

# Package ‘treeio’

January 21, 2025

**Title** Base Classes and Functions for Phylogenetic Tree Input and Output

**Version** 1.31.0

**Description** 'treeio' is an R package to make it easier to import and store phylogenetic tree with associated data; and to link external data from different sources to phylogeny. It also supports exporting phylogenetic tree with heterogeneous associated data to a single tree file and can be served as a platform for merging tree with associated data and converting file formats.

**Depends** R ( $\geq 3.6.0$ )

**Imports** ape, dplyr, jsonlite, magrittr, methods, rlang, stats, tibble, tidytree ( $\geq 0.4.5$ ), utils, yulab.utils ( $\geq 0.1.6$ )

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**Encoding** UTF-8

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

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treeio-package	<i>treeio: Base Classes and Functions for Phylogenetic Tree Input and Output</i>
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## Description

'treeio' is an R package to make it easier to import and store phylogenetic tree with associated data; and to link external data from different sources to phylogeny. It also supports exporting phylogenetic tree with heterogeneous associated data to a single tree file and can be served as a platform for merging tree with associated data and converting file formats.

## Author(s)

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## See Also

Useful links:

- <https://yulab-smu.top/contribution-tree-data/>
- Report bugs at <https://github.com/YuLab-SMU/treeio/issues>

---

```
as.treedata.phylo    as.treedata
```

---

### Description

convert phylo to treedata

### Usage

```
## S3 method for class 'phylo'
as.treedata(tree, boot = NULL, ...)
```

### Arguments

tree	input tree, a phylo object
boot	optional, can be bootstrap value from ape::boot.phylo
...	additional parameters

### Details

converting phylo object to treedata object

### Author(s)

Guangchuang Yu

---

```
find.hclust    find the hierarchical cluster analysis among the nodes of graph based
                on the length of all the shortest paths in the graph.
```

---

### Description

find the hierarchical cluster analysis among the nodes of graph based on the length of all the shortest paths in the graph.

### Usage

```
find.hclust(
  x,
  graph.mst = FALSE,
  weights = NULL,
  hclust.method = "average",
  ...
)
```

**Arguments**

x	a igraph object
graph.mst	logical whether obtain the minimum spanning tree first then find.hclust, default is FALSE.
weights	a numeric vector giving edge weights or a character. If this is NULL and the graph has a weight edge attribute, then the attribute is used. If this is NA then no weights are used even if the graph has a weight attribute. If this is a character, the graph has the edge attribute which is numeric, then it will be used, default is NULL.
hclust.method	the agglomeration method to be used, This should be (an unambiguous abbreviation of) one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
...	additional parameters

**Value**

hclust object

**Examples**

```
library(igraph)
set.seed(123)
g <- igraph::sample_gnp(100, .1) %>%
  set_edge_attr(name='weight', value=abs(rnorm(E(.),3)))
tr1 <- find.hclust(g, weights = NA)
tr2 <- find.hclust(g)
tr3 <- find.hclust(g, graph.mst = TRUE)
```

---

get.placements            *get.placements*

---

**Description**

access placement information

**Usage**

```
get.placements(tree, ...)

## S3 method for class 'jplace'
get.placements(tree, by = "best", ...)
```

**Arguments**

tree	tree object
...	additional parameters
by	one of 'best' and 'all'

**Value**

placement tibble

---

get.tree	<i>get.tree</i>
----------	-----------------

---

**Description**

access phylo slot

**Usage**

```
get.tree(x, ...)
```

**Arguments**

x	tree object
...	additional parameters

**Value**

phylo object

**Author(s)**

Guangchuang Yu

---

get.treetext	<i>get.treetext method</i>
--------------	----------------------------

---

**Description**

access tree text (newick text) from tree object

**Usage**

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

**Arguments**

object	treedata object
...	additional parameter

**Value**

phylo object

---

*getNodeNum*                      *getNodeNum*

---

**Description**

calculate total number of nodes

**Usage**

`getNodeNum(tree)`

`Nnode2(tree)`

**Arguments**

`tree`                      tree object

**Value**

number

**Author(s)**

Guangchuang Yu

**Examples**

`getNodeNum(rtree(30))`  
`Nnode2(rtree(30))`

---

*is.ggtree*                      *is.ggtree*

---

**Description**

test whether input object is produced by `ggtree` function

**Usage**

`is.ggtree(x)`

**Arguments**

`x`                              object

**Value**

TRUE or FALSE

**Author(s)**

Guangchuang Yu

---

jplace-class	<i>Class "jplace" This class stores phylogenetic placements</i>
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---

**Description**

Class "jplace" This class stores phylogenetic placements

**Slots**

phylo phylo object for tree structure  
 treetext newick tree string  
 data associated data  
 extraInfo extra information, reserve for merge\_tree  
 file tree file  
 placements reserve for jplace file to store placement information  
 info extra information, e.g. metadata, software version etc.

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


---

label_branch_paml	<i>label_branch_paml</i>
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---

**Description**

label branch for PAML to infer selection pressure using branch model

**Usage**

label\_branch\_paml(tree, node, label)

**Arguments**

tree	phylo object
node	node number
label	label of branch, e.g. #1



**Value**

updated phylo object

**Author(s)**

Guangchuang Yu

---

mask	<i>mask</i>
------	-------------

---

**Description**

site mask

**Usage**

```
mask(tree_object, field, site, mask_site = FALSE)
```

**Arguments**

tree_object	tree object
field	selected field
site	site
mask_site	if TRUE, site will be masked. if FALSE, selected site will not be masked, while other sites will be masked.

**Value**

updated tree object

**Author(s)**

Guangchuang Yu

---

<code>merge_tree</code>	<i>merge_tree</i>
-------------------------	-------------------

---

**Description**

merge two tree object

**Usage**

```
merge_tree(obj1, obj2)
```

**Arguments**

<code>obj1</code>	tree object 1
<code>obj2</code>	tree object 2

**Value**

tree object

**Author(s)**

Guangchuang Yu

---

<code>print.treedataList</code>	<i>print</i>
---------------------------------	--------------

---

**Description**

print information of a list of treedata objects

**Usage**

```
## S3 method for class 'treedataList'  
print(x, ...)
```

**Arguments**

<code>x</code>	a list of treedata objects
<code>...</code>	no used

**Value**

message

---

raxml2nwk	<i>raxml2nwk</i>
-----------	------------------

---

**Description**

convert raxml bootstrap tree to newick format

**Usage**

```
raxml2nwk(infile, outfile = "raxml.tree")
```

**Arguments**

infile	input file
outfile	output file

**Value**

newick file

**Author(s)**

Guangchuang Yu

---

read.astral	<i>read.astral</i>
-------------	--------------------

---

**Description**

parse ASTRAL output newick text

**Usage**

```
read.astral(file)
```

**Arguments**

file	ASTRAL Newick file
------	--------------------

**Value**

treedata object

**Author(s)**

Guangchuang Yu

## Examples

```
tt <- paste0(
  "((species1,(species2,species3)'[pp1=0.75;pp2=0.24;pp3=0.01]':",
  "1.2003685744180805)'[pp1=0.98;pp2=0.02;pp3=0]':0.9679599282730038,",
  "((species4,species5)'[pp1=0.88;pp2=0.11;pp3=0.01]':1.2454851536484994))"
)
read.astral(textConnection(tt))
```

---

read.beast

*read.beast*

---

## Description

read.beast/mrbayes/mega Nexus output  
read.beast/mrbayes/mega newick file format

## Usage

```
read.beast(file, threads = 1, verbose = FALSE)
read.mrbayes(file, threads = 1, verbose = FALSE)
read.beast.newick(file, threads = 1, verbose = FALSE)
read.mega(file, threads = 1, verbose = FALSE)
```

## Arguments

file	newick file
threads	number of threads for multithreading (default: 1)
verbose	set TRUE to log progress (default: FALSE)

## Value

treedata object  
treedata object

## Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>  
Bradley R Jones

**Examples**

```

file <- system.file("extdata/BEAST", "beast_mcc.tree", package="treeio")
read.beast(file)
file <- system.file("extdata/MrBayes", "Gq_nxs.tre", package="treeio")
read.mrbayes(file)
tr <- read.beast.newick(
  textConnection(
    '(a[&rate=1]:2,(b[&rate=1.1]:1,c[&rate=0.9]:1)[&rate=1]:1);'
  )
)

```

---

read.codeml

*read.codeml*


---

**Description**

read baseml output

**Usage**

```
read.codeml(rstfile, mlcfile, tree = "mlc", type = "Joint")
```

**Arguments**

rstfile	rst file
mlcfile	mlc file
tree	one of 'mlc' or 'rst'
type	one of 'Marginal' or 'Joint'

**Value**

A treedata object

**Author(s)**

Guangchuang Yu

**Examples**

```

rstfile <- system.file("extdata/PAML_Codeml", "rst", package="treeio")
mlcfile <- system.file("extdata/PAML_Codeml", "mlc", package="treeio")
read.codeml(rstfile, mlcfile)

```

read.codeml\_mlc      *read.codeml\_mlc*

---

**Description**

read mlc file of codeml output

**Usage**

```
read.codeml_mlc(mlcfile)
```

**Arguments**

mlcfile      mlc file

**Value**

A codeml\_mlc object

**Author(s)**

Guangchuang Yu

**Examples**

```
mlcfile <- system.file("extdata/PAML_Codeml", "mlc", package="treeio")
read.codeml_mlc(mlcfile)
```

---

read.fasta      *read.fasta*

---

**Description**

read FASTA file

**Usage**

```
read.fasta(fasta, type = "auto")
```

**Arguments**

fasta      fasta file  
type      sequence type of the input file, one of 'NT' or 'AA'. Default is 'auto' and guess the sequence type automatically

**Details**

This function supports both DNA or AA sequences

**Value**

DNABin or AABin object

**Author(s)**

Guangchuang Yu

---

read.hyphy	<i>read.hyphy</i>
------------	-------------------

---

**Description**

read HYPHY output

**Usage**

```
read.hyphy(nwk, ancseq, tip.fasfile = NULL)
```

**Arguments**

nwk	tree file in nwk format, one of hyphy output
ancseq	ancestral sequence file in nexus format, one of hyphy output
tip.fasfile	tip sequence file

**Value**

A hyphy object

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**Examples**

```
nwk <- system.file("extdata/HYPHY", "labelledtree.tree", package="treeio")
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="treeio")
read.hyphy(nwk, ancseq)
```

read.hyphy.seq            *read.hyphy.seq*

---

**Description**

parse sequences from hyphy output

**Usage**

```
read.hyphy.seq(file)
```

**Arguments**

file                    output of hyphy ancestral sequence inference; nexus format

**Value**

DNABin object

**Author(s)**

Guangchuang Yu

**Examples**

```
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="treeio")
read.hyphy.seq(ancseq)
```

---

read.iqtree                *read.iqtree*

---

**Description**

parse IQ-TREE output

**Usage**

```
read.iqtree(file)
```

**Arguments**

file                    IQ-TREE Newick text

**Value**

treedata object



**Author(s)**

Guangchuang Yu

---

read.jplace            *read.jplace*

---

**Description**

read jplace file

**Usage**

read.jplace(file)

**Arguments**

file            jplace file

**Value**

jplace instance

**Author(s)**

Guangchuang Yu

**Examples**

```
jp <- system.file("extdata", "sample.jplace", package="treeio")
read.jplace(jp)
```

---

read.jtree            *read.jtree*

---

**Description**

Import tree data from jtree file, which is JSON-based text and probably output by write.jtree

**Usage**

read.jtree(file)

**Arguments**

file            tree file

**Value**

treedata object

**Author(s)**

Guangchuang Yu

---

read.mcmctree	<i>read.mcmctree</i>
---------------	----------------------

---

**Description**

read MCMCTree output Tree

**Usage**

```
read.mcmctree(file, force.ultrametric = FALSE)
```

**Arguments**

`file` the output tree file of MCMCTree

`force.ultrametric`

logical whether convert the tree to be ultrametric, if it is not ultrametric, default is FALSE. When the tree is ultrametric, branch times will be calculated automatically.

**Value**

treedata object

**Examples**

```
file <- system.file("extdata/MCMCTree", "mcmctree_output.tree", package="treeio")
tr <- read.mcmctree(file)
tr
```

---

read.mega_tabular	<i>read.mega_tabular</i>
-------------------	--------------------------

---

**Description**

parse tabular output of MEGA

**Usage**

```
read.mega_tabular(file)
```

**Arguments**

file	MEGA tabular file
------	-------------------

**Value**

treedata object

**Author(s)**

Guangchuang Yu

---

read.newick	<i>read.newick</i>
-------------	--------------------

---

**Description**

read newick tree

**Usage**

```
read.newick(file, node.label = "label", ...)
```

**Arguments**

file	newick file
node.label	parse node label as 'label' or 'support' value
...	additional parameter, passed to 'read.tree'

**Value**

phylo or treedata object

**Author(s)**

Guangchuang Yu

read.nextstrain.json    *read.nextstrain.json*

---

**Description**

read.nextstrain.json

**Usage**

```
read.nextstrain.json(x)
```

**Arguments**

x                    the json tree file of auspice from nextstrain.

**Value**

treedata object

**Author(s)**

Shuangbin Xu

**Examples**

```
file1 <- system.file("extdata/nextstrain.json", "minimal_v2.json", package="treeio")
tr <- read.nextstrain.json(file1)
tr
```

---

read.nhx                    *read.nhx*

---

**Description**

read.nhx tree file

**Usage**

```
read.nhx(file)
```

**Arguments**

file                    nhx file

**Value**

nhx object

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**Examples**

```
nhxfile <- system.file("extdata/NHX", "ADH.nhx", package="treeio")
read.nhx(nhxfile)
```

---

read.paml_rst	<i>read.paml_rst</i>
---------------	----------------------

---

**Description**

read rst file from paml (both baseml and codeml) output

**Usage**

```
read.paml_rst(rstfile, type = "Joint")
```

**Arguments**

rstfile	rst file
type	one of 'Marginal' or 'Joint'

**Value**

A treedata object

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**Examples**

```
rstfile <- system.file("extdata/PAML_Baseml", "rst", package="treeio")
read.paml_rst(rstfile)
```

read.phylip            *read.phylip*

---

**Description**

parsing phylip tree format

**Usage**

```
read.phylip(file)
```

**Arguments**

file            phylip file

**Value**

an instance of 'phylip'

**Author(s)**

Guangchuang Yu

**Examples**

```
phyfile <- system.file("extdata", "sample.phy", package="treeio")
read.phylip(phyfile)
```

---

read.phylip.seq        *read.phylip.seq*

---

**Description**

read aligned sequences from phylip format

**Usage**

```
read.phylip.seq(file)
```

**Arguments**

file            phylip file, currently only sequential format is supported

**Value**

DNABin object

**Author(s)**

Guangchuang Yu

**References**

<http://evolution.genetics.washington.edu/phylip/doc/sequence.html>

---

`read.phylip.tree`      *read.phylip.tree*

---

**Description**

parse tree from phylip file

**Usage**

`read.phylip.tree(file)`

**Arguments**

`file`                  phylip file

**Value**

phylo or multiPhylo object

**Author(s)**

Guangchuang Yu

---

`read.phyloxml`      *read.phyloxml*

---

**Description**

`read.phyloxml`

**Usage**

`read.phyloxml(file)`

**Arguments**

`file`                  phyloxml file

**Value**

treedata class or treedataList class

**Examples**

```
xmlfile1 <- system.file("extdata/phyloxml", "test_x2.xml", package="treeio")
px1 <- read.phyloxml(xmlfile1)
px1
xmlfile2 <- system.file("extdata/phyloxml", "phyloxml_examples.xml", package="treeio")
px2 <- read.phyloxml(xmlfile2)
px2
```

---

read.r8s

*read.r8s*

---

**Description**

parse output from r8s

**Usage**

```
read.r8s(file)
```

**Arguments**

file                    r8s output log file

**Value**

multiPhylo object

**Author(s)**

Guangchuang Yu

**Examples**

```
read.r8s(system.file("extdata/r8s", "H3_r8s_output.log", package="treeio"))
```



---

read.raxml	<i>read.raxml</i>
------------	-------------------

---

**Description**

parse RAxML bootstrapping analysis output

**Usage**

```
read.raxml(file)
```

**Arguments**

file                   RAxML bootstrapping analysis output

**Value**

treedata object

**Author(s)**

Guangchuang Yu

**Examples**

```
raxml_file <- system.file("extdata/RAxML", "RAxML_bipartitionsBranchLabels.H3", package="treeio")
read.raxml(raxml_file)
```

---

read.treeqza	<i>read.treeqza</i>
--------------	---------------------

---

**Description**

read.treeqza

**Usage**

```
read.treeqza(treeqza, node.label = "label", ...)
```

**Arguments**

treeqza               the qiime2 output file contained tree file.  
node.label            parse node label as 'label' or 'support' value.  
...                   additional parameter, passed to 'read.tree'.

**Value**

phylo tree object or treedata object when node.label was parsed 'support'.

**Examples**

```
qzaf1 <- system.file("extdata/qiime2treeqza", "fasttree-tree.qza", package="treeio")
qzaf2 <- system.file("extdata/qiime2treeqza", "iqt-tree.qza", package="treeio")
qzaf3 <- system.file("extdata/qiime2treeqza", "raxml-cat-tree.qza", package="treeio")
tr1 <- read.treeqza(qzaf1)
tr1
tr2 <- read.treeqza(qzaf2)
tr2
tr3 <- read.treeqza(qzaf3)
tr3
# parse node label as 'support' value.
qzaf4 <- system.file("extdata/qiime2treeqza", "raxml-cat-bootstrap-tree.qza", package="treeio")
tr4 <- read.treeqza(qzaf4, node.label="support")
tr4
```

---

read.treetime

*read.timetree*

---

**Description**

read timetree output

**Usage**

```
read.treetime(file)
```

```
read.timetree(file)
```

**Arguments**

file            the output tree file of timetree

**Value**

treedata object

reexports

*Objects exported from other packages***Description**

These objects are imported from other packages. Follow the links below to see their documentation.

**ape** [as.phylo](#), [is.rooted](#), [Nnode](#), [Ntip](#), [read.nexus](#), [read.tree](#), [root](#), [rtree](#), [write.nexus](#), [write.tree](#)

**dplyr** [full\\_join](#), [inner\\_join](#)

**magrittr** [%<>%](#), [%>%](#)

**rlang** [.data](#)

**tibble** [as\\_tibble](#), [tibble](#)

**tidytree** [ancestor](#), [as.phylo](#), [as.treedata](#), [child](#), [drop.tip](#), [get.data](#), [get.fields](#), [isTip](#), [MRCA](#), [nodeid](#), [nodelab](#), [offspring](#), [parent](#), [rootnode](#), [treedata](#)

rename\_taxa

*rename\_taxa***Description**

rename tip label of phylogenetic tree

**Usage**

```
rename_taxa(tree, data, key = 1, value = 2)
```

**Arguments**

tree	tree object, either treedata or phylo
data	data frame
key	column in data that match tip label (use 1st column by default)
value	column in data for rename tip label (use 2nd column by default)

**Value**

tree object

**Author(s)**

Guangchuang Yu

**Examples**

```
tree <- rtree(3)
d <- data.frame(old = paste0('t', 1:3), new = LETTERS[1:3])
rename_taxa(tree, d)
rename_taxa(tree, d, old, new)
```

---

rescale_tree	<i>rescale_tree</i>
--------------	---------------------

---

**Description**

rescale branch length of tree object

**Usage**

```
rescale_tree(tree_object, branch.length)
```

**Arguments**

tree\_object    tree object  
 branch.length    numerical features (e.g. dN/dS)

**Value**

update tree object

**Author(s)**

Guangchuang Yu

---

spt	<i>spt method</i>
-----	-------------------

---

**Description**

spt method

**Usage**

```
spt(x, from, to, weights = NULL, ...)
```

**Arguments**

x	a igraph object
from	a specific node of network.
to	other nodes of the network, length of it must be larger than 2.
weights	a numeric vector giving edge weights or a character. If this is NULL and the graph has a weight edge attribute, then the attribute is used. If this is NA then no weights are used even if the graph has a weight attribute. If this is a character, the graph has the edge attribute which is numeric, then it will be used, default is NULL.
...	additional parameters

**Value**

phylo object

**Examples**

```
library(igraph)
set.seed(123)
g <- igraph::sample_gnp(100, .1) %>%
  set_edge_attr(name='weight', value=abs(rnorm(E(.),3)))
tr1 <- spt(g, from = 6, to=V(g), weights = 'weight')
tr1
tr2 <- spt(g, from = 6, to = V(g), weights = NA)
tr2
```

---

write.beast

*write.beast*

---

**Description**

Export treedata object to BEAST NEXUS file. This function was adopted and modified from ape::write.nexus

**Usage**

```
write.beast(treedata, file = "", translate = TRUE, tree.name = NULL)
```

**Arguments**

treedata	treedata object, list of treedata, phylo, or list of phylo
file	output file. If file = "", print the output content on screen
translate	whether to translate taxa labels
tree.name	names of the trees, NULL to use existing tree names

**Value**

output file or file content on screen

**Author(s)**

Guangchuang Yu

**Examples**

```
nhxfile <- system.file("extdata/NHX", "phyldog.nhx", package="treeio")
nhx <- read.nhx(nhxfile)
write.beast(nhx)
```

---

```
write.beast.newick    write.beast.newick
```

---

**Description**

Export treedata object to BEAST Newick file. This is useful for making BEAST starting trees with metadata

**Usage**

```
write.beast.newick(
  treedata,
  file = "",
  append = FALSE,
  digits = 10,
  tree.prefix = ""
)
```

**Arguments**

treedata	treedata object
file	output file. If file = "", print the output content on screen
append	logical. Only used if the argument 'file' is the name of file (and not a connection or "lcmd"). If 'TRUE' output will be appended to 'file'; otherwise, it will overwrite the contents of file.
digits	integer, the indicating the number of decimal places, default is 10.
tree.prefix	character the tree prefix, default is "".

**Value**

output file or file content on screen

**Author(s)**

Guangchuang Yu

**Examples**

```
nhxfile <- system.file("extdata/NHX", "phyldog.nhx", package="treeio")
nhx <- read.nhx(nhxfile)
write.beast.newick(nhx)
```

---

write.jplace	<i>write.jplace</i>
--------------	---------------------

---

**Description**

Export jplace object to jplace file.

**Usage**

```
write.jplace(x, outfile)
```

**Arguments**

x	a jplace object.
outfile	the output file name

**Examples**

```
jp <- system.file("extdata", "sample.jplace", package="treeio")
tr1 <- read.jplace(jp)
outfile <- tempfile()
write.jplace(tr1, outfile)
tr2 <- read.jplace(outfile)
tr2
```

---

write.jtree	<i>write.jtree</i>
-------------	--------------------

---

**Description**

Export treedata object to json tree file

**Usage**

```
write.jtree(treedata, file = "")
```

**Arguments**

treedata        treedata object  
file            output file. If file = "", print the output content on screen

**Value**

output file or file content on screen

**Author(s)**

Guangchuang Yu



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