Package 'TreeTools'

May 7, 2026

Title Create, Modify and Analyse Phylogenetic Trees

Version 2.3.0

License GPL (>= 3)

Copyright Incorporates C/C++ code from 'ape' by Emmanuel Paradis <doi:10.1093/bioinformatics/bty633> and 'RUtreebalance' by Robert Noble <doi:10.5281/zenodo.5873857>.

Description Efficient implementations of functions for the creation, modification and analysis of phylogenetic trees.
Applications include:
generation of trees with specified shapes;
tree rearrangement;
analysis of tree shape;
rooting of trees and extraction of subtrees;
calculation and depiction of split support;
plotting the position of rogue taxa (Klopfstein & Spasojevic 2019) <doi:10.1371/journal.pone.0212942>;
calculation of ancestor-descendant relationships,
of 'stemwardness' (Asher & Smith, 2022) <doi:10.1093/sysbio/syab072>,
and of tree balance (Mir et al. 2013, Lemant et al. 2022) <doi:10.1016/j.mbs.2012.10.005>, <doi:10.1093/sysbio/syac027>;
artificial extinction (Asher & Smith, 2022) <doi:10.1093/sysbio/syab072>;
import and export of trees from Newick, Nexus (Maddison et al. 1997) <doi:10.1093/sysbio/46.4.590>,
and TNT <https://www.lillo.org.ar/phylogeny/tnt/> formats;
and analysis of splits and cladistic information.

URL https://ms609.github.io/TreeTools/,
https://github.com/ms609/TreeTools/

BugReports https://github.com/ms609/TreeTools/issues/

SystemRequirements C++17

Depends R (>= 3.6.0), ape (>= 5.6),

Imports bit64, fastmatch (>= 1.1.3), methods, PlotTools, Rdpack (>= 2.6.6),

Suggests RCurl, spelling, knitr, phangorn (>= 2.2.1), Rcpp (>= 1.0.8), rmarkdown, testthat (>= 3.0), TreeDist, TreeSearch, vdiffr (>= 1.0.0),

Config/Needs/benchmark bench, TreeDist

Config/Needs/check rcmdcheck, testthat

Config/Needs/coverage covr

Config/Needs/memcheck devtools

Config/Needs/metadata codemeta

Config/Needs/revdeps revdepcheck

Config/Needs/website pkgdown

Config/testthat/parallel false

Config/testthat/edition 3

LinkingTo Rcpp

RdMacros Rdpack

LazyData true

ByteCompile true

Encoding UTF-8

Language en-GB

VignetteBuilder knitr

RoxygenNote 7.3.3

NeedsCompilation yes

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Repository CRAN

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Contents

`AddTip` *Add a tip to a phylogenetic tree*

Description

`AddTip()` adds a tip to a phylogenetic tree at a specified location.

Usage

```
AddTip(
  tree,
  where = sample.int(tree[["Nnode"]] * 2 + 2L, size = 1) - 1L,
  label = "New tip",
  nodeLabel = "",
  edgeLength = 0,
  lengthBelow = NULL,
  nTip = NTip(tree),
  nNode = tree[["Nnode"]],
  rootNode = RootNode(tree)
)

AddTipEverywhere(tree, label = "New tip", includeRoot = FALSE)
```

Arguments

`tree`	A tree of class `phylo`.
`where`	The node or tip that should form the sister taxon to the new node. To add a new tip at the root, use `where = 0`. By default, the new tip is added to a random edge.
`label`	Character string providing the label to apply to the new tip.
`nodeLabel`	Character string providing a label to apply to the newly created node, if `tree$node.label` is specified.
`edgeLength`	Numeric specifying length of new edge. If `NULL`, defaults to `lengthBelow`. This will become the default behaviour in a future release; please manually specify the desired behaviour in your code.
`lengthBelow`	Numeric specifying length below neighbour at which to graft new edge. Values greater than the length of the edge will result in negative edge lengths. If `NULL`, the default, the new tip will be added at the midpoint of the broken edge. If inserting at the root (`where = 0`), a new edge of length `lengthBelow` will be inserted. If `NA`, the new leaf will be attached adjacent to `where`; at internal nodes, this will result in polytomy.

nTip, nNode, rootNode
: Optional integer vectors specifying number of tips and nodes in tree, and index of root node. Not checked for correctness: specifying values here yields a marginal speed increase at the cost of code safety.

includeRoot
: Logical; if TRUE, each position adjacent to the root edge is considered to represent distinct edges; if FALSE, they are treated as a single edge.

Details

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

AddTipEverywhere() adds a tip to each edge in turn.

Value

AddTip() returns a tree of class phylo with an additional tip at the desired location.

AddTipEverywhere() returns a list of class multiPhylo containing the trees produced by adding label to each edge of tree in turn.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Add one tree to another: bind.tree()

Other tree manipulation: CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
tree <- BalancedTree(10)

# Add a leaf below an internal node
plot(tree)
ape::nodelabels() # Identify node numbers
node <- 15        # Select location to add leaf
ape::nodelabels(bg = ifelse(NodeNumbers(tree) == node, "green", "grey"))

plot(AddTip(tree, 15, "NEW_TIP"))

# Add edge lengths for an ultrametric tree
tree$edge.length <- rep(c(rep(1, 5), 2, 1, 2, 2), 2)

# Add a leaf to an external edge
leaf <- 5
plot(tree)
ape::tiplabels(bg = ifelse(seq_len(NTip(tree)) == leaf, "green", "grey"))

plot(AddTip(tree, 5, "NEW_TIP", edgeLength = NULL))
```

```
# Create a polytomy, rather than a new node
plot(AddTip(tree, 5, "NEW_TIP", edgeLength = NA))

# Set up multi-panel plot
oldPar <- par(mfrow = c(2, 4), mar = rep(0.3, 4), cex = 0.9)

# Add leaf to each edge on a tree in turn
backbone <- BalancedTree(4)
# Treating the position of the root as instructive:
additions <- AddTipEverywhere(backbone, includeRoot = TRUE)
xx <- lapply(additions, plot)

par(mfrow = c(2, 3))
# Don't treat root edges as distinct:
additions <- AddTipEverywhere(backbone, includeRoot = FALSE)
xx <- lapply(additions, plot)

# Restore original plotting parameters
par(oldPar)
```

`ApeTime` *Read modification time from "ape" Nexus file*

Description

`ApeTime()` reads the time that a tree written with "ape" was modified, based on the comment in the Nexus file.

Usage

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

Arguments

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

Value

`ApeTime()` returns the time that the specified file was created by ape, in the format specified by `format`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

`ArtificialExtinction` *Artificial Extinction*

Description

Remove tokens that do not occur in a fossil "template" taxon from a living taxon, to simulate the process of fossilization in removing data from a phylogenetic dataset.

Usage

```
ArtificialExtinction(
  dataset,
  subject,
  template,
  replaceAmbiguous = "ambig",
  replaceCoded = "original",
  replaceAll = TRUE,
  sampleFrom = NULL
)

## S3 method for class 'matrix'
ArtificialExtinction(
  dataset,
  subject,
  template,
  replaceAmbiguous = "ambig",
  replaceCoded = "original",
  replaceAll = TRUE,
  sampleFrom = NULL
)

## S3 method for class 'phyDat'
ArtificialExtinction(
  dataset,
  subject,
  template,
  replaceAmbiguous = "ambig",
  replaceCoded = "original",
  replaceAll = TRUE,
  sampleFrom = NULL
)

ArtEx(
  dataset,
  subject,
  template,
  replaceAmbiguous = "ambig",
```

```
  replaceCoded = "original",
  replaceAll = TRUE,
  sampleFrom = NULL
)
```

Arguments

`dataset`	Phylogenetic dataset of class `phyDat` or `matrix`.
`subject`	Vector identifying subject taxa, by name or index.
`template`	Character or integer identifying taxon to use as a template.
`replaceAmbiguous`, `replaceCoded`	Character specifying whether tokens that are ambiguous (?) or coded (not ?) in the fossil template should be replaced with: • `original`: Their original value; i.e. no change; • `ambiguous`: The ambiguous token, ?; • `binary`: The tokens `0` or `1`, with equal probability; • `uniform`: One of the tokens present in `sampleFrom`, with equal probability; • `sample`: One of the tokens present in `sampleFrom`, sampled according to their frequency.
`replaceAll`	Logical: if `TRUE`, replace all tokens in a subject; if `FALSE`, leave any ambiguous tokens (?) ambiguous.
`sampleFrom`	Vector identifying a subset of characters from which to sample replacement tokens. If `NULL`, replacement tokens will be sampled from the initial states of all taxa not used as a template (including the subjects).

Details

Further details are provided in Asher and Smith (2022).

Note: this simple implementation does not account for character contingency, e.g. characters whose absence imposes inapplicable or absent tokens on dependent characters.

Value

A dataset with the same class as `dataset` in which entries that are ambiguous in `template` are made ambiguous in `subject`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Asher R, Smith MR (2022). "Phylogenetic signal and bias in paleontology." *Systematic Biology*, **71**(4), 986–1008. doi:10.1093/sysbio/syab072.

Examples

```
set.seed(1)
dataset <- matrix(c(sample(0:2, 4 * 8, TRUE),
                    "0", "0", rep("?", 6)), nrow = 5,
                    dimnames = list(c(LETTERS[1:4], "FOSSIL"),
                                    paste("char", 1:8)), byrow = TRUE)
artex <- ArtificialExtinction(dataset, c("A", "C"), "FOSSIL")
```

---

as.multiPhylo *Convert object to* multiPhylo *class*

Description

Converts representations of phylogenetic trees to an object of the "ape" class multiPhylo.

Usage

```
as.multiPhylo(x)

## S3 method for class 'phylo'
as.multiPhylo(x)

## S3 method for class 'list'
as.multiPhylo(x)

## S3 method for class 'phyDat'
as.multiPhylo(x)

## S3 method for class 'Splits'
as.multiPhylo(x)
```

Arguments

x	Object to be converted

Value

as.multiPhylo returns an object of class multiPhylo

as.multiPhylo.phyDat() returns a list of trees, each corresponding to the partitions implied by each non-ambiguous character in x.

See Also

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
as.multiPhylo(BalancedTree(8))
as.multiPhylo(list(BalancedTree(8), PectinateTree(8)))
data("Lobo")
as.multiPhylo(Lobo.phy)
```

---

as.Newick *Write a phylogenetic tree in Newick format*

Description

`as.Newick()` creates a character string representation of a phylogenetic tree, in the Newick format, using R's internal tip numbering. Use `RenumberTips()` to ensure that the internal numbering follows the order you expect.

Usage

```
as.Newick(x)

## S3 method for class 'phylo'
as.Newick(x)

## S3 method for class 'list'
as.Newick(x)

## S3 method for class 'multiPhylo'
as.Newick(x)
```

Arguments

x	Object to convert to Newick format. See Usage section for supported classes.

Value

`as.Newick()` returns a character string representing `tree` in Newick format.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

- Retain leaf labels: `NewickTree()`
- Change R's internal numbering of leaves: `RenumberTips()`
- Write tree to text or file: `ape::write.tree()`

Examples

```
trees <- list(BalancedTree(1:8), PectinateTree(8:1))
trees <- lapply(trees, RenumberTips, 1:8)
as.Newick(trees)
```

`brewer` *Brewer palettes*

Description

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

Usage

```
brewer
```

Format

An object of class `list` of length 12.

Source

- ColourBrewer2.org
- Martin Krzywinski

Examples

```
data("brewer", package = "TreeTools")
plot(0, type = "n", xlim = c(1, 12), ylim = c(12, 1),
     xlab = "Colour", ylab="Palette")
for (i in seq_along(brewer)) text(seq_len(i), i, col = brewer[[i]])
```

`CharacterInformation` *Character information content*

Description

`CharacterInformation()` calculates the cladistic information content (Steel and Penny 2006) of a given character, in bits. The total information in all characters gives a measure of the potential utility of a dataset (Cotton and Wilkinson 2008), which can be compared with a profile parsimony score (Faith and Trueman 2001) to evaluate the degree of homoplasy within a dataset.

Usage

```
CharacterInformation(tokens)
```

Arguments

tokens	Character vector specifying the tokens assigned to each taxon for a character. Example: `c(0, 0, 0, 1, 1, 1, "?", "-")`. Note that ambiguous tokens such as `(01)` are not supported, and should be replaced with `?`.

Value

`CharacterInformation()` returns a numeric specifying the phylogenetic information content of the character (*sensu* Steel and Penny 2006), in bits.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Cotton JA, Wilkinson M (2008). "Quantifying the potential utility of phylogenetic characters." *Taxon*, **57**(1), 131–136.

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

Steel MA, Penny D (2006). "Maximum parsimony and the phylogenetic information in multistate characters." In Albert VA (ed.), *Parsimony, Phylogeny, and Genomics*, 163–178. Oxford University Press, Oxford.

See Also

Other split information functions: `SplitInformation()`, `SplitMatchProbability()`, `TreesMatchingSplit()`, `UnrootedTreesMatchingSplit()`

Cherries *Count cherries in a tree*

Description

`Cherries()` counts the number of vertices in a binary tree whose children are both leaves.

Usage

```
Cherries(tree, nTip)

## S3 method for class 'phylo'
Cherries(tree, nTip = NTip(tree))

## S3 method for class 'numeric'
Cherries(tree, nTip)
```

Arguments

tree	A binary tree, of class phylo; or a matrix corresponding to its edge matrix.
nTip	Number of leaves in tree.

Value

Cherries() returns an integer specifying the number of nodes whose children are both leaves.

Equations for the number of cherries expected under uniform and Yule tree models are derived by McKenzie and Steel (2000).

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

McKenzie A, Steel M (2000). "Distributions of Cherries for Two Models of Trees." *Mathematical Biosciences*, **164**(1), 81–92. doi:10.1016/S00255564(99)000607.

See Also

Other tree properties: ConsensusWithout(), EdgeRatio(), LongBranch(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

CladeSizes *Clade sizes*

Description

CladeSizes() reports the number of nodes in each clade in a tree.

Usage

```
CladeSizes(tree, internal = FALSE, nodes = NULL)
```

Arguments

tree	A tree of class phylo.
internal	Logical specifying whether internal nodes should be counted towards the size of each clade.
nodes	Integer specifying indices of nodes at the base of clades whose sizes should be returned. If unspecified, counts will be provided for all nodes (including leaves).

Value

CladeSizes() returns the number of nodes (including leaves) that are descended from each node, not including the node itself.

See Also

Other tree navigation: AncestorEdge(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- BalancedTree(6)
plot(tree)
ape::nodelabels()
CladeSizes(tree, nodes = c(1, 8, 9))
```

CladisticInfo *Cladistic information content of a tree*

Description

CladisticInfo() calculates the cladistic (phylogenetic) information content of a phylogenetic object, *sensu* Thorley *et al.* (1998).

Usage

```
CladisticInfo(x)

## S3 method for class 'phylo'
CladisticInfo(x)

## S3 method for class 'Splits'
CladisticInfo(x)

## S3 method for class 'list'
CladisticInfo(x)
```

```
## S3 method for class 'multiPhylo'
CladisticInfo(x)

CladisticInformation(x)
```

Arguments

x	Tree of class phylo, or a list thereof.

Details

The CIC is the logarithm of the number of binary trees that include the specified topology. A base two logarithm gives an information content in bits.

The CIC was originally proposed by Rohlf (1982), and formalised, with an information-theoretic justification, by Thorley et al. (1998). Steel and Penny (2006) term the equivalent quantity "phylogenetic information content" in the context of individual characters.

The number of binary trees consistent with a cladogram provides a more satisfactory measure of the resolution of a tree than simply counting the number of edges resolved (Page 1992).

Value

`CladisticInfo()` returns a numeric giving the cladistic information content of the input tree(s), in bits. If passed a `Splits` object, it returns the information content of each split in turn.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Page RD (1992). "Comments on the information content of classifications." *Cladistics*, **8**(1), 87–95. doi:10.1111/j.10960031.1992.tb00054.x.

Rohlf FJ (1982). "Consensus indices for comparing classifications." *Mathematical Biosciences*, **59**(1), 131–144. doi:10.1016/00255564(82)901122.

Steel MA, Penny D (2006). "Maximum parsimony and the phylogenetic information in multistate characters." In Albert VA (ed.), *Parsimony, Phylogeny, and Genomics*, 163–178. Oxford University Press, Oxford.

Thorley JL, Wilkinson M, Charleston M (1998). "The information content of consensus trees." In Rizzi A, Vichi M, Bock H (eds.), *Advances in Data Science and Classification*, 91–98. Springer, Berlin. ISBN 978-3-540-64641-9. doi:10.1007/9783642722530.

See Also

Other tree information functions: `NRooted()`, `TreesMatchingTree()`

Other tree characterization functions: `Consensus()`, `J1Index()`, `Stemwardness`, `TotalCopheneticIndex()`

`ClusterTable` *Convert phylogenetic tree to* `ClusterTable`

Description

`as.ClusterTable()` converts a phylogenetic tree to a `ClusterTable` object, which is an internal representation of its splits suitable for rapid tree distance calculation (per Day, 1985).

Usage

```
as.ClusterTable(x, tipLabels = NULL, ...)

## S3 method for class 'phylo'
as.ClusterTable(x, tipLabels = NULL, ...)

## S3 method for class 'list'
as.ClusterTable(x, tipLabels = NULL, ...)

## S3 method for class 'multiPhylo'
as.ClusterTable(x, tipLabels = NULL, ...)
```

Arguments

`x`	Object to convert into `ClusterTable`: perhaps a tree of class `phylo`.
`tipLabels`	Character vector specifying sequence in which to order tip labels.
`...`	Unused.

Details

Each row of a cluster table relates to a clade on a tree rooted on tip 1. Tips are numbered according to the order in which they are visited in preorder: i.e., if plotted using `plot(x)`, from the top of the page downwards. A clade containing the tips 2 .. 5 would be denoted by the entry `2, 5`, in either row 2 or row 5 of the cluster table.

Value

`as.ClusterTable()` returns an object of class `ClusterTable`, or a list thereof.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Day WHE (1985). "Optimal algorithms for comparing trees with labeled leaves." *Journal of Classification*, **2**(1), 7–28. doi:10.1007/BF01908061.

See Also

S3 methods for `ClusterTable` objects.

Other utility functions: `ClusterTable-methods`, `Hamming()`, `MSTEdges()`, `SampleOne()`, `TipTimedTree()`, `UnshiftTree()`, `as.multiPhylo()`, `match,phylo,phylo-method`, `sapply64()`, `sort.multiPhylo()`

Examples

```
tree1 <- ape::read.tree(text = "(A, (B, (C, (D, E))));");
tree2 <- ape::read.tree(text = "(A, (B, (D, (C, E))));");
ct1 <- as.ClusterTable(tree1)
summary(ct1)
as.matrix(ct1)

# Tip label order must match ct1 to allow comparison
ct2 <- as.ClusterTable(tree2, tipLabels = LETTERS[1:5])

# It can thus be safer to use
ctList <- as.ClusterTable(c(tree1, tree2))
ctList[[2]]
```

`ClusterTable-methods` *S3 methods for* `ClusterTable` *objects*

Description

S3 methods for `ClusterTable` objects.

Usage

```
## S3 method for class 'ClusterTable'
as.matrix(x, ...)

## S3 method for class 'ClusterTable'
print(x, ...)

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

Arguments

`x, object`	Object of class `ClusterTable`.
`...`	Additional arguments for consistency with S3 methods.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other utility functions: ClusterTable, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
clustab <- as.ClusterTable(TreeTools::BalancedTree(6))
as.matrix(clustab)
print(clustab)
summary(clustab)
```

CollapseNode *Collapse nodes on a phylogenetic tree*

Description

Collapses specified nodes or edges on a phylogenetic tree, resulting in polytomies.

Usage

```
CollapseNode(tree, nodes)

## S3 method for class 'phylo'
CollapseNode(tree, nodes)

CollapseEdge(tree, edges)
```

Arguments

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

Value

CollapseNode() and CollapseEdge() return a tree of class phylo, corresponding to tree with the specified nodes or edges collapsed. The length of each dropped edge will (naively) be added to each descendant edge.

Author(s)

Martin R. Smith

See Also

Other tree manipulation: AddTip(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
oldPar <- par(mfrow = c(3, 1), mar = rep(0.5, 4))

tree <- as.phylo(898, 7)
tree$edge.length <- 11:22
plot(tree)
nodelabels()
edgelabels()
edgelabels(round(tree$edge.length, 2),
           cex = 0.6, frame = "n", adj = c(1, -1))

# Collapse by node number
newTree <- CollapseNode(tree, c(12, 13))
plot(newTree)
nodelabels()
edgelabels(round(newTree$edge.length, 2),
           cex = 0.6, frame = "n", adj = c(1, -1))

# Collapse by edge number
newTree <- CollapseEdge(tree, c(2, 4))
plot(newTree)

par(oldPar)
```

`Consensus` *Construct consensus trees*

Description

`Consensus()` calculates the consensus of a set of trees, using the algorithm of (Day 1985).

Usage

```
Consensus(trees, p = 1, check.labels = TRUE)
```

Arguments

`trees`	List of trees, optionally of class `multiPhylo`.
`p`	Proportion of trees that must contain a split for it to be reported in the consensus. `p = 0.5` gives the majority-rule consensus; `p = 1` (the default) gives the strict consensus.
`check.labels`	Logical specifying whether to check that all trees have identical labels. Defaults to `TRUE`, which is slower.

Value

`Consensus()` returns an object of class `phylo`, rooted as in the first entry of `trees`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Day WHE (1985). "Optimal algorithms for comparing trees with labeled leaves." *Journal of Classification*, **2**(1), 7–28. doi:10.1007/BF01908061.

See Also

`TreeDist::ConsensusInfo()` calculates the information content of a consensus tree.

Other consensus tree functions: `ConsensusWithout()`, `RoguePlot()`

Other tree characterization functions: `CladisticInfo()`, `J1Index()`, `Stemwardness`, `TotalCopheneticIndex()`

Examples

```
Consensus(as.phylo(0:2, 8))
```

ConsensusWithout *Reduced consensus, omitting specified taxa*

Description

`ConsensusWithout()` displays a consensus plot with specified taxa excluded, which can be a useful way to increase the resolution of a consensus tree when a few wildcard taxa obscure a consistent set of relationships. `MarkMissing()` adds missing taxa as loose leaves on the plot.

Usage

```
ConsensusWithout(trees, tip = character(0), ...)

## S3 method for class 'phylo'
ConsensusWithout(trees, tip = character(0), ...)

## S3 method for class 'multiPhylo'
ConsensusWithout(trees, tip = character(0), ...)

## S3 method for class 'list'
ConsensusWithout(trees, tip = character(0), ...)

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

Arguments

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

Value

ConsensusWithout() returns a consensus tree (of class phylo) without the excluded taxa.

MarkMissing() provides a null return, after plotting the specified tips as a legend.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: AddTip(), CollapseNode(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Other tree properties: Cherries(), EdgeRatio(), LongBranch(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

Other consensus tree functions: Consensus(), RoguePlot()

Examples

```
oldPar <- par(mfrow = c(1, 2), mar = rep(0.5, 4))

# Two trees differing only in placement of tip 2:
trees <- as.phylo(c(0, 53), 6)
plot(trees[[1]])
plot(trees[[2]])

# Strict consensus (left panel) lacks resolution:
plot(ape::consensus(trees))

# But omitting tip two (right panel) reveals shared structure in common:
plot(ConsensusWithout(trees, "t2"))
MarkMissing("t2")

par(oldPar)
```

ConstrainedNJ *Constrained neighbour-joining tree*

Description

Constructs an approximation to a neighbour-joining tree, modified in order to be consistent with a constraint. Zero-length branches are collapsed at random.

Usage

```
ConstrainedNJ(dataset, constraint, weight = 1L, ratio = TRUE, ambig = "mean")
```

Arguments

dataset	A phylogenetic data matrix of **phangorn** class phyDat, whose names correspond to the labels of any accompanying tree.
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, in which each node in constraint will occur in the returned tree. See vignette for further examples.
weight	Numeric specifying degree to up-weight characters in constraint.
ambig, ratio	Settings of ambig and ratio to be used when computing Hamming() distances between sequences.

Value

ConstrainedNJ() returns a tree of class phylo.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree generation functions: GenerateTree, NJTree(), TreeNumber, TrivialTree

Examples

```
dataset <- MatrixToPhyDat(matrix(
  c(0, 1, 1, 1, 0, 1,
    0, 1, 1, 0, 0, 1), ncol = 2,
  dimnames = list(letters[1:6], NULL)))
constraint <- MatrixToPhyDat(
  c(a = 0, b = 0, c = 0, d = 0, e = 1, f = 1))
plot(ConstrainedNJ(dataset, constraint))
```

`Decompose` *Decompose additive (ordered) phylogenetic characters*

Description

`Decompose()` decomposes additive characters into a series of binary characters, which is mathematically equivalent when analysed under equal weights parsimony. (This equivalence is not exact under implied weights or under probabilistic tree inference methods.)

Usage

```
Decompose(dataset, indices)
```

Arguments

`dataset`	A phylogenetic data matrix of **phangorn** class `phyDat`, whose names correspond to the labels of any accompanying tree.
`indices`	Integer or logical vector specifying indices of characters that should be decomposed

Details

An ordered (additive) character can be rewritten as a mathematically equivalent hierarchy of binary neomorphic characters (Farris et al. 1970). Two reasons to prefer the latter approach are:

- It makes explicit the evolutionary assumptions underlying an ordered character, whether the underlying ordering is linear, reticulate or branched (Mabee 1989).
- It avoids having to identify characters requiring special treatment to phylogenetic software, which requires the maintenance of an up-to-date log of which characters are treated as additive and which sequence their states occur in, a step that may be overlooked by re-users of the data.

Careful consideration is warranted when evaluating whether a group of related characteristics ought to be treated as ordered (Wilkinson 1992). On the one hand, the 'principle of indifference' states that we should treat all transformations as equally probable (/ surprising / informative); ordered characters fail this test, as larger changes are treated as less probable than smaller ones. On the other hand, ordered characters allow more opportunities for homology of different character states, and might thus be defended under the auspices of Hennig's Auxiliary Principle (Wilkinson 1992).

For a case study of how ordering phylogenetic characters can affect phylogenetic outcomes in practice, see Brady et al. (2024).

Value

`Decompose()` returns a `phyDat` object in which the specified ordered characters have been decomposed into binary characters. The attribute `originalIndex` lists the index of the character in `dataset` to which each element corresponds.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Brady PL, Castrellon Arteaga A, López-Torres S, Springer MS (2024). "The Effects of Ordered Multistate Morphological Characters on Phylogenetic Analyses of Eutherian Mammals." *Journal of Mammalian Evolution*, **31**(3), 28. doi:10.1007/s10914024097272.

Farris JS, Kluge AG, Eckardt MJ (1970). "A Numerical Approach to Phylogenetic Systematics." *Systematic Biology*, **19**(2), 172–189. doi:10.2307/2412452.

Mabee PM (1989). "Assumptions Underlying the Use of Ontogenetic Sequences for Determining Character State Order." *Transactions of the American Fisheries Society*, **118**(2), 151–158. doi:10.1577/15488659(1989)118<0151:AUTUOO>2.3.CO;2.

Wilkinson M (1992). "Ordered versus Unordered Characters." *Cladistics*, **8**(4), 375–385. doi:10.1111/j.10960031.1992.tb00079.x.

See Also

Other phylogenetic matrix conversion functions: `MatrixToPhyDat()`, `Reweight()`, `StringToPhyDat()`

Examples

```
data("Lobo")

# Identify character 11 as additive
# Character 11 will be replaced with two characters
# The present codings 0, 1 and 2 will be replaced with 00, 10, and 11.
decomposed <- Decompose(Lobo.phy, 11)

NumberOfChars <- function(x) sum(attr(x, "weight"))
NumberOfChars(Lobo.phy)   # 115 characters in original
NumberOfChars(decomposed) # 116 characters in decomposed
```

`DescendantEdges` *Identify descendant edges*

Description

`DescendantEdges()` efficiently identifies edges that are "descended" from edges in a tree.

`DescendantTips()` efficiently identifies leaves (external nodes) that are "descended" from edges in a tree.

Usage

```
DescendantEdges(
  parent,
  child,
  edge = NULL,
  node = NULL,
  nEdge = length(parent),
  includeSelf = TRUE
)

DescendantTips(parent, child, edge = NULL, node = NULL, nEdge = length(parent))
```

Arguments

parent	Integer vector corresponding to the first column of the edge matrix of a tree of class phylo, i.e. tree[["edge"]][, 1]
child	Integer vector corresponding to the second column of the edge matrix of a tree of class phylo, i.e. tree[["edge"]][, 2].
edge	Integer specifying the number of the edge whose children are required (see edgelabels()).
node	Integer specifying the number(s) of nodes whose children are required. Specify 0 to return all nodes. If NULL (the default), the edge parameter will be used instead.
nEdge	number of edges (calculated from length(parent) if not supplied).
includeSelf	Logical specifying whether to mark edge as its own descendant.

Value

DescendantEdges() returns a logical vector stating whether each edge in turn is the specified edge (if includeSelf = TRUE) or one of its descendants.

DescendantTips() returns a logical vector stating whether each leaf in turn is a descendant of the specified edge.

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- as.phylo(0, 6)
plot(tree)
desc <- DescendantEdges(tree$edge[, 1], tree$edge[, 2], edge = 5)
which(desc)
ape::edgelabels(bg = 3 + desc)
tips <- DescendantTips(tree$edge[, 1], tree$edge[, 2], edge = 5)
which(tips)
```

```
tiplabels(bg = 3 + tips)
```

`DoubleFactorial` *Double factorial*

Description

Calculate the double factorial of a number, or its logarithm.

Usage

```
DoubleFactorial(n)

DoubleFactorial64(n)

LnDoubleFactorial(n)

Log2DoubleFactorial(n)

LogDoubleFactorial(n)

LnDoubleFactorial.int(n)

LogDoubleFactorial.int(n)
```

Arguments

`n`	Vector of integers.

Value

Returns the double factorial, $n * (n - 2) * (n - 4) * (n - 6) * ...$

Functions

- `DoubleFactorial64()`: Returns the exact double factorial as a 64-bit `integer64`, for `n` < 34.
- `LnDoubleFactorial()`: Returns the logarithm of the double factorial.
- `Log2DoubleFactorial()`: Returns the logarithm of the double factorial.
- `LnDoubleFactorial.int()`: Slightly faster, when x is known to be length one and below 50001

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other double factorials: `doubleFactorials`, `logDoubleFactorials`

Examples

```
DoubleFactorial (-4:0) # Return 1 if n < 2
DoubleFactorial (2) # 2
DoubleFactorial (5) # 1 * 3 * 5
exp(LnDoubleFactorial.int (8)) # log(2 * 4 * 6 * 8)
DoubleFactorial64(31)
```

---

doubleFactorials *Double factorials*

Description

A vector with pre-calculated values of double factorials up to 300!!, and the logarithms of double factorials up to 50 000!!.

Usage

```
doubleFactorials
```

Format

An object of class `numeric` of length 300.

Details

301!! is too large to store as an integer; use `logDoubleFactorials` instead.

See Also

Other double factorials: `DoubleFactorial()`, `logDoubleFactorials`

DropTip *Drop leaves from tree*

Description

`DropTip()` removes specified leaves from a phylogenetic tree, collapsing incident branches.

Usage

```
DropTip(tree, tip, preorder = TRUE, check = TRUE)

KeepTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'phylo'
DropTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'phylo'
KeepTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'Splits'
KeepTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'Splits'
DropTip(tree, tip, preorder, check = TRUE)

DropTipPhylo(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'multiPhylo'
DropTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'multiPhylo'
KeepTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'list'
DropTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class 'list'
KeepTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class '`NULL`'
DropTip(tree, tip, preorder = TRUE, check = TRUE)

## S3 method for class '`NULL`'
KeepTip(tree, tip, preorder = TRUE, check = TRUE)

KeepTipPreorder(tree, tip)

KeepTipPostorder(tree, tip)
```

Arguments

tree	A tree of class phylo.
tip	Character vector specifying labels of leaves in tree to be dropped or kept, or integer vector specifying the indices of leaves to be dropped or kept. Specifying the index of an internal node will drop all descendants of that node.

preorder	Logical specifying whether to Preorder tree before dropping tips. Specifying FALSE saves a little time, but will result in undefined behaviour if tree is not in preorder.
check	Logical specifying whether to check validity of tip. If FALSE and tip contains entries that do not correspond to leaves of the tree, undefined behaviour may occur.

Details

This function differs from ape::drop.tip(), which roots unrooted trees, and which can crash when trees' internal numbering follows unexpected schema.

Value

DropTip() returns a tree of class phylo, with the requested leaves removed. The edges of the tree will be numbered in preorder, but their sequence may not conform to the conventions of Preorder().

KeepTip() returns tree with all leaves not in tip removed, in preorder.

Functions

- DropTipPhylo(): Direct call to DropTip.phylo(), to avoid overhead of querying object's class.
- KeepTipPreorder(): Faster version with no checks. Does not retain labels or edge weights. Edges must be listed in preorder. May crash if improper input is specified.
- KeepTipPostorder(): Faster version with no checks. Does not retain labels or edge weights. Edges must be listed in postorder. May crash if improper input is specified.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Other split manipulation functions: SplitConsistent(), Subsplit(), TrivialSplits()

Examples

```
tree <- BalancedTree(9)
plot(tree)
plot(DropTip(tree, c("t5", "t6")))

unrooted <- UnrootTree(tree)
plot(unrooted)
plot(DropTip(unrooted, 4:5))

summary(DropTip(as.Splits(tree), 4:5))
```

EdgeAncestry *Ancestors of an edge*

Description

Quickly identify edges that are "ancestral" to a particular edge in a tree.

Usage

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

Arguments

edge	Integer specifying the number of the edge whose child edges should be returned.
parent	Integer vector corresponding to the first column of the edge matrix of a tree of class phylo, i.e. tree[["edge"]][, 1]
child	Integer vector corresponding to the second column of the edge matrix of a tree of class phylo, i.e. tree[["edge"]][, 2].
stopAt	Integer or logical vector specifying the edge(s) at which to terminate the search; defaults to the edges with the smallest parent, which will be the root edges if nodes are numbered Cladewise or in Preorder.

Value

EdgeAncestry() returns a logical vector stating whether each edge in turn is a descendant of the specified edge.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- PectinateTree(6)
plot(tree)
ape::edgelabels()
parent <- tree$edge[, 1]
child <- tree$edge[, 2]
EdgeAncestry(7, parent, child)
which(EdgeAncestry(7, parent, child, stopAt = 4))
```

EdgeDistances *Distance between edges*

Description

Number of nodes that must be traversed to navigate from each edge to each other edge within a tree

Usage

```
EdgeDistances(tree)
```

Arguments

tree	A tree of class phylo.

Value

EdgeDistances() returns a symmetrical matrix listing the number of edges that must be traversed to travel from each numbered edge to each other. The two edges straddling the root of a rooted tree are treated as a single edge. Add a "root" tip using AddTip() if the position of the root is significant.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- BalancedTree(5)
plot(tree)
ape::edgelabels()

EdgeDistances(tree)
```

EdgeRatio *Ratio of external:internal edge length*

Description

Reports the ratio of tree length associated with external edges (i.e. edges whose child is a leaf) and internal edges. Where tree length is dominated by internal edges, variation between tips is dominantly controlled by phylogenetic history.

Usage

```
EdgeRatio(x)

## S3 method for class 'phylo'
EdgeRatio(x)
```

Arguments

x	A tree of class phylo.

Value

EdgeRatio() returns a numeric specifying the ratio of external to internal edge length (> 1 means the length of a tree is predominantly in external edges), with attributes external, internal, and total specifying the total length associated with edges of that nature.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: Cherries(), ConsensusWithout(), LongBranch(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

edge_to_splits *Efficiently convert edge matrix to splits*

Description

Wrapper for internal C++ function for maximum efficiency. Improper input may crash R. Behaviour not guaranteed. It is advisable to contact the package maintainers before relying on this function.

Usage

```
edge_to_splits(
  edge,
  edgeOrder,
  tipLabels = NULL,
  asSplits = TRUE,
  nTip = NTip(edge),
  ...
)
```

Arguments

edge	A matrix with two columns, with each row listing the parent and child node of an edge in a phylogenetic tree. Property edge of objects of class phylo.
edgeOrder	Integer vector such that edge[edgeOrder,] returns a postorder ordering of edges.
tipLabels	Character vector specifying sequence in which to order tip labels. Label order must (currently) match to combine or compare separate Splits objects.
asSplits	Logical specifying whether to return a Splits object, or an unannotated two-dimensional array (useful where performance is paramount).
nTip	Integer specifying number of leaves in tree.
...	Presently unused.

Value

edge_to_splits() uses the same return format as as.Splits().

See Also

as.Splits() offers a safe access point to this function that should be suitable for most users.

EndSentence *Add full stop to end of a sentence*

Description

Add full stop to end of a sentence

Usage

```
EndSentence(string)
```

Arguments

string	Input string

Value

EndSentence() returns string, punctuated with a final full stop (period).‘

Author(s)

Martin R. Smith

See Also

Other string parsing functions: MatchStrings(), MorphoBankDecode(), RightmostCharacter(), Unquote()

Examples

```
EndSentence("Hello World") # "Hello World."
```

GenerateTree *Generate pectinate, balanced or random trees*

Description

RandomTree(), PectinateTree(), BalancedTree() and StarTree() generate trees with the specified shapes and leaf labels.

Usage

```
RandomTree(tips, root = FALSE, nodes, lengths = NULL)

YuleTree(tips, addInTurn = FALSE, root = TRUE, lengths = NULL)

PectinateTree(tips, lengths = NULL)

BalancedTree(tips, lengths = NULL)

StarTree(tips, lengths = NULL)
```

Arguments

tips	An integer specifying the number of tips, or a character vector naming the tips, or any other object from which TipLabels() can extract leaf labels.
root	Character or integer specifying tip to use as root; or TRUE to root the tree on a random edge; or FALSE to return an unrooted tree.
nodes	Number of nodes to generate. The default and maximum, tips - 1, generates a binary tree; setting a lower value will induce polytomies.
lengths	a numeric vector specifying the edge lengths of the tree.
addInTurn	Logical specifying whether to add leaves in the order of tips. If FALSE, leaves will be added in a random order.

Value

Each function returns an unweighted binary tree of class `phylo` with the specified leaf labels. Trees are rooted unless `root = FALSE`.

`RandomTree()` returns a topology drawn at random from the uniform distribution (i.e. each binary tree is drawn with equal probability). Trees are generated by inserting each tip in term at a randomly selected edge in the tree. Random numbers are generated using a Mersenne Twister. If `root = FALSE`, the tree will be unrooted, with the first tip in a basal position. Otherwise, the tree will be rooted on `root`.

`YuleTree()` returns a topology generated by the Yule process (Steel and McKenzie 2001), i.e. adding leaves in turn adjacent to a randomly-chosen existing leaf.

`PectinateTree()` returns a pectinate (caterpillar) tree.

`BalancedTree()` returns a balanced (symmetrical) tree, in preorder.

`StarTree()` returns a completely unresolved (star) tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Steel MA, McKenzie A (2001). "Properties of Phylogenetic Trees Generated by Yule-type Speciation Models." *Mathematical Biosciences*, **170**(1), 91–112. doi:10.1016/S00255564(00)000614.()

See Also

Other tree generation functions: `ConstrainedNJ()`, `NJTree()`, `TreeNumber`, `TrivialTree`

Examples

```
RandomTree(LETTERS[1:10])

data("Lobo")
RandomTree(Lobo.phy)

YuleTree(LETTERS[1:10])

plot(PectinateTree(LETTERS[1:10]))

plot(BalancedTree(LETTERS[1:10]))
plot(StarTree(LETTERS[1:10]))
```

Hamming *Hamming distance between taxa in a phylogenetic dataset*

Description

The Hamming distance between a pair of taxa is the number of characters with a different coding, i.e. the smallest number of evolutionary steps that must have occurred since their common ancestor.

Usage

```
Hamming(
  dataset,
  ratio = TRUE,
  ambig = c("median", "mean", "zero", "one", "na", "nan")
)
```

Arguments

dataset	Object of class phyDat.
ratio	Logical specifying whether to weight distance against maximum possible, given that a token that is ambiguous in either of two taxa cannot contribute to the total distance between the pair.
ambig	Character specifying value to return when a pair of taxa have a zero maximum distance (perhaps due to a preponderance of ambiguous tokens). "median", the default, take the median of all other distance values; "mean", the mean; "zero" sets to zero; "one" to one; "NA" to NA_integer_; and "NaN" to NaN.

Details

Tokens that contain the inapplicable state are treated as requiring no steps to transform into any applicable token.

Value

Hamming() returns an object of class dist listing the Hamming distance between each pair of taxa.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Used to construct neighbour joining trees in NJTree().

dist.hamming() in the **phangorn** package provides an alternative implementation.

Other utility functions: ClusterTable, ClusterTable-methods, MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
tokens <- matrix(c(0, 0, "0", 0, "?",
                   0, 0, "1", 0, 1,
                   0, 0, "1", 0, 1,
                   0, 0, "2", 0, 1,
                   1, 1, "-", "?", 0,
                   1, 1, "2", 1, "{01}"),
                   nrow = 6, ncol = 5, byrow = TRUE,
                   dimnames = list(
                     paste0("Taxon_", LETTERS[1:6]),
                     paste0("Char_", 1:5)))

dataset <- MatrixToPhyDat(tokens)
Hamming(dataset)
```

ImposeConstraint *Force a tree to match a constraint*

Description

Modify a tree such that it matches a specified constraint. This is at present a somewhat crude implementation that attempts to retain much of the structure of `tree` whilst guaranteeing compatibility with each entry in `constraint`.

Usage

```
ImposeConstraint(tree, constraint)

AddUnconstrained(constraint, toAdd, asPhyDat = TRUE)
```

Arguments

`tree`	A tree of class `phylo`.
`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`, in which each node in `constraint` will occur in the returned tree. See vignette for further examples.
`toAdd`	Character vector specifying taxa to add to constraint.
`asPhyDat`	Logical: if `TRUE`, return a `phyDat` object; if `FALSE`, return a matrix.

Value

`ImposeConstraint()` returns a tree of class `phylo`, consistent with `constraint`.

Functions

- `AddUnconstrained()`: Expand a constraint to include unconstrained taxa.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
tips <- letters[1:9]
tree <- as.phylo(1, 9, tips)
plot(tree)

constraint <- StringToPhyDat("0000?1111 000111111 0000??110", tips, FALSE)
plot(ImposeConstraint(tree, constraint))
```

---

is.TreeNumber *Is an object a* TreeNumber *object?*

Description

Is an object a TreeNumber object?

Usage

```
is.TreeNumber(x)
```

Arguments

x	R object.

Value

is.TreeNumber() returns a logical vector of length one specifying whether x inherits the class "TreeNumber".

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other 'TreeNumber' utilities: TreeNumber, print.TreeNumber()

Examples

```
is.TreeNumber(FALSE) # FALSE
is.TreeNumber(as.TreeNumber(BalancedTree(5))) # TRUE
```

J1Index *Robust universal tree balance index*

Description

Calculate tree balance index J^1 (when nonRootDominance = FALSE) or J^{1c} (when nonRootDominance = TRUE) from (Lemant et al. 2022).

Usage

```
J1Index(tree, q = 1, nonRootDominance = FALSE)

JQIndex(tree, q = 1, nonRootDominance = FALSE)
```

Arguments

tree	Either an object of class 'phylo', or a dataframe with column names Parent, Identity and (optionally) Population. The latter is similar to tree$edge, where tree is an object of class 'phylo'; the differences are in class (data.frame versus matrix) and column names. The dataframe may (but isn't required to) include a row for the root node. If population sizes are omitted then internal nodes will be assigned population size zero and leaves will be assigned population size one.
q	Numeric between zero and one specifying sensitivity to type frequencies. If q < 1, the J^q index - based on generalized entropy - will be returned; see Lemant et al. (2022), page 1223.
nonRootDominance	Logical specifying whether to use non-root dominance factor.

Details

If population sizes are not provided, then the function assigns size 0 to internal nodes, and size 1 to leaves.

Value

J1Index() returns a numeric specifying the J^1 index of tree. $J^1(T) = 1$ for a perfectly balanced tree; $J^1(T) = 0$ for a pectinate (linear / caterpillar) tree.

Author(s)

Rob Noble, adapted by Martin R. Smith

References

Lemant J, Le Sueur C, Manojlović V, Noble R (2022). "Robust, Universal Tree Balance Indices." *Systematic Biology*, **71**(5), 1210–1224. doi:10.1093/sysbio/syac027.

See Also

Other tree characterization functions: CladisticInfo(), Consensus(), Stemwardness, TotalCopheneticIndex()

Examples

```
# Using phylo object as input:
phylo_tree <- read.tree(text="((a:0.1)A:0.5,(b1:0.2,b2:0.1)B:0.2);")
J1Index(phylo_tree)
phylo_tree2 <- read.tree(text='((A, B), ((C, D), (E, F)));')
J1Index(phylo_tree2)

# Using edges lists as input:
tree1 <- data.frame(Parent = c(1, 1, 1, 1, 2, 3, 4),
                    Identity = 1:7,
                    Population = c(1, rep(5, 6)))
J1Index(tree1)
tree2 <- data.frame(Parent = c(1, 1, 1, 1, 2, 3, 4),
                    Identity = 1:7,
                    Population = c(rep(0, 4), rep(1, 3)))
J1Index(tree2)
tree3 <- data.frame(Parent = c(1, 1, 1, 1, 2, 3, 4),
                    Identity = 1:7,
                    Population = c(0, rep(1, 3), rep(0, 3)))
J1Index(tree3)
cat_tree <- data.frame(Parent = c(1, 1:14, 1:15, 15),
                       Identity = 1:31,
                       Population = c(rep(0, 15), rep(1, 16)))
J1Index(cat_tree)

# If population sizes are omitted then internal nodes are assigned population
# size zero and leaves are assigned population size one:
sym_tree1 <- data.frame(Parent = c(1, rep(1:15, each = 2)),
                       Identity = 1:31,
                       Population = c(rep(0, 15), rep(1, 16)))
# Equivalently:
sym_tree2 <- data.frame(Parent = c(1, rep(1:15, each = 2)),
                       Identity = 1:31)
J1Index(sym_tree1)
J1Index(sym_tree2)
```

KeptPaths *Paths present in reduced tree*

Description

Lists which paths present in a master tree are present when leaves are dropped.

Usage

```
KeptPaths(paths, keptVerts, all = TRUE)

## S3 method for class 'data.frame'
KeptPaths(paths, keptVerts, all = TRUE)

## S3 method for class 'matrix'
KeptPaths(paths, keptVerts, all = TRUE)
```

Arguments

paths	data.frame of paths in master tree, perhaps generated using PathLengths().
keptVerts	Logical specifying whether each entry is retained in the reduced tree, perhaps generated using KeptVerts().
all	Logical: if TRUE, return all paths that occur in the reduced tree; if FALSE, return only those paths that correspond to a single edge. that correspond to edges in the reduced tree. Ignored if paths is a matrix.

Value

KeptPaths() returns a logical vector specifying whether each path in paths occurs when keptVerts vertices are retained.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
master <- BalancedTree(9)
paths <- PathLengths(master)
keptTips <- c(1, 5, 7, 9)
keptVerts <- KeptVerts(master, keptTips)
KeptPaths(paths, keptVerts)
paths[KeptPaths(paths, keptVerts, all = FALSE), ]
```

KeptVerts *Identify vertices retained when leaves are dropped*

Description

Identify vertices retained when leaves are dropped

Usage

```
KeptVerts(tree, keptTips, tipLabels = TipLabels(tree))

## S3 method for class 'phylo'
KeptVerts(tree, keptTips, tipLabels = TipLabels(tree))

## S3 method for class 'numeric'
KeptVerts(tree, keptTips, tipLabels = TipLabels(tree))
```

Arguments

tree	Original tree of class phylo, in Preorder.
keptTips	Either: • a logical vector stating whether each leaf should be retained, in a sequence corresponding to tree[["tip.label"]]; or • a character vector listing the leaf labels to retain; or • a numeric vector listing the indices of leaves to retain.
tipLabels	Optional character vector naming the leaves of tree, if keptTips is not logical. Inferred from tree if unspecified.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
master <- BalancedTree(12)
master <- Preorder(master) # Nodes must be listed in Preorder sequence
plot(master)
nodelabels()

allTips <- master[["tip.label"]]
keptTips <- sample(allTips, 8)
```

```
plot(KeepTip(master, keptTips))
kept <- KeptVerts(master, allTips %in% keptTips)

map <- which(kept)
# Node `i` in the reduced tree corresponds to node `map[i]` in the original.
```

`LabelSplits` *Label splits*

Description

Labels the edges associated with each split on a plotted tree.

Usage

```
LabelSplits(tree, labels = NULL, unit = "", ...)
```

Arguments

`tree`	A tree of class `phylo`.
`labels`	Named vector listing annotations for each split. Names should correspond to the node associated with each split; see `as.Splits()` for details. If `NULL`, each splits will be labelled with its associated node.
`unit`	Character specifying units of `labels`, if desired. Include a leading space if necessary.
`...`	Additional parameters to `ape::edgelabels()`.

Details

As the two root edges of a rooted tree denote the same split, only the rightmost (plotted at the bottom, by default) edge will be labelled. If the position of the root is significant, add a tip at the root using `AddTip()`.

Value

`LabelSplits()` returns `invisible()`, after plotting `labels` on each relevant edge of a plot (which should already have been produced using `plot(tree)`).

See Also

Calculate split support: `SplitFrequency()`

Colour labels according to value: `SupportColour()`

Other Splits operations: `NSplits()`, `NTip()`, `PolarizeSplits()`, `SplitFrequency()`, `Splits`, `SplitsInBinaryTree()`, `TipLabels()`, `TipsInSplits()`, `match,Splits,Splits-method`, `xor()`

Examples

```
tree <- BalancedTree(LETTERS[1:5])
splits <- as.Splits(tree)
plot(tree)
LabelSplits(tree, as.character(splits), frame = "none", pos = 3L)
LabelSplits(tree, TipsInSplits(splits), unit = " tips", frame = "none",
            pos = 1L)

# An example forest of 100 trees, some identical
forest <- as.phylo(c(1, rep(10, 79), rep(100, 15), rep(1000, 5)), nTip = 9)

# Generate an 80% consensus tree
cons <- ape::consensus(forest, p = 0.8)
plot(cons)

# Calculate split frequencies
splitFreqs <- SplitFrequency(cons, forest)

# Optionally, colour edges by corresponding frequency.
# Note that not all edges are associated with a unique split
# (and two root edges may be associated with one split - not handled here)
edgeSupport <- rep(1, nrow(cons$edge)) # Initialize trivial splits to 1
childNode <- cons$edge[, 2]
edgeSupport[match(names(splitFreqs), childNode)] <- splitFreqs / 100

plot(cons, edge.col = SupportColour(edgeSupport), edge.width = 3)

# Annotate nodes by frequency
LabelSplits(cons, splitFreqs, unit = "%",
            col = SupportColor(splitFreqs / 100),
            frame = "none", pos = 3L)
```

LeafLabelInterchange *Leaf label interchange*

Description

`LeafLabelInterchange()` exchanges the position of leaves within a tree.

Usage

```
LeafLabelInterchange(tree, n = 2L)
```

Arguments

`tree`	A tree of class `phylo`.
`n`	Integer specifying number of leaves whose positions should be exchanged.

Details

Modifies a tree by switching the positions of *n* leaves. To avoid later swaps undoing earlier exchanges, all *n* leaves are guaranteed to change position. Note, however, that no attempt is made to avoid swapping equivalent leaves, for example, a pair that are each others' closest relatives. As such, the relationships within a tree are not guaranteed to be changed.

Value

`LeafLabelInterchange()` returns a tree of class `phylo` on which the position of `n` leaves have been exchanged. The tree's internal topology will not change.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: `AddTip()`, `CollapseNode()`, `ConsensusWithout()`, `DropTip()`, `ImposeConstraint()`, `KeptPaths()`, `KeptVerts()`, `MakeTreeBinary()`, `Renumber()`, `RenumberTips()`, `RenumberTree()`, `RootTree()`, `SortTree()`, `Subtree()`, `TipTimedTree()`, `TrivialTree`

Examples

```
tree <- PectinateTree(8)
plot(LeafLabelInterchange(tree, 3L))
```

`ListAncestors` *List ancestors*

Description

`ListAncestors()` reports all ancestors of a given node.

Usage

```
ListAncestors(parent, child, node = NULL)

AllAncestors(parent, child)
```

Arguments

`parent`	Integer vector corresponding to the first column of the edge matrix of a tree of class `phylo`, i.e. `tree[["edge"]][, 1]`
`child`	Integer vector corresponding to the second column of the edge matrix of a tree of class `phylo`, i.e. `tree[["edge"]][, 2]`.
`node`	Integer giving the index of the node or tip whose ancestors are required, or `NULL` to return ancestors of all nodes.

Details

Note that if node = NULL, the tree's edges must be listed such that each internal node (except the root) is listed as a child before it is listed as a parent, i.e. its index in child is less than its index in parent. This will be true of trees listed in Preorder.

Value

If node = NULL, ListAncestors() returns a list. Each entry *i* contains a vector containing, in order, the nodes encountered when traversing the tree from node *i* to the root node. The last entry of each member of the list is therefore the root node, with the exception of the entry for the root node itself, which is a zero-length integer.

If node is an integer, ListAncestors() returns a vector of the numbers of the nodes ancestral to the given node, including the root node.

Functions

- AllAncestors(): Alias for ListAncestors(node = NULL).

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Implemented less efficiently in phangorn:::Ancestors, on which this code is based.

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- PectinateTree(5)
edge <- tree[["edge"]]

# Identify desired node with:
plot(tree)
nodelabels()
tiplabels()

# Ancestors of specific nodes:
ListAncestors(edge[, 1], edge[, 2], 4L)
ListAncestors(edge[, 1], edge[, 2], 8L)

# Ancestors of each node, if tree numbering system is uncertain:
lapply(seq_len(max(edge)), ListAncestors,
       parent = edge[, 1], child = edge[, 2])
```

```
# Ancestors of each node, if tree is in preorder:
ListAncestors(edge[, 1], edge[, 2])

# Alias:
AllAncestors(edge[, 1], edge[, 2])
```

`Lobo.data` *Data from Zhang et al. 2016*

Description

Phylogenetic data from Zhang et al. (2016) in raw (`Lobo.data`) and `phyDat` (`Lobo.phy`) formats.

Usage

```
Lobo.data

Lobo.phy
```

Format

An object of class `list` of length 48.

An object of class `phyDat` of length 48.

Source

Zhang et al. (2016)

References

Zhang X, Smith MR, Yang J, Hou J (2016). "Onychophoran-like musculature in a phosphatized Cambrian lobopodian." *Biology Letters*, **12**(9), 20160492. doi:10.1098/rsbl.2016.0492.

Examples

```
data("Lobo", package = "TreeTools")
Lobo.data
Lobo.phy
```

logDoubleFactorials *Natural logarithms of double factorials*

Description

logDoubleFactorials is a numeric vector with pre-calculated values of double factorials up to 50 000!!.

Usage

```
logDoubleFactorials
```

Format

An object of class numeric of length 50000.

See Also

Other double factorials: DoubleFactorial(), doubleFactorials

LongBranch *Identify taxa with long branches*

Description

The long branch (LB) score (Struck 2014) measures the deviation of the average pairwise patristic distance of a leaf from all other leaves in a tree, relative to the average leaf-to-leaf distance.

Usage

```
LongBranch(tree)
```

Arguments

tree	A tree of class phylo, or a list of trees of class list or multiPhylo.

Details

Struck (2014) proposes the standard deviation of LB scores as a measure of heterogeneity that can be compared between trees; and the upper quartile of LB scores as "a representative value for the taxa with the longest branches".

Value

LongBranch() returns a vector giving the long branch score for each leaf in tree, or a list of such vectors if tree is a list. Results are given as raw deviations, without multiplying by 100 as proposed by Struck (2014).

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: Cherries(), ConsensusWithout(), EdgeRatio(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

Examples

```
tree <- BalancedTree(8, lengths = c(rep(2, 4), 5:7, rep(2, 4), rep(1, 3)))
lb <- LongBranch(tree)
tree$tip.label <- paste(tree$tip.label, signif(lb, 3), sep = ": ")
plot(tree, tip.col = SupportColour((1 - lb) / 2), font = 2)

# Standard deviation of LB scores allows comparison with other trees
sd(lb)
evenLengths <- BalancedTree(8, lengths = jitter(rep(1, 14)))
sd(LongBranch(evenLengths))

# Upper quartile identifies taxa with longest branches
threshold <- quantile(lb, 0.75)
tree$tip.label[lb > threshold]
```

MakeTreeBinary *Generate binary tree by collapsing polytomies*

Description

MakeTreeBinary() resolves, at random, all polytomies in a tree or set of trees, such that all trees compatible with the input topology are drawn with equal probability. Edge lengths are not yet supported, so are removed.

Usage

```
MakeTreeBinary(tree)
```

Arguments

tree	A tree of class phylo.

Value

MakeTreeBinary() returns a rooted binary tree of class phylo, corresponding to tree uniformly selected from all those compatible with the input tree topologies.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Since ape v5.5, this functionality is available through `ape::multi2di()`; previous versions of "ape" did not return topologies in equal frequencies. `MakeTreeBinary()` is often somewhat faster; `multi2di()` retains edge lengths.

Other tree manipulation: `AddTip()`, `CollapseNode()`, `ConsensusWithout()`, `DropTip()`, `ImposeConstraint()`, `KeptPaths()`, `KeptVerts()`, `LeafLabelInterchange()`, `Renumber()`, `RenumberTips()`, `RenumberTree()`, `RootTree()`, `SortTree()`, `Subtree()`, `TipTimedTree()`, `TrivialTree`

Examples

```
MakeTreeBinary(CollapseNode(PectinateTree(7), c(9, 11, 13)))
UnrootTree(MakeTreeBinary(StarTree(5)))
```

---

match,phylo,phylo-method

Tree matching

Description

`match()` returns a vector of the positions of (first) matches of trees in its first argument in its second. `%in%` is a more intuitive interface as a binary operator, which returns a logical vector indicating whether there is a match or not for each tree in its left operand.

Usage

```
## S4 method for signature 'phylo,phylo'
match(x, table, nomatch = NA_integer_, incomparables = NULL)

## S4 method for signature 'multiPhylo,phylo'
match(x, table, nomatch = NA_integer_, incomparables = NULL)

## S4 method for signature 'phylo,multiPhylo'
match(x, table, nomatch = NA_integer_, incomparables = NULL)

## S4 method for signature 'multiPhylo,multiPhylo'
match(x, table, nomatch = NA_integer_, incomparables = NULL)

## S4 method for signature 'multiPhylo,multiPhylo'
x %in% table

## S4 method for signature 'multiPhylo,phylo'
x %in% table
```

```
## S4 method for signature 'phylo,multiPhylo'
x %in% table

## S4 method for signature 'phylo,phylo'
x %in% table
```

Arguments

x, table	Object of class phylo or multiPhylo.
nomatch	Integer value that will be used in place of NA in the case where no match is found.
incomparables	Ignored. (Included for consistency with generic.)

Value

match() returns an integer vector specifying the position in table that matches each element in x, or nomatch if no match is found.

See Also

Corresponding base functions are documented in match().

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), sapply64(), sort.multiPhylo()

Examples

```
tree1 <- BalancedTree(7)
trees <- c(PectinateTree(7), BalancedTree(7))

match(tree1, trees)
```

---

match,Splits,Splits-method

Split matching

Description

match() returns a vector of the positions of (first) matches of splits in its first argument in its second. %in% is a more intuitive interface as a binary operator, which returns a logical vector indicating whether there is a match or not for each split in its left operand.

Usage

```
## S4 method for signature 'Splits,Splits'
match(x, table, nomatch = NA_integer_, incomparables = NULL)

match(x, table, nomatch = NA_integer_, incomparables = NULL)
```

```
## S4 method for signature 'Splits,Splits'
x %in% table

FirstMatchingSplit(x, table, nomatch, return = c("x", "table", "both"))
```

Arguments

x, table	Splits objects
nomatch	Integer value that will be used in place of NA in the case where no match is found.
incomparables	Ignored. (Included for consistency with generic.)
return	Which index to return: in x, in table, or both

Value

match() returns an integer vector specifying the position in table that matches each element in x, or nomatch if no match is found.

FirstMatchingSplit() returns an integer (or length-2 integer if return = "both") specifying the first split in x to have a match in table (return = "x"), or the index of that match (return = "table"). nomatch (default 0) is returned in the absence of a match.

See Also

Corresponding base functions are documented in match().

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipLabels(), TipsInSplits(), xor()

Examples

```
splits1 <- as.Splits(BalancedTree(7))
splits2 <- as.Splits(PectinateTree(7))

match(splits1, splits2)
```

MatchEdges *Match nodes and edges between trees*

Description

MatchNodes() and MatchEdges() matches nodes or edges in one tree to entries in the second that denote a clade with identical tip labels.

Usage

```
MatchEdges(x, table, nomatch = NA_integer_)

MatchNodes(x, table, nomatch = NA_integer_, tips = FALSE)
```

Arguments

x	Tree whose nodes are to be matched.
table	Tree containing nodes to be matched against.
nomatch	Integer value that will be used in place of NA in the case where no match is found.
tips	Logical specifying whether to return matches for tips; unless TRUE, only the matches for internal nodes will be returned.

Details

The current implementation is potentially inefficient. Please contact the maintainer to request a more efficient implementation if this function is proving a bottleneck.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Other tree properties: Cherries(), ConsensusWithout(), EdgeRatio(), LongBranch(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

Examples

```
MatchNodes(BalancedTree(8), RootTree(BalancedTree(8)))
```

MatchStrings *Check for mismatch between character vectors*

Description

Checks that entries in one character vector occur in another, suggesting corrections for mismatched elements.

Usage

```
MatchStrings(x, table, Fail = stop, max.distance = 0.5, ...)
```

Arguments

x, table	Character vectors, in which all elements of x are expected to occur in table.
Fail	Function to call if a mismatch is found.
max.distance, ...	Arguments to agrep(), used to propose possible matches to the user.

Value

MatchStrings() returns the elements of x that occur in table.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other string parsing functions: EndSentence(), MorphoBankDecode(), RightmostCharacter(), Unquote()

Examples

```
tree <- BalancedTree(8)
MatchStrings(c("t1", "tip2", "t3"), TipLabels(tree), Fail = message)
```

MatrixToPhyDat *Convert between matrices and* phyDat *objects*

Description

MatrixToPhyDat() converts a matrix of tokens to a phyDat object; PhyDatToMatrix() converts a phyDat object to a matrix of tokens.

Usage

```
MatrixToPhyDat(tokens, tipLabels = rownames(tokens))

PhyDatToMatrix(
  dataset,
  ambigNA = FALSE,
  inappNA = ambigNA,
  parentheses = c("{", "}"),
  sep = ""
)
```

Arguments

tokens	Matrix of tokens, possibly created with ReadCharacters() or ReadTntCharacters(). Row names should correspond to leaf labels; column names may optionally correspond to character labels.
tipLabels	Optionally, an object providing labels for leaves, via TipLabels(); will override rownames(tokens).
dataset	A dataset of class phyDat.

ambigNA, inappNA
: Logical specifying whether to denote ambiguous / inapplicable characters as NA values.

parentheses
: Character vector specifying style of parentheses with which to enclose ambiguous characters. c("[", "]") or "[]" will render [01]. NULL will use the token specified in the phyDat object; but beware that this will be treated as a distinct (non-ambiguous) token if re-encoding with PhyDatToMatrix().

sep
: Character with which to separate ambiguous tokens, e.g. ',' will render [0,1].

Value

MatrixToPhyDat() returns an object of class phyDat.

PhyDatToMatrix() returns a matrix corresponding to the uncompressed character states within a phyDat object.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other phylogenetic matrix conversion functions: Decompose(), Reweight(), StringToPhyDat()

Examples

```
tokens <- matrix(c(0, 0, "0", 0, 0,
                   0, 0, "1", 0, 1,
                   0, 0, "1", 0, 1,
                   0, 0, "2", 0, 1,
                   1, 1, "-", 1, 0,
                   1, 1, "2", 1, "{01}"),
                   nrow = 6, ncol = 5, byrow = TRUE,
                   dimnames = list(
                     paste0("Taxon_", LETTERS[1:6]),
                     paste0("Char_", 1:5)))

MatrixToPhyDat(tokens)
data("Lobo", package = "TreeTools")
head(PhyDatToMatrix(Lobo.phy)[, 91:93])
```

MorphoBankDecode *Decode MorphoBank text*

Description

Converts strings from MorphoBank notes into a Latex-compatible format.

Usage

```
MorphoBankDecode(string)
```

Arguments

string	String to process

Value

MorphoBankDecode() returns a string with new lines and punctuation reformatted.

Author(s)

Martin R. Smith

See Also

Other string parsing functions: EndSentence(), MatchStrings(), RightmostCharacter(), Unquote()

MRCA *Most recent common ancestor*

Description

MRCA() calculates the last common ancestor of specified nodes.

Usage

```
MRCA(x1, x2, ancestors)
```

Arguments

x1, x2	Integer specifying index of leaves or nodes whose most recent common ancestor should be found.
ancestors	List of ancestors for each node in a tree. Perhaps produced by ListAncestors().

Details

MRCA() requires that node values within a tree increase away from the root, which will be true of trees listed in Preorder. No warnings will be given if trees do not fulfil this requirement.

Value

MRCA() returns an integer specifying the node number of the last common ancestor of x1 and x2.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- BalancedTree(7)

# Verify that node numbering increases away from root
plot(tree)
nodelabels()

# ListAncestors expects a tree in Preorder
tree <- Preorder(tree)
edge <- tree$edge
ancestors <- ListAncestors(edge[, 1], edge[, 2])
MRCA(1, 4, ancestors)

# If a tree must be in postorder, use:
tree <- Postorder(tree)
edge <- tree$edge
ancestors <- lapply(seq_len(max(edge)), ListAncestors,
                    parent = edge[, 1], child = edge[, 2])
```

MSTEdges *Minimum spanning tree*

Description

Calculate or plot the minimum spanning tree (Gower and Ross 1969) of a distance matrix.

Usage

```
MSTEdges(distances, plot = FALSE, x = NULL, y = NULL, ...)

MSTLength(distances, mst = NULL)
```

Arguments

distances	Either a matrix that can be interpreted as a distance matrix, or an object of class dist.
plot	Logical specifying whether to add the minimum spanning tree to an existing plot.
x, y	Numeric vectors specifying the X and Y coordinates of each element in distances. Necessary only if plot = TRUE.
...	Additional parameters to send to [lines()].

mst — Optional parameter specifying the minimum spanning tree in the format returned by MSTEdges(); if NULL, calculated from distances.

Value

MSTEdges() returns a matrix in which each row corresponds to an edge of the minimum spanning tree, listed in non-decreasing order of length. The two columns contain the indices of the entries in distances that each edge connects, with the lower value listed first.

MSTLength() returns the length of the minimum spanning tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Gower JC, Ross GJS (1969). "Minimum spanning trees and single linkage cluster analysis." *Journal of the Royal Statistical Society. Series C (Applied Statistics)*, **18**(1), 54–64. doi:10.2307/2346439.

See Also

Slow implementation returning the association matrix of the minimum spanning tree: ape::mst().

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
# Corners of an almost-regular octahedron
points <- matrix(c(0, 0, 2, 2, 1.1, 1,
                   0, 2, 0, 2, 1, 1.1,
                   0, 0, 0, 0, 1, -1), 6)
distances <- dist(points)
mst <- MSTEdges(distances)
MSTLength(distances, mst)
plot(points[, 1:2], ann = FALSE, asp = 1)
MSTEdges(distances, TRUE, x = points[, 1], y = points[, 2], lwd = 2)
```

N1Spr *Number of trees one SPR step away*

Description

N1Spr() calculates the number of trees one subtree prune-and-regraft operation away from a binary input tree using the formula given by Allen and Steel (2001); IC1Spr() calculates the information content of trees at this distance: i.e. the entropy corresponding to the proportion of all possible *n*-tip trees whose SPR distance is at most one from a specified tree.

Usage

```
N1Spr(n)

IC1Spr(n)
```

Arguments

n	Integer vector specifying the number of tips in a tree.

Value

`N1Spr()` returns an integer vector denoting the number of trees one SPR rearrangement away from the input tree..

`IC1Spr()` returns an numeric vector giving the phylogenetic information content of trees 0 or 1 SPR rearrangement from an *n*-leaf tree, in bits.

References

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

Examples

```
N1Spr(4:6)
IC1Spr(5)
```

NDescendants *Count descendants for each node in a tree*

Description

`NDescendants()` counts the number of nodes (including leaves) directly descended from each node in a tree.

Usage

```
NDescendants(tree)
```

Arguments

tree	A tree of class phylo.

Value

`NDescendants()` returns an integer listing the number of direct descendants (leaves or internal nodes) for each node in a tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NodeDepth(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- CollapseNode(BalancedTree(8), 12:15)
NDescendants(tree)
plot(tree)
nodelabels(NDescendants(tree))
```

NewickTree *Write Newick Tree*

Description

NewickTree() encodes a tree as a Newick-format string. This differs from write.tree() in the encoding of spaces as spaces, rather than underscores.

Usage

```
NewickTree(tree)
```

Arguments

tree	A tree of class phylo.

Value

NewickTree() returns a character string denoting tree in Newick format.

See Also

Use tip numbers, rather than leaf labels: as.Newick

Examples

```
NewickTree(BalancedTree(LETTERS[4:9]))
```

NJTree *Generate a neighbour joining tree*

Description

NJTree() generates a rooted neighbour joining tree from a phylogenetic dataset.

Usage

```
NJTree(dataset, edgeLengths = FALSE, ratio = TRUE, ambig = "mean")
```

Arguments

dataset	A phylogenetic data matrix of **phangorn** class phyDat, whose names correspond to the labels of any accompanying tree.
edgeLengths	Logical specifying whether to include edge lengths.
ambig, ratio	Settings of ambig and ratio to be used when computing Hamming() distances between sequences.

Value

NJTree returns an object of class phylo.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree generation functions: ConstrainedNJ(), GenerateTree, TreeNumber, TrivialTree

Examples

```
data("Lobo")
NJTree(Lobo.phy)
```

NodeDepth *Distance of each node from tree exterior*

Description

NodeDepth() evaluates how "deep" each node is within a tree.

Usage

```
NodeDepth(x, shortest = FALSE, includeTips = TRUE)
```

Arguments

x	A tree of class phylo, its $edge property, or a list thereof.
shortest	Logical specifying whether to calculate the length of the shortest away-from-root path to a leaf. If FALSE, the length of the longest such route will be returned.
includeTips	Logical specifying whether to include leaves (each of depth zero) in return value.

Details

For a rooted tree, the depth of a node is the minimum (if shortest = TRUE) or maximum (shortest = FALSE) number of edges that must be traversed, moving away from the root, to reach a leaf.

Unrooted trees are treated as if a root node occurs in the "middle" of the tree, meaning the position that will minimise the maximum node depth.

Value

NodeDepth() returns an integer vector specifying the depth of each external and internal node in x.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

ape::node.depth returns the number of tips descended from a node.

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeNumbers(), NodeOrder(), RootNode()

Examples

```
tree <- CollapseNode(BalancedTree(10), c(12:13, 19))
plot(tree)
nodelabels(NodeDepth(tree, includeTips = FALSE))
```

NodeNumbers — *Numeric index of each node in a tree* NodeNumbers() *returns a sequence corresponding to the nodes in a tree*

Description

Numeric index of each node in a tree `NodeNumbers()` returns a sequence corresponding to the nodes in a tree

Usage

```
NodeNumbers(tree, tips = FALSE)
```

Arguments

`tree`	A tree of class `phylo`.
`tips`	Logical specifying whether to also include the indices of leaves.

Value

`NodeNumbers()` returns an integer vector corresponding to the indices of nodes within a tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: `Cherries()`, `ConsensusWithout()`, `EdgeRatio()`, `LongBranch()`, `MatchEdges()`, `NSplits()`, `NTip()`, `PathLengths()`, `SplitsInBinaryTree()`, `TipLabels()`, `TreeIsRooted()`, `Treeness()`

Other tree navigation: `AncestorEdge()`, `CladeSizes()`, `DescendantEdges()`, `EdgeAncestry()`, `EdgeDistances()`, `ListAncestors()`, `MRCA()`, `MatchEdges()`, `NDescendants()`, `NodeDepth()`, `NodeOrder()`, `RootNode()`

NodeOrder — *Number of edges incident to each node in a tree*

Description

`NodeOrder()` calculates the order of each node: the number of edges incident to it in a tree. This value includes the root edge in rooted trees.

Usage

```
NodeOrder(x, includeAncestor = TRUE, internalOnly = FALSE)
```

Arguments

x	A tree of class phylo, its $edge property, or a list thereof.
includeAncestor	Logical specifying whether to count edge leading to ancestral node in calculation of order.
internalOnly	Logical specifying whether to restrict to results to internal nodes, i.e. to omit leaves. Irrelevant if includeAncestor = FALSE.

Value

NodeOrder() returns an integer listing the order of each node; entries are named with the number of each node.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), RootNode()

Examples

```
tree <- CollapseNode(BalancedTree(8), 12:15)
NodeOrder(tree)
plot(tree)
nodelabels(NodeOrder(tree, internalOnly = TRUE))
```

NPartitionPairs *Distributions of tips consistent with a partition pair*

Description

NPartitionPairs() calculates the number of terminal arrangements matching a specified configuration of two splits.

Usage

```
NPartitionPairs(configuration)
```

Arguments

configuration	Integer vector of length four specifying the number of terminals that occur in both (1) splits A1 and A2; (2) splits A1 and B2; (3) splits B1 and A2; (4) splits B1 and B2.

Details

Consider splits that divide eight terminals, labelled A to H.

Bipartition 1:	ABCD:EFGH	A1 = ABCD	B1 = EFGH
Bipartition 2:	ABE:CDFGH	A2 = ABE	B2 = CDFGH

This can be represented by an association matrix:

	A2	*B2*
A1	AB	C
B1	E	FGH

The cells in this matrix contain 2, 1, 1 and 3 terminals respectively; this four-element vector (`c(2, 1, 1, 3)`) is the `configuration` implied by this pair of bipartition splits.

Value

The number of ways to distribute `sum(configuration)` taxa according to the specified pattern.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

Examples

```
NPartitionPairs(c(2, 1, 1, 3))
```

`NRooted` *Number of trees*

Description

These functions return the number of rooted or unrooted binary trees consistent with a given pattern of splits.

Usage

```
NRooted(tips)

NUnrooted(tips)

NRooted64(tips)

NUnrooted64(tips)

LnUnrooted(tips)
```

```
LnUnrooted.int(tips)

Log2Unrooted(tips)

Log2Unrooted.int(tips)

LnRooted(tips)

LnRooted.int(tips)

Log2Rooted(tips)

Log2Rooted.int(tips)

LnUnrootedSplits(...)

Log2UnrootedSplits(...)

NUnrootedSplits(...)

LnUnrootedMult(...)

Log2UnrootedMult(...)

NUnrootedMult(...)
```

Arguments

tips	Integer specifying the number of leaves.
...	Integer vector, or series of integers, listing the number of leaves in each split.

Details

Functions starting N return the number of rooted or unrooted trees. Replace this initial N with Ln for the natural logarithm of this number; or Log2 for its base 2 logarithm.

Calculations follow Cavalli-Sforza and Edwards (1967) and Carter et al. (1990), Theorem 2.

Functions

- NUnrooted(): Number of unrooted trees
- NRooted64(): Exact number of rooted trees as 64-bit integer (13 < nTip < 19)
- NUnrooted64(): Exact number of unrooted trees as 64-bit integer (14 < nTip < 20)
- LnUnrooted(): Log Number of unrooted trees
- LnUnrooted.int(): Log Number of unrooted trees (as integer)
- LnRooted(): Log Number of rooted trees
- LnRooted.int(): Log Number of rooted trees (as integer)

- `NUnrootedSplits()`: Number of unrooted trees consistent with a bipartition split.
- `NUnrootedMult()`: Number of unrooted trees consistent with a multi-partition split.

Author(s)

Martin R. Smith (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.

Cavalli-Sforza LL, Edwards AWF (1967). "Phylogenetic analysis: models and estimation procedures." *Evolution*, **21**(3), 550–570. ISSN 00143820. doi:10.1111/j.15585646.1967.tb03411.x.

See Also

Other tree information functions: `CladisticInfo()`, `TreesMatchingTree()`

Examples

```
NRooted(10)
NUnrooted(10)
LnRooted(10)
LnUnrooted(10)
Log2Unrooted(10)
# Number of trees consistent with a character whose states are
# 00000 11111 222
NUnrootedMult(c(5,5,3))

NUnrooted64(18)
LnUnrootedSplits(c(2,4))
LnUnrootedSplits(3, 3)
Log2UnrootedSplits(c(2,4))
Log2UnrootedSplits(3, 3)
NUnrootedSplits(c(2,4))
NUnrootedSplits(3, 3)
```

`nRootedShapes` *Number of rooted / unrooted tree shapes*

Description

`nRootedShapes` and `nUnrootedShapes` give the number of (un)rooted binary trees on *n* unlabelled leaves.

Usage

```
nRootedShapes

nUnrootedShapes
```

Format

An object of class `integer64` of length 55.

An object of class `integer64` of length 60.

Source

`nRootedShapes` corresponds to the Wedderburn-Etherington numbers, OEIS A001190

`nUnrootedShapes` is OEIS A000672

NSplits *Number of distinct splits*

Description

`NSplits()` counts the unique bipartition splits in a tree or object.

Usage

```
NSplits(x)

NPartitions(x)

## S3 method for class 'phylo'
NSplits(x)

## S3 method for class 'list'
NSplits(x)

## S3 method for class 'multiPhylo'
NSplits(x)

## S3 method for class 'Splits'
NSplits(x)

## S3 method for class 'numeric'
NSplits(x)

## S3 method for class '`NULL`'
NSplits(x)
```

```
## S3 method for class 'ClusterTable'
NSplits(x)

## S3 method for class 'character'
NSplits(x)
```

Arguments

x	A phylogenetic tree of class phylo; a list of such trees (of class list or multiPhylo); a Splits object; a vector of integers; or a character vector listing tips of a tree, or a character of length one specifying a tree in Newick format.

Value

NSplits() returns an integer specifying the number of bipartitions in the specified objects, or in a binary tree with x tips.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: Cherries(), ConsensusWithout(), EdgeRatio(), LongBranch(), MatchEdges(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TipLabels(), TreeIsRooted(), Treeness()

Other Splits operations: LabelSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipLabels(), TipsInSplits(), match,Splits,Splits-method, xor()

Examples

```
NSplits(8L)
NSplits(PectinateTree(8))
NSplits(as.Splits(BalancedTree(8)))
```

NTip *Number of leaves in a phylogenetic tree*

Description

NTip() extends ape::Ntip() to handle objects of class Splits and list, and edge matrices (equivalent to tree$edge).

Usage

```
NTip(phy)

## Default S3 method:
NTip(phy)

## S3 method for class 'Splits'
NTip(phy)

## S3 method for class 'list'
NTip(phy)

## S3 method for class 'phylo'
NTip(phy)

## S3 method for class 'multiPhylo'
NTip(phy)

## S3 method for class 'phyDat'
NTip(phy)

## S3 method for class 'matrix'
NTip(phy)
```

Arguments

phy	Object representing one or more phylogenetic trees.

Value

`NTip()` returns an integer specifying the number of tips in each object in phy.

See Also

Other tree properties: `Cherries()`, `ConsensusWithout()`, `EdgeRatio()`, `LongBranch()`, `MatchEdges()`, `NSplits()`, `NodeNumbers()`, `PathLengths()`, `SplitsInBinaryTree()`, `TipLabels()`, `TreeIsRooted()`, `Treeness()`

Other Splits operations: `LabelSplits()`, `NSplits()`, `PolarizeSplits()`, `SplitFrequency()`, `Splits`, `SplitsInBinaryTree()`, `TipLabels()`, `TipsInSplits()`, `match,Splits,Splits-method`, `xor()`

PairwiseDistances *Distances between each pair of trees*

Description

Distances between each pair of trees

Usage

```
PairwiseDistances(trees, Func, valueLength = 1L, ...)
```

Arguments

trees	List of trees of class phylo.
Func	Function returning a distance between two trees.
valueLength	Integer specifying expected length of the value returned by Func.
...	Additional arguments to Func.

Value

Matrix detailing distance between each pair of trees. Identical trees are assumed to have zero distance.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

Examples

```
trees <- list(BalancedTree(8), PectinateTree(8), StarTree(8))
TCIDiff <- function(tree1, tree2) {
  TotalCopheneticIndex(tree1) - TotalCopheneticIndex(tree2)
}
PairwiseDistances(trees, TCIDiff, 1)
TCIRange <- function(tree1, tree2) {
  range(TotalCopheneticIndex(tree1), TotalCopheneticIndex(tree2))
}
PairwiseDistances(trees, TCIRange, 2)
```

PathLengths *Calculate length of paths between each pair of vertices within tree*

Description

Given a weighted rooted tree tree, PathLengths() returns the distance from each vertex to each of its descendant vertices.

Usage

```
PathLengths(tree, fullMatrix = FALSE, use.na = TRUE)
```

Arguments

tree	Original tree of class phylo, in Preorder.
fullMatrix	Logical specifying return format; see "value" section‘.
use.na	Logical specifying whether to set non-existent paths to NA, or to leave uninitialized. Set to FALSE to maximize performance.

Value

If `fullMatrix = TRUE`, `PathLengths()` returns a square matrix in which entry `[i, j]` denotes the distance from internal node `i` to the descendant vertex `j`. Vertex pairs without a continuous directed path are denoted `NA` if `use.na` is `TRUE`. If `fullMatrix = FALSE`, `PathLengths()` returns a `data.frame` with three columns: `start` lists the deepest node in each path (i.e. that closest to the root); `end` lists the shallowest node (i.e. that closest to a leaf); `length` lists the total length of that path.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: `Cherries()`, `ConsensusWithout()`, `EdgeRatio()`, `LongBranch()`, `MatchEdges()`, `NSplits()`, `NTip()`, `NodeNumbers()`, `SplitsInBinaryTree()`, `TipLabels()`, `TreeIsRooted()`, `Treeness()`

Examples

```
tree <- rtree(6)
plot(tree)
add.scale.bar()
nodelabels()
tiplabels()
PathLengths(tree)
```

PolarizeSplits *Polarize splits on a single taxon*

Description

Polarize splits on a single taxon

Usage

```
PolarizeSplits(x, pole = 1L)
```

Arguments

`x`	Object that can be coerced into class `Splits`.
`pole`	Numeric, character or logical vector identifying tip that will polarize each split.

Value

`PolarizeSplits()` returns a `Splits` object in which `pole` is represented by a zero bit

See Also

Other Splits operations: LabelSplits(), NSplits(), NTip(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipLabels(), TipsInSplits(), match,Splits,Splits-method, xor()

`print.TreeNumber` *Print* `TreeNumber` *object*

Description

S3 method for objects of class `TreeNumber`.

Usage

```
## S3 method for class 'TreeNumber'
print(x, ...)
```

Arguments

`x`	Object of class `TreeNumber`.
`...`	Additional arguments for consistency with S3 method (unused).

See Also

Other 'TreeNumber' utilities: TreeNumber, is.TreeNumber()

`ReadCharacters` *Read phylogenetic characters from file*

Description

Parse a Nexus (Maddison et al. 1997) or TNT (Goloboff et al. 2008) file, reading character states and names.

Usage

```
ReadCharacters(filepath, character_num = NULL, encoding = "UTF8")

ReadTntCharacters(
  filepath,
  character_num = NULL,
  type = NULL,
  encoding = "UTF8"
)

ReadTNTCharacters(
```

```
  filepath,
  character_num = NULL,
  type = NULL,
  encoding = "UTF8"
)

ReadNotes(filepath, encoding = "UTF8")

ReadAsPhyDat(...)

ReadTntAsPhyDat(...)

ReadTNTAsPhyDat(...)

PhyDat(dataset)
```

Arguments

`filepath`	character string specifying location of file, or a connection to the file.
`character_num`	Index of character(s) to return. `NULL`, the default, returns all characters.
`encoding`	Character encoding of input file.
`type`	Character vector specifying categories of data to extract from file. Setting `type = c("num", "dna")` will return only characters following a `&[num]` or `&[dna]` tag in a TNT input file, listing `num` character blocks before `dna` characters. Leave as `NULL` (the default) to return all characters in their original sequence.
`...`	Parameters to pass to `Read[Tnt]Characters()`.
`dataset`	list of taxa and characters, in the format produced by `read.nexus.data()`: a list of sequences each made of a single character vector, and named with the taxon name.

Details

Tested with matrices downloaded from MorphoBank (O'Leary and Kaufman 2011), but should also work more widely; please report incompletely or incorrectly parsed files.

Matrices must contain only continuous or only discrete characters; maximum one matrix per file. Continuous characters will be read as strings (i.e. base type "character").

The encoding of an input file will be automatically determined by R. Errors pertaining to an `invalid multibyte string` or `string invalid at that locale` indicate that R has failed to detect the appropriate encoding. Either re-save the file in a supported encoding (`UTF-8` is a good choice) or specify the file encoding (which you can find by, for example, opening in Notepad++ and identifying the highlighted option in the "Encoding" menu) following the example below.

Value

`ReadCharacters()` and `ReadTNTCharacters()` return a matrix whose row names correspond to tip labels, and column names correspond to character labels, with the attribute `state.labels` listing

the state labels for each character; or a list of length one containing a character string explaining why the function call was unsuccessful.

`ReadAsPhyDat()` and `ReadTntAsPhyDat()` return a `phyDat` object.

`ReadNotes()` returns a list in which each entry corresponds to a single character, and itself contains a list of with two elements:

1. A single character object listing any notes associated with the character
2. A named character vector listing the notes associated with each taxon for that character, named with the names of each note-bearing taxon.

Functions

- `PhyDat()`: A convenient wrapper for **phangorn**'s `phyDat()`, which converts a **list** of morphological characters into a `phyDat` object. If your morphological characters are in the form of a **matrix**, perhaps because they have been read using `read.table()`, try `MatrixToPhyDat()` instead.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Goloboff PA, Farris JS, Nixon KC (2008). "TNT, a free program for phylogenetic analysis." *Cladistics*, **24**(5), 774–786.

Maddison DR, Swofford DL, Maddison WP (1997). "Nexus: an extensible file format for systematic information." *Systematic Biology*, **46**, 590–621. doi:10.1093/sysbio/46.4.590.

O'Leary MA, Kaufman S (2011). "MorphoBank: phylophenomics in the "cloud"." *Cladistics*, **27**(5), 529–537.

See Also

- Convert between matrices and `phyDat` objects: `MatrixToPhyDat()`
- Write characters to TNT-format file: `WriteTntCharacters()`

Examples

```
fileName <- paste0(system.file(package = "TreeTools"),
                   "/extdata/input/dataset.nex")
ReadCharacters(fileName)

fileName <- paste0(system.file(package = "TreeTools"),
                   "/extdata/tests/continuous.nex")

continuous <- ReadCharacters(fileName, encoding = "UTF8")

# To convert from strings to numbers:
at <- attributes(continuous)
```

```
continuous <- suppressWarnings(as.numeric(continuous))
attributes(continuous) <- at
continuous
```

`ReadMrBayesTrees` *Read posterior tree sample produced by MrBayes*

Description

Read posterior trees from 'MrBayes' output files, discarding burn-in generations.

Usage

```
ReadMrBayesTrees(filepath, n = NULL, burninFrac = NULL)

ReadMrBayes(filepath, n = NULL, burninFrac = NULL)

MrBayesTrees(filepath, n = NULL, burninFrac = NULL)
```

Arguments

`filepath`	character string specifying path to `.nex` input file used to initialize the MrBayes analysis, relative to the R working directory (visible with `getwd()`).
`n`	Integer specifying number of trees to sample from posterior.
`burninFrac`	Fraction of trees to discard from each run as burn-in. If `NULL` (the default), this will be read from the last `mcmc` or `mcmcp` command in `filepath`.

Details

`ReadMrBayesTrees()` samples trees from the posterior distributions computed using the Bayesian inference software 'MrBayes'

Value

`ReadMrBayesTrees()` returns a 'multiPhylo' object containing `n` trees sampled evenly from all runs generated by analysis of `filepath`, or `NULL` if no trees are found.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree import functions: `ReadTntTree()`

Examples

```
## Not run:  # Download will take a few seconds
  url <-
  "https://raw.githubusercontent.com/ms609/hyoliths/master/MrBayes/hyo.nex"
  trees <- ReadMrBayesTrees(url, n = 40)
  plot(Consensus(trees, p = 0.5))

## End(Not run)
```

`ReadTntTree` *Parse TNT Tree*

Description

Read a tree from TNT's parenthetical output.

Usage

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

TntText2Tree(treeText)

TNTText2Tree(treeText)
```

Arguments

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

Details

`ReadTntTree()` imports trees generated by the parsimony analysis program TNT into R, including node labels written with the `ttags` command. Tree files must have been saved by TNT in parenthetical notation, using the TNT command `tsave *`. Trees are easiest to load into R if taxa have been saved using their names (TNT command `taxname =`). In this case, the TNT `.tre` file contains tip labels and can be parsed directly. The downside is that the uncompressed `.tre` files will have a larger file size.

ReadTntTree() can also read .tre files in which taxa have been saved using their numbers (taxname -). Such files contain a hard-coded link to the matrix file that was used to generate the trees, in the first line of the .tre file. This poses problems for portability: if the matrix file is moved, or the .tre file is accessed on another computer, the taxon names may be lost. As such, it is important to check that the matrix file exists in the expected location – if it does not, either use the relativePath argument to point to its new location, or specify tipLabels to manually specify the tip labels.

TntText2Tree() converts text representation of a tree in TNT to an object of class phylo.

Value

ReadTntTree() returns a tree of class phylo in TNT order, corresponding to the tree in filepath, or NULL if no trees are found.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree import functions: ReadMrBayesTrees()

Examples

```
# In the examples below, TNT has read a matrix from
# "c:/TreeTools/input/dataset.nex"
# The results of an analysis were written to
# "c:/TreeTools/output/results1.tnt"
#
# results1.tnt will contain a hard-coded reference to
# "c:/TreeTools/input/dataset.nex".

# On the original machine (but not elsewhere), it would be possible to read
# this hard-coded reference from results.tnt:
# ReadTntTree("output/results1.tnt")

# These datasets are provided with the "TreeTools" package, which will
# probably not be located at c:/TreeTools on your machine:

oldWD <- getwd() # Remember the current working directory
setwd(system.file(package = "TreeTools"))

# If taxon names were saved within the file (using `taxname=` in TNT),
# then our job is easy:
ReadTntTree("extdata/output/named.tre")

# But if taxa were compressed to numbers (using `taxname-`), we need to
# look up the original matrix in order to dereference the tip names.
#
# We need to extract the relevant file path from the end of the
# hard-coded path in the original file.
#
```

```
# We are interested in the last two elements of
# c:/TreeTools/input/dataset.nex
#                2      1
#
# "." means "relative to the current directory"
ReadTntTree("extdata/output/numbered.tre", "./extdata", 2)

# If working in a lower subdirectory
setwd("./extdata/otherfolder")

# then it will be necessary to navigate up the directory path with "..":
ReadTntTree("../output/numbered.tre", "..", 2)


setwd(oldWD) # Restore original working directory

TNTText2Tree("(A (B (C (D E ))));")
```

`Renumber` *Renumber a tree's nodes and tips*

Description

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

Usage

```
Renumber(tree)
```

Arguments

`tree`	A tree of class `phylo`.

Details

The **ape** class `phylo` is not formally defined, but expects trees' internal representation to conform to certain principles: for example, nodes should be numbered sequentially, with values increasing away from the root.

`Renumber()` attempts to reformat any tree into a representation that will not cause **ape** functions to produce unwanted results or to crash R.

Value

`Renumber()` returns a tree of class `phylo`, numbered in a Cladewise fashion consistent with the expectations of **ape** functions.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Preorder() provides a faster and simpler alternative, but also rotates nodes.

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
tree <- RandomTree(letters[1:10])
Renumber(tree)
```

RenumberTips *Renumber a tree's tips*

Description

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

Usage

```
RenumberTips(tree, tipOrder)

## S3 method for class 'phylo'
RenumberTips(tree, tipOrder)

## S3 method for class 'Splits'
RenumberTips(tree, tipOrder)

## S3 method for class 'multiPhylo'
RenumberTips(tree, tipOrder)

## S3 method for class 'list'
RenumberTips(tree, tipOrder)

## S3 method for class '`NULL`'
RenumberTips(tree, tipOrder)
```

Arguments

tree	A tree of class phylo.
tipOrder	A character vector containing the values of tree[["tip.label"]] in the desired sort order, an object (perhaps of class phylo or Splits) with tip labels, or a numeric specifying the desired order.

Value

`RenumberTips()` returns `tree`, with the tips' internal representation numbered to match `tipOrder`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: `AddTip()`, `CollapseNode()`, `ConsensusWithout()`, `DropTip()`, `ImposeConstraint()`, `KeptPaths()`, `KeptVerts()`, `LeafLabelInterchange()`, `MakeTreeBinary()`, `Renumber()`, `RenumberTree()`, `RootTree()`, `SortTree()`, `Subtree()`, `TipTimedTree()`, `TrivialTree`

Examples

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

Reweight *Reweight phylogenetic characters*

Description

`Reweight()` allows the weights of specific characters in phylogenetic datasets to be arbitrarily adjusted.

Usage

```
Reweight(dataset, weights)
```

Arguments

`dataset`	A phylogenetic data matrix of **phangorn** class `phyDat`, or as a matrix in the format produced by `PhyDatToMatrix()`.
`weights`	Unnamed integer vector specifying desired weight of each character in turn; or named integer vector specifying weights of each character; unnamed entries will be assigned weight 1.

Details

This functionality should be employed with care. The underlying principle of parsimony is that all evolutionary steps are equivalent. Setting different weights to different characters is at odds with that principle, so analysis of a re-weighted matrix using a parsimony-based framework is arguably no longer parsimony analysis; on the most permissive view, the criteria used to determine a weighting scheme will always be arbitrary.

It can be useful to relax the criterion that all evolutionary steps are equivalent – for example, implied weighting (Goloboff 1997) typically recovers better trees than equal-weights parsimony (Smith 2019). This said, assigning different weights to different characters tacitly imposes a model of evolution that differs from that implicit in equal-weights parsimony. Whereas probabilistic models can be evaluated by various methods (e.g. fit, marginal likelihood, posterior predictive power), there are no principled methods of comparing different models under a parsimony framework.

As such, `Reweight()` is likely to be useful for a narrow set of uses. Examples may include:

- informal robustness testing, to explore whether certain characters are more or less influential on the resulting tree;
- Imposing constraints on a dataset, by adding each constraint as a column in a dataset whose weight exceeds the total amount of data.

Value

`Reweight()` returns `dataset` after adjusting the weights of the specified characters. For a matrix, this is attained by repeating each column the `weights` times. For a `phyDat` object, the "weight" attribute will be modified.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Goloboff PA (1997). "Self-Weighted Optimization: Tree Searches and Character State Reconstructions under Implied Transformation Costs." *Cladistics*, **13**(3), 225–245. doi:10.1111/j.1096-0031.1997.tb00317.x.

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

Other phylogenetic matrix conversion functions: `Decompose()`, `MatrixToPhyDat()`, `StringToPhyDat()`

Examples

```
mat <- rbind(a = c(0, 2, 0), b = c(0, 2, 0), c = c(1, 3, 0), d = c(1, 3, 0))
dat <- MatrixToPhyDat(mat)

 # Set character 1 to weight 1, character 2 to weight 2; omit character 3
Reweight(mat, c(1, 2, 0))
# Equivalently:
Reweight(dat, c("3" = 0, "2" = 2))
```

RightmostCharacter *Rightmost character of string*

Description

RightmostCharacter() is a convenience function that returns the final character of a string.

Usage

```
RightmostCharacter(string, len = nchar(string))
```

Arguments

string	Character string.
len	(Optional) Integer specifying number of characters in string.

Value

RightmostCharacter() returns the rightmost character of a string.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other string parsing functions: EndSentence(), MatchStrings(), MorphoBankDecode(), Unquote()

Examples

```
RightmostCharacter("Hello, World!")
```

RoguePlot *Visualize position of rogue taxa*

Description

Plots a consensus of trees with a rogue taxon omitted, with edges coloured according to the proportion of trees in which the taxon attaches to that edge, after Klopfstein and Spasojevic (2019).

Usage

```
RoguePlot(
  trees,
  tip,
  p = 1,
  plot = TRUE,
  Palette = colorRampPalette(c(par("fg"), "#009E73"), space = "Lab"),
  nullCol = rgb(colorRamp(unlist(par(c("fg", "bg"))), space = "Lab")(0.8)/255),
  edgeLength = NULL,
  thin = par("lwd"),
  fat = thin + 1L,
  outgroupTips,
  sort = FALSE,
  legend = "none",
  legend.inset = 0,
  ...
)
```

Arguments

`trees`	List or `multiPhylo` object containing phylogenetic trees of class `phylo` to be summarized.
`tip`	Numeric or character identifying rogue leaf, in format accepted by `DropTip()`.
`p`	A numeric value between 0.5 and 1 giving the proportion for a clade to be represented in the consensus tree (see `Consensus()`).
`plot`	Logical specifying whether to plot the tree.
`Palette`	Function that takes a parameter `n` and generates a colour palette with `n` entries.
`nullCol`	Colour to paint regions of the tree on which the rogue is never found.
`edgeLength`	Numeric specifying edge lengths of consensus tree; `NULL` aligns tips by scaling edges proportional to clade size; `1` sets all edges to unit length.
`thin`, `fat`	Numeric specifying width to plot edges if the rogue tip never / sometimes does attach to them.
`outgroupTips`	Vector of type character, integer or logical, specifying the names or indices of the tips to include in the outgroup. If `outgroupTips` is a of type character, and a tree contains multiple tips with a matching label, the first will be used.
`sort`	Logical specifying whether to sort consensus tree using `SortTree()`.
`legend`	Character vector specifying position of legend (e.g. `"bottomleft"`), or `"none"` to suppress legend. For fine-grained control of legend, use `PlotTools::SpectrumLegend()`.
`legend.inset`	Numeric specifying fraction of plot width / height by which the legend's position should be inset.
`...`	Additional parameters to `plot.phylo()`.

Details

Rogue taxa can be identified using the package **Rogue** (Smith 2022).

Value

`RoguePlot()` invisibly returns a list whose elements are:

- `cons`: The reduced consensus tree, sorted if `sort = TRUE`, otherwise in preorder;
- `onEdge`: a vector of integers specifying the number of trees in `trees` in which the rogue leaf is attached to each edge in turn of the consensus tree;
- `atNode`: a vector of integers specifying the number of trees in `trees` in which the rogue leaf is attached to an edge collapsed into each node of the consensus tree.
- `legendLabels`: A character vector suggesting labels for a plot legend; suitable for `PlotTools::SpectrumLegend(lege = x$legendLabels)`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Klopfstein S, Spasojevic T (2019). "Illustrating phylogenetic placement of fossils using RoguePlots: An example from ichneumonid parasitoid wasps (Hymenoptera, Ichneumonidae) and an extensive morphological matrix." *PLOS ONE*, **14**(4), e0212942. doi:10.1371/journal.pone.0212942.

Smith MR (2022). "Using information theory to detect rogue taxa and improve consensus trees." *Systematic Biology*, **71**(5), 986–1008. doi:10.1093/sysbio/syab099.

See Also

Other consensus tree functions: `Consensus()`, `ConsensusWithout()`

Examples

```
trees <- list(read.tree(text = "(a, (b, (c, (rogue, (d, (e, f))))));"),
              read.tree(text = "(a, (b, (c, (rogue, (d, (e, f))))));"),
              read.tree(text = "(a, (b, (c, (rogue, (d, (e, f))))));"),
              read.tree(text = "(a, (b, (c, (rogue, (d, (e, f))))));"),
              read.tree(text = "(rogue, (a, (b, (c, (d, (e, f))))));"),
              read.tree(text = "((rogue, a), (b, (c, (d, (e, f)))));"),
              read.tree(text = "(a, (b, ((c, d), (rogue, (e, f)))));"),
              read.tree(text = "(a, (b, ((c, (rogue, d)), (e, f))));"),
              read.tree(text = "(a, (b, (c, (d, (rogue, (e, f))))));"))
plotted <- RoguePlot(trees, "rogue", legend = "topleft", legend.inset = 0.02)
PlotTools::SpectrumLegend(
  "bottomleft",
  palette = colorRampPalette(c(par("fg"), "#009E73"), space = "Lab")(100),
  legend = plotted$legendLabels,
  cex = 0.4
)
```

RootNode *Which node is a tree's root?*

Description

RootNode() identifies the root node of a (rooted or unrooted) phylogenetic tree. Unrooted trees are represented internally by a rooted tree with a polytomy at the root.

Usage

```
RootNode(x)
```

Arguments

x	A tree of class phylo, or its edge matrix; or a list or multiPhylo object containing multiple trees.

Value

RootNode() returns an integer denoting the root node for each tree. Badly conformed trees trigger an error.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Test whether a tree is rooted: TreeIsRooted()

phangorn::getRoot()

Other tree navigation: AncestorEdge(), CladeSizes(), DescendantEdges(), EdgeAncestry(), EdgeDistances(), ListAncestors(), MRCA(), MatchEdges(), NDescendants(), NodeDepth(), NodeNumbers(), NodeOrder()

Examples

```
RootNode(BalancedTree(8))
RootNode(UnrootTree(BalancedTree(8)))
```

RootTree *Root or unroot a phylogenetic tree*

Description

RootTree() roots a tree on the smallest clade containing the specified tips; RootOnNode() roots a tree on a specified internal node; UnrootTree() collapses a root node, without the undefined behaviour encountered when using ape::unroot() on trees in preorder.

Usage

```
RootTree(tree, outgroupTips, fallback = NULL)

RootOnNode(tree, node, resolveRoot = FALSE)

UnrootTree(tree)
```

Arguments

tree	A tree of class phylo, or a list of trees of class list or multiPhylo.
outgroupTips	Vector of type character, integer or logical, specifying the names or indices of the tips to include in the outgroup. If outgroupTips is a of type character, and a tree contains multiple tips with a matching label, the first will be used.
fallback	Vector corresponding to outgroupTips determining behaviour when outgroupTips do not root a tree. Where the smallest clade that contains outgroupTips includes all taxa, RootTree() will not change the topology of a tree. If fallback = NULL, RootTree() will return tree. Otherwise, taxa will be excluded from outgroupTips in the sequence specified (fallback[1] first) by until the clade containing all outgroup tips is smaller than tree.
node	Integer specifying node (internal or tip) to set as the root.
resolveRoot	Logical specifying whether to resolve the root node.

Value

RootTree() returns a tree of class phylo, rooted on the smallest clade that contains the specified tips, with edges and nodes numbered in preorder. Node labels are not retained.

RootOnNode() returns a tree of class phylo, rooted on the requested node and ordered in Preorder.

UnrootTree() returns tree, in preorder, having collapsed the first child of the root node in each tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

- ape::root()

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), SortTree(), Subtree(), TipTimedTree(), TrivialTree

Examples

```
tree <- PectinateTree(8)
plot(tree)
ape::nodelabels()

plot(RootTree(tree, c("t6", "t7")))

plot(RootOnNode(tree, 12))
plot(RootOnNode(tree, 2))
```

SampleOne *Select element at random*

Description

SampleOne() is a fast alternative to sample() that avoids some checks.

Usage

```
SampleOne(x, len = length(x))
```

Arguments

x	A vector to sample.
len	(Optional) Integer specifying length of x.

Value

SampleOne() returns a length one vector, randomly sampled from x.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
SampleOne(9:10)
SampleOne(letters[1:4])
```

---

sapply64 *Apply a function that returns 64-bit integers over a list or vector*

Description

Wrappers for members of the `lapply()` family intended for use when a function `FUN` returns a vector of `integer64` objects. `vapply()`, `sapply()` or `replicate()` drop the `integer64` class, resulting in a vector of numerics that require conversion back to 64-bit integers. These functions restore the missing `class` attribute.

Usage

```
sapply64(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)

vapply64(X, FUN, FUN.LEN = 1, ...)

replicate64(n, expr, simplify = "array")
```

Arguments

`X`	a vector (atomic or list) or an `expression` object. Other objects (including classed objects) will be coerced by `base::as.list`.
`FUN`	the function to be applied to each element of `X`: see 'Details'. In the case of functions like `+`, `%*%`, the function name must be backquoted or quoted.
`...`	optional arguments to `FUN`.
`simplify`	logical or character string; should the result be simplified to a vector, matrix or higher dimensional array if possible? For `sapply` it must be named and not abbreviated. The default value, `TRUE`, returns a vector or matrix if appropriate, whereas if `simplify = "array"` the result may be an `array` of "rank" (=`length(dim(.))`) one higher than the result of `FUN(X[[i]])`.
`USE.NAMES`	logical; if `TRUE` and if `X` is character, use `X` as `names` for the result unless it had names already. Since this argument follows `...` its name cannot be abbreviated.
`FUN.LEN`	Integer specifying the length of the output of `FUN`.
`n`	integer: the number of replications.
`expr`	the expression (a language object, usually a call) to evaluate repeatedly.

Details

For details of the underlying functions, see `base::lapply()`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

integer64()

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sort.multiPhylo()

Examples

```
sapply64(as.phylo(1:6, 6), as.TreeNumber)
vapply64(as.phylo(1:6, 6), as.TreeNumber, 1)
set.seed(0)
replicate64(6, as.TreeNumber(RandomTree(6)))
```

---

sort.multiPhylo *Sort a list of phylogenetic trees*

Description

Trees are sorted by their mixed base representation, treating their leaves in the order of their labels (i.e. alphabetically, if leaves are labelled with text).

Usage

```
## S3 method for class 'multiPhylo'
sort(x, decreasing = FALSE, na.last = NA, ...)

## S3 method for class 'phylo'
e1 == e2

## S3 method for class 'phylo'
e1 < e2

## S3 method for class 'phylo'
e1 > e2

## S3 method for class 'MixedBase'
e1 == e2

## S3 method for class 'MixedBase'
e1 < e2

## S3 method for class 'MixedBase'
e1 > e2
```

Arguments

x, decreasing, na.last, ...	As in sort().
e1, e2	Objects to be compared.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64()

Examples

```
sort(as.phylo(5:0, 7))
```

SortTree *Sort tree*

Description

SortTree() sorts each node into a consistent order, so that node rotation does not obscure similarities between similar trees.

Usage

```
SortTree(tree, how = "cladesize", order = TipLabels(tree))

## S3 method for class 'phylo'
SortTree(tree, how = "cladesize", order = TipLabels(tree))

## S3 method for class 'list'
SortTree(tree, how = "cladesize", order = TipLabels(tree[[1]]))

## S3 method for class 'multiPhylo'
SortTree(tree, how = "cladesize", order = TipLabels(tree[[1]]))
```

Arguments

tree	One or more trees of class phylo, optionally as a list or a multiPhylo object.
how	Character vector specifying sort method: "Cladesize" rotates each node such that the larger clade is first, thus appearing lower when plotted; "TipLabels" rotates nodes such that labels listed sooner in order are listed first, and thus plot lower.
order	Character vector listing tip labels in sequence they should appear on tree. Clades containing a taxon earlier in this list will be listed sooner and thus plot lower on a tree. Taxa not listed in order will be treated as if they were last in the list.

Details

At each node, clades will be listed in `tree[["edge"]]` in decreasing size order.

Clades that contain the same number of leaves are sorted in decreasing order of minimum leaf number, so (2, 3) will occur before (1, 4).

As trees are plotted from "bottom up", the largest clades will "sink" to the bottom of a plotted tree.

Value

`SortTree()` returns tree in the format of `tree`, with each node in each tree sorted

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

`Preorder()` also rearranges trees into a consistent shape, based on the index of leaves.

`sort.multiPhylo()` sorts a list of trees stored as a `multiPhylo` object.

Other tree manipulation: `AddTip()`, `CollapseNode()`, `ConsensusWithout()`, `DropTip()`, `ImposeConstraint()`, `KeptPaths()`, `KeptVerts()`, `LeafLabelInterchange()`, `MakeTreeBinary()`, `Renumber()`, `RenumberTips()`, `RenumberTree()`, `RootTree()`, `Subtree()`, `TipTimedTree()`, `TrivialTree`

Examples

```
messyTree <- as.phylo(10, 6)
plot(messyTree)

sorted <- SortTree(messyTree)
plot(sorted)
ape::nodelabels()
ape::edgelabels()
ape::tiplabels(adj = c(2, 1/3))

plot(SortTree(messyTree, how = "tip"))
```

SplitConsistent *Identify consistent / conflicting splits*

Description

`SplitConsistent()` and `SplitConflict()` determine whether a series of splits `haystack` are consistent with or contradict the focal split `needle`.

Usage

```
SplitConsistent(needle, haystack)

SplitConflicts(needle, haystack)
```

Arguments

needle	Splits object containing the single split to evaluate
haystack	Splits object, or list thereof, containing the splits to compare against needle.

Value

SplitConsistent() returns a list of logical vectors. Each list item corresponds to an entry in haystack, reporting whether each split is consistent with (TRUE) or in conflict with (FALSE) needle. SplitConflicts() returns the inverse.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other split manipulation functions: DropTip(), Subsplit(), TrivialSplits()

Examples

```
splits1 <- as.Splits(BalancedTree(8))
splits2 <- as.Splits(PectinateTree(8))
summary(splits1[[4]])
SplitConsistent(splits1[[4]], splits2)
SplitConflicts(splits1[[4]], list(splits1, splits2))
```

SplitFrequency *Frequency of splits*

Description

SplitFrequency() provides a simple way to count the number of times that bipartition splits, as defined by a reference tree, occur in a forest of trees. May be used to calculate edge ("node") support for majority consensus or bootstrap trees.

Usage

```
SplitFrequency(reference, forest = NULL)
```

Arguments

reference	A tree of class phylo, a Splits object. If NULL, the frequencies of all splits in forest will be returned.
forest	A list of trees of class phylo, or a multiPhylo object; or a Splits object. See vignette for possible methods of loading trees into R.

Details

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

Value

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

If `reference` is `NULL`, then `SplitFrequency()` returns a list of splits (in the order encountered in forest) with attribute `"count"` stating the number of times each split occurs in `forest`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other Splits operations: `LabelSplits()`, `NSplits()`, `NTip()`, `PolarizeSplits()`, `Splits`, `SplitsInBinaryTree()`, `TipLabels()`, `TipsInSplits()`, `match,Splits,Splits-method`, `xor()`

Examples

```
# An example forest of 100 trees, some identical
forest <- as.phylo(c(1, rep(10, 79), rep(100, 15), rep(1000, 5)), nTip = 9)

# Generate an 80% consensus tree
cons <- ape::consensus(forest, p = 0.8)
plot(cons)

# Calculate split frequencies
splitFreqs <- SplitFrequency(cons, forest)

# Optionally, colour edges by corresponding frequency.
# Note that not all edges are associated with a unique split
# (and two root edges may be associated with one split - not handled here)
edgeSupport <- rep(1, nrow(cons$edge)) # Initialize trivial splits to 1
childNode <- cons$edge[, 2]
edgeSupport[match(names(splitFreqs), childNode)] <- splitFreqs / 100

plot(cons, edge.col = SupportColour(edgeSupport), edge.width = 3)

# Annotate nodes by frequency
LabelSplits(cons, splitFreqs, unit = "%",
            col = SupportColor(splitFreqs / 100),
            frame = "none", pos = 3L)
```

`SplitInformation` *Phylogenetic information content of splitting leaves into two partitions*

Description

Calculate the phylogenetic information content (*sensu* Steel and Penny 2006) of a split, which reflects the probability that a uniformly selected random tree will contain the split: a split that is consistent with a smaller number of trees will have a higher information content.

Usage

```
SplitInformation(A, B = A[1])

## S3 method for class 'numeric'
SplitInformation(A, B = A[1])

## S3 method for class 'Splits'
SplitInformation(A, B)

## S3 method for class 'phylo'
SplitInformation(A, B)

MultiSplitInformation(partitionSizes)
```

Arguments

`A, B`	Integer specifying the number of taxa in each partition.
`partitionSizes`	Integer vector specifying the number of taxa in each partition of a multi-partition split.

Details

`SplitInformation()` addresses bipartition splits, which correspond to edges in an unrooted phylogeny; `MultiSplitInformation()` supports splits that subdivide taxa into multiple partitions, which may correspond to multi-state characters in a phylogenetic matrix.

A simple way to characterise trees is to count the number of edges. (Edges are almost, but not quite, equivalent to nodes.) Counting edges (or nodes) provides a quick measure of a tree's resolution, and underpins the Robinson-Foulds tree distance measure. Not all edges, however, are created equal.

An edge splits the leaves of a tree into two subdivisions. The more equal these subdivisions are in size, the more instructive this edge is. Intuitively, the division of mammals from reptiles is a profound revelation that underpins much of zoology; recognizing that two species of bat are more closely related to each other than to any other mammal or reptile is still instructive, but somewhat less fundamental.

Formally, the phylogenetic (Shannon) information content of a split S, $h(S)$, corresponds to the probability that a uniformly selected random tree will contain the split, $P(S)$: $h(S) = -\log P(S)$. Base 2 logarithms are typically employed to yield an information content in bits.

As an example, the split AB|CDEF occurs in 15 of the 105 six-leaf trees; h(AB|CDEF) = -log P(AB|CDEF) = -log(15/105) ~ 2.81 bits. The split ABC|DEF subdivides the leaves more evenly, and is thus more instructive: it occurs in just nine of the 105 six-leaf trees, and h(ABC|DEF) = -log(9/105) ~ 3.54 bits.

As the number of leaves increases, a single even split may contain more information than multiple uneven splits – see the examples section below.

Summing the information content of all splits within a tree, perhaps using the 'TreeDist' function `SplitwiseInfo()`, arguably gives a more instructive picture of its resolution than simply counting the number of splits that are present – though with the caveat that splits within a tree are not independent of one another, so some information may be double counted. (This same charge applies to simply counting nodes, too.)

Alternatives would be to count the number of quartets that are resolved, perhaps using the 'Quartet' function `QuartetStates()`, or to use a different take on the information contained within a split, the clustering information: see the 'TreeDist' function `ClusteringInfo()` for details.

Value

`SplitInformation()` and `MultiSplitInformation()` return the phylogenetic information content, in bits, of a split that subdivides leaves into partitions of the specified sizes.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Steel MA, Penny D (2006). "Maximum parsimony and the phylogenetic information in multistate characters." In Albert VA (ed.), *Parsimony, Phylogeny, and Genomics*, 163–178. Oxford University Press, Oxford.

See Also

Sum the phylogenetic information content of splits within a tree: `TreeDist::SplitwiseInfo()`

Sum the clustering information content of splits within a tree: `TreeDist::ClusteringInfo()`

Other split information functions: `CharacterInformation()`, `SplitMatchProbability()`, `TreesMatchingSplit()`, `UnrootedTreesMatchingSplit()`

Examples

```
# Eight leaves can be split evenly:
SplitInformation(4, 4)

# or unevenly, which is less informative:
SplitInformation(2, 6)

# A single split that evenly subdivides 50 leaves contains more information
# that seven maximally uneven splits on the same leaves:
SplitInformation(25, 25)
7 * SplitInformation(2, 48)
# Three ways to split eight leaves into multiple partitions:
```

```
MultiSplitInformation(c(2, 2, 4))
MultiSplitInformation(c(2, 3, 3))
MultiSplitInformation(rep(2, 4))
```

SplitMatchProbability *Probability of matching this well*

Description

(Ln)SplitMatchProbability()calculates the probability that two random splits of the sizes provided will be at least as similar as the two specified.

Usage

```
SplitMatchProbability(split1, split2)

LnSplitMatchProbability(split1, split2)
```

Arguments

split1, split2	Logical vectors listing terminals in same order, such that each terminal is identified as a member of the ingroup (TRUE) or outgroup (FALSE) of the respective bipartition split.

Value

SplitMatchProbability() returns a numeric giving the proportion of permissible non-trivial splits that divide the terminals into bipartitions of the sizes given, that match as well as split1 and split2 do.

LnSplitMatchProbability() returns the natural logarithm of the probability.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other split information functions: CharacterInformation(), SplitInformation(), TreesMatchingSplit(), UnrootedTreesMatchingSplit()

Examples

```
split1 <- as.Splits(c(rep(TRUE, 4), rep(FALSE, 4)))
split2 <- as.Splits(c(rep(TRUE, 3), rep(FALSE, 5)))
SplitMatchProbability(split1, split2)
LnSplitMatchProbability(split1, split2)
```

`Splits` *Convert object to* `Splits`

Description

`as.Splits()` converts a phylogenetic tree to a `Splits` object representing its constituent bipartition splits.

Usage

```
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'phylo'
as.Splits(x, tipLabels = NULL, asSplits = TRUE, ...)

## S3 method for class 'multiPhylo'
as.Splits(x, tipLabels = unique(unlist(TipLabels(x))), asSplits = TRUE, ...)

## S3 method for class 'Splits'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'list'
as.Splits(x, tipLabels = NULL, asSplits = TRUE, ...)

## S3 method for class 'matrix'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'integer'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'numeric'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'logical'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'character'
as.Splits(x, tipLabels = NULL, ...)

## S3 method for class 'Splits'
as.logical(x, tipLabels = attr(x, "tip.label"), ...)
```

Arguments

`x`	Object to convert into splits: perhaps a tree of class `phylo`. If a logical matrix is provided, each row will be considered as a separate split. If an integer matrix is provided, entries assigned the same integer will be assigned to the same split.

tipLabels	Character vector specifying sequence in which to order tip labels. Label order must (currently) match to combine or compare separate Splits objects.
...	Presently unused.
asSplits	Logical specifying whether to return a Splits object, or an unannotated two-dimensional array (useful where performance is paramount).

Value

as.Splits() returns an object of class Splits, or (if asSplits = FALSE) a two-dimensional array of raw objects, with each bit specifying whether or not the leaf corresponding to the respective bit position is a member of the split. Splits are named according to the node at the non-root end of the edge that defines them. In rooted trees, the child of the rightmost root edge names the split.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), SplitsInBinaryTree(), TipLabels(), TipsInSplits(), match,Splits,Splits-method, xor()

Examples

```
splits <- as.Splits(BalancedTree(letters[1:6]))
summary(splits)
TipsInSplits(splits)
summary(!splits)
TipsInSplits(!splits)

length(splits + !splits)
length(unique(splits + !splits))

summary(c(splits[[2:3]], !splits[[1:2]]))

moreSplits <- as.Splits(PectinateTree(letters[6:1]), tipLabel = splits)
print(moreSplits, details = TRUE)
match(splits, moreSplits)
moreSplits %in% splits

as.Splits("....**", letters[1:6])
```

SplitsInBinaryTree *Maximum splits in an* n*-leaf tree*

Description

SplitsInBinaryTree() is a convenience function to calculate the number of splits in a fully-resolved (binary) tree with *n* leaves.

Usage

```
SplitsInBinaryTree(tree)

## S3 method for class 'list'
SplitsInBinaryTree(tree)

## S3 method for class 'multiPhylo'
SplitsInBinaryTree(tree)

## S3 method for class 'numeric'
SplitsInBinaryTree(tree)

## S3 method for class '`NULL`'
SplitsInBinaryTree(tree)

## Default S3 method:
SplitsInBinaryTree(tree)

## S3 method for class 'Splits'
SplitsInBinaryTree(tree)

## S3 method for class 'phylo'
SplitsInBinaryTree(tree)
```

Arguments

tree	An object of a supported format that represents a tree or set of trees, from which the number of leaves will be calculated.

Value

SplitsInBinaryTree() returns an integer vector detailing the number of unique non-trivial splits in a binary tree with *n* leaves.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: Cherries(), ConsensusWithout(), EdgeRatio(), LongBranch(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), TipLabels(), TreeIsRooted(), Treeness()

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, TipLabels(), TipsInSplits(), match,Splits,Splits-method, xor()

Examples

```
tree <- BalancedTree(8)
SplitsInBinaryTree(tree)
SplitsInBinaryTree(as.Splits(tree))
SplitsInBinaryTree(8)
SplitsInBinaryTree(list(tree, tree))
```

Stemwardness *"Stemwardness" of a leaf*

Description

Functions to describe the position of a leaf relative to the root. "Stemmier" leaves ought to exhibit a smaller root-node distance and a larger sister size.

Usage

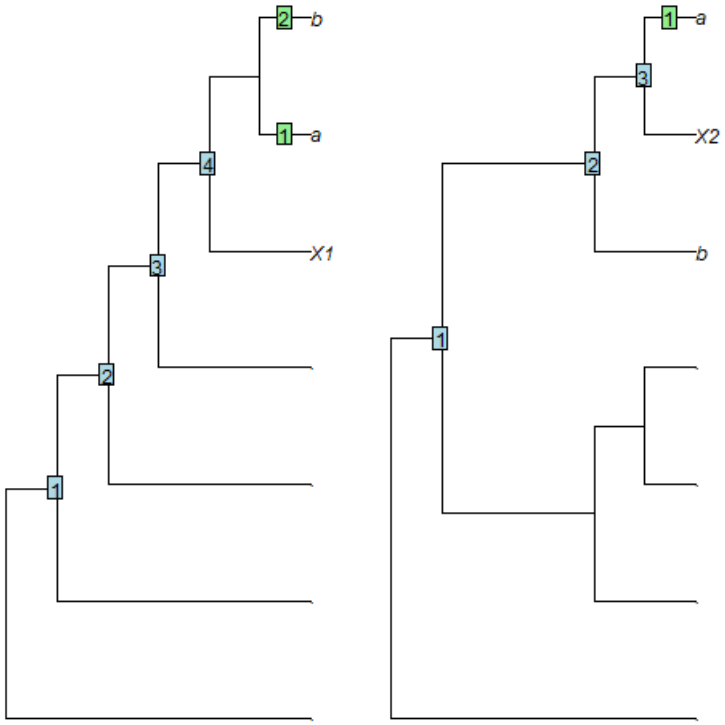
```
SisterSize(tree, tip)

## S3 method for class 'numeric'
SisterSize(tree, tip)

## S3 method for class 'character'
SisterSize(tree, tip)

RootNodeDistance(tree, tip)

## S3 method for class 'numeric'
RootNodeDistance(tree, tip)

## S3 method for class 'character'
RootNodeDistance(tree, tip)

RootNodeDist(tree, tip)
```

Arguments

tree	A tree of class phylo.
tip	Either a numeric specifying the index of a single tip, or a character specifying its label.

Details

`RootNodeDistance()` calculates the number of nodes between the chosen leaf and the root of `tree`. This is an unsatisfactory measure, as the range of possible distances is a function of the shape of the tree (Asher and Smith 2022). As an example, leaf *X1* in the tree `(.,(.,(.,(.,(X1,(a,b))))))` falls outside the clade *(a, b)* and has a root-node distance of 4, whereas leaf *X2* in the tree `(.,((.,(.,.)),(b,(X2,a))))` falls within the clade *(a, b)*, so should be considered more "crownwards", yet has a smaller root-node distance (3).



`SisterSize()` measures the number of leaves in the clade that is sister to the chosen leaf, as proposed by Asher and Smith (2022). In the examples above, *X1* has a sister size of 2 leaves, whereas *X2*, which is "more crownwards", has a smaller sister size (1 leaf), as desired.

Value

`SisterSize()` returns an integer specifying the number of leaves in the clade that is sister to `tip`. `RootNodeDist()` returns an integer specifying the number of nodes between `tip` and the root node of `tree`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Asher R, Smith MR (2022). "Phylogenetic signal and bias in paleontology." *Systematic Biology*, **71**(4), 986–1008. doi:10.1093/sysbio/syab072.

See Also

Other tree characterization functions: `CladisticInfo()`, `Consensus()`, `J1Index()`, `TotalCopheneticIndex()`

Examples

```
bal8 <- BalancedTree(8)
pec8 <- PectinateTree(8)

SisterSize(bal8, 3)
SisterSize(pec8, "t3")
SisterSize(RootTree(pec8, "t3"), "t3")

RootNodeDist(bal8, 3)
RootNodeDist(pec8, "t3")
RootNodeDist(RootTree(pec8, "t3"), "t3")
```

StringToPhyDat *Convert between strings and* phyDat *objects*

Description

`PhyDatToString()` converts a `phyDat` object as a string; `StringToPhyDat()` converts a string of character data to a `phyDat` object.

Usage

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

StringToPhydat(string, tips, byTaxon = TRUE)

PhyToString(
  phy,
  parentheses = "{",
  collapse = "",
  ps = "",
  useIndex = TRUE,
  byTaxon = TRUE,
  concatenate = TRUE
)

PhyDatToString(
  phy,
  parentheses = "{",
```

```
  collapse = "",
  ps = "",
  useIndex = TRUE,
  byTaxon = TRUE,
  concatenate = TRUE
)

PhydatToString(
  phy,
  parentheses = "{",
  collapse = "",
  ps = "",
  useIndex = TRUE,
  byTaxon = TRUE,
  concatenate = TRUE
)
```

Arguments

string	String of tokens, optionally containing whitespace, with no terminating semi-colon.
tips	(Optional) Character vector corresponding to the names (in order) of each taxon in the matrix, or an object such as a tree from which tip labels can be extracted.
byTaxon	Logical. If TRUE, write one taxon followed by the next. If FALSE, write one character followed by the next.
phy	An object of class phyDat.
parentheses	Character specifying format of parentheses with which to surround ambiguous tokens. Choose from: { (default), [, (, <.
collapse	Character specifying text, perhaps ,, with which to separate multiple tokens within parentheses.
ps	Character specifying text, perhaps ;, to append to the end of each string.
useIndex	Logical (default: TRUE) specifying whether to print duplicate characters multiple times, as they appeared in the original matrix.
concatenate	Logical specifying whether to concatenate all characters/taxa into a single string, or to return a separate string for each entry.

Value

StringToPhyDat() returns an object of class phyDat.

PhyToString() returns a character vector listing a text representation of the phylogenetic character state for each taxon in turn.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other phylogenetic matrix conversion functions: Decompose(), MatrixToPhyDat(), Reweight()

Examples

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

fileName <- paste0(system.file(package = "TreeTools"),
                   "/extdata/input/dataset.nex")
phyDat <- ReadAsPhyDat(fileName)
PhyToString(phyDat, concatenate = FALSE)
```

Subsplit *Subset of a split on fewer leaves*

Description

Subsplit() removes leaves from a Splits object.

Usage

```
Subsplit(splits, tips, keepAll = FALSE, unique = TRUE)
```

Arguments

splits	An object of class Splits.
tips	A vector specifying a subset of the leaf labels applied to split.
keepAll	logical specifying whether to keep entries that define trivial splits (i.e. splits of zero or one leaf) on the subset of leaves.
unique	logical specifying whether to remove duplicate splits.

Value

Subsplit() returns an object of class Splits, defined on the leaves tips.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

KeepTip() is a less flexible but faster equivalent.

Other split manipulation functions: DropTip(), SplitConsistent(), TrivialSplits()

Examples

```
splits <- as.Splits(PectinateTree(letters[1:9]))
splits
efgh <- Subsplit(splits, tips = letters[5:8], keepAll = TRUE)
summary(efgh)

TrivialSplits(efgh)

summary(Subsplit(splits, tips = letters[5:8], keepAll = FALSE))
```

Subtree *Extract a subtree*

Description

`Subtree()` safely extracts a clade from a phylogenetic tree.

Usage

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

Arguments

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

Details

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

Value

`Subtree()` returns a tree of class `phylo` that represents a clade extracted from the original tree.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree manipulation: `AddTip()`, `CollapseNode()`, `ConsensusWithout()`, `DropTip()`, `ImposeConstraint()`, `KeptPaths()`, `KeptVerts()`, `LeafLabelInterchange()`, `MakeTreeBinary()`, `Renumber()`, `RenumberTips()`, `RenumberTree()`, `RootTree()`, `SortTree()`, `TipTimedTree()`, `TrivialTree`

Examples

```
tree <- Preorder(BalancedTree(8))
plot(tree)
ape::nodelabels()
ape::nodelabels(13, 13, bg="yellow")

plot(Subtree(tree, 13))
```

SupportColour *Colour for node support value*

Description

Colour value with which to display node support.

Usage

```
SupportColour(
  support,
  show1 = TRUE,
  scale = colorRampPalette(c("#D33F6A", "#e2e2e2", "#4A6FE3"))(101),
  outOfRange = "red"
)

SupportColor(
  support,
  show1 = TRUE,
  scale = colorRampPalette(c("#D33F6A", "#e2e2e2", "#4A6FE3"))(101),
  outOfRange = "red"
)
```

Arguments

support	A numeric vector of values in the range 0–1.
show1	Logical specifying whether to display values of 1. A transparent white will be returned if FALSE.
scale	101-element vector listing colours in sequence. Defaults to a diverging HCL scale.
outOfRange	Colour to use if results are outside the range 0–1.

Value

SupportColour() returns the appropriate value from scale, or outOfRange if a value is outwith the valid range.

See Also

Use in conjunction with LabelSplits() to colour split labels, possibly calculated using SplitFrequency().

Examples

```
SupportColour((-1):4 / 4, show1 = FALSE)

# An example forest of 100 trees, some identical
forest <- as.phylo(c(1, rep(10, 79), rep(100, 15), rep(1000, 5)), nTip = 9)

# Generate an 80% consensus tree
cons <- ape::consensus(forest, p = 0.8)
plot(cons)

# Calculate split frequencies
splitFreqs <- SplitFrequency(cons, forest)

# Optionally, colour edges by corresponding frequency.
# Note that not all edges are associated with a unique split
# (and two root edges may be associated with one split - not handled here)
edgeSupport <- rep(1, nrow(cons$edge)) # Initialize trivial splits to 1
childNode <- cons$edge[, 2]
edgeSupport[match(names(splitFreqs), childNode)] <- splitFreqs / 100

plot(cons, edge.col = SupportColour(edgeSupport), edge.width = 3)

# Annotate nodes by frequency
LabelSplits(cons, splitFreqs, unit = "%",
            col = SupportColor(splitFreqs / 100),
            frame = "none", pos = 3L)
```

TipLabels *Extract tip labels*

Description

TipLabels() extracts labels from an object: for example, names of taxa in a phylogenetic tree or data matrix. AllTipLabels() extracts all labels, where entries of a list of trees may pertain to different taxa.

Usage

```
TipLabels(x, single = TRUE)

## Default S3 method:
TipLabels(x, single = TRUE)

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

```
TipLabels(x, single = TRUE)

## S3 method for class 'logical'
TipLabels(x, single = TRUE)

## S3 method for class 'phylo'
TipLabels(x, single = TRUE)

## S3 method for class 'phyDat'
TipLabels(x, single = TRUE)

## S3 method for class 'MixedBase'
TipLabels(x, single = TRUE)

## S3 method for class 'TreeNumber'
TipLabels(x, single = TRUE)

## S3 method for class 'Splits'
TipLabels(x, single = TRUE)

## S3 method for class 'list'
TipLabels(x, single = FALSE)

## S3 method for class 'multiPhylo'
TipLabels(x, single = FALSE)

## S3 method for class 'character'
TipLabels(x, single = TRUE)

## S3 method for class 'numeric'
TipLabels(x, single = TRUE)

## S3 method for class 'phyDat'
TipLabels(x, single = TRUE)

AllTipLabels(x)

## S3 method for class 'list'
AllTipLabels(x)

## S3 method for class 'multiPhylo'
AllTipLabels(x)

## S3 method for class 'phylo'
AllTipLabels(x)

## S3 method for class 'Splits'
AllTipLabels(x)
```

```
## S3 method for class 'TreeNumber'
AllTipLabels(x)

## S3 method for class 'matrix'
AllTipLabels(x)
```

Arguments

x	An object of a supported class (see Usage section above).
single	Logical specifying whether to report the labels for the first object only (TRUE), or for each object in a list (FALSE).

Value

TipLabels() returns a character vector listing the tip labels appropriate to x. If x is a single integer, this will be a vector t1, t2 ... tx, to match the default of rtree().

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: Cherries(), ConsensusWithout(), EdgeRatio(), LongBranch(), MatchEdges(), NSplits(), NTip(), NodeNumbers(), PathLengths(), SplitsInBinaryTree(), TreeIsRooted(), Treeness()

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipsInSplits(), match,Splits,Splits-method, xor()

Examples

```
TipLabels(BalancedTree(letters[5:1]))
TipLabels(5)

data("Lobo")
head(TipLabels(Lobo.phy))

AllTipLabels(c(BalancedTree(4), PectinateTree(8)))
```

TipsInSplits *Tips contained within splits*

Description

TipsInSplits() specifies the number of tips that occur within each bipartition split in a Splits object.

Usage

```
TipsInSplits(splits, keep.names = TRUE, smallest = FALSE, ...)

## S3 method for class 'Splits'
TipsInSplits(splits, keep.names = TRUE, smallest = FALSE, ...)

## S3 method for class 'phylo'
TipsInSplits(splits, keep.names = TRUE, smallest = FALSE, ...)

SplitImbalance(splits, keep.names = TRUE, ...)

## S3 method for class 'Splits'
SplitImbalance(splits, keep.names = TRUE, ...)

## S3 method for class 'phylo'
SplitImbalance(splits, keep.names = TRUE, ...)
```

Arguments

splits	Object of class Splits or phylo.
keep.names	Logical specifying whether to include the names of splits in the output.
smallest	Logical; if TRUE, return the number of leaves in the smaller bipartition.
...	Additional parameters to pass to as.Splits().

Value

TipsInSplits() returns a named vector of integers, specifying the number of tips contained within each split in splits.

SplitImbalance() returns a named vector of integers, specifying the number of leaves within a split that are not "balanced" by a leaf outside it; i.e. a split that divides leaves evenly has an imbalance of zero; one that splits two tips from ten has an imbalance of 10 - 2 = 8.

See Also

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipLabels(), match,Splits,Splits-method, xor()

Examples

```
tree <- PectinateTree(8)
splits <- as.Splits(tree)
TipsInSplits(splits)

plot(tree)
LabelSplits(tree, as.character(splits), frame = "none", pos = 3L, cex = 0.7)
LabelSplits(tree, TipsInSplits(splits), unit = " tips", frame = "none",
            pos = 1L)
```

TipTimedTree *Display time-calibrated tree using tip information only*

Description

TipTimedTree() plots a phylogenetic tree against time using an *ad hoc* approach based on dates associated with the leaves. Nodes are dated to the youngest possible value, plus an additional "buffer" (specified with minEdge) to ensure that branching order is readable.

Usage

```
TipTimedTree(tree, tipAge, minEdge = 1)
```

Arguments

tree	A tree of class phylo.
tipAge	Numeric vector specifying the age (in units-of-time ago) associated with each tip in tree$tip.label in turn. Older ages signify earlier tips.
minEdge	Minimum length of edge to allow (in units-of-time)

Details

This experimental function is liable to change its behaviour, or to be deprecated, in coming releases. Please contact the maintainer if you find it useful, so that a production-ready version can be prioritized.

Value

TipTimedTree() returns a tree with edge lengths set based on the ages of each tip.

See Also

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), UnshiftTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TrivialTree

Examples

```
tree <- BalancedTree(6)
plot(TipTimedTree(tree, tipAge = 1:6, minEdge = 2))
```

TopologyOnly *Remove metadata from trees*

Description

`TopologyOnly()` removes all information from trees except for their topologies and leaf labels.

Usage

```
TopologyOnly(tree)
```

Arguments

`tree`	A tree of class `phylo`.

Value

Returns `tree`, with each tree in `Preorder`, with edge lengths, node labels and other attributes removed.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

TotalCopheneticIndex *Total Cophenetic Index*

Description

`TotalCopheneticIndex()` calculates the total cophenetic index (Mir et al. 2013) for any tree, a measure of its balance; `TCIContext()` lists its possible values.

Usage

```
TotalCopheneticIndex(x)

TCIContext(x)

## S3 method for class 'numeric'
TCIContext(x)
```

Arguments

`x`	A tree of class `phylo`, its `$edge` property, or a list thereof.

Details

The Total Cophenetic Index is a measure of tree balance – i.e. whether a (phylogenetic) tree comprises symmetric pairs of nodes, or has a pectinate "caterpillar" shape. The index has a greater resolution power than Sackin's and Colless' indices, and can be applied to trees that are not perfectly resolved.

For a tree with n leaves, the Total Cophenetic Index can take values of 0 to `choose(n, 3)`. The minimum value is higher for a perfectly resolved (i.e. dichotomous) tree (see Lemma 14 of Mir *et al.* 2013). Formulae to calculate the expected values under the Yule and Uniform models of evolution are given in Theorems 17 and 23.

Full details are provided by Mir et al. (2013).

The J^1 index (Lemant et al. 2022) has advantages over the Total Cophenetic Index, particularly when comparing trees with different numbers of leaves, or where the population size of nodes is meaningful; see `J1Index()`.

Value

`TotalCopheneticIndex()` returns an integer denoting the total cophenetic index.

`TCIContext()` returns a data frame detailing the maximum and minimum value obtainable for the Total Cophenetic Index for rooted binary trees with the number of leaves of the given tree, and the expected value under the Yule and Uniform models. The variance of the expected value is given under the Yule model, but cannot be obtained by calculation for the Uniform model.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Lemant J, Le Sueur C, Manojlović V, Noble R (2022). "Robust, Universal Tree Balance Indices." *Systematic Biology*, **71**(5), 1210–1224. doi:10.1093/sysbio/syac027.

Mir A, Rosselló F, Rotger LA (2013). "A new balance index for phylogenetic trees." *Mathematical Biosciences*, **241**(1), 125–136. doi:10.1016/j.mbs.2012.10.005.

See Also

- `J1Index()` provides a more robust, universal tree balance index.
- `cophen.index()` in the package **CollessLike** provides an alternative implementation of this index and its predecessors.

Other tree characterization functions: `CladisticInfo()`, `Consensus()`, `J1Index()`, `Stemwardness`

Examples

```
# Balanced trees have the minimum index for a binary tree;
# Pectinate trees the maximum:
TCIContext(8)
TotalCopheneticIndex(PectinateTree(8))
```

```
TotalCopheneticIndex(BalancedTree(8))
TotalCopheneticIndex(StarTree(8))


# Examples from Mir et al. (2013):
tree12 <- ape::read.tree(text="(1, (2, (3, (4, 5))));")  #Fig. 4, tree 12
TotalCopheneticIndex(tree12) # 10
tree8  <- ape::read.tree(text="((1, 2, 3, 4), 5);")      #Fig. 4, tree 8
TotalCopheneticIndex(tree8)  # 6
TCIContext(tree8)
TCIContext(5L) # Context for a tree with 5 leaves.
```

`TreeIsRooted` *Is tree rooted?*

Description

`TreeIsRooted()` is a fast alternative to `ape::is.rooted()`.

Usage

```
TreeIsRooted(tree)
```

Arguments

`tree`	A phylogenetic tree of class `phylo`.

Value

`TreeIsRooted()` returns a logical specifying whether a root node is resolved.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree properties: `Cherries()`, `ConsensusWithout()`, `EdgeRatio()`, `LongBranch()`, `MatchEdges()`, `NSplits()`, `NTip()`, `NodeNumbers()`, `PathLengths()`, `SplitsInBinaryTree()`, `TipLabels()`, `Treeness()`

Examples

```
TreeIsRooted(BalancedTree(6))
TreeIsRooted(UnrootTree(BalancedTree(6)))
```

`Treeness` *Relative length of internal branches*

Description

Treeness (also termed stemminess) is the proportion of a tree's length found on internal branches (Lanyon 1988). Insofar as external branches do not contain phylogenetic (grouping) signal, trees with a high treeness can be interpreted as containing a higher signal:noise ratio (Phillips and Penny 2003-08).

Usage

```
Treeness(tree)

Stemminess(tree)
```

Arguments

`tree`	A tree of class `phylo`, or a list of trees of class `list` or `multiPhylo`.

Value

`Treeness()` returns a numeric vector reporting the treeness of each `tree`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Lanyon SM (1988). "The Stochastic Mode of Molecular Evolution: What Consequences for Systematic Investigations?" *The Auk*, **105**(3), 565–573. doi:10.1093/auk/105.3.565.

Phillips MJ, Penny D (2003-08). "The Root of the Mammalian Tree Inferred from Whole Mitochondrial Genomes." *Molecular Phylogenetics and Evolution*, **28**(2), 171–185. doi:10.1016/S10557903(03)000575.

See Also

Other tree properties: `Cherries()`, `ConsensusWithout()`, `EdgeRatio()`, `LongBranch()`, `MatchEdges()`, `NSplits()`, `NTip()`, `NodeNumbers()`, `PathLengths()`, `SplitsInBinaryTree()`, `TipLabels()`, `TreeIsRooted()`

Examples

```
lowTree <- BalancedTree(6, lengths = c(1, 1, 4, 4, 4, 1, 1, 4, 4, 4))
plot(lowTree)
Treeness(lowTree)
highTree <- BalancedTree(6, lengths = c(6, 6, 1, 1, 1, 6, 6, 1, 1, 1))
plot(highTree)
Treeness(c(lowTree, highTree))
```

TreeNumber *Unique integer indices for bifurcating tree topologies*

Description

Functions converting between phylogenetic trees and their unique decimal representation, based on a concept by John Tromp, employed in Li et al. (1996).

Usage

```
as.TreeNumber(x, ...)

## S3 method for class 'phylo'
as.TreeNumber(x, ...)

## S3 method for class 'multiPhylo'
as.TreeNumber(x, ...)

## S3 method for class 'character'
as.TreeNumber(x, nTip, tipLabels = TipLabels(nTip), ...)

## S3 method for class 'TreeNumber'
as.TreeNumber(x, ...)

## S3 method for class 'MixedBase'
as.TreeNumber(x, ...)

## S3 method for class 'TreeNumber'
as.MixedBase(x, ...)

## S3 method for class 'integer64'
as.MixedBase(x, tipLabels = NULL, ...)

## S3 method for class 'numeric'
as.MixedBase(x, tipLabels = NULL, ...)

## S3 method for class 'numeric'
as.phylo(x, nTip = attr(x, "nTip"), tipLabels = attr(x, "tip.label"), ...)
```

```
## S3 method for class 'TreeNumber'
as.phylo(x, nTip = attr(x, "nTip"), tipLabels = attr(x, "tip.label"), ...)

as.MixedBase(x, ...)

## S3 method for class 'MixedBase'
as.MixedBase(x, ...)

## S3 method for class 'phylo'
as.MixedBase(x, ...)

## S3 method for class 'multiPhylo'
as.MixedBase(x, ...)

## S3 method for class 'MixedBase'
as.phylo(x, nTip = attr(x, "nTip"), tipLabels = attr(x, "tip.label"), ...)
```

Arguments

x	Integer identifying the tree (see details).
...	Additional parameters for consistency with S3 methods (unused).
nTip	Integer specifying number of leaves in the tree.
tipLabels	Character vector listing the labels assigned to each tip in a tree, perhaps obtained using TipLabels().

Details

There are NUnrooted(n) unrooted trees with n leaves. As such, each n-leaf tree can be uniquely identified by a non-negative integer $x <$ NUnrooted(n).

This integer can be converted by a tree by treating it as a mixed-base number, with bases 1, 3, 5, 7, ... (2 n - 5).

Each digit of this mixed base number corresponds to a leaf, and determines the location on a growing tree to which that leaf should be added.

We start with a two-leaf tree, and treat 0 as the origin of the tree.

```
0 ---- 1
```

We add leaf 2 by breaking an edge and inserting a node (numbered 2 + nTip - 1). In this example, we'll work up to a six-leaf tree; this node will be numbered 2 + 6 - 1 = 7. There is only one edge on which leaf 2 can be added. Let's add node 7 and leaf 2:

```
0 ---- 7 ---- 1
       |
       |
       2
```

There are now three edges on which leaf 3 can be added. Our options are:

Option 0: the edge leading to 1;

Option 1: the edge leading to 2;

Option 2: the edge leading to 7.

If we select option 1, we produce:

```
0 ---- 7 ---- 1
       |
       |
       8 ---- 2
       |
       |
       3
```

1 is now the final digit of our mixed-base number.

There are five places to add leaf 4:

Option 0: the edge leading to 1;

Option 1: the edge leading to 2;

Option 2: the edge leading to 3;

Option 3: the edge leading to 7;

Option 4: the edge leading to 8.

If we chose option 3, then 3 would be the penultimate digit of our mixed-base number.

If we chose option 0 for the next two additions, we could specify this tree with the mixed-base number 0021. We can convert this into decimal:

$0 \times (1 \times 3 \times 5 \times 9) +$

$0 \times (1 \times 3 \times 5) +$

$3 \times (1 \times 3) +$

$1 \times (1)$

$= 10$

`as.TreeNumber()` supports up to 51 leaves. For trees with at most 19 leaves, the number fits in a 64-bit integer and the `TreeNumber` is stored as an `integer64` (via the `bit64` package), enabling arithmetic and exact round-tripping via `as.MixedBase()`. For trees with 20–51 leaves, there are more than 2^64 distinct topologies, so the tree number is stored as a decimal character string instead.

Package developers can use the C++ header `TreeTools/tree_number.h` (via `LinkingTo: TreeTools`) for the underlying 256-bit encoding (`tree_num_t`) directly.

Value

`as.TreeNumber()` returns an object of class `TreeNumber` with attributes `nTip` and `tip.label`. For trees with at most 19 leaves the underlying storage is a single `integer64` value (class `c("TreeNumber", "integer64")`), enabling `integer64` arithmetic and exact round-tripping through `as.MixedBase()`.

For trees with 20–51 leaves the number exceeds 2^64, so it is stored as a decimal character string (class `c("TreeNumber", "character")`). If `x` is a list of trees or a `multiPhylo` object, `as.TreeNumber()` returns a corresponding list of `TreeNumber` objects.

`as.phylo.numeric()` returns a tree of class `phylo`.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

References

Li M, Tromp J, Zhang L (1996). "Some notes on the nearest neighbour interchange distance." In Goos G, Hartmanis J, Leeuwen J, Cai J, Wong CK (eds.), *Computing and Combinatorics*, volume 1090, 343–351. Springer, Berlin, Heidelberg. ISBN 978-3-540-61332-9. doi:10.1007/354061332-3_168.

See Also

Describe the shape of a tree topology, independent of leaf labels: `TreeShape()`

Other tree generation functions: `ConstrainedNJ()`, `GenerateTree`, `NJTree()`, `TrivialTree`

Other 'TreeNumber' utilities: `is.TreeNumber()`, `print.TreeNumber()`

Examples

```
tree <- as.phylo(10, nTip = 6)
plot(tree)
as.TreeNumber(tree)

# Trees with 20--51 leaves are stored as decimal strings:
as.TreeNumber(BalancedTree(19))  # integer64-backed
as.TreeNumber(BalancedTree(51))  # character-backed

# If > 9 digits, represent the tree number as a string.
treeNumber <- as.TreeNumber("1234567890123", nTip = 14)
tree <- as.phylo(treeNumber)
as.phylo(0:2, nTip = 6, tipLabels = letters[1:6])
```

TreesMatchingSplit *Number of trees matching a bipartition split*

Description

Calculates the number of unrooted bifurcated trees that are consistent with a bipartition split that divides taxa into groups of size `A` and `B`.

Usage

```
TreesMatchingSplit(A, B = A[2])

LnTreesMatchingSplit(A, B = A[2])

Log2TreesMatchingSplit(A, B = A[2])
```

Arguments

A, B	Integer specifying the number of taxa in each partition.

Value

`TreesMatchingSplit()` returns a numeric specifying the number of trees that are compatible with the given split.

`LnTreesMatchingSplit()` and `Log2TreesMatchingSplit()` give the natural and base-2 logarithms of this number.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other split information functions: `CharacterInformation()`, `SplitInformation()`, `SplitMatchProbability()`, `UnrootedTreesMatchingSplit()`

Examples

```
TreesMatchingSplit(5, 6)
LnTreesMatchingSplit(5, 6)
Log2TreesMatchingSplit(5, 6)
```

TreesMatchingTree *Number of trees containing a tree*

Description

`TreesMatchingTree()` calculates the number of unrooted binary trees that are consistent with a tree topology on the same leaves.

Usage

```
TreesMatchingTree(tree)

LnTreesMatchingTree(tree)

Log2TreesMatchingTree(tree)
```

Arguments

tree	A tree of class phylo.

Details

Remember to unroot a tree first if the position of its root is arbitrary.

Value

TreesMatchingTree() returns a numeric specifying the number of unrooted binary trees that contain all the edges present in the input tree.

LnTreesMatchingTree() gives the natural logarithm of this number.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other tree information functions: CladisticInfo(), NRooted()

Examples

```
partiallyResolvedTree <- CollapseNode(BalancedTree(8), 12:15)
TreesMatchingTree(partiallyResolvedTree)
LnTreesMatchingTree(partiallyResolvedTree)

# Number of rooted trees:
rootedTree <- AddTip(partiallyResolvedTree, where = 0)
TreesMatchingTree(partiallyResolvedTree)
```

TrivialSplits *Identify and remove trivial splits*

Description

TrivialSplits() identifies trivial splits (which separate one or zero leaves from all others); WithoutTrivialSplits() removes them from a Splits object.

Usage

```
TrivialSplits(splits, nTip = attr(splits, "nTip"))

WithoutTrivialSplits(splits, nTip = attr(splits, "nTip"))
```

Arguments

splits	An object of class Splits.
nTip	Integer specifying number of tips (leaves).

Value

`TrivialSplits()` returns a logical vector specifying whether each split in `splits` is trivial, i.e. includes or excludes only a single tip or no tips at all.

`WithoutTrivialSplits()` returns a `Splits` object with trivial splits removed.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

Other split manipulation functions: `DropTip()`, `SplitConsistent()`, `Subsplit()`

Examples

```
splits <- as.Splits(PectinateTree(letters[1:9]))
efgh <- Subsplit(splits, tips = letters[5:8], keepAll = TRUE)
summary(efgh)

TrivialSplits(efgh)
summary(WithoutTrivialSplits(efgh))
```

TrivialTree *Generate trivial trees*

Description

`SingleTaxonTree()` creates a phylogenetic "tree" that contains a single taxon. `ZeroTaxonTree()` creates an empty `phylo` object with zero leaves or edges.

Usage

```
SingleTaxonTree(label = "t1", lengths = NULL)

ZeroTaxonTree()
```

Arguments

`label`	a character vector specifying the label of the tip.
`lengths`	a numeric vector specifying the edge lengths of the tree.

Value

`SingleTaxonTree()` returns a `phylo` object containing a single tip with the specified label.

`ZeroTaxonTree()` returns an empty `phylo` object.

See Also

Other tree manipulation: AddTip(), CollapseNode(), ConsensusWithout(), DropTip(), ImposeConstraint(), KeptPaths(), KeptVerts(), LeafLabelInterchange(), MakeTreeBinary(), Renumber(), RenumberTips(), RenumberTree(), RootTree(), SortTree(), Subtree(), TipTimedTree()

Other tree generation functions: ConstrainedNJ(), GenerateTree, NJTree(), TreeNumber

Examples

```
SingleTaxonTree("Homo_sapiens")
plot(SingleTaxonTree("root") + BalancedTree(4))

ZeroTaxonTree()
```

Unquote *Remove quotation marks from a string*

Description

Remove quotation marks from a string

Usage

```
Unquote(string)
```

Arguments

string	Input string

Value

Unquote() returns string, with any matched punctuation marks and trailing whitespace removed.

Author(s)

Martin R. Smith

See Also

Other string parsing functions: EndSentence(), MatchStrings(), MorphoBankDecode(), RightmostCharacter()

Examples

```
Unquote("'Hello World'")
```

`UnrootedTreesMatchingSplit`
Number of trees consistent with split

Description

Calculates the number of unrooted bifurcating trees consistent with the specified multi-partition split, using theorem two of Carter et al. (1990).

Usage

```
UnrootedTreesMatchingSplit(...)

LnUnrootedTreesMatchingSplit(...)

Log2UnrootedTreesMatchingSplit(...)
```

Arguments

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

Value

`UnrootedTreesMatchingSplit()` returns an integer specifying the number of unrooted bifurcating trees consistent with the specified split.

Author(s)

Martin R. Smith (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

Other split information functions: `CharacterInformation()`, `SplitInformation()`, `SplitMatchProbability()`, `TreesMatchingSplit()`

Examples

```
UnrootedTreesMatchingSplit(c(3, 5))
UnrootedTreesMatchingSplit(3, 2, 1, 2)
```

UnshiftTree *Add tree to start of list*

Description

UnshiftTree() adds a phylogenetic tree to the start of a list of trees. This is useful where the class of a list of trees is unknown, or where names of trees should be retained.

Usage

```
UnshiftTree(add, treeList)
```

Arguments

add	Tree to add to the list, of class phylo.
treeList	A list of trees, of class list, multiPhylo, or, if a single tree, phylo.

Details

Caution: adding a tree to a multiPhylo object whose own attributes apply to all trees, for example trees read from a Nexus file, causes data to be lost.

Value

UnshiftTree() returns a list of class list or multiPhylo (following the original class of treeList), whose first element is the tree specified as 'add.

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

c() joins a tree or series of trees to a multiPhylo object, but loses names and does not handle lists of trees.

Other utility functions: ClusterTable, ClusterTable-methods, Hamming(), MSTEdges(), SampleOne(), TipTimedTree(), as.multiPhylo(), match,phylo,phylo-method, sapply64(), sort.multiPhylo()

Examples

```
forest <- as.phylo(0:5, 6)
tree <- BalancedTree(6)

UnshiftTree(tree, forest)
UnshiftTree(tree, tree)
```

`WriteTntCharacters` *Write morphological character matrix to TNT file*

Description

Write morphological character matrix to TNT file

Usage

```
WriteTntCharacters(
  dataset,
  filepath = NULL,
  comment = "Dataset written by `TreeTools::WriteTntCharacters()`",
  types = NULL,
  pre = "",
  post = ""
)

## S3 method for class 'phyDat'
WriteTntCharacters(
  dataset,
  filepath = NULL,
  comment = "Dataset written by `TreeTools::WriteTntCharacters()`",
  types = NULL,
  pre = "",
  post = ""
)

## S3 method for class 'matrix'
WriteTntCharacters(
  dataset,
  filepath = NULL,
  comment = "Dataset written by `TreeTools::WriteTntCharacters()`",
  types = NULL,
  pre = "",
  post = ""
)
```

Arguments

`dataset`	Morphological dataset of class `phyDat` or `matrix`.
`filepath`	Path to file; if `NULL`, returns a character vector.
`comment`	Optional comment with which to entitle matrix.
`types`	Optional list specifying where different data types begin. `c(num = 1, dna = 10)` sets characters 1..9 as numeric, 10..end as DNA.

pre, post — Character vector listing text to print before and after the character matrix. Specify pre = 'piwe=; if the matrix is to be analysed using extended implied weighting (xpiwe=).

Author(s)

Martin R. Smith (martin.smith@durham.ac.uk)

See Also

ReadTntCharacters()

Examples

```
data("Lobo", package = "TreeTools")

WriteTntCharacters(Lobo.phy)

# Read with extended implied weighting
WriteTntCharacters(Lobo.phy, pre = "piwe=10;", post = "xpiwe=;")

# Write to a file with:
# WriteTntCharacters(Lobo.phy, "example_file.tnt")
```

---

xor *Exclusive OR operation*

Description

Exclusive OR operation

Usage

```
xor(x, y)

## S4 method for signature 'Splits,Splits'
xor(x, y)
```

Arguments

x, y — Objects to be compared.

See Also

Other Splits operations: LabelSplits(), NSplits(), NTip(), PolarizeSplits(), SplitFrequency(), Splits, SplitsInBinaryTree(), TipLabels(), TipsInSplits(), match,Splits,Splits-method

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