

Package: treeio (via r-universe)

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Title Base Classes and Functions for Phylogenetic Tree Input and Output

Version 1.37.1

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 (>= 3.6.0)

Imports ape, dplyr, jsonlite, magrittr, methods, rlang, stats, tibble, tidytree (>= 0.4.5), utils, yulab.utils (>= 0.1.6)

Suggests Biostrings, cli, ggplot2, ggtree, igraph, knitr, rmarkdown, phangorn, prettydoc, purrr, testthat, tidyr, vroom, xml2, yaml

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

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

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

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as.treedata.phylo	<i>as.treedata</i>
-------------------	--------------------

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

edgeNum2nodeNum	<i>edgeNum2nodeNum</i>
-----------------	------------------------

Description

convert edge number to node number for EPA/pplacer output

Usage

```
edgeNum2nodeNum(jp, edgeNum)
```

Arguments

- jp a jplace object
- edgeNum the edge number of a placement, the edge_num column of a jplace file. EPA and pplacer number the edges by a post-order traversal, they are not the row numbers of jp@phylo\$edge

Value

the node number of the reference tree, NA for an edge number that is not in the tree

Author(s)

Guangchuang Yu

Examples

```
jpfile <- system.file("extdata", "sample.jplace", package="treeio")
jp <- read.jplace(jpfile)
edgeNum2nodeNum(jp, c(0, 1, 2))
```

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	<i>get.placements</i>
----------------	-----------------------

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'

Details

The node column is the node number of the reference tree, that is the node the branch leads to (a tip or an internal node, numbered 1:Ntip for the tips and Ntip+1:Ntip+Nnode for the internal nodes). It is translated from the edge_num of the jplace file, which EPA and pplacer number by a post-order traversal of the tree; edgeNum2nodeNum() does that translation, #22

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	<i>getNodeNum</i>
------------	-------------------

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	<i>is.ggtree</i>
-----------	------------------

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>
--------------	---

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>
-------------------	--------------------------

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`*raxml2nwk*

Description

convert raxml bootstrap tree to newick format

Usage

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

Arguments

<code>infile</code>	input file
<code>outfile</code>	output file

Value

newick file

Author(s)

Guangchuang Yu

`read.astral`*read.astral*

Description

parse ASTRAL output newick text

Usage

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

Arguments

<code>file</code>	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)

```

<code>read.codeml_mlc</code>	<i>read.codeml_mlc</i>
------------------------------	------------------------

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)
```

<code>read.fasta</code>	<i>read.fasta</i>
-------------------------	-------------------

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

read.hyphy

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

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	<i>read.iqtree</i>
-------------	--------------------

Description

parse IQ-TREE output

Usage

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

Arguments

file	IQ-TREE Newick text
------	---------------------

Details

`read.iqtree()` parses the tree file of an IQ-TREE run (e.g. *.treefile, the report file *.iqtree is not a tree file) and splits the node labels into the SH-aLRT and the UFBoot support values. The two values are expected to be separated by a /, which is what IQ-TREE writes when both were requested. If the branch support was assessed with a single method (e.g. the standard non-parametric bootstrap or SH-aLRT alone), the node label holds one value only and there is no way to tell which method produced it; the value is then stored in both columns and a message is emitted. Use `read.newick()` to import such a tree without guessing.

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	<i>read.jtree</i>
------------	-------------------

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.

Details

The node age is not reported by MCMCTree, it is derived from the branch lengths and stored in the reltime column. The credibility interval of a node age, [$95\% = \{lower, upper\}$] in the file, is stored in the reltime_0.95_CI column and can be plotted with `geom_range(range='reltime_0.95_CI', center='reltime')`.

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	<i>read.nhx</i>
----------	-----------------

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 phyip file

Value

an instance of 'phyip'

Author(s)

Guangchuang Yu

Examples

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

read.phylip.seq	<i>read.phylip.seq</i>
-----------------	------------------------

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	<i>read.phylip.tree</i>
------------------	-------------------------

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	<i>read.phyloxml</i>
---------------	----------------------

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	<i>read.r8s</i>
----------	-----------------

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

read.raxml

Description

parse RAxML bootstrapping analysis output

Usage

```
read.raxml(file = NULL, text = NULL)
```

Arguments

file	RAxML bootstrapping analysis output
text	alternatively, the content of the file as a character string or a connection; 'file' is ignored when 'text' is given

Value

treedata object

Author(s)

Guangchuang Yu

Examples

```
raxml_file <- system.file("extdata/RAxML", "RAxML_bipartitionsBranchLabels.H3", package="treeio")
read.raxml(raxml_file)
read.raxml(text = "(a:0.1,b:0.2)90:0.3;")
```

<code>read.treeqza</code>	<i><code>read.treeqza</code></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", "iq-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
```

<code>read.treetime</code>	<i><code>read.timetree</code></i>
----------------------------	-----------------------------------

Description

read timetree output

Usage

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

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

Arguments

file the output tree file of timetree

Value

treedata object

rename_taxa	<i>rename_taxa</i>
-------------	--------------------

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

<code>treedata</code>	treedata object, list of treedata, phylo, or list of phylo
<code>file</code>	output file. If file = "", print the output content on screen
<code>translate</code>	whether to translate taxa labels
<code>tree.name</code>	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	<i>write.beast.newick</i>
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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>
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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>
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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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