

Package ‘treeio’

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Title Base Classes and Functions for Phylogenetic Tree Input and Output

Version 1.14.3

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, tibble, tidytree (>= 0.3.0), utils

Suggests Biostrings, ggplot2, ggtree, igraph, knitr, phangorn, prettydoc, testthat, tidyr, vroom, xml2

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

Encoding UTF-8

URL <https://github.com/YuLab-SMU/treeio> (devel),
<https://docs.ropensci.org/treeio/> (docs),
<https://yulab-smu.top/treedata-book/> (book)

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

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as.treedata.phylo *as.treedata*

Description

convert phylo to treedata

Usage

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

```
## S3 method for class 'pml'
as.treedata(tree, type = "ml", ...)
```

Arguments

tree	input tree, a phylo object
boot	optional, can be bootstrap value from ape::boot.phylo
...	additional parameters
type	one of 'ml' and 'bayes' for inferring ancestral sequences

Details

converting phylo object to treedata object

Author(s)

Guangchuang Yu
Yu Guangchuang

drop.tip *drop.tip method*

Description

drop.tip method
drop.tip method

Usage

```
drop.tip(object, tip, ...)
```

```
drop.tip(object, tip, ...)
```

```
## S4 method for signature 'phylo'
drop.tip(object, tip, ...)
```

Arguments

object	A treedata or phylo object
tip	a vector of mode numeric or character specifying the tips to delete
...	additional parameters

Value

updated object

Author(s)

Casey Dunn <http://dunnlab.org> and Guangchuang Yu <https://guangchuangyu.github.io>

Source

drop.tip for phylo object is a wrapper method of ape::drop.tip from the ape package. The documentation you should read for the drop.tip function can be found here: [drop.tip](#)

See Also

[drop.tip](#)

Examples

```
nhxfile <- system.file("extdata/NHX", "ADH.nhx", package="treeio")
nhx <- read.nhx(nhxfile)
drop.tip(nhx, c("ADH2", "ADH1"))
```

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`*get.tree*

Description

access phylo slot

Usage

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

Arguments

x	tree object
...	additional parameters

Value

phylo object

Author(s)

Guangchuang Yu

`get.treetext`*get.treetext method*

Description

access tree text (newick text) from tree object

Usage

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

```
## S4 method for signature 'treedata'  
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

isTip	<i>isTip</i>
-------	--------------

Description

whether the node is a tip

Usage

```
isTip(.data, .node, ...)

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

## S3 method for class 'phylo'
isTip(.data, .node, ...)

## S3 method for class 'treedata'
isTip(.data, .node, ...)
```

Arguments

.data	phylo, treedata or tbl_tree object
.node	node number
...	additional parameters

Value

logical value

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

merge_tree

merge_tree

Description

merge two tree object

Usage

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

Arguments

obj1 tree object 1

obj2 tree object 2

Value

tree object

Author(s)

Guangchuang Yu

Nnode.treedata

Nnode

Description

number of nodes

Usage

```
## S3 method for class 'treedata'
Nnode(phy, internal.only = TRUE, ...)
```

Arguments

phy treedata object

internal.only whether only count internal nodes

... additional parameters

Value

number of nodes

Author(s)

Guangchuang Yu

Examples

```
Nnode(rtree(30))
```

```
print.treedataList    print
```

Description

print information of a list of treedata objects

Usage

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

Arguments

x	a list of treedata objects
...	no used

Value

message

```
raxml2nwk            raxml2nwk
```

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

Usage

```
read.beast(file)
```

```
read.mrbayes(file)
```

```
read.mega(file)
```

Arguments

file beast file

Value

treedata object

Author(s)

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

Examples

```
file <- system.file("extdata/BEAST", "beast_mcc.tree", package="treeio")
read.beast(file)
```

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	<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)
```

read.fasta

read.fasta

Description

read FASTA file

Usage

```
read.fasta(fasta)
```

Arguments

fasta fasta file

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

Value

treedata object

Author(s)

Guangchuang Yu

read.jplace	<i>read.jplace</i>
-------------	--------------------

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.mega_tabular` *read.mega_tabular*

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` *read.newick*

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

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

Description

parse tree from phyloxml file

Usage

read.phyloxml.tree(file)

Arguments

file phyloxml 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 multitreedata class

Examples

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

read.raxml

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)
```

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

root.phylo	<i>root</i>
------------	-------------

Description

re-root a tree

Usage

```
## S3 method for class 'phylo'
root(phy, outgroup, node = NULL, resolve.root = TRUE, ...)
```

```
## S3 method for class 'treedata'
root(phy, outgroup, node = NULL, resolve.root = TRUE, ...)
```

Arguments

phy	tree object
outgroup	a vector of mode numeric or character specifying the new outgroup
node	node to reroot
resolve.root	a logical specifying whether to resolve the new root as a bifurcating node
...	additional parameters passed to ape::root.phylo

Value

rerooted tree

Author(s)

Guangchuang Yu

tree_subset

Subset tree objects by related nodes

Description

This function allows for a tree object to be subset by specifying a node and returns all related nodes within a selected number of levels

Usage

```
tree_subset(  
  tree,  
  node,  
  levels_back = 5,  
  group_node = TRUE,  
  group_name = "group",  
  root_edge = TRUE  
)  
  
## S3 method for class 'phylo'  
tree_subset(  
  tree,  
  node,  
  levels_back = 5,  
  group_node = TRUE,  
  group_name = "group",  
  root_edge = TRUE  
)  
  
## S3 method for class 'treedata'  
tree_subset(  
  tree,  
  node,  
  levels_back = 5,  
  group_node = TRUE,  
  group_name = "group",  
  root_edge = TRUE  
)
```

Arguments

tree	a tree object of class phylo
node	either a tip label or a node number for the given tree that will be the focus of the subsetted tree

levels_back	a number specifying how many nodes back from the selected node the subsetted tree should include
group_node	whether add grouping information of selected node
group_name	group name (default 'group') for storing grouping information if group_node = TRUE
root_edge	If TRUE (by default), set root.edge to path length of original root to the root of subset tree

Details

This function will take a tree and a specified node from that tree and subset the tree showing all relatives back to a specified number of nodes. This function allows for a combination of ancestor and offspring to return a subsetted tree that is of class phylo. This allows for easy graphing of the tree with ggtree

Examples

```
## Not run:
nwk <- system.file("extdata", "sample.nwk", package="treeio")
tree <- read.tree(nwk)

sub_tree <- tree_subset(tree, node = "A", levels_back = 3)
ggtree(sub_tree) + geom_tiplab() + geom_nodelab()

## End(Not run)

## Not run:
nwk <- system.file("extdata", "sample.nwk", package="treeio")
tree <- read.tree(nwk)

sub_tree <- tree_subset(tree, node = "A", levels_back = 3)
ggtree(sub_tree) + geom_tiplab() + geom_nodelab()

## End(Not run)
```

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 = "UNTITLED")
```

Arguments

treedata	treedata object
file	output file. If file = "", print the output content on screen
translate	whether translate taxa labels
tree.name	name of the tree

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.jtree

write.jtree

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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