Package 'tidytree'

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Title A Tidy Tool for Phylogenetic Tree Data Manipulation

Version 0.4.9

Description Phylogenetic trees contain components such as nodes, edges, branches, and associated data. As the core data manipulation tool in the 'ggtree' ecosystem, 'tidytree' provides tools for converting tree objects to tidy data frames and tidy interfaces for manipulating, analyzing, and visualizing tree data.

Depends R (>= 3.4.0)

Imports ape, dplyr, lazyeval, magrittr, methods, rlang, tibble, tidyr, tidyselect, yulab.utils (>= 0.1.5), pillar, cli

Suggests testthat

ByteCompile true

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URL https://yulab-smu.top/contribution-tree-data/

BugReports https://github.com/YuLab-SMU/tidytree/issues

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`ancestor` *ancestor*

Description

access ancestor data

Usage

```
ancestor(.data, .node, ...)

## S3 method for class 'tbl_tree'
ancestor(.data, .node, ...)
```

Arguments

.data	phylo or tbl_tree object
.node	node number
...	additional parameters

Value

ancestor data

Author(s)

Guangchuang Yu

Examples

```
library(ape)
tree <- rtree(4)
x <- as_tibble(tree)
ancestor(x, 3)
```

---

as.treedata *as.treedata*

Description

convert a tree object to treedata object

Usage

```
as.treedata(tree, ...)

## S3 method for class 'tbl_tree'
as.treedata(tree, ...)
```

Arguments

tree	tree object
...	additional parameters

Value

treedata object

Examples

```
library(ape)
set.seed(2017)
tree <- rtree(4)
d <- tibble(label = paste0('t', 1:4),
            trait = rnorm(4))
x <- as_tibble(tree)
full_join(x, d, by = 'label') %>% as.treedata
```

`as.ultrametric` *as.ultrametric*

Description

as.ultrametric

Usage

```
as.ultrametric(tree, ...)
```

Arguments

`tree`	tree object
`...`	additional parameters

Value

treedata or phylo object

`child` *child*

Description

access child data

Usage

```
child(.data, .node, ...)

## S3 method for class 'tbl_tree'
child(.data, .node, ...)
```

Arguments

.data	phylo or tbl_tree object
.node	node number
...	additional parameters

Value

child data

Author(s)

Guangchuang Yu

Examples

```
library(ape)
tree <- rtree(4)
x <- as_tibble(tree)
child(x, 4)
```

---

drop.tip *drop.tip method*

Description

drop.tip method

Usage

```
drop.tip(object, tip, ...)

keep.tip(object, tip, ...)

## S4 method for signature 'treedata'
drop.tip(object, tip, ...)

## S4 method for signature 'phylo'
drop.tip(object, tip, ...)

## S4 method for signature 'treedata'
keep.tip(object, tip, ...)

## S4 method for signature 'phylo'
keep.tip(object, tip, ...)
```

Arguments

object	A treedata or phylo object
tip	a vector of mode numeric or character specifying the tips to delete
...	additional parameters

Value

updated object

Author(s)

Casey Dunn http://dunnlab.org and Guangchuang Yu https://guangchuangyu.github.io

Source

drop.tip for phylo object is a wrapper method of ape::drop.tip from the ape package. The documentation you should read for the drop.tip function can be found here: ape::drop.tip()

See Also

ape::drop.tip()

Examples

```
library(tidytree)
set.seed(123)
tr <- ape::rtree(6)
da <- data.frame(id=tip.label(tr), value = letters[seq_len(6)])
trda <- tr %>% dplyr::left_join(da, by = c('label'='id'))
tr1 <- drop.tip(tr, c("t2", "t1"))
tr2 <- keep.tip(tr, c("t2", "t1"))
```

---

get.data *get.data method*

Description

get.data method

get.data method

Usage

```
get.data(object, ...)

## S4 method for signature 'treedata'
get.data(object)
```

Arguments

object	treedata object
...	additional parameter

Value

associated data of phylogeny

---

get.fields *get.fields method*

Description

get.fields method

Usage

```
get.fields(object, ...)

## S4 method for signature 'treedata'
get.fields(object)
```

Arguments

object	treedata object
...	additional parameter

Value

available annotation variables

---

get.treetext *get.treetext method*

Description

access tree text (newick text) from tree object

Usage

```
get.treetext(object, ...)

## S4 method for signature 'treedata'
get.treetext(object)
```

Arguments

object	treedata object
...	additional parameter

Value

phylo object

`getNodeNum` *getNodeNum*

Description

calculate total number of nodes

Usage

```
getNodeNum(tree)
```

Arguments

tree	tree object

Value

number

Author(s)

Guangchuang Yu

Examples

```
getNodeNum(rtree(30))
```

get_tree_data *get_tree_data*

Description

get associated data stored in treedata object

Usage

```
get_tree_data(tree_object)
```

Arguments

tree_object	a treedata object

Value

tbl_df

Author(s)

guangchuang yu

groupClade *groupClade*

Description

grouping clades

Usage

```
groupClade(.data, .node, group_name = "group", overlap = "overwrite", ...)
```

Arguments

.data	tree object (phylo, treedata, tbl_tree, ggtree etc.)
.node	selected nodes
group_name	character the name of the group cluster, default is group.
overlap	character one of overwrite, origin and abandon, default is overwrite.
...	additional parameter

Value

updated tree with group information or group index

Author(s)

Guangchuang Yu

`groupOTU` *groupOTU*

Description

grouping OTUs

Usage

```
groupOTU(.data, .node, group_name = "group", ...)
```

Arguments

`.data`	tree object (phylo, treedata, tbl_tree, ggtree etc.)
`.node`	selected nodes
`group_name`	character the name of the group cluster, default is `group`.
`...`	additional parameter

Value

updated tree with group information or group index

Author(s)

Guangchuang Yu

`isTip` *isTip*

Description

whether the node is a tip

Usage

```
isTip(.data, .node, ...)

## S3 method for class 'tbl_tree'
isTip(.data, .node, ...)

## S3 method for class 'phylo'
isTip(.data, .node, ...)

## S3 method for class 'treedata'
isTip(.data, .node, ...)
```

Arguments

`.data`	phylo, treedata or tbl_tree object
`.node`	node number
`...`	additional parameters

Value

logical value

Author(s)

Guangchuang Yu

`MRCA` *MRCA*

Description

access most recent common ancestor data

Usage

```
MRCA(.data, ...)
```

Arguments

`.data`	phylo or tbl_tree object
`...`	additional parameters

Value

MRCA data

Author(s)

Guangchuang Yu

Nnode.treedata *Nnode*

Description

number of nodes

Usage

```
## S3 method for class 'treedata'
Nnode(phy, internal.only = TRUE, ...)
```

Arguments

phy	treedata object
internal.only	whether only count internal nodes
...	additional parameters

Value

number of nodes

Author(s)

Guangchuang Yu

Examples

```
Nnode(rtree(30))
```

node.label *extract the node label of phylo, treedata or tbl_tree*

Description

extract the node label of phylo, treedata or tbl_tree

Usage

```
node.label(x, node = "internal", ...)
```

Arguments

x	object, should be one of treedata, phylo or tbl_tree.
node	character, to extract which type node label, default is internal, should be one of internal, external, all, tip.
...	additional parameters.

Value

label character vector.

`nodeid` *nodeid*

Description

convert tree label to internal node number

Usage

```
nodeid(tree, label)
```

Arguments

`tree`	tree object
`label`	tip/node label(s)

Value

node number

Author(s)

Guangchuang Yu

`nodelab` *nodelab*

Description

convert internal node number tip/node label

Usage

```
nodelab(tree, id)
```

Arguments

`tree`	tree object
`id`	node number

Value

tip/node label(s)

Author(s)

Guangchuang Yu

`offspring` *offspring*

Description

access offspring data

Usage

```
offspring(.data, .node, tiponly, self_include, ...)

## S3 method for class 'tbl_tree'
offspring(.data, .node, tiponly = FALSE, self_include = FALSE, ...)
```

Arguments

`.data`	phylo or tbl_tree object
`.node`	node number
`tiponly`	whether only return tip nodes
`self_include`	whether include the input node, only applicable for tiponly = FALSE
`...`	additional parameters

Value

offspring data

Author(s)

Guangchuang Yu

Examples

```
library(ape)
tree <- rtree(4)
x <- as_tibble(tree)
offspring(x, 4)
```

offspring_bulk *Descendants of many nodes in one pass*

Description

offspring() walks one subtree per call. Calling it once per node is O(n^2): 1.3 s at 1000 tips and 3 s at 2000. This function computes the descendants of every requested node in a single post-order pass, which is about 50 times faster for that pattern.

Usage

```
offspring_bulk(tree, nodes = NULL, tips_only = FALSE)
```

Arguments

tree	a tree object: tbl_tree, phylo or treedata.
nodes	node ids to compute descendants for. NULL computes every internal node.
tips_only	logical. If TRUE, keep only tip ids, matching offspring(tree, node, tiponly = TRUE).

Value

A named list, one element per node id. The descendants **do not include the node itself**; add it with c(node, result[[node]]) if you need it.

Examples

```
library(ape)
tr <- rtree(6)
x <- as_tibble(tr)
offspring_bulk(x, nodes = c(7, 8))
```

parent *parent*

Description

access parent data

Usage

```
parent(.data, .node, ...)

## S3 method for class 'tbl_tree'
parent(.data, .node, ...)
```

Arguments

.data	phylo or tbl_tree object
.node	node number
...	additional parameters

Value

parent data

Author(s)

Guangchuang Yu

Examples

```
library(ape)
tree <- rtree(4)
x <- as_tibble(tree)
parent(x, 2)
```

---

root.treedata *root*

Description

re-root a tree

Usage

```
## S3 method for class 'treedata'
root(phy, outgroup, node = NULL, edgelabel = TRUE, ...)
```

Arguments

phy	tree object
outgroup	a vector of mode numeric or character specifying the new outgroup
node	node to reroot
edgelabel	a logical value specifying whether to treat node labels as edge labels and thus eventually switching them so that they are associated with the correct edges.
...	additional parameters passed to ape::root.phylo

Value

rerooted treedata

rootnode *rootnode*

Description

access root node data

Usage

```
rootnode(.data, ...)
```

Arguments

.data	phylo or tbl_tree object
...	additional parameters

Value

root node data

Author(s)

Guangchuang Yu

show *show method*

Description

show method for treedata instance

Usage

```
show(object)
```

Arguments

object	treedata object

Value

print info

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

sibling *sibling*

Description

access sibling data

Usage

```
sibling(.data, ...)
```

Arguments

.data	phylo or tbl_tree object
...	additional parameters

Value

sibling

Author(s)

Guangchuang Yu

td-label-assign *the tip or internal node label assign of tbl_tree phylo and treedata*

Description

the tip or internal node label assign of tbl_tree phylo and treedata

Usage

```
tip.label(x) <- value

node.label(x) <- value

## S3 replacement method for class 'phylo'
node.label(x) <- value

## S3 replacement method for class 'treedata'
node.label(x) <- value

## S3 replacement method for class 'tbl_tree'
node.label(x) <- value
```

```
## S3 replacement method for class 'phylo'
tip.label(x) <- value

## S3 replacement method for class 'treedata'
tip.label(x) <- value

## S3 replacement method for class 'tbl_tree'
tip.label(x) <- value
```

Arguments

x	object, should be one of tbl_tree, phylo or treedata
value	character, the character vector

---

tip.label *extract the tip label of phylo treedata or tbl_tree*

Description

extract the tip label of phylo treedata or tbl_tree

Usage

```
tip.label(x, ...)
```

Arguments

x	object, should be one of treedata, phylo or tbl_tree.
...	additional parameters.

---

treedata *treedata*

Description

treedata object contructor

Usage

```
treedata(...)
```

Arguments

...	parameters

Value

treedata object

Author(s)

guangchuang yu

`treedata-class` *Class "treedata" This class stores phylogenetic tree with associated data*

Description

Class "treedata" This class stores phylogenetic tree with associated data

Slots

`file` tree file

`treetext` newick tree string

`phylo` phylo object for tree structure

`data` associated data

`extraInfo` extra information, reserve for merge_tree

`tip_seq` tip sequences

`anc_seq` ancestral sequences

`seq_type` sequence type, one of NT or AA

`tipseq_file` tip sequence file

`ancseq_file` ancestral sequence file

`info` extra information, e.g. metadata, software version etc.

Author(s)

Guangchuang Yu https://guangchuangyu.github.io

tree_subset *Subset tree objects by related nodes*

Description

This function allows for a tree object to be subset by specifying a node and returns all related nodes within a selected number of levels

Usage

```
tree_subset(
  tree,
  node,
  levels_back = 5,
  group_node = TRUE,
  group_name = "group",
  root_edge = TRUE
)

## S3 method for class 'phylo'
tree_subset(
  tree,
  node,
  levels_back = 5,
  group_node = TRUE,
  group_name = "group",
  root_edge = TRUE
)

## S3 method for class 'treedata'
tree_subset(
  tree,
  node,
  levels_back = 5,
  group_node = TRUE,
  group_name = "group",
  root_edge = TRUE
)
```

Arguments

tree	a tree object of class phylo
node	either a tip label or a node number for the given tree that will be the focus of the subsetted tree
levels_back	a number specifying how many nodes back from the selected node the subsetted tree should include

group_node	whether add grouping information of selected node
group_name	group name (default 'group') for storing grouping information if group_node = TRUE
root_edge	If TRUE (by default), set root.edge to path length of orginal root to the root of subset tree

Details

This function will take a tree and a specified node from that tree and subset the tree showing all relatives back to a specified number of nodes. This function allows for a combination of `ancestor` and `offspring` to return a subsetted tree that is of class phylo. This allows for easy graphing of the tree with `ggtree`

Examples

```
set.seed(123)
tree <- ape::rtree(6)
sub_tree <- tree_subset(tree, node = "t1", levels_back = 2)
```

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