Package: phylogram (via r-universe)

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Type Package

Title Dendrograms for Evolutionary Analysis

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Description Contains functions for developing phylogenetic trees as deeply-nested lists (``dendrogram" objects). Enables bi-directional conversion between dendrogram and ``phylo" objects (see Paradis et al (2004) <doi:10.1093/bioinformatics/btg412>), and features several tools for command-line tree manipulation and import/export via Newick parenthetic text.

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LazyData TRUE

URL https://docs.ropensci.org/phylogram, http://github.com/ropensci/phylogram

BugReports http://github.com/ropensci/phylogram/issues

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Imports ape (>= 4.0), methods, stats

Suggests dendextend, knitr, rmarkdown, testthat

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`as.cladogram` *Apply unweighted branch lengths.*

Description

This function sets the 'height' attributes of all leaf nodes to zero and progressively resets the heights of the inner nodes by single incremental units in a bottom-up fashion.

Usage

```
as.cladogram(x)
```

Arguments

`x`	an object of class `"dendrogram"`.

Value

an object of class `"dendrogram"`.

Author(s)

Shaun Wilkinson

Examples

```
x <- read.dendrogram(text = "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);")
plot(x, horiz = TRUE)
x <- as.cladogram(x)
plot(x, horiz = TRUE)
```

`as.dendrogram.phylo` *Convert a "phylo" object to a dendrogram.*

Description

This function converts a "phylo" object (Paradis et al 2004) to a dendrogram.

Usage

```
## S3 method for class 'phylo'
as.dendrogram(object, ...)
```

Arguments

`object`	an object of class "phylo".
`...`	further arguments to be passed between methods.

Value

an object of class "dendrogram".

Author(s)

Shaun Wilkinson

References

Paradis E, Claude J, Strimmer K, (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* **20**, 289-290.

Paradis E (2008) Definition of Formats for Coding Phylogenetic Trees in R. http://ape-package.ird.fr/misc/FormatTreeR_24Oct2012.pdf

Paradis E (2012) Analysis of Phylogenetics and Evolution with R (Second Edition). Springer, New York.

Examples

```
newick <- "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);"
x <- read.dendrogram(text = newick)
y <- as.phylo(x)
z <- as.dendrogram(y)
identical(x, z)
```

`as.phylo.dendrogram` *Convert a dendrogram to a "phylo" object.*

Description

This function converts a dendrogram into an object of class "phylo" (see Paradis et al 2004).

Usage

```
## S3 method for class 'dendrogram'
as.phylo(x, ...)
```

Arguments

`x`	a dendrogram.
`...`	further arguments to be passed between methods.

Value

an object of class "phylo".

Author(s)

Shaun Wilkinson

References

Paradis E, Claude J, Strimmer K, (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* **20**, 289-290.

Paradis E (2008) Definition of Formats for Coding Phylogenetic Trees in R. http://ape-package.ird.fr/misc/FormatTreeR_24Oct2012.pdf

Paradis E (2012) Analysis of Phylogenetics and Evolution with R (Second Edition). Springer, New York.

Examples

```
newick <- "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);"
x <- read.dendrogram(text = newick)
y <- as.phylo(x)
z <- as.dendrogram(y)
```

ladder *Reorder tree branches in ladderized pattern.*

Description

This function ladderizes the branches of a dendrogram object to aid in visual interpretation.

Usage

```
ladder(x, decreasing = FALSE)
```

Arguments

x	an object of class "dendrogram".
decreasing	logical indicating whether the tree should be ladderized upwards or downwards. Defaults to FALSE (downwards).

Details

This function is the dendrogram analogue of the ladderize function in the ape package (Paradis et al 2004, 2012).

Value

Returns an object of class dendrogram.

Author(s)

Shaun Wilkinson

References

Paradis E, Claude J, Strimmer K, (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* **20**, 289-290.

Paradis E (2012) Analysis of Phylogenetics and Evolution with R (Second Edition). Springer, New York.

See Also

The ladderize function in the ape package performs a similar operation for objects of class "phylo".

Examples

```
x <- read.dendrogram(text = "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);")
plot(x, horiz = TRUE)
x <- ladder(x, decreasing = TRUE)
plot(x, horiz = TRUE)
```

phylogram *Dendrograms for evolutionary analysis.*

Description

The **phylogram** R package is a tool for for developing phylogenetic trees as deeply-nested lists known as "dendrogram" objects. It provides functions for conversion between "dendrogram" and "phylo" class objects, as well as several tools for command-line tree manipulation and import/export via Newick parenthetic text. This improves accessibility to the comprehensive range of object-specific analytical and tree-visualization functions found across a wide array of bioinformatic R packages.

Functions

A brief description of the primary **phylogram** functions are provided with links to their help pages below.

File import/export

- `read.dendrogram` reads a Newick parenthetic text string from a file or text connection and creates an object of class `"dendrogram"`
- `write.dendrogram` outputs an object of class `"dendrogram"` to a text string or file in Newick format

Object conversion

- `as.phylo.dendrogram` converts a dendrogram to an object of class "phylo" `"dendrogram"`
- `as.dendrogram.phylo` converts a "phylo" object to a dendrogram

Tree editing and manipulation

- `prune` remove branches from a `dendrogram` object based on regular expression pattern matching
- `ladder` reorders the branches of a `dendrogram` object to aid visualization
- `remidpoint` recursively sets "midpoint" and "members" attributes for a nested list/`dendrogram` object
- `reposition` shifts a `dendrogram` object up or down (or sideways if plotted horizontally)
- `as.cladogram` modifies the "height" attributes of the nodes such that all leaves terminate at zero

prune *Remove tree nodes by regular expression pattern matching.*

Description

"prune" takes an object of class "dendrogram" and removes all branches whose branch labels match a given regular expression.

Usage

```
prune(tree, pattern, keep = FALSE, ...)
```

Arguments

tree	an object of class "dendrogram".
pattern	a regular expression.
keep	logical indicating whether the nodes whose labels match the regular expression provided in "pattern" should be kept and the remainder discarded. Defaults to FALSE. Note that nodes without "label" attributes are ignored.
...	further arguments to be passed to grepl and gsub.

Details

This function recursively tests the "label" attribute of each dendrogram node (including non-leaf inner nodes if applicable) for the specified pattern, removing those that register a positive hit. Note that positive matching inner nodes are removed along with all of their sub-nodes, regardless of whether the "label" attributes of the sub-nodes match the pattern.

Value

Returns an object of class "dendrogram".

Author(s)

Shaun Wilkinson

See Also

The drop.tip function in the ape package performs a similar operation for objects of class "phylo". See regex for help with compiling regular expressions.

Examples

```
x <- read.dendrogram(text = "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);")
plot(x, horiz = TRUE)
x <- prune(x, pattern = "^A$")
plot(x, horiz = TRUE)
```

`read.dendrogram` *Read a dendrogram from parenthetic text.*

Description

This function wraps the `read.tree` parser from the `ape` package to read a phylogenetic tree from parenthetic text in the Newick/New Hampshire format, and converts it to object of class "dendrogram".

Usage

```
read.dendrogram(file = "", text = NULL, ...)
```

Arguments

`file`	character string giving a valid path to the file from which to read the data.
`text`	optional character string in lieu of a "file" argument. If a text argument is provided instead of a file path, the data are read via a text connection.
`...`	further arguments to be passed to `read.tree` (which may then be passed on to `scan`).

Value

an object of class `"dendrogram"`.

Author(s)

Shaun Wilkinson

References

Felsenstein J (1986) The Newick tree format. http://evolution.genetics.washington.edu/phylip/newicktree.html

Olsen G (1990) Interpretation of the "Newick's 8:45" tree format standard. http://evolution.genetics.washington.edu/phylip/newick_doc.html

Paradis E, Claude J, Strimmer K, (2004) APE: analyses of phylogenetics and evolution in R language. *Bioinformatics* **20**, 289-290.

Paradis E (2008) Definition of Formats for Coding Phylogenetic Trees in R. http://ape-package.ird.fr/misc/FormatTreeR_24Oct2012.pdf

Paradis E (2012) Analysis of Phylogenetics and Evolution with R (Second Edition). Springer, New York.

See Also

`write.dendrogram` writes an object of class `"dendrogram"` to a Newick text string. The `read.tree` function in the `ape` package parses objects of class `"phylo"` and `"multiPhylo"`.

Examples

```
x <- read.dendrogram(text = "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);")
plot(x, horiz = TRUE)
```

`remidpoint` *Set dendrogram attributes for a nested list.*

Description

`remidpoint` is a helper function used for manually creating `"dendrogram"` objects from nested lists. The function recursively assigns the necessary 'midpoint', 'members', and 'leaf' attributes at each node.

Usage

```
remidpoint(x)
```

Arguments

`x`	a nested list, possibly of class `"dendrogram"`

Value

returns a nested list, or an object of class `"dendrogram"` depending on the class of the input object.

Author(s)

Shaun Wilkinson

Examples

```
## manually create a small dendrogram with three members, A, B and C
x <- list("A", list("B", "C"))
attr(x[[1]], "leaf") <- TRUE
attr(x[[2]][[1]], "leaf") <- TRUE
attr(x[[2]][[2]], "leaf") <- TRUE
attr(x[[1]], "label") <- "A"
attr(x[[2]][[1]], "label") <- "B"
attr(x[[2]][[2]], "label") <- "C"
attr(x, "height") <- 1
attr(x[[1]], "height") <- 0
attr(x[[2]], "height") <- 0.5
attr(x[[2]][[1]], "height") <- 0
attr(x[[2]][[2]], "height") <- 0
x <- remidpoint(x)
class(x) <- "dendrogram"
plot(x, horiz = TRUE)
```

reposition *Reset dendrogram height attributes.*

Description

reposition is a helper function used for manually creating "dendrogram" objects from nested lists. The function recursively reassigns the 'height' attributes at each node by a given constant.

Usage

```
reposition(x, shift = "reset")
```

Arguments

x	an object of class "dendrogram".
shift	either the character string "reset" (shift the graph so that the height of the farthest leaf from the root is zero), or a numeric value giving the amount to shift the graph along the primary axis.

Value

Returns an object of class "dendrogram".

Author(s)

Shaun Wilkinson

Examples

```
x <- read.dendrogram(text = "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);")
plot(x, horiz = TRUE)
x <- reposition(x)
plot(x, horiz = TRUE)
```

write.dendrogram *Write a dendrogram object to parenthetic text.*

Description

This function exports a dendrogram object as a Newick/New Hampshire text string.

Usage

```
write.dendrogram(x, file = "", append = FALSE, edges = TRUE, ...)
```

Arguments

x	an object of class "dendrogram".
file	a character string naming a file or connection to write the output to. If no file path is specified or file = "" the result is printed to the console.
append	logical indicating whether the output should be appended to the file. If append = FALSE the contents of the file will be overwritten (the default setting).
edges	logical indicating whether edge weights should be included in the output string.
...	further arguments to be passed to format. Used to specify the numbering style of the edge weights (if edges = TRUE).

References

Felsenstein J (1986) The Newick tree format. http://evolution.genetics.washington.edu/phylip/newicktree.html

Olsen G (1990) Interpretation of the "Newick's 8:45" tree format standard. http://evolution.genetics.washington.edu/phylip/newick_doc.html

See Also

read.dendrogram to parse a "dendrogram" object from a text file. The write.tree function in the ape package performs a similar operation for "phylo" and "multiPhylo" objects.

Examples

```
newick <- "(A:0.1,B:0.2,(C:0.3,D:0.4):0.5);"
x <- read.dendrogram(text = newick)
write.dendrogram(x, edges = TRUE)
```

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