Package ‘treeio’

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Title Base Classes and Functions for Phylogenetic Tree Input and Output

Version 1.28.0

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, stats, tibble, tidytree (>= 0.4.5), utils, yulab.utils (> 0.1.1)

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

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://www.amazon.com/Integration-Manipulation-Visualization-Phylogenetic-Computational-ebook/dp/B0B5NLZR1Z/ (book), https://doi.org/10.1093/molbev/msz240 (paper)

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

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

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Author Guangchuang Yu [aut, cre] (<https://orcid.org/0000-0002-6485-8781>),
Tommy Tsan-Yuk Lam [ctb, ths],
Shuangbin Xu [ctb] (<https://orcid.org/0000-0003-3513-5362>),
Bradley Jones [ctb],
Casey Dunn [ctb],
Tyler Bradley [ctb],
Konstantinos Geles [ctb]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

Contents

`treeio-package` *treeio: Base Classes and Functions for Phylogenetic Tree Input and Output*

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)

Maintainer: Guangchuang Yu <guangchuangyu@gmail.com> (ORCID)

Other contributors:

- Tommy Tsan-Yuk Lam <tylam.tommy@gmail.com> [contributor, thesis advisor]
- Shuangbin Xu <xshuangbin@163.com> (ORCID) [contributor]
- Bradley Jones <brj1@sfu.ca> [contributor]
- Casey Dunn <casey_dunn@brown.edu> [contributor]
- Tyler Bradley <tcb85@drexel.edu> [contributor]
- Konstantinos Geles <konstantinos.geles@studenti.unicz.it> [contributor]

See Also

Useful links:

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

- https://www.amazon.com/Integration-Manipulation-Visualization-Phylogenetic-Computational-ebook/dp/B0B5NLZR1Z/(book)
- doi:10.1093/molbev/msz240 (paper)
- 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 *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, ...)
```

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` *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 *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 *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_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

---

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 *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]':",
  "1.2003685744180805)'[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)

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

```
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 *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 *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 *read.mcmctree*

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 *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.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 *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

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 *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 *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'.

Value

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

Examples

```
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)
tr1
tr2 <- read.treeqza(qzafile2)
tr2
tr3 <- read.treeqza(qzafile3)
tr3
# 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")
tr4
```

---

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` *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

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 *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 "|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.jplace *write.jplace*

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 *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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