

Package ‘treeio’

December 6, 2017

Title Base Classes and Functions for Phylogenetic Tree Input and Output

Version 1.3.2

Description Base classes and functions for parsing and exporting phylogenetic trees.

Depends R (>= 3.4.0)

Imports ape, dplyr, ggplot2, jsonlite, magrittr, methods, rvcheck, tibble

Suggests ggtree, knitr, prettydoc, testthat

VignetteBuilder knitr

ByteCompile true

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URL <https://guangchuangyu.github.io/treeio>

BugReports <https://github.com/GuangchuangYu/treeio/issues>

Encoding UTF-8

LazyData true

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

RoxygenNote 6.0.1

NeedsCompilation no

Author Guangchuang Yu [aut, cre] (0000-0002-6485-8781),
Tommy Tsan-Yuk Lam [aut, ths],
Casey Dunn [ctb],
Bradley Jones [ctb]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

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

Description

converting phylo object to treedata object

Usage

```
as.treedata(tree, ...)

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

Arguments

tree	tree object
...	additional parameters
boot	optional, can be bootstrap value from ape::boot.phylo

Value

treedata object

Author(s)

guangchuang yu

codeml-class	<i>Class "codeml" This class stores information of output from codeml</i>
--------------	---

Description

Class "codeml" This class stores information of output from codeml

Slots

mlc	A code_mlc object
rst	A paml_rst object
extraInfo	extra information

See Also

[codeml_mlc](#) [paml_rst](#)

codeml_mlc-class	<i>Class "codeml_mlc" This class stores information of mlc file frm codeml output</i>
------------------	---

Description

Class "codeml_mlc" This class stores information of mlc file frm codeml output

Slots

fields available features
 treetext tree text
 phylo phylo object
 dNdS dN dS information
 mlcfile mlc file
 extraInfo extra information

Author(s)

Guangchuang Yu

See Also

[paml_rst codeml](#)

drop.tip	<i>drop.tip method</i>
----------	------------------------

Description

drop.tip method

Usage

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

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

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

Arguments

object	An nhx 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.fields	<i>get.fields method</i>
------------	--------------------------

Description

get.fields method

Usage

```
get.fields(object, ...)

## S4 method for signature 'codeml'
get.fields(object, ...)

## S4 method for signature 'paml_rst'
get.fields(object)

## S4 method for signature 'codeml_mlc'
get.fields(object)

## S4 method for signature 'treedata'
get.fields(object)

## S4 method for signature 'phangorn'
get.fields(object, ...)
```

Arguments

object	one of jplace, beast, hyphy, codeml, codeml_mlc, paml_rst object
...	additional parameter

Value

available annotation variables

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'

Value

placement tibble

get.subs	<i>get.subs method</i>
----------	------------------------

Description

get substitution information

Usage

```
get.subs(object, type, ...)

## S4 method for signature 'codeml'
get.subs(object, type, ...)

## S4 method for signature 'paml_rst'
get.subs(object, type, ...)

## S4 method for signature 'phangorn'
get.subs(object, type, ...)
```

Arguments

object	paml_rst object
type	one of 'marginal_subs', 'marginal_AA_subs', 'joint_subs' or 'joint_AA_subs'.
...	additional parameter

Value

data.frame

get.tipseq	<i>get.tipseq method</i>
------------	--------------------------

Description

get tipseq

Usage

```
get.tipseq(object, ...)

## S4 method for signature 'codeml'
get.tipseq(object, ...)

## S4 method for signature 'paml_rst'
get.tipseq(object, ...)
```

Arguments

object	one of paml_rst or codeml object
...	additional parameter

Value

character

get.tree	<i>get.tree method</i>
----------	------------------------

Description

get.tree method

Usage

```

get.tree(object, ...)

## S4 method for signature 'treedata'
get.tree(object, ...)

## S4 method for signature 'codeml'
get.tree(object, by = "rst", ...)

## S4 method for signature 'phylip'
get.tree(object, ...)

## S4 method for signature 'phylo'
get.tree(object, ...)

## S4 method for signature 'paml_rst'
get.tree(object)

## S4 method for signature 'phangorn'
get.tree(object, ...)

## S4 method for signature 'codeml_mlc'
get.tree(object, ...)

```

Arguments

object	one of phylo, jplace, nhx, phangorn, hyphy, codeml, codeml_mlc, paml_rst object
...	additional parameter
by	one of rst or mlc

Value

phylo object

Author(s)

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

get.treetext	<i>get.treetext method</i>
--------------	----------------------------

Description

access tree text (newick text) from tree object

Usage

```

get.treetext(object, ...)

```


Arguments

object	one of phylo, jplace, beast, hyphy, codeml, codeml_mlc, paml_rst 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))
```

getRoot	<i>getRoot</i>
---------	----------------

Description

get the root number

Usage

```
getRoot(tr)
```

Arguments

tr	phylo object
----	--------------

Value

root number

Author(s)

Guangchuang Yu

Examples

```
getRoot(rtree(10))
```

groupClade	<i>groupClade method</i>
------------	--------------------------

Description

group selected clade

Usage

```
groupClade(object, node, group_name = "group", ...)
```

```
## S4 method for signature 'codeml'
groupClade(object, node, group_name = "group")
```

```
## S4 method for signature 'treedata'
groupClade(object, node, group_name = "group")
```

```
## S4 method for signature 'phylip'
groupClade(object, node, group_name = "group")
```

```
## S4 method for signature 'phylo'
groupClade(object, node, group_name = "group")
```

```
## S4 method for signature 'phangorn'
groupClade(object, node, group_name = "group")
```

Arguments

object	supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy
node	a internal node or a vector of internal nodes
group_name	name of the group, 'group' by default
...	additional parameter

Value

group index

groupOTU	<i>groupOTU method</i>
----------	------------------------

Description

group tree based on selected OTU, will traceback to MRCA

Usage

```
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'codeml'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'codeml_mlc'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'treedata'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'phangorn'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'phylip'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'paml_rst'
groupOTU(object, focus, group_name = "group", ...)

## S4 method for signature 'phylo'
groupOTU(object, focus, group_name = "group", ...)
```

Arguments

object	supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy
focus	a vector of tip (label or number) or a list of tips.
group_name	name of the group, 'group' by default
...	additional parameter

Value

group index

groupOTU.phylo	<i>groupOTU.phylo</i>
----------------	-----------------------

Description

group OTU

Usage

```
groupOTU.phylo(phy, focus, group_name = "group", ...)
```

Arguments

phy	tree object
focus	tip list
group_name	name of the group
...	additional parameters

Value

phylo object

Author(s)

ygc

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

Examples

```
library(ggtree)
p <- ggtree(rtree(30))
is.ggtree(p)
```

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
 translation tip number to name translation in nexus 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	<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	<i>merge_tree</i>
------------	-------------------

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	<i>Nnode</i>
-------	--------------

Description

number of nodes

Usage

Nnode(tree, internal.only = TRUE)

Arguments

tree	tree object
internal.only	whether only count internal nodes

Value

number of nodes

Author(s)

guangchuang yu

Examples

Nnode(rtree(30))

Ntip	<i>Ntip</i>
------	-------------

Description

number of tips

Usage

Ntip(tree)

Arguments

tree	tree object
------	-------------

Value

number of tips

Author(s)

guangchuang yu

guangchuang yu

Examples

```
Ntip(rtree(30))
```

paml_rst-class

Class "paml_rst" This class stores information of rst file from PAML output

Description

Class "paml_rst" This class stores information of rst file from PAML output

Slots

fields availabel attributes

treetext tree text

phylo phylo object

seq_type one of "NT" and "AA"

tip_seq sequences of tips

marginal_ancseq Marginal reconstruction of ancestral sequences

joint_ancseq Joint reconstruction of ancestral sequences

marginal_subs sequence substitutions based on marginal_ancseq

joint_subs sequence substitutions based on joint_ancseq

marginal_AA_subs Amino acid sequence substitutions based on marginal_ancseq

joint_AA_subs Amino acid sequence substitutions based on joint_ancseq

rstfile rst file

extraInfo extra information

Author(s)

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

See Also

[codeml](#) [codeml_mlc](#)

phangorn-class	<i>Class "phangorn" This class stores ancestral sequences inferred from 'phangorn'</i>
----------------	--

Description

Class "phangorn" This class stores ancestral sequences inferred from 'phangorn'

Slots

fields available attributes
 phylo phylo object
 seq_type one of "NT" and "AA"
 tip_seq sequences of tips
 ancseq ancestral sequences
 subs sequence substitution
 AA_subs Amino acid sequence substitution
 extraInfo extra information

Author(s)

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

See Also

[paml_rst](#)

phylip-class	<i>Class "phylip" This class stores phylip tree(s)</i>
--------------	--

Description

Class "phylip" This class stores phylip tree(s)

Slots

file input file
 fields available feature
 phylo phylo or multiPhylo
 ntree number of trees
 sequence sequences
 extraInfo extra information

Author(s)

Guangchuang Yu

phyPML	<i>treeAnno.pml</i>
--------	---------------------

Description

tree annotation of sequence substitution by comparing to parent node

Usage

```
phyPML(pmlTree, type = "ml")
```

Arguments

pmlTree	tree in pml object, output of phangorn::optim.pml
type	one of 'ml' and 'bayes' for inferring ancestral sequences

Value

phangorn object

Author(s)

Yu Guangchuang

pmlToSeq	<i>pmlToSeq</i>
----------	-----------------

Description

convert pml object to XStringSet object

Usage

```
pmlToSeq(pml, type = "ml", includeAncestor = TRUE)
```

Arguments

pml	pml object
type	one of "marginal", "ml", "bayes"
includeAncestor	logical

Value

XStringSet

Author(s)

ygc

print.beastList	<i>print</i>
-----------------	--------------

Description

print information of a list of beast trees

Usage

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

Arguments

x	a list of beast object
...	no used

Value

message

Author(s)

Guangchuang Yu

raxml2nwk	<i>raxml2nwk</i>
-----------	------------------

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.baseml	<i>read.baseml</i>
-------------	--------------------

Description

read rst and mlb file from baseml output

Usage

```
read.baseml(rstfile, mlbfile)
```

Arguments

rstfile	rst file
mlbfile	mlb file

Value

A paml_rst object

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

```
rstfile <- system.file("extdata/PAML_Baseml", "rst", package="treeio")
mlbfile <- system.file("extdata/PAML_Baseml", "mlb", package="treeio")
read.baseml(rstfile, mlbfile)
```

read.beast	<i>read.beast</i>
------------	-------------------

Description

read beast output

Usage

```
read.beast(file)

read.mrbayes(file)
```

Arguments

file	beast file
------	------------

Value

beast 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	<i>read.codeml</i>
-------------	--------------------

Description

read baseml output

Usage

```
read.codeml(rstfile, mlcfile)
```

Arguments

rstfile	rst file
mlcfile	mlc file

Value

A codeml object

Author(s)

ygc

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)

ygc

Examples

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

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

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 <http://ygc.name>

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

Description

read jplace file

Usage

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

Arguments

file	jplace file
------	-------------

Value

jplace instance

Author(s)

ygc

Examples

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

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`*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 output

Usage

```
read.paml_rst(rstfile)
```

Arguments

rstfile rst file

Value

A paml_rst object

Author(s)

Guangchuang Yu <http://ygc.name>

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.phyloT	<i>read.phyloT</i>
-------------	--------------------

Description

parse output from phyloT

Usage

```
read.phyloT(file, ...)
```

Arguments

file newick tree file
... additional parameters to read.tree

Value

phylo object

Author(s)

guangchuang yu

References<http://phylot.biobyte.de/>

`read.r8s`*read.r8s*

Description

parse output from r8s

Usage`read.r8s(file)`**Arguments**

<code>file</code>	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**

<code>file</code>	RAxML bootstrapping analysis output
-------------------	-------------------------------------

Value

raxml object

Author(s)

Guangchuang Yu

Examples

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

show	<i>show method</i>
------	--------------------

Description

show method for treedata instance

Usage

```
show(object)

## S4 method for signature 'codeml'
show(object)

## S4 method for signature 'codeml_mlc'
show(object)

## S4 method for signature 'phylip'
show(object)

## S4 method for signature 'paml_rst'
show(object)
```

Arguments

object treedata object

Value

print info

Author(s)

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

Examples

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

taxa_rename	<i>taxa_rename</i>
-------------	--------------------

Description

rename taxa

Usage

```
taxa_rename(tree, name)
```

Arguments

tree	tree object
name	a two column data.frame contains original name in 1st column and new name in 2nd column

Value

updated tree object with new taxa name

Author(s)

guangchuang yu

treedata-class	<i>Class "treedata" This class stores phylogenetic tree with associated data</i>
----------------	--

Description

Class "treedata" This class stores phylogenetic tree with associated data

Slots

file tree file
 treetext newick tree string
 phylo phylo object for tree structure
 translation tip number to name translation in nexus file
 data associated data
 extraInfo extra information, reserve for merge_tree
 tip_seq tip sequences
 anc_seq ancestral sequences
 seq_type sequence type, one of NT or AA
 tipseq_file tip sequence file
 ancseq_file ancestral sequence file
 info extra information, e.g. metadata, software version etc.

Author(s)

guangchuang yu <https://guangchuangyu.github.io>

write.jplace	<i>write.jplace</i>
--------------	---------------------

Description

generate jplace file

Usage

```
write.jplace(nwk, data, outfile)
```

Arguments

nwk	tree in newick format
data	annotation data
outfile	jplace output file

Value

jplace file

Author(s)

ygc

Examples

```
tree <- system.file("extdata", "pa.nwk", package="treeio")
data <- read.csv(system.file("extdata", "pa_subs.csv", package="treeio"),
  stringsAsFactor=FALSE)
outfile <- tempfile()
write.jplace(tree, data, outfile)
```

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*Topic **codeml**

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