Package ‘ggtree’

October 9, 2015

Type Package

Title a phylogenetic tree viewer for different types of tree annotations

Version 1.0.21

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Description ggtree extends the ggplot2 plotting system which implemented the grammar of graphics. ggtree is designed for visualizing phylogenetic tree and different types of associated annotation data.

Depends R (>= 3.1.0)

Imports ape, Biostrings, colorspace, EBImage, ggplot2, grid, gridExtra, jsonlite, magrittr, methods, reshape2, stats4

Suggests phylobase, phytools, BiocStyle, knitr, testthat, rmarkdown

VignetteBuilder knitr

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URL `https://github.com/GuangchuangYu/ggtree`

BugReports `https://github.com/GuangchuangYu/ggtree/issues`

biocViews Software, Annotation, Clustering, DataImport, Visualization

NeedsCompilation no

R topics documented:

. .

Description

capture name of variable

Usage

```
.(..., .env = parent.frame())
```

Arguments

`...`	expression
`.env`	environment

Value

expression

Examples

```
x <- 1
eval(.(x)[[1]])
```

`add_colorbar` *add_colorbar*

Description

add colorbar legend

Usage

```
add_colorbar(p, color, x = NULL, ymin = NULL, ymax = NULL,
  font.size = 4)
```

Arguments

`p`	tree view
`color`	output of scale_color function
`x`	x position
`ymin`	ymin
`ymax`	ymax
`font.size`	font size

Value

ggplot2 object

Author(s)

Guangchuang Yu

`add_legend` *add_legend*

Description

add evolution distance legend

Usage

```
add_legend(p, width = NULL, x = NULL, y = NULL, offset = NULL,
  font.size = 4, ...)
```

Arguments

`p`	tree view
`width`	width of legend
`x`	x position
`y`	y position
`offset`	offset of text and line
`font.size`	font size
`...`	additional parameter

Value

tree view

Author(s)

Guangchuang Yu

`aes` *creates a lists of unevaluated expressions*

Description

creates a lists of unevaluated expressions

Usage

```
aes(x, y, ...)
```

Arguments

`x`	name values
`y`	name values
`...`	additional name values

Source

This is just the imported function from the ggplot2 package. The documentation you should read for the aes function can be found here: aes

See Also

aes

`annotation_clade` *annotation_clade*

Description

annotate a selected clade with internal node number

Usage

```
annotation_clade(tree_view, node, label, bar.size = 2, font.size = 4,
  offset = 0, offset.text = NULL, ...)
```

Arguments

`tree_view`	tree view
`node`	node number
`label`	clade label
`bar.size`	bar size
`font.size`	font size
`offset`	offset of bar from the tree
`offset.text`	offset of label from bar
`...`	additional parameter

Value

ggplot2

Author(s)

Guangchuang Yu

`annotation_clade2` *annotation_clade2*

Description

annotate a clade with selected upper and lower tips

Usage

```
annotation_clade2(tree_view, tip1, tip2, label, bar.size = 2, font.size = 4,
  offset = 0, offset.text = NULL, ...)
```

Arguments

`tree_view`	tree view
`tip1`	tip1 label or id
`tip2`	tip2 label or id
`label`	clade label
`bar.size`	bar size
`font.size`	font size
`offset`	offset of bar from the tree
`offset.text`	offset of label from bar
`...`	additional parameter

Value

ggplot2

Author(s)

Guangchuang Yu

`annotation_image` *annotation_image*

Description

annotation taxa with images

Usage

```
annotation_image(tree_view, img_info, width = 0.1, align = TRUE,
  linetype = "dotted", linesize = 1, offset = 0)
```

Arguments

`tree_view`	tree view
`img_info`	data.frame with first column of taxa name and second column of image names
`width`	width of the image to be plotted in image
`align`	logical
`linetype`	line type if align = TRUE
`linesize`	line size if align = TRUE
`offset`	offset of image from the tree view

Value

tree view

Author(s)

Guangchuang Yu

`as.binary` *as.binary*

Description

as.binary

as.binary method for `phylo` object

Usage

```
as.binary(tree, ...)

## S3 method for class 'phylo'
as.binary(tree, ...)
```

Arguments

`tree`	phylo, object
`...`	additional parameter

Value

binary tree

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

```
require(ape)
tr <- read.tree(text="((A, B, C), D);")
is.binary.tree(tr)
tr2 <- as.binary(tr)
is.binary.tree(tr2)
```

`as.data.frame.phylo` *as.data.frame*

Description

as.data.frame

Usage

```
## S3 method for class 'phylo'
as.data.frame(x, row.names, optional, layout = "rectangular",
  ...)
```

Arguments

`x`	phylo object
`row.names`	omitted here
`optional`	omitted here
`layout`	layout
`...`	additional parameter

Value

data.frame

Author(s)

Yu Guangchuang

`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://ygc.name`

See Also

`show` `get.fields` `ggtree`

`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

`collapse` *collapse*

Description

collapse a clade

Usage

```
collapse(tree_view, node)
```

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

expand

`Date2decimal` *Date2decimal*

Description

convert Date to decimal format, eg "2014-05-05" to "2014.34"

Usage

```
Date2decimal(x)
```

Arguments

`x`	Date

Value

numeric

Author(s)

Guangchuang Yu

`decimal2Date` *decimal2Date*

Description

convert decimal format to Date, eg "2014.34" to "2014-05-05"

Usage

```
decimal2Date(x)
```

Arguments

`x`	numerical number, eg 2014.34

Value

Date

Author(s)

Guangchuang Yu

`download.phylopic` *download.phylopic*

Description

download phylopic

Usage

```
download.phylopic(id, size = 512, color = "black", alpha = 1)
```

Arguments

`id`	phyopic id
`size`	size of phylopic
`color`	color
`alpha`	alpha

Value

matrix

Author(s)

Guangchuang Yu

`expand` *expand*

Description

expand collased clade

Usage

```
expand(tree_view, node)
```

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

collapse

`flip` *flip*

Description

flip position of two selected branches

Usage

```
flip(tree_view, node1, node2)
```

Arguments

`tree_view`	tree view
`node1`	node number of branch 1
`node2`	node number of branch 2

Value

ggplot2 object

Author(s)

Guangchuang Yu

`fortify.phylo` *fortify*

Description

fortify

Usage

```
## S3 method for class 'phylo'
fortify(model, data, layout = "rectangular",
  ladderize = TRUE, right = FALSE, mrsd = NULL, as.Date = FALSE, ...)
```

Arguments

`model`	phylo object
`data`	not use here
`layout`	layout
`ladderize`	ladderize, logical
`right`	logical
`mrsd`	most recent sampling date
`as.Date`	logical whether using Date class in time tree
`...`	additional parameter

Value

data.frame

Author(s)

Yu Guangchuang

`geom_aline` *geom_aline*

Description

add horizontal align lines

Usage

```
geom_aline(mapping = NULL, linetype = "dotted", size = 1, ...)
```

Arguments

`mapping`	aes mapping
`linetype`	line type
`size`	line size
`...`	additional parameter

Value

aline layer

Author(s)

Yu Guangchuang

`geom_hilight` *geom_hilight*

Description

hilight clade with rectangle

Usage

```
geom_hilight(tree_object, node, ...)
```

Arguments

`tree_object`	supported tree object
`node`	internal node
`...`	additional parameters

Value

ggplot layer

Author(s)

Guangchuang Yu

`geom_nodepoint` *geom_nodepoint*

Description

add node point

Usage

```
geom_nodepoint(mapping = NULL, ...)
```

Arguments

`mapping`	aes mapping
`...`	additional parameter

Value

node point layer

Author(s)

Guangchuang Yu

`geom_rootpoint` *geom_rootpoint*

Description

add root point

Usage

```
geom_rootpoint(mapping = NULL, ...)
```

Arguments

`mapping`	aes mapping
`...`	additional parameter

Value

root point layer

Author(s)

Guangchuang Yu

`geom_text` *text annotations*

Description

text annotations

Usage

```
geom_text(mapping = NULL, data = NULL, stat = "identity",
  position = "identity", parse = FALSE, ...)
```

Arguments

`mapping`	the aesthetic mapping
`data`	A layer specific dataset - only needed if you want to override he plot defaults.
`stat`	The statistical transformation to use on the data for this layer
`position`	The position adjustment to use for overlapping points on this layer
`parse`	if TRUE, the labels will be passd into expressions
`...`	other arguments passed on to 'layer'

Source

This is just the imported function from the ggplot2 package. The documentation you should read for the geom_text function can be found here: geom_text

See Also

geom_text

`geom_tiplab` *geom_tiplab*

Description

add tip label layer

Usage

```
geom_tiplab(mapping = NULL, hjust = 0, align = FALSE,
  linetype = "dotted", linesize = 1, ...)
```

Arguments

`mapping`	aes mapping
`hjust`	horizontal adjustment
`align`	align tip lab or not, logical
`linetype`	linetype for adding line if align = TRUE
`linesize`	line size of line if align = TRUE
`...`	additional parameter

Value

tip label layer

Author(s)

Yu Guangchuang

Examples

```
require(ape)
tr <- rtree(10)
ggtree(tr) + geom_tiplab()
```

`geom_tippoint` *geom_tippoint*

Description

add tip point

Usage

```
geom_tippoint(mapping = NULL, ...)
```

Arguments

`mapping`	aes mapping
`...`	additional parameter

Value

tip point layer

Author(s)

Guangchuang Yu

`geom_tree` *geom_tree*

Description

add tree layer

Usage

```
geom_tree(layout = "rectangular", ...)
```

Arguments

`layout`	one of 'rectangular', 'slanted', 'circular', 'radial' or 'unrooted'
`...`	additional parameter

Value

tree layer

Author(s)

Yu Guangchuang

Examples

```
require(ape)
tr <- rtree(10)
require(ggplot2)
ggplot(tr) + geom_tree()
```

`get.fields` *get.fields method*

Description

get.fields method

get.fields method

Usage

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

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

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

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

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

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

get.fields(object, ...)

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

## S4 method for signature 'r8s'
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="ggtree")
jp <- read.jplace(jp)
get.fields(jp)
```

`get.offspring.tip` *get.offspring.tip*

Description

extract offspring tips

Usage

```
get.offspring.tip(tr, node)
```

Arguments

`tr`	tree
`node`	node

Value

tip label

Author(s)

ygc

`get.path` *get.path*

Description

path from start node to end node

Usage

```
get.path(phylo, from, to)
```

Arguments

`phylo`	phylo object
`from`	start node
`to`	end node

Value

node vectot

Author(s)

Guangchuang Yu

`get.phylopic` *get.phylopic*

Description

download phylopic and convert to grob object

Usage

```
get.phylopic(id, size = 512, color = "black", alpha = 1)
```

Arguments

`id`	phylopic id
`size`	size of the phylopic
`color`	color
`alpha`	alpha

Value

grob object

Author(s)

Guangchuang Yu

`get.placements` *get.placements method*

Description

get.placements method

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="ggtree")
jp <- read.jplace(jp)
get.placements(jp, by="all")
```

`get.subs` *get.subs method*

Description

get.subs method

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, ...)
```

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

`get.tipseq` *get.tipseq method*

Description

get.tipseq method

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

get.tree method

Usage

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

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

get.tree(object, ...)

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

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

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

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

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

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

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

Arguments

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

Value

phylo object

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`get.treeinfo` *get.treeinfo method*

Description

get.treeinfo method

get.treeinfo method

Usage

```
get.treeinfo(object, layout = "phylogram", ladderize = TRUE,
  right = FALSE, ...)

get.treeinfo(object, layout, ladderize, right, ...)
```

Arguments

`object`	jplace object
`layout`	layout
`ladderize`	ladderize, logical
`right`	logical, parameter for ladderize
`...`	additional parameter

Value

data.frame

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`get.treetext` *get.treetext method*

Description

get.treetext method

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="ggtree")
jp <- read.jplace(jp)
get.treetext(jp)
```

`getNodeNum` *getNodeNum*

Description

calculate total number of nodes

Usage

```
getNodeNum(tr)
```

Arguments

`tr`	phylo object

Value

number

Author(s)

Guangchuang Yu

`getRoot` *getRoot*

Description

get the root number

Usage

```
getRoot(tr)
```

Arguments

`tr`	phylo object

Value

root number

Author(s)

Guangchuang Yu

`get_taxa_name` *get_taxa_name*

Description

get taxa name of a selected node

Usage

```
get_taxa_name(tree_view, node)
```

Arguments

`tree_view`	tree view
`node`	node

Value

taxa name vector

Author(s)

Guangchuang Yu

`ggplotGrob` *generate a ggplot2 plot grob*

Description

generate a ggplot2 plot grob

Usage

```
ggplotGrob(x)
```

Arguments

`x`	ggplot2 object

Source

This is just the imported function from the ggplot2 package. The documentation you should read for the ggplotGrob function can be found here: ggplotGrob

See Also

ggplotGrob

`ggtree` *visualizing phylogenetic tree and heterogenous associated data based on grammar of graphics* `ggtree` *provides functions for visualizing phylogenetic tree and its associated data in R.*

Description

visualizing phylogenetic tree and heterogenous associated data based on grammar of graphics `ggtree` provides functions for visualizing phylogenetic tree and its associated data in R.

drawing phylogenetic tree from phylo object

Usage

```
ggtree(tr, mapping = NULL, showDistance = FALSE, layout = "rectangular",
  mrsd = NULL, as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = TRUE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, ...)
```

Arguments

`tr`	phylo object
`mapping`	aes mapping
`showDistance`	add distance legend, logical
`layout`	one of 'rectangular', 'slanted', 'fan'/'circular', 'radial' or 'unrooted'
`mrsd`	most recent sampling date
`as.Date`	logical whether using Date class in time tree
`yscale`	y scale
`yscale_mapping`	yscale mapping for category variable
`ladderize`	logical
`right`	logical
`branch.length`	variable for scaling branch, if 'none' draw cladogram
`ndigits`	number of digits to round numerical annotation variable
`...`	additional parameter

Value

tree

Author(s)

Yu Guangchuang

Examples

```
require(ape)
tr <- rtree(10)
ggtree(tr)
```

`gheatmap` *gheatmap*

Description

append a heatmap of a matrix to right side of phylogenetic tree

Usage

```
gheatmap(p, data, offset = 0, width = 1, low = "green", high = "red",
  color = "white", colnames = TRUE, colnames_position = "bottom",
  font.size = 4)
```

Arguments

`p`	tree view
`data`	matrix or data.frame
`offset`	offset of heatmap to tree
`width`	total width of heatmap, compare to width of tree
`low`	color of lowest value
`high`	color of highest value
`color`	color of heatmap cell border
`colnames`	logical, add matrix colnames or not
`colnames_position`	one of 'bottom' or 'top'
`font.size`	font size of matrix colnames

Value

tree view

Author(s)

Guangchuang Yu

`gplot` *gplot*

Description

view tree and associated matrix

Usage

```
gplot(p, data, low = "green", high = "red", widths = c(0.5, 0.5),
  color = "white", font.size = 14)
```

Arguments

`p`	tree view
`data`	matrix
`low`	low color
`high`	high color
`widths`	widths of sub plot
`color`	color
`font.size`	font size

Value

list of figure

Author(s)

Guangchuang Yu http://ygc.name

Examples

```
nwk <- system.file("extdata", "sample.nwk", package="ggtree")
tree <- read.tree(nwk)
p <- ggtree(tree)
d <- matrix(abs(rnorm(52)), ncol=4)
rownames(d) <- tree$tip.label
colnames(d) <- paste0("G", 1:4)
gplot(p, d, low="green", high="red")
```

`groupClade` *groupClade method*

Description

groupClade method

Usage

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

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

## S4 method for signature 'ggplot'
groupClade(object, node, group_name)

## S4 method for signature 'gg'
groupClade(object, node, group_name)

## S4 method for signature 'hyphy'
```

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

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

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

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

## S4 method for signature 'r8s'
groupClade(object, node, group_name = "group",
  tree = "TREE")
```

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
`tree`	which tree selected

Value

group index

---

groupOTU *groupOTU method*

Description

groupOTU method

Usage

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

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

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

## S4 method for signature 'ggplot'
```

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

## S4 method for signature 'gg'
groupOTU(object, focus, group_name)

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

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

## 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 'paml_rst'
groupOTU(object, focus, group_name = "group")

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

## S4 method for signature 'jplace'
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
`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

Value

phylo object

Author(s)

ygc

`gzoom` *gzoom method*

Description

gzoom method

Usage

```
gzoom(object, focus, subtree = FALSE, widths = c(0.3, 0.7), ...)

## S4 method for signature 'raxml'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'beast'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'codeml'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'codeml_mlc'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'hyphy'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
```

```
  0.7))

## S4 method for signature 'paml_rst'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'phylo'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'r8s'
gzoom(object, focus, subtree = FALSE, widths = c(0.3, 0.7),
  tree = "TREE")
```

Arguments

`object`	supported tree objects
`focus`	selected tips
`subtree`	logical
`widths`	widths
`...`	additional parameter
`tree`	which tree selected

Value

figure

`gzoom.phylo` *gzoom*

Description

plots simultaneously a whole phylogenetic tree and a portion of it.

Usage

```
gzoom.phylo(phy, focus, subtree = FALSE, widths = c(0.3, 0.7))
```

Arguments

`phy`	phylo object
`focus`	selected tips
`subtree`	logical
`widths`	widths

Value

a list of ggplot object

Author(s)

ygc

Examples

```
require(ape)
data(chiroptera)
gzoom(chiroptera, grep("Plecotus", chiroptera$tip.label))
```

`hilight` *hilight*

Description

hilight clade with rectangle

Usage

```
hilight(tree_view, node, fill = "steelblue", alpha = 0.5, ...)
```

Arguments

`tree_view`	tree view
`node`	clade node
`fill`	fill color
`alpha`	alpha
`...`	additional parameter

Value

tree view

Author(s)

Guangchuang Yu

`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://ygc.name`

See Also

paml_rst

`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://ygc.name`

See Also

`show` `get.tree` `ggtree`

`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

`msaplot` *msaplot*

Description

multiple sequence alignment with phylogenetic tree

Usage

```
msaplot(p, fasta, offset = 0, width = 1, color = NULL, window = NULL)
```

Arguments

`p`	tree view
`fasta`	fasta file, multiple sequence alignment
`offset`	offset of MSA to tree
`width`	total width of alignment, compare to width of tree
`color`	color
`window`	specific a slice to display

Value

tree view

Author(s)

Guangchuang Yu

`NJ` *NJ*

Description

neighbor-joining method

Usage

```
NJ(X)
```

Arguments

`X`	distance matrix

Value

phylo object

Author(s)

ygc

Examples

```
## Not run:
X <- matrix(c(0,5,4,7,6,8,
5,0,7,10,9,11,
4,7,0,7,6,8,
7,10,7,0,5,9,
6,9,6,5,0,8,
8,11,8,9,8,0), ncol=6)
rownames(X) <- colnames(X) <- LETTERS[1:6]
tree <- NJ(X)
print(tree)

## End(Not run)
```

`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://ygc.name`

See Also

codeml codeml_mlc

`phylopic` *phylopic*

Description

add phylopic layer

Usage

```
phylopic(tree_view, phylopic_id, size = 512, color = "black", alpha = 0.5,
  node = NULL, x = NULL, y = NULL, width = 0.1)
```

Arguments

`tree_view`	tree view
`phylopic_id`	phylopic id
`size`	size of phylopic to download
`color`	color
`alpha`	alpha
`node`	selected node
`x`	x position
`y`	y position
`width`	width of phylopic

Value

phylopic layer

Author(s)

Guangchuang Yu

`plot` *plot method*

Description

plot method generics

Usage

```
## S4 method for signature 'beast,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "rate", ndigits = 2, annotation.size = 3,
  annotation.color = "black", ...)

## S4 method for signature 'codeml_mlc,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "dN_vs_dS", annotation.size = 3,
  annotation.color = "black", ndigits = 2, ...)

## S4 method for signature 'r8s,ANY'
plot(x, layout = "rectangular", branch.length = "TREE",
  show.tip.label = TRUE, tip.label.size = 4, tip.label.hjust = 0, ...)

## S4 method for signature 'raxml,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = 0, position = "node",
  annotation = "bootstrap", ndigits = 2, annotation.size = 4,
  annotation.color = "black", ...)

## S4 method for signature 'paml_rst,ANY'
plot(x, layout = "rectangular",
  show.tip.label = TRUE, tip.label.size = 4, tip.label.hjust = -0.1,
  position = "branch", annotation = "marginal_subs",
  annotation.color = "black", annotation.size = 3, ...)

## S4 method for signature 'hyphy,ANY'
plot(x, layout = "rectangular", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "subs", annotation.color = "black", annotation.size = 3,
  ...)

## S4 method for signature 'codeml,ANY'
plot(x, layout = "rectangular",
  branch.length = "mlc.branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "dN_vs_dS", annotation.size = 3,
  annotation.color = "black", ndigits = 2, ...)
```

Arguments

x	object

`layout`	layout
`branch.length`	branch length
`show.tip.label`	logical
`tip.label.size`	size of tip label
`tip.label.hjust`	hjust of tip.label
`position`	one of "branch" and "node"
`annotation`	one of get.fields(x)
`ndigits`	round digits
`annotation.size`	size of annotation
`annotation.color`	color of annotation
`...`	Additional argument list

Value

plot

Examples

```
file <- system.file("extdata/BEAST", "beast_mcc.tree", package="ggtree")
beast <- read.beast(file)
plot(beast, annotation="length_0.95_HPD", branch.length="none") + theme_tree()
```

`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://ygc.name`

`raxml-class` *Class "raxml" This class stores RAxML bootstrapping analysis result*

Description

Class "raxml" This class stores RAxML bootstrapping analysis result

Slots

`file` input file

`fields` available features

`treetext` tree text

`phylo` phylo object of treetext

`bootstrap` bootstrap value

`extraInfo` extra information

Author(s)

Guangchuang Yu `http://ygc.name`

`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="ggtree")
mlbfile <- system.file("extdata/PAML_Baseml", "mlb", package="ggtree")
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 `http://ygc.name`

Examples

```
file <- system.file("extdata/BEAST", "beast_mcc.tree", package="ggtree")
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="ggtree")
mlcfile <- system.file("extdata/PAML_Codeml", "mlc", package="ggtree")
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="ggtree")
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="ggtree")
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="ggtree")
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="ggtree")
read.jplace(jp)
```

`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="ggtree")
read.paml_rst(rstfile)
```

`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

`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

`read.tree` *read newick tree*

Description

read newick tree

Usage

```
read.tree(file = "", text = NULL, tree.names = NULL, skip = 0,
  comment.char = "#", keep.multi = FALSE, ...)
```

Arguments

`file`	file name
`text`	alternatively, using newick text
`tree.names`	if read several trees, specify their names
`skip`	number of lines of the input file to skip
`comment.char`	a single character, the remaining of the line after this character is ignored.
`keep.multi`	if 'TRUE' and 'tree.names = NULL' then single trees are returned in 'multiPhylo' format with any name that is present. Default is 'FALSE'
`...`	further arguments to be passed to 'scan()'.

Source

This is just the imported function from the ape package. The documentation you should read for the read.tree function can be found here: read.tree

See Also

read.tree

`reroot` *reroot method*

Description

reroot method

Usage

```
reroot(object, node, ...)

## S4 method for signature 'beast'
reroot(object, node, ...)

## S4 method for signature 'phylo'
reroot(object, node, ...)
```

Arguments

`object`	one of `phylo`, `jplace`, `beast`, `hyphy`, `codeml`, `codeml_mlc`, `paml_rst` object
`node`	internal nnode number
`...`	additional parameter

Value

tree object

`rm.singleton.newick` *rm.singleton.newick*

Description

remove singleton

Usage

```
rm.singleton.newick(nwk, outfile = NULL)
```

Arguments

`nwk`	newick file
`outfile`	output newick file

Value

tree text

Author(s)

Guangchuang Yu `http://ygc.name`

`rotate` *rotate*

Description

rotate 180 degree of a selected branch

Usage

```
rotate(tree_view, node)
```

Arguments

`tree_view`	tree view
`node`	selected node

Value

ggplot2 object

Author(s)

Guangchuang Yu

`rtree` *generate random tree*

Description

generate random tree

Usage

```
rtree(n, rooted = TRUE, tip.label = NULL, br = runif, ...)
```

Arguments

`n`	number of tips in the tree
`rooted`	logcial
`tip.label`	tip label
`br`	one of the following: (i) an R function used to generate the branch lengths ('rtree'; use 'NULL' to simulate only a topology), or the coalescence times ('rcoal'); (ii) a character to simulate a genuine coalescent tree for 'rcoal' (the default); or (iii) a numeric vector for the branch lengths or the coalescence times.
`...`	additional parameters to be passed to 'br'

Source

This is just the imported function from the ape package. The documentation you should read for the rtree function can be found here: rtree

See Also

rtree

`scaleClade` *scaleClade*

Description

scale clade

Usage

```
scaleClade(tree_view, node, scale = 1, vertical_only = TRUE)
```

Arguments

`tree_view`	tree view
`node`	clade node
`scale`	scale
`vertical_only`	logical. If TRUE, only vertical will be scaled. If FALSE, the clade will be scaled vertical and horizontally. TRUE by default.

Value

tree view

Author(s)

Guangchuang Yu

---

scale_color *scale_color method*

Description

scale_color method

Usage

```
scale_color(object, by, ...)

## S4 method for signature 'raxml'
scale_color(object, by = "bootstrap", ...)

## S4 method for signature 'beast'
scale_color(object, by, ...)

## S4 method for signature 'codeml'
scale_color(object, by, ...)

## S4 method for signature 'codeml_mlc'
scale_color(object, by, ...)

## S4 method for signature 'hyphy'
scale_color(object, by, ...)

## S4 method for signature 'jplace'
scale_color(object, by, ...)

## S4 method for signature 'paml_rst'
scale_color(object, by, ...)

## S4 method for signature 'phylo'
scale_color(object, by, ...)

## S4 method for signature 'r8s'
scale_color(object, by = "bootstrap", tree = "TREE")
```

Arguments

`object`	supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy
`by`	one of numerical attributes
`...`	additional parameter
`tree`	which tree selected

Value

color vector

`scale_x_ggtree` *scale_x_ggtree*

Description

scale x for tree with heatmap

Usage

```
scale_x_ggtree(p, breaks = NULL, labels = NULL)
```

Arguments

`p`	tree view
`breaks`	breaks for tree
`labels`	lables for corresponding breaks

Value

tree view

Author(s)

Guangchuang Yu

`show,raxml-method` *show method*

Description

show method for `jplace` instance

Usage

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

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

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

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

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

show(object)

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

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

Arguments

`object`	one of `jplace`, `beast` object

Value

print info

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`subview` *subview*

Description

add subview to mainview for ggplot2 objects

Usage

```
subview(mainview, subview, x, y, width = 0.1, height = 0.1)
```

Arguments

`mainview`	main view
`subview`	sub view
`x`	x position
`y`	y position
`width`	width of subview, [0,1]
`height`	height of subview, [0,1]

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_transparent` *theme_transparent*

Description

transparent background theme

Usage

```
theme_transparent(...)
```

Arguments

`...`	additional parameter to tweak the theme

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_tree` *theme_tree*

Description

tree theme

Usage

```
theme_tree(bgcolor = "white", fgcolor = "black", ...)
```

Arguments

`bgcolor`	background color
`fgcolor`	foreground color
`...`	additional parameter

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

```
require(ape)
tr <- rtree(10)
ggtree(tr) + theme_tree()
```

`theme_tree2` *theme_tree2*

Description

tree2 theme

Usage

```
theme_tree2(bgcolor = "white", fgcolor = "black", ...)
```

Arguments

`bgcolor`	background color
`fgcolor`	foreground color
`...`	additional parameter

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

```
require(ape)
tr <- rtree(10)
ggtree(tr) + theme_tree2()
```

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

`%<+%` *%<+%*

Description

add annotation data to a tree

Usage

```
pg %<+% data
```

Arguments

`pg`	ggplot2 object
`data`	annotation data

Value

ggplot object with annotation data added

Author(s)

Yu Guangchuang

Examples

```
nwk <- system.file("extdata", "sample.nwk", package="ggtree")
tree <- read.tree(nwk)
p <- ggtree(tree)
dd <- data.frame(taxa=LETTERS[1:13],
     place=c(rep("GZ", 5), rep("HK", 3), rep("CZ", 4), NA),
             value=round(abs(rnorm(13, mean=70, sd=10)), digits=1))
row.names(dd) <- NULL
p %<+% dd + geom_text(aes(color=place, label=label), hjust=-0.5)
```

`%>%` *pipe*

Description

pipe

Usage

```
lhs %>% rhs
```

Arguments

`lhs`	left hand side
`rhs`	right hand side

See Also

pipe

`%<%` *%<%*

Description

update tree

Usage

```
pg %<% x
```

Arguments

`pg`	ggplot2 object
`x`	update by x

Value

updated ggplot object

Author(s)

Yu Guangchuang

Examples

```
library("ggplot2")
nwk <- system.file("extdata", "sample.nwk", package="ggtree")
tree <- read.tree(nwk)
p <- ggtree(tree) + geom_tippoint(color="#b5e521", alpha=1/4, size=10)
p %<% rtree(30)
```

Index