Package 'ggtree'

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Type Package

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

Version 1.8.2

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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 (>= 3.3.2), ggplot2 (>= 2.2.0), treeio

Imports ape, grDevices, grid, magrittr, methods, rvcheck, tidyr, utils

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

VignetteBuilder knitr

ByteCompile true

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URL `https://guangchuangyu.github.io/ggtree`

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

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

RoxygenNote 5.0.1

NeedsCompilation no

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Tommy Tsan-Yuk Lam [aut, ths],
Justin Silverman [ctb]

R topics documented:

. .

Description

capture name of variable

Usage

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

Arguments

`...`	expression
`.env`	environment

Value

expression

Examples

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

`add_colorbar` *add_colorbar*

Description

add colorbar legend

Usage

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

Arguments

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

Value

ggplot2 object

Author(s)

Guangchuang Yu

`annotation_image` *annotation_image*

Description

annotation taxa with images

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`apeBoot` *apeBoot*

Description

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

Usage

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

Arguments

`phylo`	phylo
`boot`	bootstrap values

Value

an instance of 'apeBootstrap'

Author(s)

Guangchuang Yu

`applyLayoutDaylight` *applyLayoutDaylight*

Description

Apply the daylight alorithm 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.binary` *as.binary*

Description

as.binary method for `phylo` object

Usage

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

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

Arguments

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

Value

binary tree

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

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

Description

convert phylo to data.frame

Usage

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

Arguments

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

Value

data.frame

Author(s)

Yu Guangchuang

`as.polytomy` *as.polytomy*

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` *collapse*

Description

collapse a clade

Usage

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

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

expand

`Date2decimal` *Date2decimal*

Description

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

Usage

```
Date2decimal(x)
```

Arguments

`x`	Date

Value

numeric

Author(s)

Guangchuang Yu

`decimal2Date` *decimal2Date*

Description

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

Usage

```
decimal2Date(x)
```

Arguments

`x`	numerical number, eg 2014.34

Value

Date

Author(s)

Guangchuang Yu

`download.phylopic` *download.phylopic*

Description

download phylopic

Usage

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

Arguments

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

Value

matrix

Author(s)

Guangchuang Yu

`expand` *expand*

Description

expand collased clade

Usage

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

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

collapse

`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'

Value

ggplot object

Author(s)

Guangchuang Yu

`flip` *flip*

Description

flip position of two selected branches

Usage

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

Arguments

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

Value

ggplot2 object

Author(s)

Guangchuang Yu

`fortify.phylo` *fortify*

Description

fortify a phylo to data.frame

Usage

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

Arguments

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

Value

data.frame

Author(s)

Yu Guangchuang

`geom_aline` *geom_aline*

Description

add horizontal align lines

Usage

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

Arguments

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

Value

aline layer

Author(s)

Yu Guangchuang

`geom_balance` *geom_balance*

Description

highlights the two direct descendant clades of an internal node

Usage

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

Arguments

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

Details

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

Value

ggplot2

Author(s)

Justin Silverman

References

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

`geom_cladelabel` *geom_cladelabel*

Description

annotate a clade with bar and text label

Usage

```
geom_cladelabel(node, label, offset = 0, offset.text = 0, align = FALSE,
  barsize = 0.5, fontsize = 3.88, angle = 0, geom = "text", hjust = 0,
  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
`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_hilight` *geom_hilight*

Description

layer of hilight clade with rectangle

Usage

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

Arguments

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

Value

ggplot2

Author(s)

Guangchuang Yu

`geom_label2` *geom_label2*

Description

geom_label2 support aes(subset) via setup_data

Usage

```
geom_label2(mapping = NULL, data = NULL, ..., 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 he plot defaults.
`...`	other arguments passed on to 'layer'
`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 passd into expressions
`nudge_x`	horizontal adjustment
`nudge_y`	vertical adjustment
`label.padding`	Amount of padding around label.
`label.r`	Radius of rounded corners.
`label.size`	Size of label border, in mm
`na.rm`	logical
`show.legend`	logical
`inherit.aes`	logical

Value

label layer

Author(s)

Guangchuang Yu

See Also

geom_label

`geom_nodepoint` *geom_nodepoint*

Description

add node point

Usage

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

Arguments

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

Value

node point layer

Author(s)

Guangchuang Yu

`geom_point2` *geom_point2*

Description

geom_point2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

point layer

Author(s)

Guangchuang Yu

See Also

geom_point

`geom_range` *geom_range*

Description

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

Usage

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

Arguments

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

Value

ggplot layer

Author(s)

Guangchuang Yu

`geom_rootpoint` *geom_rootpoint*

Description

add root point

Usage

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

Arguments

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

Value

root point layer

Author(s)

Guangchuang Yu

`geom_segment2` *geom_segment2*

Description

geom_segment2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

add segment layer

Author(s)

Guangchuang Yu

See Also

geom_segment

`geom_strip` *geom_strip*

Description

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

Usage

```
geom_strip(taxa1, taxa2, label = NA, offset = 0, offset.text = 0,
  align = TRUE, barsize = 0.5, barextend = 0, fontsize = 3.88,
  angle = 0, geom = "text", hjust = 0, fill = NA, family = "sans",
  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
`barextend`	extend bar vertically
`fontsize`	size of text
`angle`	angle of text
`geom`	one of 'text' or 'label'
`hjust`	hjust
`fill`	fill label background, only work with geom='label'
`family`	sans by default, can be any supported font
`parse`	logical, whether parse label
`...`	additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

`geom_taxalink` *geom_taxalink*

Description

link between taxa

Usage

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

Arguments

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

Value

ggplot layer

Author(s)

Guangchuang Yu

`geom_text2` *geom_text2*

Description

geom_text2 support aes(subset) via setup_data

Usage

```
geom_text2(mapping = NULL, data = NULL, ..., position = "identity",
  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 he plot defaults.
`...`	other arguments passed on to 'layer'
`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 passd 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` *geom_tiplab*

Description

add tip label layer

Usage

```
geom_tiplab(mapping = NULL, hjust = 0, align = FALSE,
  linetype = "dotted", linesize = 1, 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' and 'label'
`offset`	tiplab offset
`...`	additional parameter

Value

tip label layer

Author(s)

Yu Guangchuang

Examples

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

`geom_tiplab2` *geom_tiplab2*

Description

add tip label for circular layout

Usage

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

Arguments

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

Value

tip label layer

Author(s)

Guangchuang Yu

References

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

`geom_tippoint` *geom_tippoint*

Description

add tip point

Usage

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

Arguments

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

Value

tip point layer

Author(s)

Guangchuang Yu

`geom_tree` *geom_tree*

Description

add tree layer

Usage

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

Arguments

`mapping`	aesthetic mapping
`data`	data
`layout`	one of ’rectangular’, ’slanted’, ’circular’, ’radial’, ’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

`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

`getChild.df` *getChild.df*

Description

Get list of child node id numbers of parent node

Usage

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

Arguments

`df`	tree data.frame
`node`	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

`df`	tree data.frame
`origin_node_id`	origin node id number
`node_id`	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.

`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)

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 and list of node ids for given subtree.

Value

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

`get_balance_position` *get_balance_position*

Description

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

Usage

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

Arguments

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

Value

data.frame

Author(s)

Justin Silverman

`get_clade_position` *get_clade_position*

Description

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

Usage

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

Arguments

`treeview`	tree view
`node`	selected node

Value

data.frame

Author(s)

Guangchuang Yu

`get_heatmap_column_position` *get_heatmap_column_position*

Description

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

Usage

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

Arguments

`treeview`	output of ‘gheatmap‘
`by`	one of ’bottom’ or ’top’

Value

data.frame

Author(s)

Guangchuang Yu

`get_taxa_name` *get_taxa_name*

Description

get taxa name of a selected node (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` *visualizing phylogenetic tree and heterogenous associated data based on grammar of graphics* `ggtree` *provides functions for visualizing phylogenetic tree and its associated data in R.*

Description

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

drawing phylogenetic tree from phylo object

Usage

```
ggtree(tr, mapping = NULL, layout = "rectangular", open.angle = 0,
  mrsd = NULL, as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = TRUE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, ...)
```

Arguments

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

Value

tree

Author(s)

Yu Guangchuang

Examples

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

`gheatmap` *gheatmap*

Description

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

Usage

```
gheatmap(p, data, offset = 0, width = 1, low = "green", high = "red",
  color = "white", colnames = TRUE, colnames_position = "bottom",
  colnames_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 righ)

Value

tree view

Author(s)

Guangchuang Yu

`groupClade` *groupClade method*

Description

groupClade method for ggtree object

Usage

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

Arguments

`object`	ggtree object
`node`	internal node number
`group_name`	name of the group

`groupOTU` *groupOTU method*

Description

groupOTU method for ggtree object

Usage

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

Arguments

`object`	ggtree object
`focus`	OTU to focus
`group_name`	name of the group
`...`	additional parameters

`gzoom` *gzoom method*

Description

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 '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 'treedata'
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))
```

Arguments

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

Value

figure

`gzoom.phylo` *gzoom*

Description

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

Usage

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

Arguments

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

Value

a list of ggplot object

Author(s)

ygc

Examples

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

`identify.gg` *identify*

Description

identify node by interactive click

Usage

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

Arguments

`x`	tree view
`...`	additional parameters

Value

node id

Author(s)

Guangchuang Yu

`inset` *inset*

Description

add insets in a tree

Usage

```
inset(tree_view, insets, width = 0.1, height = 0.1, 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` *Equal daylight layout method for unrooted trees.*

Description

#' @title

Usage

```
layoutDaylight(tree, branch.length)
```

Arguments

`tree`	phylo object
`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 aglorithm 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` *layoutEqualAngle*

Description

'Equal-angle layout algorithm for unrooted trees'

Usage

```
layoutEqualAngle(tree, branch.length)
```

Arguments

`tree`	phylo object
`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` *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

`NJ` *NJ*

Description

neighbor-joining method

Usage

```
NJ(X)
```

Arguments

`X`	distance matrix

Value

phylo object

Author(s)

ygc

Examples

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

## End(Not run)
```

`nodebar` *nodebar*

Description

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

Usage

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

Arguments

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

Value

list of ggplot objects

Author(s)

Guangchuang Yu

`nodeid` *nodeid*

Description

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

Usage

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

Arguments

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

Value

internal node number

Author(s)

Guangchuang Yu

`nodepie` *nodepie*

Description

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

Usage

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

Arguments

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

Value

list of ggplot objects

Author(s)

Guangchuang Yu

`open_tree` *open_tree*

Description

open tree with specific angle

Usage

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

Arguments

`treeview`	tree view
`angle`	angle

Value

updated tree view

Author(s)

Guangchuang Yu

`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

`print.beastList` *print*

Description

print information of a list of beast trees

Usage

```
## S3 method for class 'beastList'
print(x, ...)
```

Arguments

`x`	a list of beast object
`...`	no used

Value

message

Author(s)

Guangchuang Yu

`reroot` *reroot method*

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` *rescale_tree*

Description

rescale branch length of tree object

Usage

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

Arguments

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

Value

update tree object

Author(s)

Guangchuang Yu

`revts` *revts*

Description

reverse timescle x-axis

Usage

```
revts(treeview)
```

Arguments

`treeview`	treeview

Value

updated treeview

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

`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_treerotate_tree` *rotate_tree*

Description

rotate circular tree

Usage

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

Arguments

`treeview`	tree view
`angle`	angle

Value

updated tree view

Author(s)

Guangchuang Yu

`scaleClade` *scaleClade*

Description

scale clade

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`scale_color` *scale_color method*

Description

scale color by a numerical tree attribute

Usage

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

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

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

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

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

Arguments

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

Value

color vector

`scale_x_ggtree` *scale_x_ggtree*

Description

scale x for tree with heatmap

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`StatBalance` *StatBalance*

Description

StatBalance

StatHilight

`stat_balance` *stat_balance*

Description

stat_balance

Usage

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

Arguments

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

Value

layer

`stat_hilight` *stat_hilight*

Description

stat_hilight

Usage

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

Arguments

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

Value

layer

`subview` *subview*

Description

add subview to mainview for ggplot2 objects

Usage

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

Arguments

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

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_inset` *theme_inset*

Description

inset theme

Usage

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

Arguments

`...`	additional parameter

Details

theme for inset function

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_transparent` *theme_transparent*

Description

transparent background theme

Usage

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

Arguments

`...`	additional parameter to tweak the theme

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_tree` *theme_tree*

Description

tree theme

Usage

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

Arguments

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

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

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

`theme_tree2` *theme_tree2*

Description

tree2 theme

Usage

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

Arguments

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

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

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

`viewClade` *viewClade*

Description

view a clade of tree

Usage

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

Arguments

`tree_view`	full tree view
`node`	internal node number
`xmax_adjust`	adjust xmax

Value

clade plot

Author(s)

Guangchuang Yu

`xlim_expand` *xlim_expand*

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="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)
```

`%+>%` %+>%

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

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