Package 'ggtree'

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Type Package

Title an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data

Version 1.4.20

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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 (>= 3.2.0), ggplot2 (>= 2.0.0)

Imports ape, grDevices, grid, jsonlite, magrittr, methods, stats4, tidyr, utils

Suggests Biostrings, colorspace, EBImage, emojifont, knitr, rmarkdown, scales, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

URL http://guangchuangyu.github.io/ggtree

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

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

RoxygenNote 5.0.1

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

---

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

---

apeBoot	*apeBoot*

Description

merge phylo and output of boot.phylo to 'apeBootstrap' object

Usage

```
apeBoot(phylo, boot)
```

Arguments

phylo	phylo
boot	bootstrap values

Value

an instance of 'apeBootstrap'

Author(s)

Guangchuang Yu

---

apeBootstrap-class	*Class "apeBootstrap" This class stores ape bootstrapping analysis result*

Description

Class "apeBootstrap" This class stores ape bootstrapping analysis result

Slots

phylo phylo object of treetext

fields available features

bootstrap bootstrap value

extraInfo extra information

Author(s)

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

---

as.binary	*as.binary*

Description

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

convert phylo to 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://guangchuangyu.github.io>

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 = NULL, 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 = NULL, 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 = NULL, 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 a phylo to data.frame

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_balance *geom_balance*

Description

highlights the two direct descendant clades of an internal node

Usage

```
geom_balance(node, fill = "steelblue", color = "white", alpha = 0.5,
  extend = 0, extendto = NULL)
```

Arguments

node	selected node (balance) to highlight
fill	color fill
color	color to outline highlights and divide balance
alpha	alpha (transparency)
extend	extend xmax of the rectangle
extendto	extend xmax to extendto

Details

Particularly useful when studying neighboring clades. Note that balances that correspond to multi-chotomies will not be displayed.

Value

ggplot2

Author(s)

Justin Silverman

References

J. Silverman, et al. *A phylogenetic transform enhances analysis of compositional microbiota data.* (in preparation)

---

  geom_cladelabel   *geom_cladelabel*

Description

annotate a clade with bar and text label

Usage

```
geom_cladelabel(node, label, offset = 0, offset.text = 0, align = FALSE,
  barsize = 0.5, fontsize = 3.88, angle = 0, geom = "text", hjust = 0,
  fill = NA, family = "sans", ...)
```

Arguments

node	selected node
label	clade label
offset	offset of bar and text from the clade
offset.text	offset of text from bar
align	logical
barsize	size of bar
fontsize	size of text
angle	angle of text
geom	one of 'text' or 'label'
hjust	hjust
fill	fill label background, only work with geom='label'
family	sans by default, can be any supported font
...	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

---

geom_hilight *geom_hilight*

Description

layer of hilight clade with rectangle

Usage

```
geom_hilight(node, fill = "steelblue", alpha = 0.5, extend = 0,
  extendto = NULL)
```

Arguments

node	selected node to hilight
fill	color fill
alpha	alpha (transparency)
extend	extend xmax of the rectangle
extendto	extend xmax to extendto

Value

ggplot2

Author(s)

Guangchuang Yu

---

geom_label2   *geom_text2*

Description

geom_text2 support aes(subset) via setup_data

Usage

```
geom_label2(mapping = NULL, data = NULL, ..., parse = FALSE,
  nudge_x = 0, nudge_y = 0, label.padding = unit(0.25, "lines"),
  label.r = unit(0.15, "lines"), label.size = 0.25, na.rm = TRUE,
  show.legend = NA, inherit.aes = TRUE)
```

Arguments

mapping	the aesthetic mapping
data	A layer specific dataset - only needed if you want to override he plot defaults.
...	other arguments passed on to 'layer'
parse	if TRUE, the labels will be passd into expressions
nudge_x	horizontal adjustment
nudge_y	vertical adjustment
label.padding	Amount of padding around label.
label.r	Radius of rounded corners.
label.size	Size of label border, in mm
na.rm	logical
show.legend	logical
inherit.aes	logical

Value

label layer

Author(s)

Guangchuang Yu

See Also

[geom_label](#)

---

geom_nodepoint *geom_nodepoint*

Description

add node point

Usage

```
geom_nodepoint(mapping = NULL, data = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

mapping	aes mapping
data	data
position	position
na.rm	logical
show.legend	logical
inherit.aes	logical
...	addktional parameter

Value

node point layer

Author(s)

Guangchuang Yu

---

geom_point2 *geom_point2*

Description

geom_point2 support aes(subset) via setup_data

Usage

```
geom_point2(mapping = NULL, data = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

`mapping`	aes mapping
`data`	data
`position`	position
`na.rm`	logical
`show.legend`	logical
`inherit.aes`	logical
`...`	addktional parameter

Value

point layer

Author(s)

Guangchuang Yu

See Also

geom_point

`geom_range`	*geom_range*

Description

bar of range (HPD, range etc) to present uncertainty of evolutionary inference

Usage

```
geom_range(range = "height_0.95_HPD", ...)
```

Arguments

`range`	range, e.g. "height_0.95_HPD"
`...`	additional parameter, e.g. color, size, alpha

Value

ggplot layer

Author(s)

Guangchuang Yu

geom_rootpoint	*geom_rootpoint*

Description

add root point

Usage

```
geom_rootpoint(mapping = NULL, data = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

mapping	aes mapping
data	data
position	position
na.rm	logical
show.legend	logical
inherit.aes	logical
...	addktional parameter

Value

root point layer

Author(s)

Guangchuang Yu

geom_segment2	*geom_segment2*

Description

geom_segment2 support aes(subset) via setup_data

Usage

```
geom_segment2(mapping = NULL, data = NULL, position = "identity",
  arrow = NULL, lineend = "butt", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

Arguments

`mapping`	aes mapping
`data`	data
`position`	position
`arrow`	arrow
`lineend`	lineend
`na.rm`	logical
`show.legend`	logical
`inherit.aes`	logical
`...`	additional parameter

Value

add segment layer

Author(s)

Guangchuang Yu

See Also

geom_segment

`geom_strip`	*geom_strip*

Description

annotate associated taxa (from taxa1 to taxa2, can be Monophyletic, Polyphyletic or Paraphyletc Taxa) with bar and (optional) text label

Usage

```
geom_strip(taxa1, taxa2, label = NA, offset = 0, offset.text = 0,
  align = TRUE, barsize = 0.5, barextend = 0, fontsize = 3.88,
  angle = 0, geom = "text", hjust = 0, fill = NA, family = "sans",
  ...)
```

Arguments

`taxa1`	taxa1
`taxa2`	taxa2
`label`	optional label
`offset`	offset of bar and text from the clade
`offset.text`	offset of text from bar
`align`	logical
`barsize`	size of bar
`barextend`	extend bar vertically
`fontsize`	size of text
`angle`	angle of text
`geom`	one of 'text' or 'label'
`hjust`	hjust
`fill`	fill label background, only work with geom='label'
`family`	sans by default, can be any supported font
`...`	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

`geom_taxalink`	*geom_taxalink*

Description

link between taxa

Usage

```
geom_taxalink(taxa1, taxa2, curvature = 0.5, ...)
```

Arguments

`taxa1`	taxa1, can be label or node number
`taxa2`	taxa2, can be label or node number
`curvature`	A numeric value giving the amount of curvature. Negative values produce left-hand curves, positive values produce right-hand curves, and zero produces a straight line.
`...`	additional parameter

Value

ggplot layer

Author(s)

Guangchuang Yu

---

geom_text2   *geom_text2*

Description

geom_text2 support aes(subset) via setup_data

Usage

```
geom_text2(mapping = NULL, data = NULL, position = "identity",
  parse = FALSE, na.rm = TRUE, show.legend = NA, inherit.aes = TRUE,
  ..., nudge_x = 0, nudge_y = 0, check_overlap = FALSE)
```

Arguments

mapping	the aesthetic mapping
data	A layer specific dataset - only needed if you want to override he plot defaults.
position	The position adjustment to use for overlapping points on this layer
parse	if TRUE, the labels will be passd into expressions
na.rm	logical
show.legend	logical
inherit.aes	logical
...	other arguments passed on to 'layer'
nudge_x	horizontal adjustment
nudge_y	vertical adjustment
check_overlap	if TRUE, text that overlaps previous text in the same layer will not be plotted

Value

text layer

Author(s)

Guangchuang Yu

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, geom = "text", ...)
```

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
geom	one of 'text' and 'label'
...	additional parameter

Value

tip label layer

Author(s)

Yu Guangchuang

Examples

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

---

geom_tiplab2   *geom_tiplab2*

Description

add tip label for circular layout

Usage

```
geom_tiplab2(mapping = NULL, hjust = 0, ...)
```

Arguments

mapping	aes mapping
hjust	horizontal adjustment
...	additional parameter, see geom_tiplab

Value

tip label layer

Author(s)

Guangchuang Yu

References

<https://groups.google.com/forum/#!topic/bioc-ggtree/o35PV3iHO-0>

---

geom_tippoint   *geom_tippoint*

Description

add tip point

Usage

```
geom_tippoint(mapping = NULL, data = NULL, position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

`mapping`	aes mapping
`data`	data
`position`	position
`na.rm`	logical
`show.legend`	logical
`inherit.aes`	logical
`...`	addktional parameter

Value

tip point layer

Author(s)

Guangchuang Yu

`geom_tree`	*geom_tree*

Description

add tree layer

Usage

```
geom_tree(mapping = NULL, data = NULL, layout = "rectangular",
  multiPhylo = FALSE, ...)
```

Arguments

`mapping`	aesthetic mapping
`data`	data
`layout`	one of 'rectangular', 'slanted', 'circular', 'radial' or 'unrooted'
`multiPhylo`	logical
`...`	additional parameter

Value

tree layer

Author(s)

Yu Guangchuang

geom_tree2   *geom_tree2*

Description

add tree layer

Usage

```
geom_tree2(layout = "rectangular", ...)
```

Arguments

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

Value

tree layer

Author(s)

Yu Guangchuang

geom_treescale   *geom_treescale*

Description

add tree scale

Usage

```
geom_treescale(x = NULL, y = NULL, width = NULL, offset = NULL,
  color = "black", linesize = 0.5, fontsize = 3.88, family = "sans")
```

Arguments

x	x position
y	y position
width	width of scale
offset	offset of text to line
color	color
linesize	size of line
fontsize	size of text
family	sans by default, can be any supported font

Value

ggplot layers

Author(s)

Guangchuang Yu

---

get.fields *get.fields method*

Description

get.fields method

Usage

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

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

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

## S4 method for signature 'apeBootstrap'
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 'phangorn'
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.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 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="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

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, ...)

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

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

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

```
## S4 method for signature 'apeBootstrap'
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 'nhx'
get.tree(object)

## 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 '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="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

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

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_balance_position *get_balance_position*

Description

get position of balance (xmin, xmax, ymin, ymax)

Usage

```
get_balance_position(treeview, node, direction)
```

Arguments

treeview   tree view
node   selected node
direction   either (1 for 'up' or 2 for 'down')

Value

data.frame

Author(s)

Justin Silverman

---

get_clade_position   *get_clade_position*

Description

get position of clade (xmin, xmax, ymin, ymax)

Usage

```
get_clade_position(treeview, node)
```

Arguments

treeview	tree view
node	selected node

Value

data.frame

Author(s)

Guangchuang Yu

---

get_heatmap_column_position

get_heatmap_column_position

Description

return a data.frame that contains position information for labeling column names of heatmap produced by 'gheatmap' function

Usage

```
get_heatmap_column_position(treeview, by = "bottom")
```

Arguments

treeview   output of 'gheatmap'

by   one of 'bottom' or 'top'

Value

data.frame

Author(s)

Guangchuang Yu

---

get_taxa_name   *get_taxa_name*

Description

get taxa name of a selected node

Usage

```
get_taxa_name(tree_view = NULL, node)
```

Arguments

tree_view   tree view

node   node

Value

taxa name vector

Author(s)

Guangchuang Yu

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, layout = "rectangular", open.angle = 0,
  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
`layout`	one of 'rectangular', 'slanted', 'fan', 'circular', 'radial' or 'unrooted'
`open.angle`	open angle, only for 'fan' layout
`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",
  colnames_level = NULL, 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'
colnames_level	levels of colnames
font.size	font size of matrix colnames

Value

tree view

Author(s)

Guangchuang Yu

---

groupClade   *groupClade method*

Description

group selected clade

Usage

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

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

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

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

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

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

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

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

## S4 method for signature 'phangorn'
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

group tree based on selected OTU, will traceback to MRCA

Usage

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

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

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

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

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

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

## S4 method for signature 'nhx'
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

Value

phylo object

Author(s)

ygc

gzoom   *gzoom method*

Description

zoom selected subtree

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 '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 'gg'
gzoom(object, focus, widths = c(0.3, 0.7), xmax_adjust = 0)

## S4 method for signature 'apeBootstrap'
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 'nhx'
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 'phangorn'
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
xmax_adjust	adjust xmax (xlim[2])
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))
```

---

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](#)

---

identify.gg *identify*

Description

identify node by interactive click

Usage

```
## S3 method for class 'gg'
identify(x, ...)
```

Arguments

x	tree view
...	additional parameters

Value

node id

Author(s)

Guangchuang Yu

---

inset	*inset*

Description

add insets in a tree

Usage

```
inset(tree_view, insets, width = 0.05, height = 0.05, hjust = 0,
  vjust = 0, x = "node")
```

Arguments

tree_view	tree view
insets	a list of ggplot objects, named by node number
width	width of inset
height	height of inset
hjust	horizontal adjustment
vjust	vertical adjustment
x	x position, one of 'node' and 'branch'

Value

tree view with insets

Author(s)

Guangchuang Yu

---

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 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

MRCA   *MRCA*

Description

Find Most Recent Common Ancestor among a vector of tips

Usage

```
MRCA(obj, tip)
```

Arguments

obj	supported tree object or ggplot object
tip	a vector of mode numeric or character specifying the tips

Value

MRCA of two or more tips

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

---

multiplot *multiplot*

Description

plot multiple ggplot objects in one page

Usage

```
multiplot(..., plotlist = NULL, ncol, widths = rep_len(1, ncol),
  labels = NULL, label_size = 5)
```

Arguments

...	plots
plotlist	plot list
ncol	number of column
widths	widths of plots
labels	labels for labeling the plots
label_size	font size of label

Value

plot

Author(s)

Guangchuang Yu

---

nhx-class *Class "nhx" This class stores nhx tree*

Description

Class "nhx" This class stores nhx tree

Slots

file input file

fields available feature

phylo phylo object

nhx_tags tag information in nhx file

extraInfo extra information

Author(s)

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

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)
```

---

nodebar   *nodebar*

Description

generate a list of bar charts for results of ancestral state reconstruction

Usage

```
nodebar(data, cols, color, alpha = 1, position = "stack")
```

Arguments

data	a data.frame of stats with an additional column of node number
cols	column of stats
color	color of bar
alpha	alpha
position	position of bar, one of 'stack' and 'dodge'

Value

list of ggplot objects

Author(s)

Guangchuang Yu

---

nodeid   *nodeid*

Description

convert tip or node label(s) to internal node number

Usage

```
nodeid(x, label)
```

Arguments

x	tree object or graphic object return by ggtree
label	tip or node label(s)

Value

internal node number

Author(s)

Guangchuang Yu

---

nodepie *nodepie*

Description

generate a list of pie charts for results of ancestral stat reconstruction

Usage

```
nodepie(data, cols, color, alpha = 1)
```

Arguments

data	a data.frame of stats with an additional column of node number
cols	column of stats
color	color of bar
alpha	alpha

Value

list of ggplot objects

Author(s)

Guangchuang Yu

---

open_tree *open_tree*

Description

open tree with specific angle

Usage

```
open_tree(treeview, angle)
```

Arguments

treeview	tree view
angle	angle

Value

updated tree view

Author(s)

Guangchuang Yu

---

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

---

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

---

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

---

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()
```

---

pmlToSeq   *pmlToSeq*

Description

convert pml object to XStringSet object

Usage

```
pmlToSeq(pml, includeAncestor = TRUE)
```

Arguments

pml   pml object

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>

---

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://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="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.nhx   *read.nhx*

Description

read nhx tree file

Usage

```
read.nhx(file)
```

Arguments

file   nhx file

Value

nhx object

Author(s)

Guangchuang Yu http://ygc.name

---

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.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

---

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

---

reroot   *reroot method*

Description

reroot a tree

Usage

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

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

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

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

Arguments

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

Value

tree object

---

rescale_tree	*rescale_tree*

Description

rescale branch length of tree object

Usage

```
rescale_tree(tree_object, branch.length)
```

Arguments

tree_object	tree object
branch.length	numerical features (e.g. dN/dS)

Value

update tree object

Author(s)

Guangchuang Yu

---

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 = NULL, node)
```

Arguments

tree_view	tree view
node	selected node

Value

ggplot2 object

Author(s)

Guangchuang Yu

rotate_tree	*rotate_tree*

Description

rotate circular tree

Usage

```
rotate_tree(treeview, angle)
```

Arguments

treeview	tree view
angle	angle

Value

updated tree view

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 = NULL, 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 by a numerical tree attribute

Usage

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

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

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

## 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 'beast'
scale_color(object, by, ...)

## S4 method for signature 'nhx'
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 'phangorn'
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(tree_view, breaks = NULL, labels = NULL)
```

Arguments

`tree_view`	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 'apeBootstrap'
show(object)

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

## 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 'nhx'
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 'phangorn'
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)
```

StatBalance	*StatBalance*

Description

StatBalance

StatHilight

---

stat_balance	*stat_balance*

Description

stat_balance

Usage

```
stat_balance(mapping = NULL, data = NULL, geom = "rect",
  position = "identity", node, show.legend = NA, inherit.aes = FALSE,
  fill, color, alpha, extend = 0, extendto = NULL, ...)
```

Arguments

mapping	aes mapping
data	data
geom	geometric object
position	position
node	node number
show.legend	show legend
inherit.aes	logical

fill	fill color
color	color to outline highlights and divide balance
alpha	transparency
extend	extend xmax of the rectangle
extendto	extend xmax to extendto
...	additional parameter

Value

layer

---

stat_hilight	*stat_hilight*

Description

stat_hilight

Usage

```
stat_hilight(mapping = NULL, data = NULL, geom = "rect",
  position = "identity", node, show.legend = NA, inherit.aes = FALSE,
  fill, alpha, extend = 0, extendto = NULL, ...)
```

Arguments

mapping	aes mapping
data	data
geom	geometric object
position	position
node	node number
show.legend	show legend
inherit.aes	logical
fill	fill color
alpha	transparency
extend	extend xmax of the rectangle
extendto	extend xmax to extendto
...	additional parameter

Value

layer

---

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	a ggplot or grob object
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_inset   *theme_inset*

Description

inset theme

Usage

```
theme_inset(...)
```

Arguments

...	additional parameter

Details

theme for inset function

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()
```

---

viewClade   *viewClade*

Description

view a clade of tree

Usage

```
viewClade(tree_view = NULL, node, xmax_adjust = 0)
```

Arguments

tree_view	full tree view
node	internal node number
xmax_adjust	adjust xmax

Value

clade plot

Author(s)

Guangchuang Yu

---

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)
```

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