

Package ‘ggtree’

April 23, 2016

Type Package

Title a phylogenetic tree viewer for different types of tree annotations

Version 1.2.17

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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, Biostrings, grid, jsonlite, magrittr, methods, stats4, tidyrr

Suggests colorspace, EBImage, gridExtra, knitr, phylobase, phytools, phangorn, rmarkdown, scales, testthat

VignetteBuilder knitr

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URL <https://github.com/GuangchuangYu/ggtree>

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

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

RoxygenNote 5.0.1

NeedsCompilation no

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Description

capture name of variable

Usage

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

Arguments

...	expression
.env	environment

Value

expression

Examples

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

add_colorbar	<i>add_colorbar</i>
--------------	---------------------

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	<i>annotation_image</i>
------------------	-------------------------

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	<i>apeBoot</i>
---------	----------------

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	<i>Class "apeBootstrap" This class stores ape bootstrapping analysis result</i>
--------------------	---

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	<i>as.binary</i>
-----------	------------------

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	<i>as.data.frame</i>
---------------------	----------------------

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

Description

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

Slots

mlc A code_mlc object

rst A paml_rst object

extraInfo extra information

See Also

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

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

Description

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

Slots

fields available features

treetext tree text

phylo phylo object

dNdS dN dS information

mlcfile mlc file

extraInfo extra information

Author(s)

Guangchuang Yu

See Also

[paml_rst](#) [codeml](#)

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 phylopic 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	<i>flip</i>
------	-------------

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	<i>fortify</i>
---------------	----------------

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_cladelabel	<i>geom_cladelabel</i>
-----------------	------------------------

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, ...)
```

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'
...	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

geom_highlight *geom_highlight*

Description

layer of highlight clade with rectangle

Usage

```
geom_highlight(node, fill = "steelblue", alpha = 0.5)
```

Arguments

node	selected node to highlight
fill	color fill
alpha	alpha (transparency)

Value

ggplot2

Author(s)

Guangchuang Yu

geom_nodepoint *geom_nodepoint*

Description

add node point

Usage

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

Arguments

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

Value

node point layer

Author(s)

Guangchuang Yu

geom_point2	<i>geom_point2</i>
-------------	--------------------

Description

geom_point2 support aes(subset) via setup_data

Usage

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

Arguments

mapping	aes mapping
data	data
stat	stat
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_rootpoint	<i>geom_rootpoint</i>
----------------	-----------------------

Description

add root point

Usage

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

Arguments

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

Value

root point layer

Author(s)

Guangchuang Yu

geom_segment2	<i>geom_segment2</i>
---------------	----------------------

Description

geom_segment2 support aes(subset) via setup_data

Usage

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

Arguments

mapping	aes mapping
data	data
stat	stat
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_text2`*geom_text2*

Description

`geom_text2` support `aes(subset)` via `setup_data`

Usage

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

Arguments

<code>mapping</code>	the aesthetic mapping
<code>data</code>	A layer specific dataset - only needed if you want to override the plot defaults.
<code>stat</code>	The statistical transformation to use on the data for this layer
<code>position</code>	The position adjustment to use for overlapping points on this layer
<code>parse</code>	if TRUE, the labels will be passed into expressions
<code>na.rm</code>	logical
<code>show.legend</code>	logical
<code>inherit.aes</code>	logical
<code>...</code>	other arguments passed on to 'layer'
<code>nudge_x</code>	horizontal adjustment
<code>nudge_y</code>	vertical adjustment
<code>check_overlap</code>	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	<i>geom_tiplab</i>
-------------	--------------------

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	<i>geom_tippoint</i>
---------------	----------------------

Description

add tip point

Usage

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

Arguments

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

Value

tip point layer

Author(s)

Guangchuang Yu

geom_tree	<i>geom_tree</i>
-----------	------------------

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	<i>geom_treescale</i>
----------------	-----------------------

Description

add tree scale

Usage

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

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

Value

ggplot layers

Author(s)

Guangchuang Yu

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

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

Description

get.tipseq

Usage

```

get.tipseq(object, ...)

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

```

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

Arguments

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

Value

```
character
```

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

Description

```
get.tree method
```

Usage

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

## S4 method for signature '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 'paml_rst'  
get.tree(object)  
  
## S4 method for signature 'phangorn'  
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, 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	<i>get.treeinfo method</i>
--------------	----------------------------

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

Description

get.treetext method

Usage

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

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

Arguments

object	one of phylo, jplace, beast, hyphy, codeml, codeml_mlc, pam1_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

<code>get_clade_position</code>	<i>get_clade_position</i>
---------------------------------	---------------------------

Description

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

Usage`get_clade_position(treeview, node)`**Arguments**

<code>treeview</code>	tree view
<code>node</code>	selected node

Value

data.frame

Author(s)

Guangchuang Yu

<code>get_heatmap_column_position</code>	<i>get_heatmap_column_position</i>
--	------------------------------------

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**

<code>treeview</code>	output of 'gheatmap'
<code>by</code>	one of 'bottom' or 'top'

Value

data.frame

Author(s)

Guangchuang Yu

get_taxa_name	<i>get_taxa_name</i>
---------------	----------------------

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	<i>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.</i>
--------	--

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", mrsd = NULL,  
       as.Date = FALSE, yscale = "none", yscale_mapping = NULL,  
       ladderize = TRUE, right = FALSE, branch.length = "branch.length",  
       ndigits = NULL, ...)
```

Arguments

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

Value

tree

Author(s)

Yu Guangchuang

Examples

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

gheatmap	<i>gheatmap</i>
----------	-----------------

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

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

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

Description

group tree based on selected OTU, will traceback to MRCA

Usage

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

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

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

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

## S4 method for signature 'beast'
group0TU(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	<i>groupOTU.phylo</i>
----------------	-----------------------

Description

group OTU

Usage

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

Arguments

phy	tree object
focus	tip list
group_name	name of the group

Value

phylo object

Author(s)

ygc

gzoom	<i>gzoom method</i>
-------	---------------------

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

<i>gzoom.phylo</i>	<i>gzoom</i>
--------------------	--------------

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

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](#)

inset	<i>inset</i>
-------	--------------

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	<i>mask</i>
------	-------------

Description

site mask

Usage

```
mask(tree_object, field, site, mask_site = FALSE)
```

Arguments

tree_object	tree object
field	selected field
site	site
mask_site	if TRUE, site will be masked. if FALSE, selected site will not be masked, while other sites will be masked.

Value

updated tree object

Author(s)

Guangchuang Yu

merge_tree	<i>merge_tree</i>
------------	-------------------

Description

merge two tree object

Usage

```
merge_tree(obj1, obj2)
```

Arguments

obj1	tree object 1
obj2	tree object 2

Value

tree object

Author(s)

Guangchuang Yu

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

nodepie	<i>nodepie</i>
---------	----------------

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

paml_rst-class	<i>Class "paml_rst" This class stores information of rst file from PAML output</i>
----------------	--

Description

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

Slots

fields	availabel attributes
treetext	tree text
phylo	phylo object
seq_type	one of "NT" and "AA"
tip_seq	sequences of tips
marginal_ancseq	Marginal reconstruction of ancestral sequences
joint_ancseq	Joint reconstruction of ancestral sequences

marginal_subs sequence substitutions based on marginal_ancseq
joint_subs sequence substitutions based on joint_ancseq
marginal_AA_subs Amino acid sequence substitutions based on marginal_ancseq
joint_AA_subs Amino acid sequence substitutions based on joint_ancseq
rstfile rst file
extraInfo extra information

Author(s)

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

See Also

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

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

Description

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

Slots

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

Author(s)

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

See Also

[paml_rst](#)

phylip-class *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

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

Description

read HYPHY output

Usage

```
read.hyphy(nwk, ancseq, tip.fasfile = NULL)
```

Arguments

nwk	tree file in nwk format, one of hyphy output
ancseq	ancestral sequence file in nexus format, one of hyphy output
tip.fasfile	tip sequence file

Value

A hyphy object

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

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

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

Description

read jplace file

Usage

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

Arguments

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

Value

jplace instance

Author(s)

ygc

Examples

```
jp <- system.file("extdata", "sample.jplace", package="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	<i>read.paml_rst</i>
---------------	----------------------

Description

read rst file from paml output

Usage

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

Arguments

rstfile rst file

Value

A paml_rst object

Author(s)

Guangchuang Yu <http://ygc.name>

Examples

```
rstfile <- system.file("extdata/PAML_Baseml", "rst", package="ggtree")
read.paml_rst(rstfile)
```

read.phylip	<i>read.phylip</i>
-------------	--------------------

Description

parsing phylip tree format

Usage

```
read.phylip(file)
```

Arguments

file phylip file

Value

an instance of 'phylip'

Author(s)

Guangchuang Yu

`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	<i>read newick tree</i>
-----------	-------------------------

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 'multi-Phylo' 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	<i>reroot method</i>
--------	----------------------

Description

reroot a tree

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

Value

tree object

rescale_tree	<i>rescale_tree</i>
--------------	---------------------

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

rtree	<i>generate random tree</i>
-------	-----------------------------

Description

generate random tree

Usage

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

Arguments

n	number of tips in the tree
rooted	logical
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	<i>scaleClade</i>
------------	-------------------

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	<i>scale_color method</i>
-------------	---------------------------

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 'phangorn'
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	<i>scale_x_ggtree</i>
----------------	-----------------------

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 'codeml_mlc'  
show(object)  
  
## S4 method for signature 'hyphy'  
show(object)  
  
## S4 method for signature 'beast'  
show(object)  
  
## S4 method for signature 'codeml'  
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 'phangorn'  
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)
```

StatHilight

StatHilight

Description

StatHilight

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, ...)
```

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
...	additional parameter

Value

layer

subview	<i>subview</i>
---------	----------------

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	<i>theme_tree</i>
------------	-------------------

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	<i>theme_tree2</i>
-------------	--------------------

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

Description

generate jplace file

Usage

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

Arguments

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

Value

jplace file

Author(s)

ygc

Examples

```
tree <- system.file("extdata", "pa.nwk", package="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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