

# Package ‘tidytree’

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

**Version** 0.1.8

**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, tibble

**Suggests** ggtree, knitr, prettydoc, testthat, treeio

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://github.com/GuangchuangYu/tidytree>

**BugReports** <https://github.com/GuangchuangYu/tidytree/issues>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**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_data_frame(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_data_frame(tree)
full_join(x, d, by = 'label') %>% as.treedata
```

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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_data_frame(tree)  
child(x, 4)
```

---

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

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

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<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

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get_tree_data	<i>get_tree_data</i>
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**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

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groupClade	<i>groupClade</i>
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**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

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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

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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

offspring                      *offspring*

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**Description**

access offspring data

**Usage**

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

**Arguments**

<code>.data</code>	phylo or <code>tbl_tree</code> object
<code>.node</code>	node number
<code>...</code>	additional parameters

**Value**

offspring data

**Author(s)**

guangchuang yu

**Examples**

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

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parent                      *parent*

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**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_data_frame(tree)  
parent(x, 2)
```

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rootnode

*rootnode*

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**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

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`show`*show method*

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**Description**

show method for treedata instance

**Usage**`show(object)`**Arguments**`object` treedata object**Value**

print info

**Author(s)**Guangchuang Yu <https://guangchuangyu.github.io>

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`sibling`*sibling*

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**Description**

access sibling data

**Usage**`sibling(.data, ...)`**Arguments**`.data` phylo or tbl\_tree object  
`...` additional parameters**Value**

sibling

**Author(s)**

guangchuang yu

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treedata	<i>treedata</i>
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**Description**

treedata object constructor

**Usage**

treedata(...)

**Arguments**

... parameters

**Value**

treedata object

**Author(s)**

guangchuang yu

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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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