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 1.6.11

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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 (>= 3.3.1), ggplot2 (>= 2.2.0)

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

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

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

URL `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

R topics documented:

. .

Description

capture name of variable

Usage

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

Arguments

`...`	expression
`.env`	environment

Value

expression

Examples

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

`add_colorbar` *add_colorbar*

Description

add colorbar legend

Usage

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

Arguments

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

Value

ggplot2 object

Author(s)

Guangchuang Yu

`annotation_image` *annotation_image*

Description

annotation taxa with images

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`apeBoot` *apeBoot*

Description

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

Usage

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

Arguments

`phylo`	phylo
`boot`	bootstrap values

Value

an instance of 'apeBootstrap'

Author(s)

Guangchuang Yu

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

Description

Class "apeBootstrap" This class stores ape bootstrapping analysis result

Slots

`phylo` phylo object of treetext

`fields` available features

`bootstrap` bootstrap value

`extraInfo` extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

`as.binary` *as.binary*

Description

as.binary method for `phylo` object

Usage

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

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

Arguments

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

Value

binary tree

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

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

Description

convert phylo to data.frame

Usage

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

Arguments

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

Value

data.frame

Author(s)

Yu Guangchuang

`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

`beast-class` *Class "beast" This class stores information of beast output*

Description

Class "beast" This class stores information of beast output

Slots

`fields` beast statistic variables

`treetext` tree text in beast file

`phylo` tree phylo object

`translation` tip number to name translation in beast file

`stats` beast statistics

`file` beast file, nexus format

`extraInfo` extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

`show` `get.fields` `ggtree`

`codeml-class` *Class "codeml" This class stores information of output from codeml*

Description

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

Slots

`mlc` A `code_mlc` object

`rst` A `paml_rst` object

`extraInfo` extra information

See Also

codeml_mlc paml_rst

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

Description

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

Slots

`fields` available features

`treetext` tree text

`phylo` phylo object

`dNdS` dN dS information

`mlcfile` mlc file

`extraInfo` extra information

Author(s)

Guangchuang Yu

See Also

paml_rst codeml

`collapse` *collapse*

Description

collapse a clade

Usage

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

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

expand

`Date2decimal` *Date2decimal*

Description

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

Usage

```
Date2decimal(x)
```

Arguments

`x`	Date

Value

numeric

Author(s)

Guangchuang Yu

`decimal2Date` *decimal2Date*

Description

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

Usage

```
decimal2Date(x)
```

Arguments

`x`	numerical number, eg 2014.34

Value

Date

Author(s)

Guangchuang Yu

`download.phylopic` *download.phylopic*

Description

download phylopic

Usage

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

Arguments

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

Value

matrix

Author(s)

Guangchuang Yu

`expand` *expand*

Description

expand collased clade

Usage

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

Arguments

`tree_view`	tree view
`node`	clade node

Value

tree view

Author(s)

Guangchuang Yu

See Also

collapse

`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_text2*

Description

geom_text2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

label layer

Author(s)

Guangchuang Yu

See Also

geom_label

`geom_nodepoint` *geom_nodepoint*

Description

add node point

Usage

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

Arguments

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

Value

node point layer

Author(s)

Guangchuang Yu

`geom_point2` *geom_point2*

Description

geom_point2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

point layer

Author(s)

Guangchuang Yu

See Also

geom_point

`geom_range` *geom_range*

Description

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

Usage

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

Arguments

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

Value

ggplot layer

Author(s)

Guangchuang Yu

`geom_rootpoint` *geom_rootpoint*

Description

add root point

Usage

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

Arguments

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

Value

root point layer

Author(s)

Guangchuang Yu

`geom_segment2` *geom_segment2*

Description

geom_segment2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

add segment layer

Author(s)

Guangchuang Yu

See Also

geom_segment

`geom_strip` *geom_strip*

Description

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

Usage

```
geom_strip(taxa1, taxa2, label = NA, offset = 0, offset.text = 0,
  align = TRUE, barsize = 0.5, barextend = 0, fontsize = 3.88,
  angle = 0, geom = "text", hjust = 0, fill = NA, family = "sans",
  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",
  parse = FALSE, na.rm = TRUE, show.legend = NA, inherit.aes = TRUE,
  ..., nudge_x = 0, nudge_y = 0, check_overlap = FALSE)
```

Arguments

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

Value

text layer

Author(s)

Guangchuang Yu

See Also

geom_text

`geom_tiplab` *geom_tiplab*

Description

add tip label layer

Usage

```
geom_tiplab(mapping = NULL, hjust = 0, align = FALSE,
  linetype = "dotted", linesize = 1, geom = "text", 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' or 'unrooted'
`multiPhylo`	logical
`...`	additional parameter

Value

tree layer

Author(s)

Yu Guangchuang

`geom_tree2` *geom_tree2*

Description

add tree layer

Usage

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

Arguments

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

Value

tree layer

Author(s)

Yu Guangchuang

`geom_treescale` *geom_treescale*

Description

add tree scale

Usage

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

Arguments

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

Value

ggplot layers

Author(s)

Guangchuang Yu

`get.fields` *get.fields method*

Description

get.fields method

Usage

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

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

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

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

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

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

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

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

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

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

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

## S4 method for signature 'r8s'
get.fields(object, ...)
```

Arguments

`object`	one of `jplace`, `beast`, `hyphy`, `codeml`, `codeml_mlc`, `paml_rst` object
`...`	additional parameter

Value

available annotation variables

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
jp <- read.jplace(jp)
get.fields(jp)
```

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

Description

extract offspring tips

Usage

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

Arguments

`tr`	tree
`node`	node

Value

tip label

Author(s)

ygc

`get.path` *get.path*

Description

path from start node to end node

Usage

```
get.path(phylo, from, to)
```

Arguments

`phylo`	phylo object
`from`	start node
`to`	end node

Value

node vectot

Author(s)

Guangchuang Yu

`get.phylopic` *get.phylopic*

Description

download phylopic and convert to grob object

Usage

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

Arguments

`id`	phylopic id
`size`	size of the phylopic
`color`	color
`alpha`	alpha

Value

grob object

Author(s)

Guangchuang Yu

`get.placements` *get.placements method*

Description

get.placement method

Usage

```
get.placements(object, by, ...)

get.placements(object, by, ...)
```

Arguments

`object`	jplace object
`by`	get best hit or others
`...`	additional parameter

Value

data.frame

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
jp <- read.jplace(jp)
get.placements(jp, by="all")
```

`get.subs` *get.subs method*

Description

get substitution information

Usage

```
get.subs(object, type, ...)

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

## S4 method for signature 'hyphy'
get.subs(object, type, ...)
```

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

## S4 method for signature 'phangorn'
get.subs(object, type, ...)
```

Arguments

`object`	paml_rst object
`type`	one of 'marginal_subs', 'marginal_AA_subs', 'joint_subs' or 'joint_AA_subs'.
`...`	additional parameter

Value

data.frame

Examples

```
nwk <- system.file("extdata/HYPHY", "labelledtree.tree", package="ggtree")
ancseq <- system.file("extdata/HYPHY", "ancseq.nex", package="ggtree")
tipfas <- system.file("extdata", "pa.fas", package="ggtree")
hy <- read.hyphy(nwk, ancseq, tipfas)
get.subs(hy, type="AA_subs")
```

`get.tipseq` *get.tipseq method*

Description

get tipseq

Usage

```
get.tipseq(object, ...)

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

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

Arguments

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

Value

character

`get.tree` *get.tree method*

Description

get.tree method

Usage

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

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

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

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

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

get.tree(object, ...)

## S4 method for signature 'codeml'
get.tree(object, by = "rst", ...)

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

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

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

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

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

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

## S4 method for signature 'r8s'
get.tree(object, ...)
```

Arguments

`object`	one of `phylo`, `jplace`, `nhx`, `phangorn`, `beast`, `hyphy`, `codeml`, `codeml_mlc`, `paml_rst` object
`...`	additional parameter
`by`	one of rst or mlc

Value

phylo object

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

Examples

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

`get.treeinfo` *get.treeinfo method*

Description

get.treeinfo method

Usage

```
get.treeinfo(object, layout = "phylogram", ladderize = TRUE,
  right = FALSE, ...)

get.treeinfo(object, layout, ladderize, right, ...)
```

Arguments

`object`	jplace object
`layout`	layout
`ladderize`	ladderize, logical
`right`	logical, parameter for ladderize
`...`	additional parameter

Value

data.frame

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
jp <- read.jplace(jp)
get.treeinfo(jp)
```

`get.treetext` *get.treetext method*

Description

get.treetext method

Usage

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

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

Arguments

`object`	one of `phylo`, `jplace`, `beast`, `hyphy`, `codeml`, `codeml_mlc`, `paml_rst` object
`...`	additional parameter

Value

phylo object

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
jp <- read.jplace(jp)
get.treetext(jp)
```

`getNodeNum` *getNodeNum*

Description

calculate total number of nodes

Usage

```
getNodeNum(tr)
```

Arguments

`tr`	phylo object

Value

number

Author(s)

Guangchuang Yu

`getRoot` *getRoot*

Description

get the root number

Usage

```
getRoot(tr)
```

Arguments

`tr`	phylo object

Value

root number

Author(s)

Guangchuang Yu

`get_balance_position` *get_balance_position*

Description

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

Usage

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

Arguments

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

Value

data.frame

Author(s)

Justin Silverman

`get_clade_position` *get_clade_position*

Description

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

Usage

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

Arguments

`treeview`	tree view
`node`	selected node

Value

data.frame

Author(s)

Guangchuang Yu

`get_heatmap_column_position` *get_heatmap_column_position*

Description

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

Usage

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

Arguments

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

Value

data.frame

Author(s)

Guangchuang Yu

`get_taxa_name` *get_taxa_name*

Description

get taxa name of a selected node

Usage

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

Arguments

`tree_view`	tree view
`node`	node

Value

taxa name vector

Author(s)

Guangchuang Yu

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

Description

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

drawing phylogenetic tree from phylo object

Usage

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

Arguments

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

Value

tree

Author(s)

Yu Guangchuang

Examples

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

`gheatmap` *gheatmap*

Description

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

Usage

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

group selected clade

Usage

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

## S4 method for signature 'r8s'
groupClade(object, node, group_name = "group",
  tree = "TREE")
```

Arguments

`object`	supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy
`node`	a internal node or a vector of internal nodes
`group_name`	name of the group, 'group' by default
`...`	additional parameter
`tree`	which tree selected

Value

group index

`groupOTU` *groupOTU method*

Description

group tree based on selected OTU, will traceback to MRCA

Usage

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

## S4 method for signature 'r8s'
groupOTU(object, focus, group_name = "group", tree = "TREE")
```

Arguments

`object`	supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy
`focus`	a vector of tip (label or number) or a list of tips.
`group_name`	name of the group, 'group' by default
`...`	additional parameter
`tree`	which tree selected

Value

group index

`groupOTU.phylo` *groupOTU.phylo*

Description

group OTU

Usage

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

Arguments

`phy`	tree object
`focus`	tip list
`group_name`	name of the group

Value

phylo object

Author(s)

ygc

`gzoom` *gzoom method*

Description

zoom selected subtree

Usage

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

## S4 method for signature 'raxml'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'codeml_mlc'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'hyphy'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

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

## S4 method for signature 'apeBootstrap'
gzoom(object, focus, subtree = FALSE,
  widths = c(0.3, 0.7))

## S4 method for signature 'beast'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'codeml'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'nhx'
gzoom(object, focus, subtree = FALSE, widths = c(0.3, 0.7))

## S4 method for signature 'paml_rst'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'phylo'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
  0.7))

## S4 method for signature 'phangorn'
gzoom(object, focus, subtree = FALSE, widths = c(0.3,
```

```
  0.7))

## S4 method for signature 'r8s'
gzoom(object, focus, subtree = FALSE, widths = c(0.3, 0.7),
  tree = "TREE")
```

Arguments

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

Value

figure

`gzoom.phylo` *gzoom*

Description

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

Usage

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

Arguments

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

Value

a list of ggplot object

Author(s)

ygc

Examples

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

`hyphy-class` *Class "hyphy" This class stores information of HYPHY output*

Description

Class "hyphy" This class stores information of HYPHY output

Slots

`fields`	available features
`treetext`	tree text
`phylo`	phylo object
`seq_type`	one of "NT" and "AA"
`subs`	sequence substitutions
`AA_subs`	Amino acid sequence substitution
`ancseq`	ancestral sequences
`tip_seq`	tip sequences
`tip.fasfile`	fasta file of tip sequences
`tree.file`	tree file
`ancseq.file`	ancestral sequence file, nexus format
`extraInfo`	extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

paml_rst

`identify.gg` *identify*

Description

identify node by interactive click

Usage

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

Arguments

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

Value

node id

Author(s)

Guangchuang Yu

`inset` *inset*

Description

add insets in a tree

Usage

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

Arguments

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

Value

tree view with insets

Author(s)

Guangchuang Yu

`jplace-class` *Class "jplace" This class stores information of jplace file.*

Description

Class "jplace" This class stores information of jplace file.

Slots

`fields` colnames of first variable of placements

`treetext` tree text

`phylo` tree phylo object

`placements` placement information

`version` version

`metadata` metadata

`file` jplace file

`extraInfo` extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

`show` `get.tree` `ggtree`

`mask` *mask*

Description

site mask

Usage

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

Arguments

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

Value

updated tree object

Author(s)

Guangchuang Yu

`merge_tree` *merge_tree*

Description

merge two tree object

Usage

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

Arguments

`obj1`	tree object 1
`obj2`	tree object 2

Value

tree object

Author(s)

Guangchuang Yu

`MRCA` *MRCA*

Description

Find Most Recent Common Ancestor among a vector of tips

Usage

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

Arguments

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

Value

MRCA of two or more tips

Author(s)

Guangchuang Yu

`msaplot` *msaplot*

Description

multiple sequence alignment with phylogenetic tree

Usage

```
msaplot(p, fasta, offset = 0, width = 1, color = NULL, window = NULL)
```

Arguments

`p`	tree view
`fasta`	fasta file, multiple sequence alignment
`offset`	offset of MSA to tree
`width`	total width of alignment, compare to width of tree
`color`	color
`window`	specific a slice to display

Value

tree view

Author(s)

Guangchuang Yu

`multiplot` *multiplot*

Description

plot multiple ggplot objects in one page

Usage

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

Arguments

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

Value

plot

Author(s)

Guangchuang Yu

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

Description

Class "nhx" This class stores nhx tree

Slots

- `file` input file
- `fields` available feature
- `phylo` phylo object
- `nhx_tags` tag information in nhx file
- `extraInfo` extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

`NJ` *NJ*

Description

neighbor-joining method

Usage

```
NJ(X)
```

Arguments

`X`	distance matrix

Value

phylo object

Author(s)

ygc

Examples

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

## End(Not run)
```

`nodebar` *nodebar*

Description

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

Usage

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

Arguments

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

Value

list of ggplot objects

Author(s)

Guangchuang Yu

`nodeid` *nodeid*

Description

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

Usage

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

Arguments

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

Value

internal node number

Author(s)

Guangchuang Yu

`nodepie` *nodepie*

Description

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

Usage

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

Arguments

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

Value

list of ggplot objects

Author(s)

Guangchuang Yu

`open_tree` *open_tree*

Description

open tree with specific angle

Usage

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

Arguments

`treeview`	tree view
`angle`	angle

Value

updated tree view

Author(s)

Guangchuang Yu

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

Description

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

Slots

- `fields` availabel attributes
- `treetext` tree text
- `phylo` phylo object
- `seq_type` one of "NT" and "AA"
- `tip_seq` sequences of tips
- `marginal_ancseq` Marginal reconstruction of ancestral sequences
- `joint_ancseq` Joint reconstruction of ancestral sequences
- `marginal_subs` sequence substitutions based on marginal_ancseq
- `joint_subs` sequence substitutions based on joint_ancseq
- `marginal_AA_subs` Amino acid sequence substitutions based on marginal_ancseq
- `joint_AA_subs` Amino acid sequence substitutions based on joint_ancseq
- `rstfile` rst file
- `extraInfo` extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

codeml codeml_mlc

`phangorn-class` *Class "phangorn" This class stores ancestral sequences inferred from 'phangorn'*

Description

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

Slots

`fields` available attributes

`phylo` phylo object

`seq_type` one of "NT" and "AA"

`tip_seq` sequences of tips

`ancseq` ancenstral sequences

`subs` sequence substitution

`AA_subs` Amino acid sequence substitution

`extraInfo` extra information

Author(s)

Guangchuang Yu `http://guangchuangyu.github.io`

See Also

paml_rst

`phylip-class` *Class "phylip" This class stores phylip tree(s)*

Description

Class "phylip" This class stores phylip tree(s)

Slots

`file` input file

`fields` available feature

`phylo` phylo or multiPhylo

`ntree` number of trees

`sequence` sequences

`extraInfo` extra information

Author(s)

Guangchuang Yu

`phylopic` *phylopic*

Description

add phylopic layer

Usage

```
phylopic(tree_view, phylopic_id, size = 512, color = "black", alpha = 0.5,
  node = NULL, x = NULL, y = NULL, width = 0.1)
```

Arguments

`tree_view`	tree view
`phylopic_id`	phylopic id
`size`	size of phylopic to download
`color`	color
`alpha`	alpha
`node`	selected node
`x`	x position
`y`	y position
`width`	width of phylopic

Value

phylopic layer

Author(s)

Guangchuang Yu

`phyPML` *treeAnno.pml*

Description

tree annotation of sequence substitution by comparing to parent node

Usage

```
phyPML(pmlTree, type = "ml")
```

Arguments

`pmlTree`	tree in pml object, output of phangorn::optim.pml
`type`	one of 'ml' and 'bayes' for inferring ancestral sequences

Value

phangorn object

Author(s)

Yu Guangchuang

`plot` *plot method*

Description

plot method generics

Usage

```
## S4 method for signature 'beast,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "rate", ndigits = 2, annotation.size = 3,
  annotation.color = "black", ...)

## S4 method for signature 'codeml_mlc,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "dN_vs_dS", annotation.size = 3,
  annotation.color = "black", ndigits = 2, ...)

## S4 method for signature 'r8s,ANY'
plot(x, layout = "rectangular", branch.length = "TREE",
```

```
  show.tip.label = TRUE, tip.label.size = 4, tip.label.hjust = 0, ...)

## S4 method for signature 'raxml,ANY'
plot(x, layout = "rectangular",
  branch.length = "branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = 0, position = "node",
  annotation = "bootstrap", ndigits = 2, annotation.size = 4,
  annotation.color = "black", ...)

## S4 method for signature 'paml_rst,ANY'
plot(x, layout = "rectangular",
  show.tip.label = TRUE, tip.label.size = 4, tip.label.hjust = -0.1,
  position = "branch", annotation = "marginal_subs",
  annotation.color = "black", annotation.size = 3, ...)

## S4 method for signature 'hyphy,ANY'
plot(x, layout = "rectangular", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "subs", annotation.color = "black", annotation.size = 3,
  ...)

## S4 method for signature 'codeml,ANY'
plot(x, layout = "rectangular",
  branch.length = "mlc.branch.length", show.tip.label = TRUE,
  tip.label.size = 4, tip.label.hjust = -0.1, position = "branch",
  annotation = "dN_vs_dS", annotation.size = 3,
  annotation.color = "black", ndigits = 2, ...)
```

Arguments

`x`	object
`layout`	layout
`branch.length`	branch length
`show.tip.label`	logical
`tip.label.size`	size of tip label
`tip.label.hjust`	hjust of tip.label
`position`	one of "branch" and "node"
`annotation`	one of get.fields(x)
`ndigits`	round digits
`annotation.size`	size of annotation
`annotation.color`	color of annotation
`...`	Additional argument list

Value

plot

Examples

```
file <- system.file("extdata/BEAST", "beast_mcc.tree", package="ggtree")
beast <- read.beast(file)
plot(beast, annotation="length_0.95_HPD", branch.length="none") + theme_tree()
```

`pmlToSeq` *pmlToSeq*

Description

convert pml object to XStringSet object

Usage

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

Arguments

`pml`	pml object
`includeAncestor`	logical

Value

XStringSet

Author(s)

ygc

`print.beastList` *print*

Description

print information of a list of beast trees

Usage

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

Arguments

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

Value

message

Author(s)

Guangchuang Yu

`r8s-class` *Class "r8s" This class stores output info from r8s*

Description

Class "r8s" This class stores output info from r8s

Slots

`file` input file

`fields` available feature

`treetext` tree text

`phylo` multiPhylo, time tree, rate tree and absolute substitution tree

`extraInfo` extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

`raxml-class` *Class "raxml" This class stores RAxML bootstrapping analysis result*

Description

Class "raxml" This class stores RAxML bootstrapping analysis result

Slots

`file` input file

`fields` available features

`treetext` tree text

`phylo` phylo object of treetext

`bootstrap` bootstrap value

`extraInfo` extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

`raxml2nwk` *raxml2nwk*

Description

convert raxml bootstrap tree to newick format

Usage

```
raxml2nwk(infile, outfile = "raxml.tree")
```

Arguments

`infile`	input file
`outfile`	output file

Value

newick file

Author(s)

Guangchuang Yu

`read.baseml` *read.baseml*

Description

read rst and mlb file from baseml output

Usage

```
read.baseml(rstfile, mlbfile)
```

Arguments

`rstfile`	rst file
`mlbfile`	mlb file

Value

A `paml_rst` object

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`read.beast` *read.beast*

Description

read beast output

Usage

```
read.beast(file)
```

Arguments

`file`	beast file

Value

`beast` object

Author(s)

Guangchuang Yu http://ygc.name

Examples

```
file <- system.file("extdata/BEAST", "beast_mcc.tree", package="ggtree")
read.beast(file)
```

`read.codeml` *read.codeml*

Description

read baseml output

Usage

```
read.codeml(rstfile, mlcfile)
```

Arguments

`rstfile`	rst file
`mlcfile`	mlc file

Value

A `codeml` object

Author(s)

ygc

Examples

```
rstfile <- system.file("extdata/PAML_Codeml", "rst", package="ggtree")
mlcfile <- system.file("extdata/PAML_Codeml", "mlc", package="ggtree")
read.codeml(rstfile, mlcfile)
```

`read.codeml_mlc` *read.codeml_mlc*

Description

read mlc file of codeml output

Usage

```
read.codeml_mlc(mlcfile)
```

Arguments

`mlcfile`	mlc file

Value

A `codeml_mlc` object

Author(s)

ygc

Examples

```
mlcfile <- system.file("extdata/PAML_Codeml", "mlc", package="ggtree")
read.codeml_mlc(mlcfile)
```

`read.hyphy` *read.hyphy*

Description

read HYPHY output

Usage

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

Arguments

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

Value

A hyphy object

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`read.jplace` *read.jplace*

Description

read jplace file

Usage

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

Arguments

`file`	jplace file

Value

`jplace` instance

Author(s)

ygc

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
read.jplace(jp)
```

`read.nhx` *read.nhx*

Description

read nhx tree file

Usage

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

Arguments

`file`	nhx file

Value

nhx object

Author(s)

Guangchuang Yu `http://ygc.name`

`read.paml_rst` *read.paml_rst*

Description

read rst file from paml output

Usage

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

Arguments

`rstfile`	rst file

Value

A `paml_rst` object

Author(s)

Guangchuang Yu `http://ygc.name`

Examples

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

`read.phylip` *read.phylip*

Description

parsing phylip tree format

Usage

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

Arguments

`file`	phylip file

Value

an instance of 'phylip'

Author(s)

Guangchuang Yu

`read.phyloT` *read.phyloT*

Description

parse output from phyloT

Usage

```
read.phyloT(file, ...)
```

Arguments

`file`	newick tree file
`...`	additional parameters to read.tree

Value

phylo object

Author(s)

guangchuang yu

References

`http://phylot.biobyte.de/`

`read.r8s` *read.r8s*

Description

parse output from r8s

Usage

```
read.r8s(file)
```

Arguments

`file`	r8s output log file

Value

r8s instance

Author(s)

Guangchuang Yu

`read.raxml` *read.raxml*

Description

parse RAxML bootstrapping analysis output

Usage

```
read.raxml(file)
```

Arguments

`file`	RAxML bootstrapping analysis output

Value

raxml object

Author(s)

Guangchuang Yu

`reroot` *reroot method*

Description

reroot a tree

Usage

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

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

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

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

Arguments

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

Value

tree object

`rescale_tree` *rescale_tree*

Description

rescale branch length of tree object

Usage

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

Arguments

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

Value

update tree object

Author(s)

Guangchuang Yu

`rm.singleton.newick` *rm.singleton.newick*

Description

remove singleton

Usage

```
rm.singleton.newick(nwk, outfile = NULL)
```

Arguments

`nwk`	newick file
`outfile`	output newick file

Value

tree text

Author(s)

Guangchuang Yu http://ygc.name

`rotate` *rotate*

Description

rotate 180 degree of a selected branch

Usage

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

Arguments

`tree_view`	tree view
`node`	selected node

Value

ggplot2 object

Author(s)

Guangchuang Yu

`rotate_tree` *rotate_tree*

Description

rotate circular tree

Usage

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

Arguments

`treeview`	tree view
`angle`	angle

Value

updated tree view

Author(s)

Guangchuang Yu

`rtree` *generate random tree*

Description

generate random tree

Usage

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

Arguments

`n`	number of tips in the tree
`rooted`	logcial
`tip.label`	tip label
`br`	one of the following: (i) an R function used to generate the branch lengths ('rtree'; use 'NULL' to simulate only a topology), or the coalescence times ('rcoal'); (ii) a character to simulate a genuine coalescent tree for 'rcoal' (the default); or (iii) a numeric vector for the branch lengths or the coalescence times.
`...`	additional parameters to be passed to 'br'

Source

This is just the imported function from the ape package. The documentation you should read for the rtree function can be found here: rtree

See Also

rtree

`scaleClade` *scaleClade*

Description

scale clade

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`scale_color` *scale_color method*

Description

scale color by a numerical tree attribute

Usage

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

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

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

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

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

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

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

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

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

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

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

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

## S4 method for signature 'r8s'
scale_color(object, by = "bootstrap", tree = "TREE")
```

Arguments

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

Value

color vector

`scale_x_ggtree` *scale_x_ggtree*

Description

scale x for tree with heatmap

Usage

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

Arguments

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

Value

tree view

Author(s)

Guangchuang Yu

`show,raxml-method` *show method*

Description

show method for `jplace` instance

Usage

```
## S4 method for signature 'raxml'
show(object)

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

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

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

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

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

show(object)

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

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

## S4 method for signature 'paml_rst'
show(object)
```

```
## S4 method for signature 'r8s'
show(object)

## S4 method for signature 'phangorn'
show(object)
```

Arguments

`object`	one of `jplace`, `beast` object

Value

print info

Author(s)

Guangchuang Yu http://ygc.name

Examples

```
jp <- system.file("extdata", "sample.jplace", package="ggtree")
jp <- read.jplace(jp)
show(jp)
```

`StatBalance` *StatBalance*

Description

StatBalance

StatHilight

`stat_balance` *stat_balance*

Description

stat_balance

Usage

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

Arguments

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

Value

layer

`stat_hilight` *stat_hilight*

Description

stat_hilight

Usage

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

Arguments

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

Value

layer

`subview` *subview*

Description

add subview to mainview for ggplot2 objects

Usage

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

Arguments

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

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_inset` *theme_inset*

Description

inset theme

Usage

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

Arguments

`...`	additional parameter

Details

theme for inset function

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_transparent` *theme_transparent*

Description

transparent background theme

Usage

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

Arguments

`...`	additional parameter to tweak the theme

Value

ggplot object

Author(s)

Guangchuang Yu

`theme_tree` *theme_tree*

Description

tree theme

Usage

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

Arguments

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

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

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

`theme_tree2` *theme_tree2*

Description

tree2 theme

Usage

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

Arguments

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

Value

updated ggplot object with new theme

Author(s)

Yu Guangchuang

Examples

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

`viewClade` *viewClade*

Description

view a clade of tree

Usage

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

Arguments

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

Value

clade plot

Author(s)

Guangchuang Yu

`write.jplace` *write.jplace*

Description

generate jplace file

Usage

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

Arguments

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

Value

jplace file

Author(s)

ygc

Examples

```
tree <- system.file("extdata", "pa.nwk", package="ggtree")
data <- read.csv(system.file("extdata", "pa_subs.csv", package="ggtree"),
                stringsAsFactor=FALSE)
outfile <- tempfile()
write.jplace(tree, data, outfile)
```

`%<+%` %<+%

Description

add annotation data to a tree

Usage

```
pg %<+% data
```

Arguments

`pg`	ggplot2 object
`data`	annotation data

Value

ggplot object with annotation data added

Author(s)

Yu Guangchuang

Examples

```
nwk <- system.file("extdata", "sample.nwk", package="ggtree")
tree <- read.tree(nwk)
p <- ggtree(tree)
dd <- data.frame(taxa=LETTERS[1:13],
     place=c(rep("GZ", 5), rep("HK", 3), rep("CZ", 4), NA),
             value=round(abs(rnorm(13, mean=70, sd=10)), digits=1))
row.names(dd) <- NULL
p %<+% dd + geom_text(aes(color=place, label=label), hjust=-0.5)
```

`%+>%` *%+>%*

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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