

# Package ‘tidytree’

September 26, 2022

**Title** A Tidy Tool for Phylogenetic Tree Data Manipulation

**Version** 0.4.1

**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), pillar

**Suggests** knitr, rmarkdown, prettydoc, testthat, utils

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://www.amazon.com/Integration-Manipulation-Visualization-Phylogenetic-Computational-ebook/dp/B0B5NLZR1Z/>

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

**Encoding** UTF-8

**RoxygenNote** 7.2.1

**NeedsCompilation** no

**Author** Guangchuang Yu [aut, cre, cph]  
(<https://orcid.org/0000-0002-6485-8781>),  
Bradley Jones [ctb],  
Zebulun Arendsee [ctb]

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

**Repository** CRAN

**Date/Publication** 2022-09-26 10:10:02 UTC

**R topics documented:**

ancestor . . . . .	2
as.treedata . . . . .	3
child . . . . .	4
get.data . . . . .	4
get.fields . . . . .	5
get_tree_data . . . . .	6
groupClade . . . . .	6
groupOTU . . . . .	7
MRCA . . . . .	7
nodeid . . . . .	8
nodelab . . . . .	8
offspring . . . . .	9
parent . . . . .	10
rootnode . . . . .	10
show . . . . .	11
sibling . . . . .	12
treedata . . . . .	12
treedata-class . . . . .	13

<b>Index</b>	<b>14</b>
--------------	-----------

---

ancestor	<i>ancestor</i>
----------	-----------------

---

**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>
-------	--------------

---

**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>
----------	------------------------

---

**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>
-------------------	--------------------------

---

**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>
-----------	------------------

---

**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**

<code>.data</code>	phylo or <code>tbl_tree</code> object
<code>.node</code>	node number
<code>tiponly</code>	whether only return tip nodes
<code>self_include</code>	whether include the input node, only applicable for <code>tiponly = FALSE</code>
<code>...</code>	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 <i>tbl_tree</i> 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>
----------------	--

---

**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>

# Index

## \* classes

treedata-class, 13

ancestor, 2

as.treedata, 3

child, 4

get.data, 4

get.data, treedata-method (get.data), 4

get.fields, 5

get.fields, treedata (get.fields), 5

get.fields, treedata-method  
(get.fields), 5

get\_tree\_data, 6

groupClade, 6

groupOTU, 7

MRCA, 7

nodeid, 8

nodelab, 8

offspring, 9

parent, 10

rootnode, 10

show, 11

show, treedata-method (treedata-class),  
13

sibling, 12

treedata, 12

treedata-class, 13