

# Package ‘treeio’

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**Title** Base Classes and Functions for Phylogenetic Tree Input and Output

**Version** 1.2.2

**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** 6.0.1

**NeedsCompilation** no

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

**Value**

treedata object

**Author(s)**

guangchuang yu

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beast-class	<i>Class "beast" This class stores information of beast output</i>
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**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](#)

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

*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	<i>get.placements method</i>
----------------	------------------------------

---

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

---

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

---

### 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)
```

---

<i>getNodeNum</i>	<i>getNodeNum</i>
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---

**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

---

group0TU	<i>groupOTU method</i>
----------	------------------------

---

### Description

group tree based on selected OTU, will traceback to MRCA

### Usage

```
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'beast'
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'codeml'
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'codeml_mlc'
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'jplace'
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'treedata'
group0TU(object, focus, group_name = "group", ...)

## S4 method for signature 'phangorn'
group0TU(object, focus, group_name = "group", ...)
```

```
## S4 method for signature 'phylo'
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	<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

---

hyphy-class	<i>Class "hyphy" This class stores information of HYPHY output</i>
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---

**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	<i>is.ggtree</i>
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---

**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	<i>label_branch_paml</i>
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---

**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

*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	<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>
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---

**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	<i>Class "r8s" This class stores output info from r8s</i>
-----------	---

---

**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	<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)
```

**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      *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	<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	<i>read.newick</i>
-------------	--------------------

---

**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	<i>read.paml_rst</i>
---------------	----------------------

---

**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	<i>read.r8s</i>
----------	-----------------

---

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

---

**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)**

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

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)**

ycg

**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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