the specified concavity constant.

## Author(s)

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

## 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).

Goloboff PA (1993). "Estimating character weights during tree search." *Cladistics*, **9**(1), 83–91. doi:[10.1111/j.10960031.1993.tb00209.x](https://doi.org/10.1111/j.10960031.1993.tb00209.x).

Goloboff PA, Torres A, Arias JS (2018). "Weighted parsimony outperforms other methods of phylogenetic inference under models appropriate for morphology." *Cladistics*, **34**(4), 407–437. doi:[10.1111/cla.12205](https://doi.org/10.1111/cla.12205).

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Smith MR (2019). "Bayesian and parsimony approaches reconstruct informative trees from simulated morphological datasets." *Biology Letters*, **15**(2), 20180632. doi:[10.1098/rsbl.2018.0632](https://doi.org/10.1098/rsbl.2018.0632).

## See Also

Other tree scoring: [CharacterLength\(\)](#), [IWScore\(\)](#), [MinimumLength\(\)](#), [MorphyTreeLength\(\)](#)

## Examples

```
trees <- inapplicable.trees[["Vinther2008"]]
dataset <- inapplicable.phyData[["Vinther2008"]]
char <- dataset[, 11]
added <- LengthAdded(trees, char)
```

```
PlotCharacter(
```

```

tree = trees[[1]],
dataset = char,
tip.color = 1 + added[trees[[1]]$tip.label] # Colour by added steps
) -> XX # Suppress return value; display plot only

```

---

MaximizeParsimony      *Find most parsimonious trees*

---

### Description

Search for most parsimonious trees using the parsimony ratchet and TBR rearrangements, treating inapplicable data as such using the algorithm of Brazeau et al. (2019).

Tree search will be conducted from a specified or automatically-generated starting tree in order to find a tree with an optimal parsimony score, under implied or equal weights, treating inapplicable characters as such in order to avoid the artefacts of the standard Fitch algorithm (see Maddison 1993; Brazeau et al. 2019). Tree length is calculated using the MorphyLib C library (Brazeau et al. 2017).

### Usage

```

MaximizeParsimony(
  dataset,
  tree,
  ratchIter = 7L,
  tbrIter = 2L,
  startIter = 2L,
  finalIter = 1L,
  maxHits = NTip(dataset) * 1.8,
  maxTime = 60,
  quickHits = 1/3,
  concavity = Inf,
  tolerance = sqrt(.Machine$double.eps),
  constraint,
  verbosity = 3L
)

```

```

Resample(
  dataset,
  tree,
  method = "jack",
  proportion = 2/3,
  ratchIter = 1L,
  tbrIter = 8L,
  finalIter = 3L,
  maxHits = 12L,
  concavity = Inf,

```

```

    tolerance = sqrt(.Machine$double.eps),
    constraint,
    verbosity = 2L,
    ...
)

EasyTrees()

EasyTreesy()

```

### Arguments

|           |   |
|-----------|---|
| dataset   | A phylogenetic data matrix of <b>phangorn</b> class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree.  |
| tree      | (optional) A bifurcating tree of class <code>phylo</code> , containing only the tips listed in dataset, from which the search should begin. If unspecified, an <b>addition tree</b> will be generated from dataset, respecting any supplied constraint. Edge lengths are not supported and will be deleted.   |
| ratchIter | Numeric specifying number of iterations of the parsimony ratchet (Nixon 1999) to conduct.   |
| tbrIter   | Numeric specifying the maximum number of TBR break points to evaluate before concluding each search. The counter is reset to zero each time tree score improves. The counter is reset to zero each time tree score improves. One "iteration" comprises breaking a single branch and evaluating all possible reconnections.  |
| startIter | Numeric: an initial round of tree search with <code>startIter × tbrIter</code> TBR break points is conducted in order to locate a local optimum before beginning ratchet searches.  |
| finalIter | Numeric: a final round of tree search will evaluate <code>finalIter × tbrIter</code> TBR break points, in order to sample the final optimal neighbourhood more intensely.   |
| maxHits   | Numeric specifying the maximum times that an optimal parsimony score may be hit before concluding a ratchet iteration or final search concluded.  |
| maxTime   | Numeric: after <code>maxTime</code> minutes, stop tree search at the next opportunity.  |
| quickHits | Numeric: iterations on subsampled datasets will retain <code>quickHits × maxHits</code> trees with the best score.  |
| concavity | Numeric specifying concavity constant for implied step weighting. The most appropriate value will depend on the dataset, but values around 10–15 often perform well (Goloboff et al. 2018; Smith 2019). The character string "profile" employs an approximation of profile parsimony (Faith and Trueman 2001). Set as <code>Inf</code> for equal step weights, which underperforms step weighting approaches (Goloboff et al. 2008; Goloboff et al. 2018; Goloboff and Arias 2019; Smith 2019). |
| tolerance | Numeric specifying degree of suboptimality to tolerate before rejecting a tree. The default, <code>sqrt(.Machine\$double.eps)</code> , retains trees that may be equally parsimonious but for rounding errors. Setting to larger values will include trees suboptimal by up to <code>tolerance</code> in search results, which may improve the accuracy of the consensus tree (at the expense of resolution) (Smith 2019).  |



|            |  |
|------------|--|
| constraint | Either an object of class phyDat, in which case returned trees will be perfectly compatible with each character in constraint; or a tree of class phylo, all of whose nodes will occur in any output tree. See <a href="#">ImposeConstraint()</a> and <a href="#">vignette</a> for further examples. |
| verbosity  | Integer specifying level of messaging; higher values give more detailed commentary on search progress. Set to 0 to run silently.   |
| method     | Unambiguous abbreviation of jackknife or bootstrap specifying how to re-sample characters. Note that jackknife is considered to give more meaningful results.  |
| proportion | Numeric between 0 and 1 specifying what proportion of characters to retain under jackknife resampling.   |
| ...        | Additional parameters to MaximizeParsimony().  |

### Details

Tree search commences with ratchIter iterations of the parsimony ratchet (Nixon 1999), which bootstraps the input dataset in order to escape local optima. A final round of tree bisection and reconnection (TBR) is conducted to broaden the sampling of trees.

This function can be called using the R command line / terminal, or through the "shiny" graphical user interface app (type EasyTrees() to launch).

For detailed documentation of the "TreeSearch" package, including full instructions for loading phylogenetic data into R and initiating and configuring tree search, see the [package documentation](#).

### Value

MaximizeParsimony() returns a list of trees with class multiPhylo. This lists all trees found during each search step that are within tolerance of the optimal score, listed in the sequence that they were first visited, and named according to the step in which they were first found; it may contain more than maxHits elements. Note that the default search parameters may need to be increased in order for these trees to be the globally optimal trees; examine the messages printed during tree search to evaluate whether the optimal score has stabilized.

The return value has the attribute firstHit, a named integer vector listing the number of optimal trees visited for the first time in each stage of the tree search. Stages are named:

- seed: starting trees;
- start: Initial TBR search;
- ratchN: Ratchet iteration N;
- final: Final TBR search. The first tree hit for the first time in ratchet iteration three is named ratch3\_1.

Resample() returns a multiPhylo object containing a list of trees obtained by tree search using a resampled version of dataset.

## Resampling

Note that bootstrap support is a measure of the amount of data supporting a split, rather than the amount of confidence that should be afforded the grouping. "Bootstrap support of 100% is not enough, the tree must also be correct" (Phillips et al. 2004). See discussion in Egan (2006); Wagele et al. (2009); (Simmons and Freudenstein 2011); Kumar et al. (2012).

For a discussion of suitable search parameters in resampling estimates, see Muller (2005). The user should decide whether to start each resampling from the optimal tree (which may be quicker, but result in overestimated support values as searches get stuck in local optima close to the optimal tree) or a random tree (which may take longer as more rearrangements are necessary to find an optimal tree on each iteration).

For other ways to estimate clade concordance, see [SiteConcordance\(\)](#).

## Author(s)

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

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### See Also

Tree search *via* graphical user interface: [EasyTrees\(\)](#)

Other split support functions: [JackLabels\(\)](#), [Jackknife\(\)](#), [SiteConcordance](#)

### Examples

```
## Only run examples in interactive R sessions
if (interactive()) {
  # launch "shiny" point-and-click interface
  EasyTrees()

  # Here too, use the "continue search" function to ensure that tree score
  # has stabilized and a global optimum has been found
}

# Load data for analysis in R
library("TreeTools")
data("congreveLamsdellMatrices", package = "TreeSearch")
dataset <- congreveLamsdellMatrices[[42]]

# A very quick run for demonstration purposes
trees <- MaximizeParsimony(dataset, ratchIter = 0, startIter = 0,
                           tbrIter = 1, maxHits = 4, maxTime = 1/100,
                           concavity = 10, verbosity = 4)

names(trees)

# In actual use, be sure to check that the score has converged on a global
# optimum, conducting additional iterations and runs as necessary.
```

```

if (interactive()) {
# Jackknife resampling
nReplicates <- 10
jackTrees <- replicate(nReplicates,
  #c() ensures that each replicate returns a list of trees
  c(Resample(dataset, trees, ratchIter = 0, tbrIter = 2, startIter = 1,
    maxHits = 5, maxTime = 1 / 10,
    concavity = 10, verbosity = 0))
)

# In a serious analysis, more replicates would be conducted, and each
# search would undergo more iterations.

# Now we must decide what to do with the multiple optimal trees from
# each replicate.

# Treat each tree equally
JackLabels(ape::consensus(trees), unlist(jackTrees, recursive = FALSE))

# Take the strict consensus of all trees for each replicate
JackLabels(ape::consensus(trees), lapply(jackTrees, ape::consensus))

# Take a single tree from each replicate (the first; order's irrelevant)
JackLabels(ape::consensus(trees), lapply(jackTrees, `[`, 1))
}

# Tree search with a constraint
constraint <- MatrixToPhyDat(c(a = 1, b = 1, c = 0, d = 0, e = 0, f = 0))
characters <- MatrixToPhyDat(matrix(
  c(0, 1, 1, 1, 0, 0,
    1, 1, 1, 0, 0, 0), ncol = 2,
  dimnames = list(letters[1:6], NULL)))
MaximizeParsimony(characters, constraint = constraint, verbosity = 0)

```

---

MinimumLength

*Minimum length*


---

### Description

The smallest length that a character can obtain on any tree.

### Usage

```
MinimumLength(x, compress = FALSE)
```

```
## S3 method for class 'phyDat'
MinimumLength(x, compress = FALSE)
```

```
## S3 method for class 'numeric'
```

```

MinimumLength(x, compress = NA)

## S3 method for class 'character'
MinimumLength(x, compress = TRUE)

MinimumSteps(x)

```

### Arguments

|          |   |
|----------|---|
| x        | An object of class phyDat; or a string to be coerced to a phyDat object via <code>TreeTools::StringToPhyDat()</code> ; or an 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 (= $2^0 + 2^1 + 2^3$ ) means that the tip may have tokens 0, 1 or 3.<br>Inapplicable tokens should be denoted with the integer 0 (not $2^0$ ). |
| compress | Logical specifying whether to retain the compression of a phyDat object or to return a vector specifying to each individual character, decompressed using the dataset's index attribute.  |

### Value

MinimumLength() returns a vector of integers specifying the minimum number of steps that each character must contain.

### Author(s)

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### See Also

Other tree scoring: [CharacterLength\(\)](#), [IWScore\(\)](#), [LengthAdded\(\)](#), [MorphyTreeLength\(\)](#)

### Examples

```

data("inapplicable.datasets")
myPhyDat <- inapplicable.phyData[[4]]

# load your own data with
# my.PhyDat <- as.phyDat(read.nexus.data("filepath"))
# or Windows users can select a file interactively using:
# my.PhyDat <- as.phyDat(read.nexus.data(choose.files()))

class(myPhyDat) # phyDat object

# Minimum length of each character in turn
MinimumLength(myPhyDat)

# Collapse duplicate characters, per phyDat compression
MinimumLength(myPhyDat, compress = TRUE)

# Calculate length of a single character from its textual representation

```

```
MinimumLength("-{-1}{-2}{-3}2233")
```

---

|                 |                          |
|-----------------|--------------------------|
| MorphyBootstrap | <i>Parsimony Ratchet</i> |
|-----------------|--------------------------|

---

### Description

Ratchet() uses the parsimony ratchet (Nixon 1999) to search for a more parsimonious tree using custom optimality criteria.

### Usage

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

Ratchet(
  tree,
  dataset,
  InitializeData = PhyDat2Morph,
  CleanupData = UnloadMorph,
  TreeScorer = MorphyLength,
  Bootstrapper = MorphyBootstrap,
  swappers = list(TBRSwap, SPRSwap, NNISwap),
  BootstrapSwapper = if (is.list(swappers)) swappers[[length(swappers)]] else swappers,
  returnAll = FALSE,
  stopAtScore = NULL,
  stopAtPeak = FALSE,
  stopAtPlateau = 0L,
  ratchIter = 100,
  ratchHits = 10,
  searchIter = 4000,
  searchHits = 42,
  bootstrapIter = searchIter,
  bootstrapHits = searchHits,
  verbosity = 1L,
  suboptimal = sqrt(.Machine$double.eps),
  ...
)
```

```

MultiRatchet(
  tree,
  dataset,
  ratchHits = 10,
  searchIter = 500,
  searchHits = 20,
  verbosity = 0L,
  swappers = list(RootedNNISwap),
  nSearch = 10,
  stopAtScore = NULL,
  ...
)

RatchetConsensus(
  tree,
  dataset,
  ratchHits = 10,
  searchIter = 500,
  searchHits = 20,
  verbosity = 0L,
  swappers = list(RootedNNISwap),
  nSearch = 10,
  stopAtScore = NULL,
  ...
)

```

### 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 |
| morphyObj     | Object of class morphy, perhaps created with <a href="#">PhyDat2Morphy()</a> .   |
| EdgeSwapper   | a function that rearranges a parent and child vector, and returns a list with modified vectors; for example <a href="#">SPRSwap()</a> .  |
| maxIter       | Numeric specifying maximum number of iterations to perform in tree search.   |
| maxHits       | Numeric specifying maximum number of hits to accomplish in tree search.  |
| verbosity     | Numeric specifying 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. Will be overridden if a passed function has an attribute stopAtPeak set by <code>attr(FileName, "stopAtPeak") &lt;- TRUE</code> .   |
| stopAtPlateau | Integer. If > 0, tree search will terminate if the score has not improved after stopAtPlateau iterations. Will be overridden if a passed function has an attribute stopAtPlateau set by <code>attr(FileName, "stopAtPlateau") &lt;- TRUE</code> .                                      |

|                               |   |
|-------------------------------|---|
| ...                           | further arguments to pass to <code>TreeScorer()</code> , e.g. <code>dataset = .</code>  |
| <code>tree</code>             | A tree of class <code>phylo</code> .  |
| <code>dataset</code>          | a dataset in the format required by <code>TreeScorer()</code> .   |
| <code>InitializeData</code>   | Function that sets up data object to prepare for tree search. The function will be passed the <code>dataset</code> parameter. Its return value will be passed to <code>TreeScorer()</code> and <code>CleanUpData()</code> .   |
| <code>CleanUpData</code>      | Function to destroy data object on function exit. The function will be passed the value returned by <code>InitializeData()</code> .   |
| <code>TreeScorer</code>       | 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.   |
| <code>Bootstrapper</code>     | Function to perform bootstrapped rearrangements of tree. First arguments will be an <code>edgeList</code> and a dataset, initialized using <code>InitializeData()</code> . Should return a rearranged <code>edgeList</code> .   |
| <code>swappers</code>         | A list of functions to use to conduct edge rearrangement during tree search. Provide functions like <code>NNISwap</code> to shuffle root position, or <code>RootedTBRSwap</code> if the position of the root should be retained. You may wish to use extreme swappers (such as TBR) early in the list, and a more subtle rearranger (such as NNI) later in the list to make incremental tinkering once an almost-optimal tree has been found. |
| <code>BootstrapSwapper</code> | Function such as <code>RootedNNISwap</code> to use to rearrange trees within <code>Bootstrapper()</code> .  |
| <code>returnAll</code>        | Set to TRUE to report all MPTs encountered during the search, perhaps to analyse consensus.   |
| <code>stopAtScore</code>      | stop search as soon as this score is hit or beaten.   |
| <code>ratchIter</code>        | Stop when this many ratchet iterations have been performed.   |
| <code>ratchHits</code>        | Stop when this many ratchet iterations have found the same best score.  |
| <code>searchIter</code>       | Integer specifying maximum rearrangements to perform on each bootstrap or ratchet iteration. To override this value for a single swapper function, set e.g. <code>attr(SwapperFunction, "searchIter") &lt;- 99</code>   |
| <code>searchHits</code>       | Integer specifying maximum times to hit best score before terminating a tree search within a ratchet iteration. To override this value for a single swapper function, set e.g. <code>attr(SwapperFunction, "searchHits") &lt;- 99</code>  |
| <code>bootstrapIter</code>    | Integer specifying maximum rearrangements to perform on each bootstrap iteration (default: <code>searchIter</code> ).   |
| <code>bootstrapHits</code>    | Integer specifying maximum times to hit best score on each bootstrap iteration (default: <code>searchHits</code> ).   |
| <code>suboptimal</code>       | retain trees that are suboptimal by this score. Defaults to a small value that will counter rounding errors.  |
| <code>nSearch</code>          | Number of Ratchet searches to conduct (for <code>RatchetConsensus()</code> )  |

## Details

For usage pointers, see the [vignette](#).



**Value**

MorphyBootstrap() returns a tree that is optimal under a random sampling of the original characters.

Ratchet() returns a tree modified by parsimony ratchet iterations.

MultiRatchet() returns a list of optimal trees produced by nSearch ratchet searches, from which a consensus tree can be generated using `ape::consensus()` or `TreeTools::ConsensusWithout()`.

**Functions**

- RatchetConsensus(): deprecated alias for MultiRatchet()

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**References**

Nixon KC (1999). "The Parsimony Ratchet, a new method for rapid parsimony analysis." *Cladistics*, **15**(4), 407–414. ISSN 0748-3007, doi:10.1111/j.10960031.1999.tb00277.x.

**See Also**

- Adapted from `pratchet()` in the **phangorn** package.

Other custom search functions: `EdgeListSearch()`, `Jackknife()`, `SuccessiveApproximations()`

**Examples**

```
data("Lobo", package = "TreeTools")
njtree <- TreeTools::NJTree(Lobo.phy)
# Increase value of ratchIter and searchHits to do a proper search
quickResult <- Ratchet(njtree, Lobo.phy, ratchIter = 2, searchHits = 3)

# Plot result (legibly)
oldPar <- par(mar = rep(0, 4), cex = 0.75)
plot(quickResult)
par(oldPar)
```

---

MorphyWeights

*Set and get the character weightings associated with a Morphy object.*


---

**Description**

MorphyWeights() details the approximate and exact weights associated with characters in a Morphy object; SetMorphyWeights() edits them.

**Usage**

```
MorphyWeights(morphObj)
```

```
SetMorphyWeights(weight, morphObj, checkInput = TRUE)
```

**Arguments**

|                         |  |
|-------------------------|--|
| <code>morphObj</code>   | Object of class <code>morphObj</code> , perhaps created with <code>PhyDat2MorphObj()</code> .          |
| <code>weight</code>     | A vector listing the new weights to be applied to each character                                       |
| <code>checkInput</code> | Whether to sanity-check input data before applying. Defaults to TRUE to protect the user from crashes. |

**Value**

`MorphyWeights()` returns a data frame with two named rows and one column per character pattern: row 1, `approx`, is a list of integers specifying the approximate (integral) weights used by `MorphObj`; row 2, `exact`, is a list of numerics specifying the exact weights specified by the user.

`SetMorphyWeights()` returns the `MorphObj` error code generated when applying `weight`.

**Author(s)**

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other `MorphObj` API functions: `GapHandler()`, `MorphObjErrorCheck()`, `PhyDat2MorphObj()`, `SingleCharMorphObj()`, `UnloadMorphObj()`, `is.morphObjPtr()`, `mpl_apply_tipdata()`, `mpl_attach_rawdata()`, `mpl_attach_symbols()`, `mpl_delete_MorphObj()`, `mpl_delete_rawdata()`, `mpl_first_down_recon()`, `mpl_first_up_recon()`, `mpl_get_charac_weight()`, `mpl_get_gaphandl()`, `mpl_get_num_charac()`, `mpl_get_num_internal_nodes()`, `mpl_get_numtaxa()`, `mpl_get_symbols()`, `mpl_init_MorphObj()`, `mpl_new_MorphObj()`, `mpl_second_down_recon()`, `mpl_second_up_recon()`, `mpl_set_charac_weight()`, `mpl_set_num_internal_nodes()`, `mpl_set_parsim_t()`, `mpl_translate_error()`, `mpl_update_lower_root()`, `mpl_update_tip()`, `summary.morphObjPtr()`

**Examples**

```
tokens <- matrix(c(
  0, 0, 0, 1, 1, 2,
  0, 0, 0, 0, 0, 0), byrow = TRUE, nrow = 2L,
  dimnames = list(letters[1:2], NULL))
pd <- TreeTools::MatrixToPhyDat(tokens)
morphObj <- PhyDat2MorphObj(pd)
MorphObjWeights(morphObj)
if (SetMorphObjWeights(c(1, 1.5, 2/3), morphObj) != 0L) message("Errored")
MorphObjWeights(morphObj)
morphObj <- UnloadMorphObj(morphObj)
```

---

NNI *Nearest neighbour interchange (NNI)*

---

### Description

NNI() performs a single iteration of the nearest-neighbour interchange algorithm; RootedNNI() retains the position of the root. These functions are based on equivalents in the **phangorn** package. cNNI() is an equivalent function coded in C, that runs much faster.

### Usage

```

NNI(tree, edgeToBreak = NULL)

cNNI(tree, edgeToBreak = NULL, whichSwitch = 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 | In (Rooted)NNI(), an optional integer specifying the index of an edge to bisect/prune, generated randomly if not specified. If -1, a complete list of all trees one step from the input tree will be returned. In cNNI(), an integer from zero to <code>nEdge(tree) - nTip(tree) - 2</code> , specifying which internal edge to break. |
| whichSwitch | Integer from zero to one, specifying which way to re-build the broken internal edge.   |
| parent      | Integer vector corresponding to the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code> .  |
| child       | Integer vector corresponding to 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

Branch lengths are not supported.

All nodes in a tree must be bifurcating; `ape::collapse.singles()` and `ape::multi2di()` may help.

**Value**

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

`cNNI()` returns a tree of class `phylo`, rooted on the same leaf, on which the specified rearrangement has been conducted.

`NNISwap()` returns 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 ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**References**

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

**See Also**

Other tree rearrangement functions: [SPR\(\)](#), [TBR\(\)](#)

**Examples**

```
tree <- TreeTools::BalancedTree(8)
# A random rearrangement
NNI(tree)
cNNI(tree)

# All trees one NNI rearrangement away
NNI(tree, edgeToBreak = -1)

# Manual random sampling
cNNI(tree, sample.int(14 - 8 - 1, 1), sample.int(2, 1))

# A specified rearrangement
cNNI(tree, 0, 0)

# If a tree may not be binary, collapse nodes with
tree <- TreeTools::MakeTreeBinary(tree)

# If a tree may be improperly rooted, use
tree <- TreeTools::RootTree(tree, 1)
```

```
# If a tree may exhibit unusual node ordering, this can be addressed with
tree <- TreeTools::Preorder(tree)
```

---

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. Once finished with the object, it should be destroyed using `UnloadMorphy()` to free the allocated memory.

### Usage

```
PhyDat2Morphy(phy, gap = "inapplicable")
```

### Arguments

|     |  |
|-----|--|
| phy | An object of <b>phangorn</b> class phyDat.   |
| gap | An unambiguous abbreviation of inapplicable, ambiguous (= missing), or extra state, specifying how gaps will be handled. |

### Value

PhyDat2Morphy() returns a pointer to an initialized Morphy object.

### Author(s)

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### See Also

Other Morphy API functions: `GapHandler()`, `MorphyErrorCheck()`, `MorphyWeights()`, `SingleCharMorphy()`, `UnloadMorphy()`, `is.morphyPtr()`, `mpl_apply_tipdata()`, `mpl_attach_rawdata()`, `mpl_attach_symbols()`, `mpl_delete_Morphy()`, `mpl_delete_rawdata()`, `mpl_first_down_recon()`, `mpl_first_up_recon()`, `mpl_get_charac_weight()`, `mpl_get_gaphandl()`, `mpl_get_num_charac()`, `mpl_get_num_internal_nodes()`, `mpl_get_numtaxa()`, `mpl_get_symbols()`, `mpl_init_Morphy()`, `mpl_new_Morphy()`, `mpl_second_down_recon()`, `mpl_second_up_recon()`, `mpl_set_charac_weight()`, `mpl_set_num_internal_nodes()`, `mpl_set_parsim_t()`, `mpl_translate_error()`, `mpl_update_lower_root()`, `mpl_update_tip()`, `summary.morphyPtr()`

### Examples

```
data("Lobo", package="TreeTools")
morphyObj <- PhyDat2Morphy(Lobo.phy)
# Set object to be destroyed at end of session or closure of function
# on.exit(morphyObj <- UnloadMorphy(morphyObj), add = TRUE)

# Do something with pointer
```

```
# ...

# Or, instead of on.exit, manually destroy morphy object and free memory:
morphyObj <- UnloadMorphy(morphyObj)
```

---

PlotCharacter

*Plot the distribution of a character on a tree*


---

### Description

Reconstructs the distribution of a character on a tree topology using the modified Fitch algorithm presented in Brazeau et al. (2019).

### Usage

```
PlotCharacter(
  tree,
  dataset,
  char = 1L,
  updateTips = FALSE,
  plot = TRUE,
  tokenCol = NULL,
  ambigCol = "grey",
  inappCol = "lightgrey",
  ambigLty = "dotted",
  inappLty = "dashed",
  plainLty = par("lty"),
  tipOffset = 1,
  unitEdge = FALSE,
  ...
)
```

### Arguments

|  |   |
|--|---|
| tree   | A tree of class <a href="#">phylo</a> .   |
| dataset  | A phylogenetic data matrix of <b>phangorn</b> class <code>phyDat</code> , whose names correspond to the labels of any accompanying tree.  |
| char   | Index of character to plot.   |
| updateTips                                       | Logical; if FALSE, tips will be labelled with their original state in dataset.  |
| plot   | Logical specifying whether to plot the output.  |
| tokenCol   | Palette specifying colours to associate with each token in turn, in the sequence listed in <code>attr(dataset, "levels")</code> .   |
| ambigCol, ambigLty, inappCol, inappLty, plainLty | Colours and line types to apply to ambiguous, inapplicable and applicable tokens. See the <a href="#">lty graphical parameter</a> for details of line styles. Overrides <code>tokenCol</code> . |

|           |  |
|-----------|--|
| tipOffset | Numeric: how much to offset tips from their labels.      |
| unitEdge  | Logical: Should all edges be plotted with a unit length? |
| ...       | Further arguments to pass to <code>plot.phylo()</code> . |

**Value**

`PlotCharacter()` invisibly returns a matrix in which each row corresponds to a numbered tip or node of tree, and each column corresponds to a token; the tokens that might parsimoniously be present at each point on a tree are denoted with TRUE.

**Author(s)**

Martin R. Smith ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**References**

Brazeau MD, Guillaume T, Smith MR (2019). "An algorithm for morphological phylogenetic analysis with inapplicable data." *Systematic Biology*, **68**(4), 619–631. doi:10.1093/sysbio/syy083.

**Examples**

```
# Set up plotting area
oPar <- par(mar = rep(0, 4))

tree <- ape::read.tree(text =
  "((((((a, b), c), d), e), f), (g, (h, (i, (j, (k, l))))));")
## A character with inapplicable data
dataset <- TreeTools::StringToPhyDat("23--1??--032", tips = tree)
plotted <- PlotCharacter(tree, dataset)
plotted

# Character from a real dataset
data("Lobo", package = "TreeTools")
dataset <- Lobo.phy
tree <- TreeTools::NJTree(dataset)
PlotCharacter(tree, dataset, 14)
par(oPar)
```

---

PrepareDataProfile      *Prepare data for Profile Parsimony*

---

**Description**

Calculates profiles for each character in a dataset. Will also simplify characters, with a warning, where they are too complex for the present implementation of profile parsimony:

- inapplicable tokens will be replaced with the ambiguous token (i.e. - → ?);
- Ambiguous tokens will be treated as fully ambiguous (i.e. {02} → ?)
- Where more than two states are informative (i.e. unambiguously present in more than one taxon), states beyond the two most informative will be ignored.

**Usage**

```
PrepareDataProfile(dataset)
```

```
PrepareDataIW(dataset)
```

**Arguments**

dataset            dataset of class phyDat

**Value**

An object of class phyDat, with additional attributes. PrepareDataProfile adds the attributes:

- `info.amounts`: details the information represented by each character when subject to N additional steps.
- `informative`: logical specifying which characters contain any phylogenetic information.
- `bootstrap`: The character vector `c("info.amounts", "split.sizes")`, indicating attributes to sample when bootstrapping the dataset (e.g. in Ratchet searches).

PrepareDataIW adds the attribute:

- `min.length`: The minimum number of steps that must be present in each transformation series.

**Functions**

- `PrepareDataIW()`: Prepare data for implied weighting

**Author(s)**

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

**See Also**

Other profile parsimony functions: [Carter1\(\)](#), [StepInformation\(\)](#), [WithOneExtraStep\(\)](#), [profiles](#)

**Examples**

```
data("congreveLamsdellMatrices")
dataset <- congreveLamsdellMatrices[[42]]
PrepareDataProfile(dataset)
```



---

 profiles

*Empirically counted profiles for small trees*


---

**Description**

The base 2 logarithm of the number of trees containing  $s$  steps, calculated by scoring a character on each  $n$ -leaf tree.

**Usage**

```
profiles
```

**Format**

A list with the structure `profiles[[number of leaves]][[number of tokens]][[tokens in smallest split]]`. The list entry returns a named numeric vector; each entry lists  $\log_2$ (proportion of  $n$ -leaf trees with  $s$  or fewer steps for this character).

**See Also**

Other profile parsimony functions: [Carter1\(\)](#), [PrepareDataProfile\(\)](#), [StepInformation\(\)](#), [WithOneExtraStep\(\)](#)

**Examples**

```
data(profiles)

# Load profile for a character of the structure 0 0 0 1 1 1 1 1
profile3.5 <- profiles[[8]][[2]][[3]]

# Number of trees with _s_ or fewer steps on that character
TreeTools::NUnrooted(8) * 2 ^ profile3.5
```

---

 QuartetResolution

*Relationship between four taxa*


---

**Description**

Relationship between four taxa

**Usage**

```
QuartetResolution(trees, tips)
```

**Arguments**

|       |  |
|-------|--|
| trees | A list of trees of class phylo, or a multiPhylo object.  |
| tips  | Vector specifying four tips whose relationship should be reported, in a format accepted by <a href="#">KeepTip()</a> . |

**Value**

A vector specifying an integer, for each tree, which of tips[-1] is most closely related to tips[1].

**See Also**

Other utility functions: [ClusterStrings\(\)](#), [WhenFirstHit\(\)](#)

**Examples**

```
trees <- inapplicable.trees[["Vinther2008"]]
tips <- c("Lingula", "Halkieria", "Wiwaxia", "Acaenoplax")
QuartetResolution(trees, tips)
```

---

RandomMorphyTree

*Random postorder tree*

---

**Description**

Random postorder tree

**Usage**

```
RandomMorphyTree(nTip)
```

**Arguments**

nTip                    Integer specifying the number of tips to include in the tree (minimum 2).

**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.

**See Also**

Other tree generation functions: [AdditionTree\(\)](#)

---

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

---

**Description**

Parsimony score of random postorder tree

**Usage**

```
RandomTreeScore(morphyObj)
```

**Arguments**

morphyObj      Object of class morphy, perhaps created with [PhyDat2Morphy\(\)](#).

**Value**

RandomTreeScore() returns the parsimony score of a random tree for the given Morphy object.

**Examples**

```
tokens <- matrix(c(
  0, "-", "-", 1, 1, 2,
  0, 1, 0, 1, 2, 2,
  0, "-", "-", 0, 0, 0), byrow = TRUE, nrow = 3L,
  dimnames = list(letters[1:3], NULL))
pd <- TreeTools::MatrixToPhyDat(tokens)
morphyObj <- PhyDat2Morphy(pd)

RandomTreeScore(morphyObj)

morphyObj <- UnloadMorphy(morphyObj)
```

---

|                |   |
|----------------|---|
| RearrangeEdges | <i>Rearrange edges of a phylogenetic tree</i> |
|----------------|---|

---

**Description**

RearrangeEdges() performs the specified edge rearrangement on 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      | Integer vector corresponding to the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code> .   |
| child       | Integer vector corresponding to the second column of the edge matrix of a tree of class <code>phylo</code> , 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 <code>parent</code> and <code>child</code> 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 <code>SPRSwap()</code> .  |
| 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   | Numeric specifying level of detail to display in console: larger numbers provide more verbose feedback to the user.   |
| ...         | further arguments to pass to <code>TreeScorer()</code> , e.g. <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", package="TreeTools")
tree <- TreeTools::NJTree(Lobo.phy)
edge <- tree$edge
parent <- edge[, 1]
child <- edge[, 2]
dataset <- PhyDat2Morpho(Lobo.phy)
RearrangeEdges(parent, child, dataset, EdgeSwapper = RootedNNISwap)
# Remember to free memory:
dataset <- UnloadMorpho(dataset)
```

---

referenceTree

*Tree topology for matrix simulation*

---

## Description

The tree topology used to generate the matrices in [congreveLamsdellMatrices](#)

## Usage

```
referenceTree
```

## Format

A single phylogenetic tree saved as an object of class phylo

## Source

Congreve & Lamsdell (2016); [doi:10.1111/pala.12236](https://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**(3), 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](https://doi.org/10.5061/dryad.7dq0j). [doi:10.5061/dryad.7dq0j](https://doi.org/10.5061/dryad.7dq0j).

## Examples

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

---

SingleCharMorphy      *Morphy object from single character*

---

### Description

Morphy object from single character

### Usage

```
SingleCharMorphy(char, gap = "inapp")
```

### Arguments

|      |  |
|------|--|
| char | State of each character at each tip in turn, in a format that will be converted to a character string by <code>paste0(char, ";", collapse="")</code> . |
| gap  | An unambiguous abbreviation of inapplicable, ambiguous (= missing), or extra state, specifying how gaps will be handled.                               |

### Value

A pointer to an object of class `morphyObj`. Don't forget to unload it when you've finished with it.

### Author(s)

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### See Also

Score a tree: [MorphyTreeLength\(\)](#)

Other Morphy API functions: [GapHandler\(\)](#), [MorphyErrorCheck\(\)](#), [MorphyWeights\(\)](#), [PhyDat2Morphy\(\)](#), [UnloadMorphy\(\)](#), [is.morphyPtr\(\)](#), [mpl\\_apply\\_tipdata\(\)](#), [mpl\\_attach\\_rawdata\(\)](#), [mpl\\_attach\\_symbols\(\)](#), [mpl\\_delete\\_Morphy\(\)](#), [mpl\\_delete\\_rawdata\(\)](#), [mpl\\_first\\_down\\_recon\(\)](#), [mpl\\_first\\_up\\_recon\(\)](#), [mpl\\_get\\_charac\\_weight\(\)](#), [mpl\\_get\\_gaphandl\(\)](#), [mpl\\_get\\_num\\_charac\(\)](#), [mpl\\_get\\_num\\_internal\\_nodes\(\)](#), [mpl\\_get\\_numtaxa\(\)](#), [mpl\\_get\\_symbols\(\)](#), [mpl\\_init\\_Morphy\(\)](#), [mpl\\_new\\_Morphy\(\)](#), [mpl\\_second\\_down\\_recon\(\)](#), [mpl\\_second\\_up\\_recon\(\)](#), [mpl\\_set\\_charac\\_weight\(\)](#), [mpl\\_set\\_num\\_internal\\_nodes\(\)](#), [mpl\\_set\\_parsim\\_t\(\)](#), [mpl\\_translate\\_error\(\)](#), [mpl\\_update\\_lower\\_root\(\)](#), [mpl\\_update\\_tip\(\)](#), [summary.morphyPtr\(\)](#)

### Examples

```
morphyObj <- SingleCharMorphy("-0-0", gap = "Extra")
RandomTreeScore(morphyObj)
morphyObj <- UnloadMorphy(morphyObj)
```

---

|                 |  |
|-----------------|--|
| SiteConcordance | <i>Calculate site concordance factor</i> |
|-----------------|--|

---

### Description

The site concordance factor (Minh et al. 2020) is a measure of the strength of support that the dataset presents for a given split in a tree.

### Usage

```
QuartetConcordance(tree, dataset = NULL)
```

```
ClusteringConcordance(tree, dataset)
```

```
PhylogeneticConcordance(tree, dataset)
```

```
MutualClusteringConcordance(tree, dataset)
```

```
SharedPhylogeneticConcordance(tree, dataset)
```

### Arguments

|         |  |
|---------|--|
| tree    | A tree of class <a href="#">phylo</a> .  |
| dataset | A phylogenetic data matrix of <b>phangorn</b> class phyDat, whose names correspond to the labels of any accompanying tree. |

### Details

QuartetConcordance() is the proportion of quartets (sets of four leaves) that are decisive for a split which are also concordant with it. For example, a quartet with the characters 0 0 0 1 is not decisive, as all relationships between those leaves are equally parsimonious. But a quartet with characters 0 0 1 1 is decisive, and is concordant with any tree that groups the first two leaves together to the exclusion of the second.

NOTE: These functions are under development, and may be incompletely tested or change without notice. Complete documentation and discussion will follow in due course.

### Author(s)

[Martin R. Smith](#) ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

### References

Minh BQ, Hahn MW, Lanfear R (2020). “New methods to calculate concordance factors for phylogenomic datasets.” *Molecular Biology and Evolution*, **37**(9), 2727–2733. [doi:10.1093/molbev/msaa106](https://doi.org/10.1093/molbev/msaa106).

**See Also**

Other split support functions: [JackLabels\(\)](#), [Jackknife\(\)](#), [MaximizeParsimony\(\)](#)

**Examples**

```
data("congreveLamsdellMatrices", package = "TreeSearch")
dataset <- congreveLamsdellMatrices[[1]][, 1:20]
tree <- referenceTree
qc <- QuartetConcordance(tree, dataset)
cc <- ClusteringConcordance(tree, dataset)
pc <- PhylogeneticConcordance(tree, dataset)
spc <- SharedPhylogeneticConcordance(tree, dataset)
mcc <- MutualClusteringConcordance(tree, dataset)

oPar <- par(mar = rep(0, 4), cex = 0.8)
plot(tree)
TreeTools::LabelSplits(tree, signif(qc, 3))
TreeTools::LabelSplits(tree, signif(cc, 3))
TreeTools::LabelSplits(tree, signif(pc, 3))
par(oPar)

pairs(cbind(qc, cc, pc, spc, mcc))
```

---

 SPR

*Subtree pruning and rearrangement (SPR)*


---

**Description**

Perform one SPR rearrangement on a tree

**Usage**

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

```
SPRMoves(tree, edgeToBreak = integer(0))
```

```
## S3 method for class 'phylo'
SPRMoves(tree, edgeToBreak = integer(0))
```

```
## S3 method for class 'matrix'
SPRMoves(tree, edgeToBreak = integer(0))
```

```
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 <a href="#">phylo</a> .   |
| 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      | Integer vector corresponding to the first column of the edge matrix of a tree of class <a href="#">phylo</a> , i.e. <code>tree\$edge[, 1]</code> .  |
| child       | Integer vector corresponding to the second column of the edge matrix of a tree of class <a href="#">phylo</a> , i.e. <code>tree\$edge[, 2]</code> . |
| nEdge       | (optional) integer specifying the number of edges of a tree of class <a href="#">phylo</a> , i.e. <code>dim(tree\$edge)[1]</code>                   |
| nNode       | (optional) Number of nodes.   |

### Details

Equivalent to `kSPR()` in the **phangorn** package, 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.

All nodes in a tree must be bifurcating; [ape::collapse.singles](#) and [ape::multi2di](#) may help.

### Value

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

`TBRMoves()` returns a list of all trees one SPR move away from `tree`, with edges and nodes in preorder, rooted on the first-labelled tip.

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.

Other tree rearrangement functions: `NNI()`, `TBR()`

**Examples**

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

---

StepInformation

*Information content of a character known to contain  $e$  steps*

---

**Description**

`StepInformation()` calculates the phylogenetic information content of a character `char` when  $e$  extra steps are present, for all possible values of  $e$ .

**Usage**

```
StepInformation(char, ambiguousTokens = c("-", "?"))
```

**Arguments**

`char`                    Vector of tokens listing states for the character in question.

`ambiguousTokens`

Vector specifying which tokens, if any, correspond to the ambiguous token (?).

**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.

**Value**

StepInformation() returns a numeric vector detailing the amount of phylogenetic information (in bits) associated with the character when 0, 1, 2... extra steps are present. The vector is named with the total number of steps associated with each entry in the vector: for example, a character with three observed tokens must exhibit two steps, so the first entry (zero extra steps) is named 2 (two steps observed).

**Author(s)**

**Martin R. Smith** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other profile parsimony functions: [Carter1\(\)](#), [PrepareDataProfile\(\)](#), [WithOneExtraStep\(\)](#), [profiles](#)

**Examples**

```
character <- rep(c(0:3, "?", "-"), c(8, 5, 1, 1, 2, 2))
StepInformation(character)
```

---

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** ([martin.smith@durham.ac.uk](mailto:martin.smith@durham.ac.uk))

**See Also**

Other Morphy API functions: `GapHandler()`, `MorphyErrorCheck()`, `MorphyWeights()`, `PhyDat2Morphy()`, `SingleCharMorphy()`, `UnloadMorphy()`, `is.morphyPtr()`, `mpl_apply_tipdata()`, `mpl_attach_rawdata()`, `mpl_attach_symbols()`, `mpl_delete_Morphy()`, `mpl_delete_rawdata()`, `mpl_first_down_recon()`, `mpl_first_up_recon()`, `mpl_get_charac_weight()`, `mpl_get_gaphandl()`, `mpl_get_num_charac()`, `mpl_get_num_internal_nodes()`, `mpl_get_numtaxa()`, `mpl_get_symbols()`, `mpl_init_Morphy()`, `mpl_new_Morphy()`, `mpl_second_down_recon()`, `mpl_second_up_recon()`, `mpl_set_charac_weight()`, `mpl_set_num_internal_nodes()`, `mpl_set_parsim_t()`, `mpl_translate_error()`, `mpl_update_lower_root()`, `mpl_update_tip()`

---

TBR

*Tree bisection and reconnection (TBR)*


---

**Description**

TBR performs a single random TBR iteration.

**Usage**

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

```
TBRMoves(tree, edgeToBreak = integer(0))
```

```
## S3 method for class 'phylo'
```

```
TBRMoves(tree, edgeToBreak = integer(0))
```

```
## S3 method for class 'matrix'
```

```
TBRMoves(tree, edgeToBreak = integer(0))
```

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

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

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

**Arguments**

|             |  |
|-------------|--|
| tree        | A bifurcating tree of class <code>phylo</code> , 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      | Integer vector corresponding to the first column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 1]</code> .  |
| child       | Integer vector corresponding to the second column of the edge matrix of a tree of class <code>phylo</code> , i.e. <code>tree\$edge[, 2]</code> .   |
| nEdge       | (optional) Number of edges.  |

**Details**

Branch lengths are not (yet) supported.

All nodes in a tree must be bifurcating; `ape::collapse.singles` and `ape::multi2di` may help.

**Value**

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

`TBRMoves()` returns a `multiPhylo` object listing all trees one TBR move away from `tree`, with edges and nodes in preorder, rooted on the first-labelled tip.

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

**Functions**

- `TBRswap()`: faster version that takes and returns parent and child parameters
- `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.

Other tree rearrangement functions: `NNI()`, `SPR()`

**Examples**

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

---

UnloadMorphy

*Destroy a Morphy object*

---

**Description**

Destroys a previously-created Morphy object.

**Usage**

```
UnloadMorphy(morphObj)
```

**Arguments**

`morphObj`      Object of class `morphy`, perhaps created with `PhyDat2Morphy()`.

**Details**

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

**Value**

Morphy error code, decipherable using `mpl_translate_error`

**Author(s)**

Martin R. Smith

**See Also**

Other Morphy API functions: `GapHandler()`, `MorphyErrorCheck()`, `MorphyWeights()`, `PhyDat2Morphy()`, `SingleCharMorphy()`, `is.morphyPtr()`, `mpl_apply_tipdata()`, `mpl_attach_rawdata()`, `mpl_attach_symbols()`, `mpl_delete_Morphy()`, `mpl_delete_rawdata()`, `mpl_first_down_recon()`, `mpl_first_up_recon()`, `mpl_get_charac_weight()`, `mpl_get_gaphandl()`, `mpl_get_num_charac()`, `mpl_get_num_internal_nodes()`, `mpl_get_numtaxa()`, `mpl_get_symbols()`, `mpl_init_Morphy()`, `mpl_new_Morphy()`, `mpl_second_down_recon()`, `mpl_second_up_recon()`, `mpl_set_charac_weight()`, `mpl_set_num_internal_nodes()`, `mpl_set_parsim_t()`, `mpl_translate_error()`, `mpl_update_lower_root()`, `mpl_update_tip()`, `summary.morphyPtr()`

---

|              |  |
|--------------|--|
| WhenFirstHit | <i>When was a tree topology first hit?</i> |
|--------------|--|

---

### Description

Reports when each tree in a list was first found by tree search. This information is read from the `firstHit` attribute if present. If not, trees are taken to be listed in the order in which they were found, and named according to the search iteration in which they were first hit - the situation when trees found by `MaximizeParsimony()` are saved to file.

### Usage

```
WhenFirstHit(trees)
```

### Arguments

`trees`            A list of trees, or a `multiPhylo` object.

### Value

`trees`, with a `firstHit` attribute listing the number of trees hit for the first time in each search iteration.

### Author(s)

[Martin R. Smith \(martin.smith@durham.ac.uk\)](mailto:martin.smith@durham.ac.uk)

### See Also

- [MaximizeParsimony\(\)](#)

Other utility functions: [ClusterStrings\(\)](#), [QuartetResolution\(\)](#)

### Examples

```
library("TreeTools", quietly = TRUE)
trees <- list(
  seed_00 = as.phylo(1, 8),
  ratch1_01 = as.phylo(2, 8),
  ratch1_02 = as.phylo(3, 8),
  ratch4_44 = as.phylo(4, 8),
  final_99 = as.phylo(5, 8)
)
attr(WhenFirstHit(trees), "firstHit")
```

---

|                  |  |
|------------------|--|
| WithOneExtraStep | <i>Number of trees with one extra step</i> |
|------------------|--|

---

**Description**

Number of trees with one extra step

**Usage**

```
WithOneExtraStep(...)
```

**Arguments**

... Vector or series of integers specifying the number of leaves bearing each distinct non-ambiguous token.

**See Also**

Other profile parsimony functions: [Carter1\(\)](#), [PrepareDataProfile\(\)](#), [StepInformation\(\)](#), [profiles](#)

**Examples**

```
WithOneExtraStep(1, 2, 3)
```



# Index

## \* Morphy API functions

- GapHandler, 11
- is.morphyPtr, 16
- MorphyWeights, 33
- PhyDat2Morphy, 37
- SingleCharMorphy, 46
- summary.morphyPtr, 51
- UnloadMorphy, 54

## \* custom search functions

- Jackknife, 18
- MorphyBootstrap, 30

## \* datasets

- congreveLamsdellMatrices, 9
- inapplicable.datasets, 12
- profiles, 41
- referenceTree, 45

## \* profile parsimony functions

- Carter1, 5
- PrepareDataProfile, 39
- profiles, 41
- StepInformation, 50
- WithOneExtraStep, 56

## \* split support functions

- Jackknife, 18
- JackLabels, 20
- MaximizeParsimony, 23
- SiteConcordance, 47

## \* tree generation functions

- AdditionTree, 3
- RandomMorphyTree, 42

## \* tree rearrangement functions

- NNI, 35
- SPR, 48
- TBR, 52

## \* tree scoring

- CharacterLength, 6
- IWScore, 16
- LengthAdded, 21
- MinimumLength, 28

## \* utility functions

- ClusterStrings, 7
- QuartetResolution, 41
- WhenFirstHit, 55

addition tree, 24

AdditionTree, 3, 42

AllSPR, 4

ape::collapse.singles, 49, 53

ape::collapse.singles(), 35

ape::consensus(), 33

ape::multi2di, 49, 53

ape::multi2di(), 35

Carter1, 5, 40, 41, 51, 56

CharacterLength, 6, 18, 22, 29

CharacterLength(), 18

ClusteringConcordance  
(SiteConcordance), 47

ClusterStrings, 7, 42, 55

cNNI (NNI), 35

ConcordantInfo (ConcordantInformation),  
8

ConcordantInformation, 8

congreveLamsdellMatrices, 9, 45

Consistency, 10

cSPR, 11

EasyTrees (MaximizeParsimony), 23

EasyTrees(), 18, 27

EasyTreesy (MaximizeParsimony), 23

EdgeListSearch, 20, 33

Evaluate (ConcordantInformation), 8

FastCharacterLength (CharacterLength), 6

Fitch (IWScore), 16

FitchSteps (CharacterLength), 6

GapHandler, 11, 16, 34, 37, 46, 52, 54

graphical parameter, 38

- ImposeConstraint(), 3, 25
- inapplicable.citations
  - (inapplicable.datasets), 12
- inapplicable.datasets, 12
- inapplicable.phyData
  - (inapplicable.datasets), 12
- inapplicable.trees
  - (inapplicable.datasets), 12
- is.morphyPtr, 12, 16, 34, 37, 46, 52, 54
- IWScore, 7, 16, 22, 29
- Jackknife, 18, 21, 27, 33, 48
- Jackknife(), 20, 21
- JackLabels, 20, 20, 27, 48
- JackLabels(), 20
- KeepTip, 42
- LengthAdded, 7, 18, 21, 29
- Log2Carter1 (Carter1), 5
- LogCarter1 (Carter1), 5
- MaximizeParsimony, 20, 21, 23, 48
- MaximizeParsimony(), 18, 55
- MinimumLength, 7, 18, 22, 28
- MinimumSteps (MinimumLength), 28
- MorphyBootstrap, 20, 30
- MorphyErrorCheck, 12, 16, 34, 37, 46, 52, 54
- MorphyTreeLength, 7, 18, 22, 29
- MorphyTreeLength(), 46
- MorphyWeights, 12, 16, 33, 37, 46, 52, 54
- mpl\_apply\_tipdata, 12, 16, 34, 37, 46, 52, 54
- mpl\_attach\_rawdata, 12, 16, 34, 37, 46, 52, 54
- mpl\_attach\_symbols, 12, 16, 34, 37, 46, 52, 54
- mpl\_delete\_Morphy, 12, 16, 34, 37, 46, 52, 54
- mpl\_delete\_rawdata, 12, 16, 34, 37, 46, 52, 54
- mpl\_first\_down\_recon, 12, 16, 34, 37, 46, 52, 54
- mpl\_first\_up\_recon, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_charac\_weight, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_gaphandl, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_num\_charac, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_num\_internal\_nodes, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_numtaxa, 12, 16, 34, 37, 46, 52, 54
- mpl\_get\_symbols, 12, 16, 34, 37, 46, 52, 54
- mpl\_init\_Morphy, 12, 16, 34, 37, 46, 52, 54
- mpl\_new\_Morphy, 12, 16, 34, 37, 46, 52, 54
- mpl\_second\_down\_recon, 12, 16, 34, 37, 46, 52, 54
- mpl\_second\_up\_recon, 12, 16, 34, 37, 46, 52, 54
- mpl\_set\_charac\_weight, 12, 16, 34, 37, 46, 52, 54
- mpl\_set\_num\_internal\_nodes, 12, 16, 34, 37, 46, 52, 54
- mpl\_set\_parsim\_t, 12, 16, 34, 37, 46, 52, 54
- mpl\_translate\_error, 12, 16, 34, 37, 46, 52, 54
- mpl\_update\_lower\_root, 12, 16, 34, 37, 46, 52, 54
- mpl\_update\_tip, 12, 16, 34, 37, 46, 52, 54
- MultiRatchet (MorphyBootstrap), 30
- MutualClusteringConcordance
  - (SiteConcordance), 47
- NNI, 35, 50, 53
- NNISwap, 32
- NNISwap (NNI), 35
- paste0, 46
- PhyDat2Morphy, 12, 16, 34, 37, 46, 52, 54
- PhyDat2Morphy(), 12, 16, 31, 34, 43, 54
- phylo, 4, 6, 8, 10, 11, 19, 20, 24, 32, 35, 38, 44, 47, 49, 53
- PhylogeneticConcordance
  - (SiteConcordance), 47
- PlotCharacter, 38
- PolEscapa (LengthAdded), 21
- pratchet(), 33
- PrepareDataIW (PrepareDataProfile), 39
- PrepareDataProfile, 6, 39, 41, 51, 56
- profiles, 6, 40, 41, 51, 56
- QuartetConcordance (SiteConcordance), 47
- QuartetResolution, 8, 41, 55
- RandomMorphyTree, 4, 42
- RandomTreeScore, 43
- Ratchet (MorphyBootstrap), 30
- RatchetConsensus (MorphyBootstrap), 30
- read.nexus.data(), 12
- RearrangeEdges, 43

referenceTree, [9](#), [45](#)  
Resample (MaximizeParsimony), [23](#)  
RootedNNI (NNI), [35](#)  
RootedNNISwap, [32](#)  
RootedNNISwap (NNI), [35](#)  
RootedSPR (SPR), [48](#)  
RootedSPR(), [50](#)  
RootedSPRSwap (SPR), [48](#)  
RootedTBR (TBR), [52](#)  
RootedTBR(), [53](#)  
RootedTBRSwap, [32](#)  
RootedTBRSwap (TBR), [52](#)  
  
SetMorphWeights (MorphWeights), [33](#)  
SharedPhylogeneticConcordance  
    (SiteConcordance), [47](#)  
SingleCharMorphy, [12](#), [16](#), [34](#), [37](#), [46](#), [52](#), [54](#)  
SiteConcordance, [20](#), [21](#), [27](#), [47](#)  
SiteConcordance(), [26](#)  
SPR, [36](#), [48](#), [53](#)  
SPRMoves (SPR), [48](#)  
SPRSwap (SPR), [48](#)  
SPRSwap(), [19](#), [31](#), [44](#)  
StepInformation, [6](#), [40](#), [41](#), [50](#), [56](#)  
SuccessiveApproximations, [20](#), [33](#)  
summary.morphyPtr, [12](#), [16](#), [34](#), [37](#), [46](#), [51](#), [54](#)  
  
TBR, [36](#), [50](#), [52](#)  
TBRMoves (TBR), [52](#)  
TBRSwap (TBR), [52](#)  
TreeLength (IWScore), [16](#)  
TreeSearch(), [18](#)  
TreeTools::ConsensusWithout(), [33](#)  
TreeTools::StringToPhyDat(), [29](#)  
  
UnloadMorphy, [12](#), [16](#), [34](#), [37](#), [46](#), [52](#), [54](#)  
UnloadMorphy(), [37](#)  
  
WhenFirstHit, [8](#), [42](#), [55](#)  
WithOneExtraStep, [6](#), [40](#), [41](#), [51](#), [56](#)