

Package ‘ggtree’

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Type Package

Title an R package for visualization of tree and annotation data

Version 2.2.4

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Description 'ggtree' extends the 'ggplot2' plotting system which implemented the grammar of graphics. 'ggtree' is designed for visualization and annotation of phylogenetic trees and other tree-like structures with their annotation data.

Depends R (>= 3.5.0)

Imports ape, aplot (>= 0.0.4), dplyr, ggplot2 (>= 3.0.0), grid, magrittr, methods, purrr, rlang, rvcheck, tidyr, tidytree (>= 0.2.6), treeio (>= 1.8.0), utils

Suggests emojiFont, ggimage, ggplotify, grDevices, knitr, prettydoc, rmarkdown, scales, stats, testthat, tibble

Remotes GuangchuangYu/treeio

VignetteBuilder knitr

ByteCompile true

Encoding UTF-8

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URL <https://yulab-smu.github.io/treedata-book/>

BugReports <https://github.com/YuLab-SMU/ggtree/issues>

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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

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

Value

tree view

Author(s)

Guangchuang Yu

`applyLayoutDaylight` *applyLayoutDaylight*

Description

Apply the daylight algorithm to adjust the spacing between the subtrees and tips of the specified node.

Usage

```
applyLayoutDaylight(df, node_id)
```

Arguments

<code>df</code>	tree data.frame
<code>node_id</code>	is id of the node from which daylight is measured to the other subtrees.

Value

list with tree data.frame with updated layout using daylight algorithm and `max_change` angle.

as.polytomy	<i>as.polytomy</i>
-------------	--------------------

Description

collapse binary tree to polytomy by applying 'fun' to 'feature'

Usage

```
as.polytomy(tree, feature, fun)
```

Arguments

tree	tree object
feature	selected feature
fun	function to select nodes to collapse

Value

polytomy tree

Author(s)

Guangchuang Yu

collapse.ggtree	<i>collapse-ggtree</i>
-----------------	------------------------

Description

collapse a clade

Usage

```
## S3 method for class 'ggtree'
collapse(x = NULL, node, mode = "none", clade_name = NULL, ...)
```

Arguments

x	tree view
node	clade node
mode	one of 'none', 'max', 'min' and 'mixed'
clade_name	set clade name. If clade_name = NULL, do nothing
...	additional parameters

Value

tree view

Author(s)

Guangchuang Yu

See Also

expand

Date2decimal	<i>Date2decimal</i>
--------------	---------------------

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	<i>decimal2Date</i>
--------------	---------------------

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

expand	<i>expand</i>
--------	---------------

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

facet_data	<i>facet_data</i>
------------	-------------------

Description

extract data used in facet_plot or geom_facet

Usage

```
facet_data(tree_view, panel)
```

Arguments

tree_view	ggtree object
panel	data plotted in specific panel. If only one dataset used in the panel, return the data frame, else return a list of data frames.

Value

data frame or a list of data frames

Author(s)

Guangchuang Yu

References

G Yu, TTY Lam, H Zhu, Y Guan (2018). Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*, 35(2):3041-3043. <https://doi.org/10.1093/molbev/msy194>

facet_labeller	<i>facet_labeller</i>
----------------	-----------------------

Description

label facet_plot output

Usage

facet_labeller(p, label)

Arguments

p	facet_plot output
label	labels of facet panels

Value

ggplot object

Author(s)

Guangchuang Yu

facet_plot	<i>facet_plot</i>
------------	-------------------

Description

plot tree associated data in an additional panel

Usage

facet_plot(p, mapping = NULL, data, geom, panel, ...)

geom_facet(mapping = NULL, data, geom, panel, ...)

Arguments

p	tree view
mapping	aes mapping for 'geom'
data	data to plot by 'geom', first column should be matched with tip label of tree
geom	geom function to plot the data
panel	panel name for plot of input data
...	additional parameters for 'geom'

Details

'facet_plot()' automatically re-arranges the input 'data' according to the tree structure, visualizes the 'data' on specific 'panel' using the 'geom' function with aesthetic 'mapping' and other parameters, and align the graph with the tree 'p' side by side. 'geom_facet' is a 'ggplot2' layer version of 'facet_plot'

Value

ggplot object

Author(s)

Guangchuang Yu

References

G Yu, TTY Lam, H Zhu, Y Guan (2018). Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*, 35(2):3041-3043. <https://doi.org/10.1093/molbev/msy194>

Examples

```
tr <- rtree(10)
dd = data.frame(id=tr$tip.label, value=abs(rnorm(10)))
p <- ggtree(tr)
facet_plot(p, 'Trait', data = dd, geom=geom_point, mapping=aes(x=value))
```

facet_widths

facet_widths

Description

set relative widths (for column only) of facet plots

Usage

```
facet_widths(p, widths)
```

Arguments

p	ggplot or ggtree object
widths	relative widths of facet panels

Value

ggplot object by redrawing the figure (not a modified version of input object)

Author(s)

Guangchuang Yu

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

geom_aline	<i>geom_aline</i>
------------	-------------------

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 and modified by Guangchuang Yu

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,  
  extend = 0,  
  align = FALSE,  
  barsize = 0.5,  
  fontsize = 3.88,  
  angle = 0,  
  geom = "text",  
  hjust = 0,  
  color = NULL,  
  fill = NA,  
  family = "sans",  
  parse = FALSE,  
  ...  
)
```

Arguments

node	selected node
label	clade label
offset	offset of bar and text from the clade
offset.text	offset of text from bar
extend	extend bar height
align	logical
barsize	size of bar
fontsize	size of text
angle	angle of text
geom	one of 'text' or 'label'
hjust	justify text horizontally
color	color for clade & label, of length 1 or 2
fill	fill label background, only work with geom='label'
family	sans by default, can be any supported font
parse	logical, whether parse label
...	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

See Also

[geom_cladelabel2](#)

geom_cladelabel2

geom_cladelabel2

Description

annotate a clade with bar and text label

Usage

```
geom_cladelabel2(  
  node,  
  label,  
  offset = 0,  
  offset.text = 0,  
  offset.bar = 0,  
  align = FALSE,  
  barsize = 0.5,  
  fontsize = 3.88,  
  hjust = 0,  
  geom = "text",  
  color = NULL,  
  family = "sans",  
  parse = FALSE,  
  ...  
)
```

Arguments

node	selected node
label	clade label
offset	offset of bar and text from the clade
offset.text	offset of text from bar
offset.bar	offset of bar from text
align	logical
barsize	size of bar
fontsize	size of text
hjust	justify text horizontally

geom	one of 'text' or 'label'
color	color for clade & label, of length 1 or 2
family	sans by default, can be any supported font
parse	logical, whether parse label
...	additional parameter

Value

ggplot layers

Author(s)

JustGitting

See Also

[geom_cladelabel](#)

geom_highlight

geom_highlight

Description

layer of highlight clade with rectangle

Usage

```
geom_highlight(node, fill = "steelblue", alpha = 0.5, extend = 0, ...)
```

```
geom_highlight(node, fill = "steelblue", alpha = 0.5, extend = 0, ...)
```

Arguments

node	selected node to highlight (required)
fill	color fill (default = steelblue)
alpha	alpha transparency, (default = 0.5)
extend	extend xmax of the rectangle (default = 0)
...	additional parameters

Value

ggplot2

Author(s)

Guangchuang Yu

geom_highlight_encircle *geom_highlight_encircle*

Description

layer of highlight clade with xspline

Usage

```
geom_highlight_encircle(
  data = NULL,
  node,
  mapping = NULL,
  fill = "steelblue",
  alpha = 0.5,
  extend = 0,
  ...
)
```

Arguments

data	data frame to calculate xspline (default = NULL)
node	selected node to highlight (required)
mapping	aesthetic mapping (default = NULL)
fill	colour fill (default = steelblue)
alpha	alpha (transparency) (default = 0.5)
extend	expands the xspline clade region only (default = 0)
...	additional parameters, including: 'spread' spread of shape? (default = 0.1), 'line-type' Line type of xspline (default = 1), 'size' Size of xspline line (default = 1), 's_shape' Corresponds to shape of xspline (default = 0.5), 's_open' Boolean switch determines if xspline shape is open or closed. (default = FALSE)

Value

ggplot2

geom_inset *geom_inset*

Description

add subplots to tree

add insets in a tree

Usage

```
geom_inset(  
  insets,  
  width = 0.1,  
  height = 0.1,  
  hjust = 0,  
  vjust = 0,  
  x = "node",  
  reverse_x = FALSE,  
  reverse_y = FALSE  
)  
  
inset(  
  tree_view,  
  insets,  
  width,  
  height,  
  hjust = 0,  
  vjust = 0,  
  x = "node",  
  reverse_x = FALSE,  
  reverse_y = FALSE  
)
```

Arguments

<code>insets</code>	a list of ggplot objects, named by node number
<code>width</code>	width of inset, relative to the range of x-axis
<code>height</code>	height of inset, relative to the range of y-axis
<code>hjust</code>	horizontal adjustment
<code>vjust</code>	vertical adjustment
<code>x</code>	x position, one of 'node' and 'branch'
<code>reverse_x</code>	whether x axis was reversed by <code>scale_x_reverse</code>
<code>reverse_y</code>	whether y axis was reversed by <code>scale_y_reverse</code>
<code>tree_view</code>	tree view

Value

inset layer
tree view with insets

Author(s)

Guangchuang Yu
Guangchuang Yu

geom_label2

*geom_label2***Description**

geom_label2 support aes(subset) via setup_data

Usage

```
geom_label2(
  mapping = NULL,
  data = NULL,
  ...,
  stat = "identity",
  position = "identity",
  family = "sans",
  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 the plot defaults.
...	other arguments passed on to 'layer'
stat	Name of stat to modify data
position	The position adjustment to use for overlapping points on this layer
family	sans by default, can be any supported font
parse	if TRUE, the labels will be parsed as 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_motif`*geom_motif*

Description

geom layer to draw aligned motif

Usage`geom_motif(mapping, data, on, label, align = "centre", ...)`**Arguments**

<code>mapping</code>	aes mapping
<code>data</code>	data
<code>on</code>	gene to center (i.e. set middle position of the on gene to 0)
<code>label</code>	specify a column to be used to label genes
<code>align</code>	where to place gene label, default is 'centre' and can be set to 'left' and 'right'
<code>...</code>	additional parameters

Value

geom layer

Author(s)

Guangchuang Yu

geom_nodelab	<i>geom_nodelab</i>
--------------	---------------------

Description

add node label layer

Usage

```
geom_nodelab(
  mapping = NULL,
  nudge_x = 0,
  nudge_y = 0,
  geom = "text",
  hjust = 0.5,
  ...
)
```

Arguments

mapping	aes mapping
nudge_x	horizontal adjustment to nudge label
nudge_y	vertical adjustment to nudge label
geom	one of 'text', 'label', 'image' and 'phylopic'
hjust	horizontal alignment, one of 0, 0.5 or 1
...	additional parameters

Value

geom layer

Author(s)

Guangchuang Yu

geom_nodelab2	@ <i>geom_nodelab2</i>
---------------	------------------------

Description

add node label for circular layout

Usage

```
geom_nodepoint2(
  mapping = NULL,
  nudge_x = 0,
  nudge_y = 0,
  geom = "text",
  hjust = 0.5,
  ...
)
```

Arguments

mapping	aes mapping
nudge_x	horizontal adjustment to nudge label
nudge_y	vertical adjustment to nudge label
geom	one of 'text', 'label', 'image' and 'phylopic'
hjust	horizontal alignment, one of 0, 0.5 or 1
...	additional parameters

Value

node label layer

Author(s)

Guangchuang Yu

geom_nodepoint	<i>geom_nodepoint</i>
----------------	-----------------------

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	<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	Name of stat to modify 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	<i>geom_range</i>
------------	-------------------

Description

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

Usage

```
geom_range(range, center = "auto", ...)
```

Arguments

range	range, e.g. "height_0.95_HPDP"
center	center of the range, mean, median or auto (default, the center of the range)
...	additional parameter, e.g. color, size, alpha

Value

ggplot layer

Author(s)

Guangchuang Yu

geom_rootedge	<i>geom_rootedge</i>
---------------	----------------------

Description

display root edge

Usage

```
geom_rootedge(rootedge = NULL, ...)
```

Arguments

rootedge length of rootedge; use phylo\$root.edge if rootedge = NULL (by default).
 ... additional parameters

Value

ggplot layer

Author(s)

Guangchuang Yu

geom_rootpoint	<i>geom_rootpoint</i>
----------------	-----------------------

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

Description

geom_segment2 support aes(subset) via setup_data

Usage

```
geom_segment2(  
  mapping = NULL,  
  data = NULL,  
  stat = "identity",  
  position = "identity",  
  lineend = "butt",  
  na.rm = FALSE,  
  show.legend = NA,  
  inherit.aes = TRUE,  
  nudge_x = 0,  
  arrow = NULL,  
  arrow.fill = NULL,  
  ...  
)
```

Arguments

mapping	aes mapping
data	data
stat	Name of stat to modify data
position	position
lineend	lineend
na.rm	logical
show.legend	logical
inherit.aes	logical
nudge_x	horizontal adjustment of x
arrow	specification for arrow heads, as created by arrow().
arrow.fill	fill color to usse for the arrow head (if closed). NULL means use colour aesthetic.
...	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 Paraphyletic Taxa) with bar and (optional) text label

Usage

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

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
extend	extend bar vertically
fontsize	size of text
angle	angle of text
geom	one of 'text' or 'label'
hjust	hjust
color	color for bar and label
fill	fill label background, only work with geom='label'
family	sans by default, can be any supported font
parse	logical, whether parse label
...	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

geom_taxalink	<i>geom_taxalink</i>
---------------	----------------------

Description

link between taxa

Usage

```
geom_taxalink(  
  taxa1,  
  taxa2,  
  curvature = 0.5,  
  arrow = NULL,  
  arrow.fill = NULL,  
  ...  
)
```

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.
arrow	specification for arrow heads, as created by arrow().
arrow.fill	fill color to use for the arrow head (if closed). NULL means use colour aesthetic.
...	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,
  ...,
  stat = "identity",
  position = "identity",
  family = "sans",
  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 the plot defaults.
...	other arguments passed on to 'layer'
stat	Name of stat to modify data
position	The position adjustment to use for overlapping points on this layer
family	sans by default, can be any supported font
parse	if TRUE, the labels will be passed into expressions
na.rm	logical
show.legend	logical
inherit.aes	logical
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	<i>geom_tiplab</i>
-------------	--------------------

Description

add tip label layer

Usage

```
geom_tiplab(  
  mapping = NULL,  
  hjust = 0,  
  align = FALSE,  
  linetype = "dotted",  
  linesize = 0.5,  
  geom = "text",  
  offset = 0,  
  ...  
)
```

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', 'label', 'image' and 'phylopic'
offset	tiplab offset
...	additional parameter

Value

tip label layer

Author(s)

Guangchuang Yu

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/o35PV3iH0-0>

See Also

[geom_tiplab](#)

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', 'fan', 'circular', 'radial', 'equal_angle', 'day-light' or 'ape'
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

<i>get.path</i>	<i>get.path</i>
-----------------	-----------------

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

getNodeAngle.df *getNodeAngle.df*

Description

Get the angle between the two nodes specified.

Usage

```
getNodeAngle.df(df, origin_node_id, node_id)
```

Arguments

<code>df</code>	tree data.frame
<code>origin_node_id</code>	origin node id number
<code>node_id</code>	end node id number

Value

angle in range [-1, 1], i.e. degrees/180, radians/pi

getNodeBreadthFirst.df
getNodeBreadthFirst.df

Description

Get the nodes of tree from root in breadth-first order.

Usage

```
getNodeBreadthFirst.df(df)
```

Arguments

<code>df</code>	tree data.frame
-----------------	-----------------

Value

list of node id's in breadth-first order.

getSubtree	<i>getSubtree</i>
------------	-------------------

Description

Get all children of node from tree, including start_node.

Usage

```
getSubtree(tree, node)
```

Arguments

tree	ape phylo tree object
node	is the tree node id from which the tree is derived.

Value

list of all child node id's from starting node.

getSubtree.df	<i>getSubtree.df</i>
---------------	----------------------

Description

Get all children of node from df tree using breath-first.

Usage

```
getSubtree.df(df, node)
```

Arguments

df	tree data.frame
node	id of starting node.

Value

list of all child node id's from starting node.

`getSubtreeUnrooted` *getSubtreeUnrooted*

Description

Get all subtrees of specified node. This includes all ancestors and relatives of node and return named list of subtrees.

Usage

```
getSubtreeUnrooted(tree, node)
```

Arguments

<code>tree</code>	ape phylo tree object
<code>node</code>	is the tree node id from which the subtrees are derived.

Value

named list of subtrees with the root id of subtree and list of node id's making up subtree.

`getSubtreeUnrooted.df` *getSubtreeUnrooted*

Description

Get all subtrees of node, as well as remaining branches of parent (ie, rest of tree structure as subtree) return named list of subtrees with list name as starting node id.

Usage

```
getSubtreeUnrooted.df(df, node)
```

Arguments

<code>df</code>	tree data.frame
<code>node</code>	is the tree node id from which the subtrees are derived.

Value

named list of subtrees with the root id of subtree and list of node id's making up subtree.

getTreeArcAngles *getTreeArcAngles*

Description

Find the right (clockwise rotation, angle from +ve x-axis to furthest subtree nodes) and left (anti-clockwise angle from +ve x-axis to subtree) Returning arc angle in [0, 2] (0 to 360) domain.

Usage

```
getTreeArcAngles(df, origin_id, subtree)
```

Arguments

df	tree data.frame
origin_id	node id from which to calculate left and right hand angles of subtree.
subtree	named list of root id of subtree (node) and list of node ids for given subtree (subtree).

Value

named list with right and left angles in range [0,2] i.e 1 = 180 degrees, 1.5 = 270 degrees.

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 (or tree if node=NULL) sorted by their position in plotting

Usage

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

Arguments

tree_view	tree view
node	node

Value

taxa name vector

Author(s)

Guangchuang Yu

ggsensitree *ggsensitree*

Description

drawing phylogenetic trees from list of phylo objects

Usage

```
ggsensitree(
  data = NULL,
  mapping = NULL,
  layout = "slanted",
  tip.order = "mds_dist",
  align.tips = TRUE,
  jitter = 0,
  ...
)
```

Arguments

data	a list of phylo objects or any object with an <code>as.phylo</code> and <code>fortify</code> method
mapping	aesthetic mapping
layout	one of 'slanted', 'rectangular', 'fan', 'circular' or 'radial' (default: 'slanted')
tip.order	the order of the tips by a character vector of taxa names; or an integer, N, to order the tips by the order of the tips in the Nth tree; 'mds' to order the tips based on MDS of the path length between the tips; or 'mds_dist' to order the tips based on MDS of the distance between the tips (default: 'mds_dist')
align.tips	TRUE to align trees by their tips and FALSE to align trees by their root (default: TRUE)
jitter	deviation to jitter tips
...	additional parameters passed to <code>fortify</code> , <code>ggtree</code> and <code>geom_tree</code>

Value

tree layer

Author(s)

Yu Guangchuang, Bradley R. Jones

Examples

```
require(ape)
require(dplyr)

# Plot multiple trees with aligned tips
trees <- list(read.tree(text="((a:1,b:1):1.5,c:2.5);"), read.tree(text="((a:1,c:1):1,b:2);"));
ggsensitree(trees) + geom_tiplab()
```

```

# Plot multiple trees with aligned tips with tip labels and separate tree colors
trees.fort <- list(trees[[1]] %>% fortify %>% mutate(tree="a"), trees[[2]] %>% fortify %>% mutate(tree="b"));
ggdensitree(trees.fort, aes(colour=tree)) + geom_tiplab(colour='black')

# Generate example data
set.seed(1)
trees <- rmtree(5, 10)
time.trees <- lapply(1:length(trees), function(i) {
  tree <- trees[[i]]
  tree$tip.label <- paste0("t", 1:10)
  dates <- estimate.dates(tree, 1:10, mu=1, nsteps=1)
  tree$edge.length <- dates[tree$edge[, 2]] - dates[tree$edge[, 1]]
  fortify(tree) %>% mutate(tree=factor(i, levels=as.character(1:10)))
})

# Plot multiple trees with aligned tips from multiple time points
ggdensitree(time.trees, aes(colour=tree), tip.order=paste0("t", 1:10)) + geom_tiplab(colour='black')

# Read example data
trees <- read.tree(system.file("examples", "ggdensitree_example.tree", package="ggtree"))

# Compute OTU
grp <- list(A = c("a.t1", "a.t2", "a.t3", "a.t4"), B = c("b.t1", "b.t2", "b.t3", "b.t4"), C = c("c.t1", "c.t2", "c.t3", "c.t4"))
trees <- lapply(trees, group0TU, grp)

# Plot multiple trees colored by OTU
ggdensitree(trees, aes(colour=group), alpha=1/6) + scale_colour_manual(values=c("black", "red", "green", "blue"))

```

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

If you use ggtree in published research, please cite: Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam. ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods in Ecology and Evolution* 2017, 8(1):28-36, doi:10.1111/2041-210X.12628

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",
    root.position = 0,
    ...
)

```

Arguments

<code>tr</code>	phylo object
<code>mapping</code>	aesthetic mapping
<code>layout</code>	one of 'rectangular', 'slanted', 'fan', 'circular', 'radial', 'equal_angle', 'day-light' or 'ape'
<code>open.angle</code>	open angle, only for 'fan' layout
<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 (default TRUE). Should the tree be re-organized to have a 'ladder' aspect?
<code>right</code>	logical. If <code>ladderize = TRUE</code> , should the ladder have the smallest clade on the right-hand side? See ape::ladderize() for more information.
<code>branch.length</code>	variable for scaling branch, if 'none' draw cladogram
<code>root.position</code>	position of the root node (default = 0)
<code>...</code>	additional parameter

Value

tree

Author(s)

Yu Guangchuang

References

1. G Yu, TTY Lam, H Zhu, Y Guan (2018). Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*, 35(2):3041-3043. <https://doi.org/10.1093/molbev/msy194>
2. G Yu, DK Smith, H Zhu, Y Guan, TTY Lam (2017). ggtree: an R package for visualization and annotation of phylogenetic trees with their covariates and other associated data. *Methods in Ecology and Evolution*, 8(1):28-36. <https://doi.org/10.1111/2041-210X.12628>

See Also

[ape::ladderize\(\)](#)

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_angle = 0,
  colnames_level = NULL,
  colnames_offset_x = 0,
  colnames_offset_y = 0,
  font.size = 4,
  family = "",
  hjust = 0.5,
  legend_title = "value"
)
```

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_angle	angle of column names
colnames_level	levels of colnames
colnames_offset_x	x offset for column names
colnames_offset_y	y offset for column names

font.size	font size of matrix colnames
family	font of matrix colnames
hjust	hjust for column names (0: align left, 0.5: align center, 1: align right)
legend_title	title of fill legend

Value

tree view

Author(s)

Guangchuang Yu

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

Description

gzoom method
gzoom method
zoom selected subtree

Usage

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

## S4 method for signature 'ggtree'
gzoom(object, focus, widths = c(0.3, 0.7), xmax_adjust = 0)

## S4 method for signature 'treedata'
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))
```

Arguments

object	supported tree objects
focus	selected tips
subtree	logical
widths	widths
...	additional parameter
xmax_adjust	adjust xmax (xlim[2])

Value

figure

gzoom.phylo	<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

identify.gg	<i>identify</i>
-------------	-----------------

Description

identify node by interactive click

Usage

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

Arguments

x	tree view
...	additional parameters

Value

node id

Author(s)

Guangchuang Yu

layoutDaylight	<i>Equal daylight layout method for unrooted trees.</i>
----------------	---

Description

#' @title

Usage

```
layoutDaylight(model, branch.length, MAX_COUNT = 5)
```

Arguments

model	tree object, e.g. phylo or treedata
branch.length	set to 'none' for edge length of 1. Otherwise the phylogenetic tree edge length is used.
MAX_COUNT	the maximum number of iterations to run (default 5)

Value

tree as data.frame with equal angle layout.

References

The following algorithm aims to implement the vague description of the "Equal-daylight Algorithm" in "Inferring Phylogenies" pp 582-584 by Joseph Felsenstein.

```
Leafs are subtrees with no children
Initialise tree using equal angle algorithm
tree_df = equal_angle(tree)
```

```
nodes = get list of nodes in tree_df breadth-first
nodes = remove tip nodes.
```

layoutEqualAngle	<i>layoutEqualAngle</i>
------------------	-------------------------

Description

'Equal-angle layout algorithm for unrooted trees'

Usage

```
layoutEqualAngle(model, branch.length = "branch.length")
```

Arguments

`model` tree object, e.g. `phylo` or `treedata`

`branch.length` set to 'none' for edge length of 1. Otherwise the phylogenetic tree edge length is used.

Value

tree as `data.frame` with equal angle layout.

References

"Inferring Phylogenies" by Joseph Felsenstein.

`layout_rectangular` *layout_rectangular*

Description

tree layout

Usage

```
layout_rectangular()  
layout_circular()  
layout_fan(angle = 180)  
layout_dendrogram()
```

Arguments

`angle` open tree at specific angle

Author(s)

Guangchuang Yu

msaplot	<i>msaplot</i>
---------	----------------

Description

multiple sequence alignment with phylogenetic tree

Usage

```
msaplot(  
  p,  
  fasta,  
  offset = 0,  
  width = 1,  
  color = NULL,  
  window = NULL,  
  bg_line = TRUE,  
  height = 0.8  
)
```

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
bg_line	whether add background line in alignment
height	height ratio of sequence

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

 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

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

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

range_format	<i>range_format</i>
--------------	---------------------

Description

format a list of range (HPD, CI, etc that has length of 2)

Usage

```
range_format(x, trans = NULL)
```

Arguments

x	input list
trans	transformation function

Value

character vector of [lower, upper]

Author(s)

Guangchuang Yu

revts	<i>revts</i>
-------	--------------

Description

reverse timescle x-axis

Usage

```
revts(treeview)
```

Arguments

treeview	treeview
----------	----------

Value

updated treeview

Author(s)

Guangchuang Yu

rotate	<i>rotate</i>
--------	---------------

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

rotateTreePoints.df	<i>rotateTreePoints.data.frame</i>
---------------------	------------------------------------

Description

Rotate the points in a tree data.frame around a pivot node by the angle specified.

Usage

```
rotateTreePoints.df(df, pivot_node, nodes, angle)
```

Arguments

df	tree data.frame
pivot_node	is the id of the pivot node.
nodes	list of node numbers that are to be rotated by angle around the pivot_node
angle	in range [0,2], ie degrees/180, radians/pi

Value

updated tree data.frame with points rotated by angle

rotate_tree	<i>rotate_tree</i>
-------------	--------------------

Description

rotate circular tree

Usage

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

Arguments

treeview	tree view
angle	angle

Value

updated tree view

Author(s)

Guangchuang Yu

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 method
scale color by a numerical tree attribute

Usage

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

```
## S4 method for signature 'treedata'
```

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

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

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

Arguments

object	treedata object
by	one of numerical attributes
...	additional parameter

Value

color vector

scale_x_ggtree	<i>scale_x_ggtree</i>
----------------	-----------------------

Description

scale x for tree with gheatmap

Usage

```
scale_x_ggtree(breaks = waiver(), labels = waiver())
```

Arguments

breaks	breaks for tree
labels	lables for corresponding breaks

Value

updated tree view

Author(s)

Guangchuang Yu

scale_x_range	<i>scale_x_range</i>
---------------	----------------------

Description

add second x-axis for geom_range

Usage

```
scale_x_range()
```

Value

ggtree object

Author(s)

Guangchuang Yu

set_highlight_legend *set_highlight_legend*

Description

set legend for multiple geom_highlight layers

Usage

```
set_highlight_legend(p, color, label, alpha = 1)
```

Arguments

p	ggtree object
color	color vector
label	label vector
alpha	transparency of color

Value

updated ggtree object

Author(s)

Guangchuang Yu

StatBalance *StatBalance*

Description

StatBalance

StatHighlight

GeomHighlight

stat_highlight	<i>stat_highlight</i>
----------------	-----------------------

Description

stat_highlight

Usage

```
stat_highlight(  
  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	<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
height	height of subview

Value

ggplot object

Author(s)

Guangchuang Yu

theme_dendrogram	<i>theme_dendrogram</i>
------------------	-------------------------

Description

dendrogram theme

Usage

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

Arguments

bgcolor	background color
fgcolor	color for axis
...	additional parameter

Author(s)

Guangchuang Yu

theme_inset	<i>theme_inset</i>
-------------	--------------------

Description

inset theme

Usage

```
theme_inset(legend.position = "none", ...)
```

Arguments

legend.position	position of legend
...	additional parameter

Details

theme for inset function

Value

ggplot object

Author(s)

Guangchuang Yu

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

Description

tree theme

Usage

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

Arguments

bgcolor	background color
...	additional parameter

Value

updated ggplot object with new theme

Author(s)

Guangchuang Yu

Examples

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

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)

Guangchuang Yu

Examples

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

viewClade	<i>viewClade</i>
-----------	------------------

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

xlim_expand	<i>xlim_expand</i>
-------------	--------------------

Description

expand x axis limits for specific panel

Usage

```
xlim_expand(xlim, panel)
```

Arguments

xlim	xlim
panel	panel

Value

updated tree view

Author(s)

Guangchuang Yu

 xlim_tree

xlim_tree

Description

set x axis limits for Tree panel

Usage

```
xlim_tree(xlim)
```

Arguments

xlim xlim

Value

updated tree view

Author(s)

Guangchuang Yu

%+>%

%+>%

Description

update data with tree info (y coordination and panel)

Usage

```
p %+>% data
```

Arguments

p tree view
data data.frame

Details

add tree information to an input data. This function will setup y coordination and panel info for data used in facet_plot and geom_facet

Value

updated data.frame

Author(s)

Guangchuang Yu

References

G Yu, TTY Lam, H Zhu, Y Guan (2018). Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*, 35(2):3041-3043. <https://doi.org/10.1093/molbev/msy194>

%<+%

%<+%

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)

Guangchuang Yu

References

G Yu, TTY Lam, H Zhu, Y Guan (2018). Two methods for mapping and visualizing associated data on phylogeny using ggtree. *Molecular Biology and Evolution*, 35(2):3041-3043. <https://doi.org/10.1093/molbev/msy194>

See Also

`geom_facet`

Examples

```
nwk <- system.file("extdata", "sample.nwk", package="treeio")
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)
```

%<%

%<%

Description

update tree

Usage

pg %<% x

Arguments

pg	ggtree object
x	tree object

Details

This operator apply the visualization directives in ggtree object (lhs) to visualize another tree object (rhs), that is similar to Format Painter.

Value

updated ggplot object

Author(s)

Guangchuang Yu

Examples

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


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