Package ‘treeio’

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Title Base Classes and Functions for Phylogenetic Tree Input and Output

Version 1.26.0

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 (>= 3.6.0)

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

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

VignetteBuilder knitr

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License Artistic-2.0

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

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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.

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See Also

Useful links:
- https://github.com/YuLab-SMU/treeio(devel)
- https://docs.ropensci.org/treeio/(docs)
as.treedata.phylo  as.treedata

Description
convert phylo to treedata

Usage
```r
## 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

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)
Usage

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

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

Arguments

tree tree object

... additional parameters

by one of 'best' and 'all'

Value

placement tibble

get.tree

Description

access phylo slot

Usage

```r
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, ...)

**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

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

Class "jplace" This class stores phylogenetic placements

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*

**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*

**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 two tree object

Description

merge two tree object

Usage

merge_tree(obj1, obj2)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>obj1</td>
<td>tree object 1</td>
</tr>
<tr>
<td>obj2</td>
<td>tree object 2</td>
</tr>
</tbody>
</table>

Value

tree object

Author(s)

Guangchuang Yu

print.treedataList

print information of a list of treedata objects

Usage

```r
## S3 method for class 'treedataList'
print(x, ...)
```
raxml2nwk

Arguments

- x: a list of treedata objects
- ...: no used

Value

- message

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

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]':",
  "1.200385744180805)'[pp1=0.98;pp2=0.02;pp3=0]' :0.967959928273038,'",
  "((species4,species5)'[pp1=0.88;pp2=0.11;pp3=0.01]' :1.2454851536484994))"
)  
read.astral(textConnection(tt))

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

Usage
read.beast(file)
read.mrbayes(file)
read.beast.newick(file)
read.mega(file)

Arguments
file newick file

Value
treedata object
treedata object

Author(s)
Guangchuang Yu https://guangchuangyu.github.io
Bradley R Jones
Examples

```r
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);'
  )
)
```

Description

read baseml output

Usage

```r
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

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

Description
read FASTA file

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

Arguments
fasta fasta file

Example: 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

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

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

Description
parse IQ-TREE output

Usage
read.iqtree(file)

Arguments
file IQ-TREE Newick text

Value
treedata object
read.jplace

Author(s)
Guangchuang Yu

Description
read jplace file

Usage
read.jplace(file)

Arguments
file jplace file

Value
jplace instance

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

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
read.mcmctree

Value

treedata object

Author(s)

Guangchuang Yu

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

**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

**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**

**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**

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

---

**read.nhx**

**Description**
read nhx tree file

**Usage**
read.nhx(file)

**Arguments**
file  
nhx file

**Value**
nhx object
**read.paml_rst**

**Author(s)**

Guangchuang Yu [https://guangchuangyu.github.io](https://guangchuangyu.github.io)

**Examples**

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

**Description**

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

**Usage**

```r
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](https://guangchuangyu.github.io)

**Examples**

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

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
**Description**

parse tree from phylip file

**Usage**

```r
read.phylip.tree(file)
```

**Arguments**

- **file** phylip file

**Value**

phylo or multiPhylo object

**Author(s)**

Guangchuang Yu

---

**Description**

read.phyloxml

**Usage**

```r
read.phyloxml(file)
```

**Arguments**

- **file** phyloxml file
Value

treedata class or treedataList class

Examples

```r
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
```

Description

parse output from r8s

Usage

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

Arguments

- `file`: r8s output log file

Value

multiPhylo object

Author(s)

Guangchuang Yu

Examples

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

**Description**

parse RAxML bootstrapping analysis output

**Usage**

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

**Arguments**

- `file`: RAxML bootstrapping analysis output

**Value**

treedata object

**Author(s)**

Guangchuang Yu

**Examples**

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

### read.treeqza

**Description**

read.treeqza

**Usage**

```r
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'.

---

**Description**

parse RAxML bootstrapping analysis output

**Usage**

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

**Arguments**

- `file`: RAxML bootstrapping analysis output

**Value**

treedata object

**Author(s)**

Guangchuang Yu

**Examples**

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

**Description**

read.treeqza

**Usage**

```r
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'.

---
rename_taxa

Value

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

Examples

```r
qzafile1 <- system.file("extdata/qiime2treeqza", "fasttree-tree.qza", package="treeio")
qzafile2 <- system.file("extdata/qiime2treeqza", "iqt-tree.qza", package="treeio")
qzafile3 <- system.file("extdata/qiime2treeqza", "raxml-cat-tree.qza", package="treeio")
tr1 <- read.treeqza(qzafile1)
tr2 <- read.treeqza(qzafile2)
tr3 <- read.treeqza(qzafile3)
# parse node label as 'support' value.
qzafile4 <- system.file("extdata/qiime2treeqza", "raxml-cat-bootstrap-tree.qza", package="treeio")
tr4 <- read.treeqza(qzafile4, node.label="support")
```

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

**Description**

rename tip label of phylogenetic tree

**Usage**

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

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)

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

spt method

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

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.beast.newick

Description

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

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

Arguments

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 "cmd"). 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

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

Description

Export treedata object to json tree file

Usage

```r
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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