

Package ‘ggtree’

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Type Package

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

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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 with their covariates and other associated data.

Depends R (>= 3.4.0)

Imports ape, dplyr, ggplot2 (>= 3.0.0), grDevices, grid, magrittr, methods, purrr, rlang, rvcheck (>= 0.1.0), scales, tibble, tidyr, tidytree (>= 0.1.9), treeio (>= 1.3.14), utils

Suggests colorspace, cowplot, emojiFont, ggimage, knitr, prettydoc, rmarkdown, testthat

Remotes GuangchuangYu/treeio

VignetteBuilder knitr

ByteCompile true

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URL <https://guangchuangyu.github.io/software/ggtree>

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

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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

applyLayoutDaylight	<i>applyLayoutDaylight</i>
---------------------	----------------------------

Description

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

Usage

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

Arguments

df	tree data.frame
node_id	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

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

Description

collapse a clade

Usage

```
## S3 method for class 'ggtree'
collapse(x = NULL, node, clade_name = NULL, ...)
```

Arguments

x	tree view
node	clade node
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_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

facet_plot

Description

plot tree associated data in an additional panel

Usage

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

Arguments

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

Value

ggplot object

Author(s)

Guangchuang Yu

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))
```

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	<i>geom_balance</i>
--------------	---------------------

Description

highlights the two direct descendant clades of an internal node

Usage

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

Arguments

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

Details

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

Value

ggplot2

Author(s)

Justin Silverman

References

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

geom_cladelabel *geom_cladelabel*

Description

annotate a clade with bar and text label

Usage

```
geom_cladelabel(node, label, offset = 0, offset.text = 0, 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	hjust
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

geom_cladelabel2	<i>geom_cladelabel2</i>
------------------	-------------------------

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	font 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

`geom_highlight` *geom_highlight*

Description

layer of highlight clade with rectangle

Usage

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

Arguments

<code>node</code>	selected node to highlight (required)
<code>fill</code>	color fill (default = steelblue)
<code>alpha</code>	alpha transparency, (default = 0.5)
<code>extend</code>	extend xmax of the rectangle (default = 0)
<code>extendto</code>	extend xmax to extendto (default = NULL)

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, expand = 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)
expand	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_label2	<i>geom_label2</i>
-------------	--------------------

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 passed into expressions
nudge_x	horizontal adjustment
nudge_y	vertical adjustment
label.padding	Amount of padding around label.
label.r	Radius of rounded corners.
label.size	Size of label border, in mm
na.rm	logical
show.legend	logical
inherit.aes	logical

Value

label layer

Author(s)

Guangchuang Yu

See Also

[geom_label](#)

geom_motif

geom_motif

Description

geom layer to draw aligned motif

Usage

```
geom_motif(mapping, data, on, ...)
```

Arguments

mapping	aes mapping
data	data
on	gene to center (i.e. set middle position of the 'on' gene to 0)
...	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_nodelab2(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
...	addktonal 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 = "length_0.95_HPD", branch.length = "branch.length",
            ...)
```

Arguments

range range, e.g. "height_0.95_HPD"
 branch.length corresponding branch.length
 ... 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 use 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 = NA, offset = 0, offset.text = 0,
  align = TRUE, barsize = 0.5, extend = 0, fontsize = 3.88,
  angle = 0, geom = "text", hjust = 0, 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
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>

geom_tippoint *geom_tippoint*

Description

add tip point

Usage

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

Arguments

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

Value

tip point layer

Author(s)

Guangchuang Yu

geom_tree

geom_tree

Description

add tree layer

Usage

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

Arguments

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

Value

tree layer

Author(s)

Yu Guangchuang

geom_tree2

geom_tree2

Description

add tree layer

Usage

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

Arguments

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

Value

tree layer

Author(s)

Yu Guangchuang

geom_treescale *geom_treescale*

Description

add tree scale

Usage

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

Arguments

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

Value

ggplot layers

Author(s)

Guangchuang Yu

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

Description

extract offspring tips

Usage

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

Arguments

<code>tr</code>	tree
<code>node</code>	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

<code>phylo</code>	phylo object
<code>from</code>	start node
<code>to</code>	end node

Value

node vectot

Author(s)

Guangchuang Yu

`getChild.df` *getChild.df*

Description

Get list of child node id numbers of parent node

Usage

```
getChild.df(df, node)
```

Arguments

<code>df</code>	tree data.frame
<code>node</code>	is the node id of child in tree.

Value

list of child node ids of parent

`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

`getNodesBreadthFirst.df`
getNodesBreadthFirst.df

Description

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

Usage

`getNodesBreadthFirst.df(df)`

Arguments

`df` tree data.frame

Value

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

`getParent.df` *getParent.df*

Description

Get parent node id of child node.

Usage

`getParent.df(df, node)`

Arguments

`df` tree data.frame
`node` is the node id of child in tree.

Value

integer node id of parent

`getSubtree`*getSubtree*

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`*getSubtree.df*

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

tree	ape phylo tree object
node	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

df	tree data.frame
node	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.

<code>getTreeArcAngles</code>	<i>getTreeArcAngles</i>
-------------------------------	-------------------------

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

<code>df</code>	tree data.frame
<code>origin_id</code>	node id from which to calculate left and right hand angles of subtree.
<code>subtree</code>	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.

<code>get_balance_position</code>	<i>get_balance_position</i>
-----------------------------------	-----------------------------

Description

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

Usage

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

Arguments

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

Value

data.frame

Author(s)

Justin Silverman

get_clade_position *get_clade_position*

Description

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

Usage

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

Arguments

treeview	tree view
node	selected node

Value

data.frame

Author(s)

Guangchuang Yu

get_heatmap_column_position
get_heatmap_column_position

Description

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

Usage

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

Arguments

treeview	output of 'gheatmap'
by	one of 'bottom' or 'top'

Value

data.frame

Author(s)

Guangchuang Yu

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

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

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

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", ...)
```

Arguments

tr	phylo object
mapping	aes mapping
layout	one of 'rectangular', 'slanted', 'fan', 'circular', 'radial', 'equal_angle' or 'day-light'
open.angle	open angle, only for 'fan' layout
mrsd	most recent sampling date
as.Date	logical whether using Date class in time tree
yscale	y scale
yscale_mapping	yscale mapping for category variable
ladderize	logical (default TRUE). Should the tree be re-organized to have a 'ladder' aspect?
right	logical. If ladderize = TRUE, should the ladder have the smallest clade on the right-hand side? See ladderize for more information.
branch.length	variable for scaling branch, if 'none' draw cladogram
...	additional parameter

Value

tree

Author(s)

Yu Guangchuang

See Also

[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, hjust = 0.5)
```

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
hjust	hjust for column names (0: align left, 0.5: align center, 1: align right)

Value

tree view

Author(s)

Guangchuang Yu

gzoom

gzoom method

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

Examples

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

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

Description

identify node by interactive click

Usage

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

Arguments

x	tree view
...	additional parameters

Value

node id

Author(s)

Guangchuang Yu

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

Description

add insets in a tree

Usage

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

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'
reverse_x	whether x axis was reversed by scale_x_reverse
reverse_y	whether y axis was reversed by scale_y_reverse

Value

tree view with insets

Author(s)

Guangchuang Yu

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

Description

#' @title

Usage

```
layoutDaylight(model, 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

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)
```

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.

MRCA	<i>MRCA</i>
------	-------------

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	<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	<i>multiplot</i>
-----------	------------------

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

nodeid	<i>nodeid</i>
--------	---------------

Description

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

Usage

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

Arguments

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

Value

internal node number

Author(s)

Guangchuang Yu

nodepie	<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

open_tree	<i>open_tree</i>
-----------	------------------

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

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

reroot	<i>reroot method</i>
--------	----------------------

Description

reroot method
reroot a tree

Usage

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

Arguments

object	treedata 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

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

Description

reverse timescale x-axis

Usage

```
revts(treeview)
```

Arguments

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

Value

updated treeview

Author(s)

guangchuang yu

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

rotateTreePoints.df

rotateTreePoints.data.fram

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 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

`set_highlight_legend` *set_highlight_legend*

Description

set legend for multiple geom_highlight layers

Usage`set_highlight_legend(p, color, label, alpha = 1)`**Arguments**

<code>p</code>	ggtree object
<code>color</code>	color vector
<code>label</code>	label vector
<code>alpha</code>	transparency of color

Value

updated ggtree object

Author(s)

guangchuang yu

`StatBalance` *StatBalance*

Description

StatBalance

StatHighlight

GeomHighlight

stat_balance	<i>stat_balance</i>
--------------	---------------------

Description

stat_balance

Usage

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

Arguments

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

Value

layer

stat_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

subview

Description

add subview to mainview for ggplot2 objects

Usage

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

Arguments

mainview	main view
subview	a ggplot or grob object
x	x position
y	y position
width	width of subview, [0,1]
height	height of subview, [0,1]

Value

ggplot object

Author(s)

Guangchuang Yu

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

Description

inset theme

Usage

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

Arguments

... 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", 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	<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

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="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 data with tree info (y coordination and panel)

Usage

p %+>% data

Arguments

p	tree view
data	data.frame

Value

updated data.frame

Author(s)

Guangchuang Yu

%>%

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

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