

Package ‘tidytree’

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Title A Tidy Tool for Phylogenetic Tree Data Manipulation

Version 0.3.7

Description Phylogenetic tree generally contains multiple components including node, edge, branch and associated data. 'tidytree' provides an approach to convert tree object to tidy data frame as well as provides tidy interfaces to manipulate tree data.

Depends R (>= 3.4.0)

Imports ape, dplyr, lazyeval, magrittr, methods, rlang, tibble, tidyr, tidyselect, yulab.utils (>= 0.0.4)

Suggests knitr, rmarkdown, prettydoc, testthat, pillar, utils

VignetteBuilder knitr

ByteCompile true

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URL <https://yulab-smu.top/treedata-book/>

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

Encoding UTF-8

RoxygenNote 7.1.2

NeedsCompilation no

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ancestor	<i>ancestor</i>
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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
```

child	<i>child</i>
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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)
```

get.data	<i>get.data method</i>
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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

<i>get.fields</i>	<i>get.fields method</i>
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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_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, ...)
```

Arguments

.data tree object (phylo, treedata, tbl_tree, ggtree etc.)
.node selected nodes
... additional parameter

Value

updated tree with group information or group index

Author(s)

Guangchuang Yu

groupOTU

groupOTU

Description

grouping OTUs

Usage

groupOTU(.data, .node, ...)

Arguments

.data	tree object (phylo, treedata, tbl_tree, ggtree etc.)
.node	selected nodes
...	additional parameter

Value

updated tree with group information or group index

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

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	<i>offspring</i>
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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)
```

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)
```

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

treedata *treedata*

Description

treedata object constructor

Usage

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

Arguments

... parameters

Value

treedata object

Author(s)

guangchuang yu

treedata-class	<i>Class "treedata" This class stores phylogenetic tree with associated data</i>
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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>

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