

# 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** 1.16.6

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**Description** 'ggtree' extends the 'ggplot2' plotting system which implemented the grammar of graphics. 'ggtree' is designed for visualization and annotation of phylogenetic trees with their covariates and other associated data.

**Depends** R (>= 3.4.0)

**Imports** ape, dplyr, ggplot2 (>= 3.0.0), grid, magrittr, methods, purrr, rlang, rvcheck (>= 0.1.0), tidyr, tidytree (>= 0.2.4), treeio (>= 1.7.3), utils

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

**Remotes** GuangchuangYu/treeio

**VignetteBuilder** knitr

**ByteCompile** true

**Encoding** UTF-8

**License** Artistic-2.0

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

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

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

**RoxygenNote** 6.1.1

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**Description**

capture name of variable

**Usage**

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

**Arguments**

...	expression
.env	environment

**Value**

expression

**Examples**

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

---

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

**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

---

 applyLayoutDaylight      *applyLayoutDaylight*


---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

list with tree data.frame with updated layout using daylight algorithm and max\_change angle.

---

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

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

polytomy tree

**Author(s)**

Guangchuang Yu

---

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

**Description**

collapse a clade

**Usage**

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

**Arguments**

x	tree view
node	clade node
clade_name	set clade name. If clade_name = NULL, do nothing
...	additional parameters

**Value**

tree view

**Author(s)**

Guangchuang Yu

**See Also**

expand

---

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

---

**Description**

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

**Usage**

Date2decimal(x)

**Arguments**

x                      Date

**Value**

numeric

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

decimal2Date(x)

**Arguments**

x                      numerical number, eg 2014.34

**Value**

Date

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

expand collased clade

**Usage**

expand(tree\_view = NULL, node)

**Arguments**

tree_view	tree view
node	clade node

**Value**

tree view

**Author(s)**

Guangchuang Yu

**See Also**

collapse

---

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

**Description**

extract data used in 'facet\_plot' or 'geom\_facet'

**Usage**

facet\_data(tree\_view, panel)

**Arguments**

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



**Value**

data frame or a list of data frames

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

label facet\_plot output

**Usage**

```
facet_labeller(p, label)
```

**Arguments**

p	facet_plot output
label	labels of facet panels

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

plot tree associated data in an additional panel

**Usage**

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

**Arguments**

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

**Details**

'facet\_plot()' automatically re-arranges the input 'data' according to the tree structure, visualizes the 'data' on specific 'panel' using the 'geom' function with aesthetic 'mapping' and other parameters, and align the graph with the tree 'p' side by side.

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

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

---

facet\_widths

*facet\_widths*

---

**Description**

set relative widths (for column only) of facet plots

**Usage**

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

**Arguments**

p	ggplot or ggtree object
widths	relative widths of facet panels

**Value**

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

**Author(s)**

Guangchuang Yu

---

 flip

*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

---

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	<i>geom_balance</i>
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---

**Description**

highlights the two direct descendant clades of an internal node

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

ggplot2

**Author(s)**

Justin Silverman

**References**

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

---

geom\_cladelabel      *geom\_cladelabel*

---

### Description

annotate a clade with bar and text label

### Usage

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

### Arguments

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

### Value

ggplot layers

### Author(s)

Guangchuang Yu

---

geom\_cladelabel2      *geom\_cladelabel2*

---

### Description

annotate a clade with bar and text label

### Usage

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

### Arguments

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

### Value

ggplot layers

### Author(s)

JustGitting

---

geom_highlight	<i>geom_highlight</i>
----------------	-----------------------

---

**Description**

layer of highlight clade with rectangle

**Usage**

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

**Arguments**

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

**Value**

ggplot2

**Author(s)**

Guangchuang Yu

---

geom_highlight_encircle	<i>geom_highlight_encircle</i>
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---

**Description**

layer of highlight clade with xspline

**Usage**

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

**Arguments**

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

**Value**

ggplot2

---

geom_label2	<i>geom_label2</i>
-------------	--------------------

---

**Description**

geom\_label2 support aes(subset) via setup\_data

**Usage**

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

**Arguments**

mapping	the aesthetic mapping
data	A layer specific dataset - only needed if you want to override the plot defaults.
...	other arguments passed on to 'layer'
stat	Name of stat to modify data
position	The position adjustment to use for overlapping points on this layer
family	sans by default, can be any supported font
parse	if TRUE, the labels will be passed into expressions
nudge_x	horizontal adjustment
nudge_y	vertical adjustment
label.padding	Amount of padding around label.
label.r	Radius of rounded corners.
label.size	Size of label border, in mm
na.rm	logical
show.legend	logical
inherit.aes	logical



**Value**

label layer

**Author(s)**

Guangchuang Yu

**See Also**

[geom\\_label](#)

---

<code>geom_motif</code>	<i>geom_motif</i>
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---

**Description**

geom layer to draw aligned motif

**Usage**

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

**Arguments**

mapping	aes mapping
data	data
on	gene to center (i.e. set middle position of the 'on' gene to 0)
...	additional parameters

**Value**

geom layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add node label layer

**Usage**

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

**Arguments**

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

**Value**

geom layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add node label for circular layout

**Usage**

```
geom_nodelab2(mapping = NULL, nudge_x = 0, nudge_y = 0,
              geom = "text", hjust = 0.5, ...)
```

**Arguments**

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

**Value**

node label layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add node point

**Usage**

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

**Arguments**

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

**Value**

node point layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

geom\_point2 support aes(subset) via setup\_data

**Usage**

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

**Arguments**

mapping	aes mapping
data	data
stat	Name of stat to modify data
position	position
na.rm	logical
show.legend	logical
inherit.aes	logical
...	addktonal parameter

**Value**

point layer

**Author(s)**

Guangchuang Yu

**See Also**

[geom\\_point](#)

---

geom_range	<i>geom_range</i>
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---

**Description**

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

**Usage**

```
geom_range(range = "length_0.95_HPD", branch.length = "branch.length",
            ...)
```

**Arguments**

<code>range</code>	range, e.g. "height_0.95_HPD"
<code>branch.length</code>	corresponding <code>branch.length</code>
<code>...</code>	additional parameter, e.g. <code>color</code> , <code>size</code> , <code>alpha</code>

**Value**

ggplot layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

display root edge

**Usage**

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

**Arguments**

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

**Value**

ggplot layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add root point

**Usage**

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

**Arguments**

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

**Value**

root point layer

**Author(s)**

Guangchuang Yu

---

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

**Description**

geom\_segment2 support aes(subset) via setup\_data

**Usage**

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

**Arguments**

mapping	aes mapping
data	data
stat	Name of stat to modify data
position	position
lineend	lineend
na.rm	logical
show.legend	logical
inherit.aes	logical
nudge_x	horizontal adjustment of x
arrow	specification for arrow heads, as created by arrow().
arrow.fill	fill color to use for the arrow head (if closed). 'NULL' means use 'colour' aesthetic.
...	additional parameter

**Value**

add segment layer

**Author(s)**

Guangchuang Yu

**See Also**

[geom\\_segment](#)

---

geom\_strip

*geom\_strip*

---

**Description**

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

**Usage**

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

**Arguments**

taxa1	taxa1
taxa2	taxa2
label	optional label
offset	offset of bar and text from the clade
offset.text	offset of text from bar
align	logical
barsize	size of bar
extend	extend bar vertically
fontsize	size of text
angle	angle of text
geom	one of 'text' or 'label'
hjust	hjust
fill	fill label background, only work with geom='label'
family	sans by default, can be any supported font
parse	logical, whether parse label
...	additional parameter

**Value**

ggplot layers

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

link between taxa

**Usage**

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

**Arguments**

taxa1	taxa1, can be label or node number
taxa2	taxa2, can be label or node number
curvature	A numeric value giving the amount of curvature. Negative values produce left-hand curves, positive values produce right-hand curves, and zero produces a straight line.
arrow	specification for arrow heads, as created by arrow().
arrow.fill	fill color to use for the arrow head (if closed). 'NULL' means use 'colour' aesthetic.
...	additional parameter



**Value**

ggplot layer

**Author(s)**

Guangchuang Yu

---

geom_text2	<i>geom_text2</i>
------------	-------------------

---

**Description**

geom\_text2 support aes(subset) via setup\_data

**Usage**

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

**Arguments**

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

**Value**

text layer

**Author(s)**

Guangchuang Yu

**See Also**

[geom\\_text](#)

---

geom_tiplab	<i>geom_tiplab</i>
-------------	--------------------

---

**Description**

add tip label layer

**Usage**

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

**Arguments**

mapping	aes mapping
hjust	horizontal adjustment
align	align tip lab or not, logical
linetype	linetype for adding line if align = TRUE
linesize	line size of line if align = TRUE
geom	one of 'text', 'label', 'image' and 'phylopic'
offset	tiplab offset
...	additional parameter

**Value**

tip label layer

**Author(s)**

Guangchuang Yu

**Examples**

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

---

geom_tiplab2	<i>geom_tiplab2</i>
--------------	---------------------

---

**Description**

add tip label for circular layout

**Usage**

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

**Arguments**

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

**Value**

tip label layer

**Author(s)**

Guangchuang Yu

**References**

<https://groups.google.com/forum/#!topic/bioc-ggtree/o35PV3iH0-0>

---

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

---

**Description**

add tip point

**Usage**

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

**Arguments**

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

**Value**

tip point layer

**Author(s)**

Guangchuang Yu

---

geom\_tree

*geom\_tree*

---

**Description**

add tree layer

**Usage**

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

**Arguments**

mapping	aesthetic mapping
data	data
layout	one of 'rectangular', 'slanted', 'fan', 'circular', 'radial', 'equal_angle' or 'day-light'
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.path`*get.path*

---

**Description**

path from start node to end node

**Usage**`get.path(phylo, from, to)`**Arguments**

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

**Value**

node vectot

**Author(s)**

Guangchuang Yu

---

`getNodeAngle.df`*getNodeAngle.df*

---

**Description**

Get the angle between the two nodes specified.

**Usage**`getNodeAngle.df(df, origin_node_id, node_id)`**Arguments**

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

**Value**

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

---

`getNodesBreadthFirst.df`  
*getNodesBreadthFirst.df*

---

**Description**

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

**Usage**

`getNodesBreadthFirst.df(df)`

**Arguments**

`df`                    tree data.frame

**Value**

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

---

`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.

---

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

---

**Description**

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

**Usage**

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

**Arguments**

<code>df</code>	tree data.frame
<code>node</code>	id of starting node.

**Value**

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

---

<code>getSubtreeUnrooted</code>	<i>getSubtreeUnrooted</i>
---------------------------------	---------------------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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



---

getSubtreeUnrooted.df *getSubtreeUnrooted*

---

### Description

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

### Usage

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

### Arguments

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) Returning arc angle in [0, 2] (0 to 360) domain.

### Usage

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

### Arguments

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

### Value

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

---

`get_balance_position`    *get\_balance\_position*

---

**Description**

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

**Usage**

`get_balance_position(treeview, node, direction)`

**Arguments**

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

**Value**

data.frame

**Author(s)**

Justin Silverman

---

`get_clade_position`    *get\_clade\_position*

---

**Description**

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

**Usage**

`get_clade_position(treeview, node)`

**Arguments**

<code>treeview</code>	tree view
<code>node</code>	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	<i>visualizing phylogenetic tree and heterogenous associated data based on grammar of graphics ggtree provides functions for visualizing phylogenetic tree and its associated data in R.</i>
--------	--

---

### Description

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

drawing phylogenetic tree from phylo object

### Usage

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

### Arguments

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

### Value

tree

### Author(s)

Yu Guangchuang

### See Also

[ladderize](#)

**Examples**

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

gheatmap

*gheatmap***Description**

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

**Usage**

```
gheatmap(p, data, offset = 0, width = 1, low = "green",
  high = "red", color = "white", colnames = TRUE,
  colnames_position = "bottom", colnames_angle = 0,
  colnames_level = NULL, colnames_offset_x = 0,
  colnames_offset_y = 0, font.size = 4, hjust = 0.5)
```

**Arguments**

p	tree view
data	matrix or data.frame
offset	offset of heatmap to tree
width	total width of heatmap, compare to width of tree
low	color of lowest value
high	color of highest value
color	color of heatmap cell border
colnames	logical, add matrix colnames or not
colnames_position	one of 'bottom' or 'top'
colnames_angle	angle of column names
colnames_level	levels of colnames
colnames_offset_x	x offset for column names
colnames_offset_y	y offset for column names
font.size	font size of matrix colnames
hjust	hjust for column names (0: align left, 0.5: align center, 1: align right)

**Value**

tree view

**Author(s)**

Guangchuang Yu

gzoom

*gzoom method***Description**

gzoom method  
 gzoom method  
 zoom selected subtree

**Usage**

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

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

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

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

**Arguments**

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

**Value**

figure

gzoom.phylo

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

---

**Description**

add insets in a tree

**Usage**

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

**Arguments**

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

**Value**

tree view with insets

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

#' @title

**Usage**

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

**Arguments**

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



**Value**

tree as data.frame with equal angle layout.

**References**

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

```

““ Leafs are subtrees with no children Initialise tree using equal angle algorithm tree_df = equal_angle(tree)
nodes = get list of nodes in tree_df breadth-first nodes = remove tip nodes.
““

```

---

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

---

**Description**

'Equal-angle layout algorithm for unrooted trees'

**Usage**

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

**Arguments**

model	tree object, e.g. phylo or treedata
branch.length	set to 'none' for edge length of 1. Otherwise the phylogenetic tree edge length is used.

**Value**

tree as data.frame with equal angle layout.

**References**

"Inferring Phylogenies" by Joseph Felsenstein.

msaplot

*msaplot*

---

**Description**

multiple sequence alignment with phylogenetic tree

**Usage**

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

**Arguments**

p	tree view
fasta	fasta file, multiple sequence alignment
offset	offset of MSA to tree
width	total width of alignment, compare to width of tree
color	color
window	specific a slice to display
bg_line	whether add background line in alignment
height	height ratio of sequence

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

multiplot

*multiplot*

---

**Description**

plot multiple ggplot objects in one page

**Usage**

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

**Arguments**

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

**Value**

plot

**Author(s)**

Guangchuang Yu

---

nodebar	<i>nodebar</i>
---------	----------------

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

list of ggplot objects

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

internal node number

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

list of ggplot objects

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

open tree with specific angle

**Usage**

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

**Arguments**

treeview	tree view
angle	angle

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add phylopic layer

**Usage**

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

**Arguments**

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

**Value**

phylopic layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

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

**Arguments**

x	input list
trans	transformation function

**Value**

character vector of '[lower, upper]'

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

reverse timescse x-axis

**Usage**

```
revts(treeview)
```

**Arguments**

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

**Value**

updated treeview

**Author(s)**

guangchuang yu

---

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

---

**Description**

rotate 180 degree of a selected branch

**Usage**

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

**Arguments**

tree_view	tree view
node	selected node

**Value**

ggplot2 object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

updated tree data.frame with points rotated by angle

---

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

---

**Description**

rotate circular tree

**Usage**

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

**Arguments**

treeview	tree view
angle	angle

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

---

scaleClade	<i>scaleClade</i>
------------	-------------------

---

**Description**

scale clade

**Usage**

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

**Arguments**

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

**Value**

tree view

**Author(s)**

Guangchuang Yu



---

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

---

**Description**

scale\_color method  
 scale color by a numerical tree attribute

**Usage**

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

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

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

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

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

**Arguments**

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

**Value**

color vector

---

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

---

**Description**

scale x for tree with heatmap

**Usage**

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

**Arguments**

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

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

set_highlight_legend	<i>set_highlight_legend</i>
----------------------	-----------------------------

---

**Description**

set legend for multiple geom\_highlight layers

**Usage**

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

**Arguments**

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

**Value**

updated ggtree object

**Author(s)**

Guangchuang Yu

---

StatBalance	<i>StatBalance</i>
-------------	--------------------

---

**Description**

StatBalance

StatHighlight

GeomHighlight

---

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

---

**Description**

stat\_balance

**Usage**

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

**Arguments**

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

**Value**

layer

---

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

---

**Description**

stat\_highlight

**Usage**

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

**Arguments**

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

**Value**

layer

---

subview

*subview*

---

**Description**

add subview to mainview for ggplot2 objects

**Usage**

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

**Arguments**

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

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

inset theme

**Usage**

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

**Arguments**

... additional parameter

**Details**

theme for inset function

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

tree theme

**Usage**

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

**Arguments**

bgcolor background color  
fgcolor foreground color  
... additional parameter

**Value**

updated ggplot object with new theme

**Author(s)**

Yu Guangchuang

**Examples**

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

---

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

---

**Description**

tree2 theme

**Usage**

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

**Arguments**

bgcolor	background color
fgcolor	foreground color
...	additional parameter

**Value**

updated ggplot object with new theme

**Author(s)**

Yu Guangchuang

**Examples**

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

---

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

---

**Description**

view a clade of tree

**Usage**

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

**Arguments**

tree_view	full tree view
node	internal node number
xmax_adjust	adjust xmax

**Value**

clade plot

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

expand x axis limits for specific panel

**Usage**

xlim\_expand(xlim, panel)

**Arguments**

xlim	xlim
panel	panel

**Value**

updated tree view

**Author(s)**

guangchuang yu

`xlim_tree`*xlim\_tree*

---

**Description**

set x axis limits for Tree panel

**Usage**

```
xlim_tree(xlim)
```

**Arguments**

`xlim` `xlim`

**Value**

updated tree view

**Author(s)**

guangchuang yu

---

%&lt;+%

%<+%

---

**Description**

add annotation data to a tree

**Usage**

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

**Arguments**

`pg` `ggplot2` object  
`data` `annotation` data

**Value**

ggplot object with annotation data added

**Author(s)**

Guangchuang Yu



**Examples**

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

---

  
%+>%%+>%  

---

**Description**

update data with tree info (y coordination and panel)

**Usage**

p %+>% data

**Arguments**

p	tree view
data	data.frame

**Value**

updated data.frame

**Author(s)**

Guangchuang Yu

---

  
%<%%<%  

---

**Description**

update tree

**Usage**

pg %<% x

**Arguments**

pg	ggplot2 object
x	update by x

**Value**

updated ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

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

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