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

ByteCompile true

License Artistic-2.0

Encoding UTF-8

URL  https://github.com/YuLab-SMU/treeio (devel),
     https://docs.ropensci.org/treeio/ (docs),

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

biocViews Software, Annotation, Clustering, DataImport,
    DataRepresentation, Alignment, MultipleSequenceAlignment, Phylogenetics

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treeio-package

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`

*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)

Description

access placement information
Usage

get.placements(tree, ...)

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

Arguments

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

Value

placement tibble

Description

access phylo slot

Usage

get.tree(x, ...)

Arguments

x tree object
...

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)

**Arguments**
- `tree` tree object

**Value**
number

**Author(s)**
Guangchuang Yu
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
newick : 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`

**Description**

merge two tree object

**Usage**

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

**Arguments**

- `obj1`: tree object 1
- `obj2`: tree object 2

**Value**

tree object

**Author(s)**

Guangchuang Yu

---

### `print.treedataList`

**Description**

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**

```r
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**

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

**Arguments**

- `file`  ASTRAL Newick file
read.beast

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

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")
system.file("extdata/MrBayes", "Gq_nxs.tre", package="treeio")
read.beast(file)
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 bsemf 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)**

Guangchuan 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)
```
**read.codeml_mlc**

**Description**

read mlc file of codeml output

**Usage**

```r
codeml_mlc(read.mlcf)
```

**Arguments**

- `mlcf` mlc file

**Value**

A `codeml_mlc` object

**Author(s)**

Guangchuang Yu

**Examples**

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

---

**read.fasta**

**Description**

read FASTA file

**Usage**

```r
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

Description

read HYPHY output

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nwk</td>
<td>tree file in nwk format, one of hyphy output</td>
</tr>
<tr>
<td>ancseq</td>
<td>ancestral sequence file in nexus format, one of hyphy output</td>
</tr>
<tr>
<td>tip.fasfile</td>
<td>tip sequence file</td>
</tr>
</tbody>
</table>

Value

A hyphy object

Author(s)

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

```r
read.jplace(file)
```

### Arguments

- **file**
  - jplace file

### Value

jplace instance

**Author(s)**

Guangchuang Yu

**Examples**

```r
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**

```r
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
Author(s)

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

Examples

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

read.paml_rst

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

Examples

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

**Description**

parsing phylip tree format

**Usage**

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

**Arguments**

- `file` : phylip file

**Value**

an instance of 'phylip'

**Author(s)**

Guangchuang Yu

**Examples**

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

---

**read.phylip.seq**

**Description**

read aligned sequences from phylip format

**Usage**

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

**Arguments**

- `file` : phylip file, currently only sequential format is supported

**Value**

DNAbin object
**read.phylip.tree**

**Author(s)**
Guangchuang Yu

**References**

**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**

**Description**
read.phyloxml

**Usage**
```
read.phyloxml(file)
```

**Arguments**
- `file` phyloxml file
Value
treedata class or treedataList class

Examples

```r
xmfile1 <- system.file("extdata/phyloxml", "test_x2.xml", package="treeio")
px1 <- read.phyloxml(xmfile1)
px1

xmfile2 <- system.file("extdata/phyloxml", "phyloxml_examples.xml", package="treeio")
px2 <- read.phyloxml(xmfile2)
px2
```

Description
parse output from r8s

Usage

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

Arguments

```r
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
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

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'.
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)
tr4 <- read.treeqza(qzafile4, node.label="support")
```

---

**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

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 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

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
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
write.jtree

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 "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

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

write.jtree

Description

Export treedata object to json tree file

Usage

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

Arguments

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

Value

treedata file output file or file content on screen

Author(s)

Guangchuang Yu
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