Package 'treeio'

October 18, 2017

Title Base Classes and Functions for Phylogenetic Tree Input and
Output

Version 1.0.2

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

Depends R (>= 3.3.2)

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

Suggests Biostrings, ggtree (>= 1.7.5), knitr, prettydoc, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

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 5.0.1

NeedsCompilation no

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R topics documented:

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as.treedata	*as.treedata*

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 parameter
boot	optional, can be bootstrap value from ape::boot.phylo

Value

treedata object

Author(s)

guangchuang yu

---

beast-class	*Class "beast" This class stores information of beast output*

Description

Class "beast" This class stores information of beast output

Slots

fields beast statistic variables

treetext tree text in beast file

phylo tree phylo object

translation tip number to name translation in beast file

stats beast statistics

file beast file, nexus format

extraInfo extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

See Also

show get.fields

---

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

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

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	*drop.tip method*

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   *get.fields method*

Description

get.fields method

Usage

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

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

get.fields(object, ...)

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

## S4 method for signature 'r8s'
get.fields(object, ...)

## S4 method for signature 'hyphy'
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

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

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

---

get.placements   *get.placements method*

Description

get.placement method

Usage

```
get.placements(object, by, ...)

get.placements(object, by, ...)
```

Arguments

object	jplace object
by	get best hit or others
...	additional parameter

Value

data.frame

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

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

---

get.subs   *get.subs method*

Description

get substitution information

Usage

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

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

## S4 method for signature 'hyphy'
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

Examples

```
nwk <- system.file("extdata/HYPHY", "labelledtree.tree", package="treeio")
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="treeio")
tipfas <- system.file("extdata", "pa.fas", package="treeio")
hy <- read.hyphy(nwk, ancseq, tipfas)
get.subs(hy, type="AA_subs")
```

---

get.tipseq   *get.tipseq method*

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   *get.tree method*

Description

get.tree method

Usage

```
get.tree(object, ...)

get.tree(object, ...)

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

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

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

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

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

## S4 method for signature 'hyphy'
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, ...)

## S4 method for signature 'r8s'
get.tree(object, ...)
```

Arguments

object	one of phylo, jplace, nhx, phangorn, beast, 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>

Examples

```
nwk <- system.file("extdata/HYPHY", "labelledtree.tree", package="treeio")
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="treeio")
hy <- read.hyphy(nwk, ancseq)
get.tree(hy)
```

---

get.treetext   *get.treetext method*

Description

get.treetext method

Usage

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

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

Arguments

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

Value

phylo object

Author(s)

Guangchuang Yu http://ygc.name

Examples

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

---

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   *getRoot*

Description

get the root number

Usage

```
getRoot(tr)
```

Arguments

tr   phylo object

Value

root number

Author(s)

Guangchuang Yu

Examples

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

---

groupClade   *groupClade method*

Description

group selected clade

Usage

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

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

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

## S4 method for signature 'jplace'
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	*groupOTU method*

Description

group tree based on selected OTU, will traceback to MRCA

Usage

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

## S4 method for signature 'beast'
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 'jplace'
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", ...)

## S4 method for signature 'r8s'
groupOTU(object, focus, group_name = "group", tree = "TREE",
  ...)
```

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
`tree`	which tree selected

Value

group index

`groupOTU.phylo`	*groupOTU.phylo*

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

hyphy-class   *Class "hyphy" This class stores information of HYPHY output*

Description

Class "hyphy" This class stores information of HYPHY output

Slots

fields available features

treetext tree text

phylo phylo object

seq_type one of "NT" and "AA"

subs sequence substitutions

AA_subs Amino acid sequence substitution

ancseq ancestral sequences

tip_seq tip sequences

tip.fasfile fasta file of tip sequences

tree.file tree file

ancseq.file ancestral sequence file, nexus format

extraInfo extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

See Also

paml_rst

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

Examples

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

---

jplace-class   *Class "jplace" This class stores information of jplace file.*

Description

Class "jplace" This class stores information of jplace file.

Slots

fields colnames of first variable of placements

treetext tree text

phylo tree phylo object

placements placement information

version version

metadata metadata

file jplace file

extraInfo extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

See Also

show get.tree

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

Nnode   *Nnode*

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	*Ntip*

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

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` ancenstral 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 *Class "phylip" This class stores phylip tree(s)*

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 *treeAnno.pml*

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   *pmlToSeq*

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   *print*

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

---

r8s-class   *Class "r8s" This class stores output info from r8s*

Description

Class "r8s" This class stores output info from r8s

Slots

file input file

fields available feature

treetext tree text

phylo multiPhylo, time tree, rate tree and absolute substitution tree

extraInfo extra information

Author(s)

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

---

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.baseml   *read.baseml*

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   *read.beast*

Description

read beast output

Usage

```
read.beast(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   *read.codeml*

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   *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)

ygc

Examples

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

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 <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.jplace	*read.jplace*

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   *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.phyloT   *read.phyloT*

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

file   r8s output log file

Value

r8s instance

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

raxml object

Author(s)

Guangchuang Yu

Examples

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

---

show,beast-method   *show method*

Description

show method for jplace instance

Usage

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

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

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

show(object)

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

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

## S4 method for signature 'r8s'
show(object)

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

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

Arguments

object   one of jplace, beast 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   *taxa_rename*

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

Description

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

Slots

phylo phylo object for tree structure

treetext newick tree string

data associated data

extraInfo extra information, reserve for merge_tree

file tree file

Author(s)

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write.jplace *write.jplace*

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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