

# Package ‘ggtree’

January 19, 2018

**Type** Package

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

**Version** 1.10.2

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

**Depends** R (>= 3.3.2), ggplot2 (>= 2.2.0), treeio

**Imports** ape, grDevices, grid, magrittr, methods, rvcheck, scales, tidy, utils

**Suggests** Biostrings, colorspace, EBImage, emojiFont, knitr, prettydoc, rmarkdown, 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** 6.0.1

**NeedsCompilation** no

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---

**Description**

capture name of variable

**Usage**

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

**Arguments**

...	expression
.env	environment

**Value**

expression

**Examples**

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

---

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

---

**Description**

add colorbar legend

**Usage**

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

**Arguments**

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

**Value**

ggplot2 object

**Author(s)**

Guangchuang Yu

---

 annotation\_image      *annotation\_image*


---

**Description**

annotation taxa with images

**Usage**

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

**Arguments**

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

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

 apeBoot      *apeBoot*


---

**Description**

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

**Usage**

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

**Arguments**

phylo	phylo
boot	bootstrap values

**Value**

an instance of 'apeBootstrap'

**Author(s)**

Guangchuang Yu

---

applyLayoutDaylight    *applyLayoutDaylight*

---

**Description**

Apply the daylight 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.binary    *as.binary*

---

**Description**

as.binary method for phylo object

**Usage**

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

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

**Arguments**

tree	phylo, object
...	additional parameter

**Value**

binary tree

**Author(s)**

Guangchuang Yu <http://ygc.name>

**Examples**

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

---

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

---

**Description**

convert phylo to data.frame

**Usage**

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

**Arguments**

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

**Value**

data.frame

**Author(s)**

Yu Guangchuang

as.polytomy                      *as.polytomy*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

polytomy tree

**Author(s)**

Guangchuang

---

collapse                              *collapse*

---

**Description**

collapse a clade

**Usage**

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

**Arguments**

tree_view	tree view
node	clade node

**Value**

tree view

**Author(s)**

Guangchuang Yu

**See Also**

expand



---

Date2decimal

*Date2decimal*

---

**Description**

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

**Usage**

Date2decimal(x)

**Arguments**

x                      Date

**Value**

numeric

**Author(s)**

Guangchuang Yu

---

decimal2Date

*decimal2Date*

---

**Description**

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

**Usage**

decimal2Date(x)

**Arguments**

x                      numerical number, eg 2014.34

**Value**

Date

**Author(s)**

Guangchuang Yu

---

download.phylopic	<i>download.phylopic</i>
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---

**Description**

download phylopic

**Usage**

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

**Arguments**

id	phylopic id
size	size of phylopic
color	color
alpha	alpha

**Value**

matrix

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

expand collapsed 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**

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

<code>tree_view</code>	tree view
<code>node1</code>	node number of branch 1
<code>node2</code>	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	<i>geom_aline</i>
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---

**Description**

add horizontal align lines

**Usage**

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

**Arguments**

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

**Value**

aline layer

**Author(s)**

Yu Guangchuang

---

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

---

**Description**

highlights the two direct descendant clades of an internal node

**Usage**

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

**Arguments**

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

**Details**

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

**Value**

ggplot2

**Author(s)**

Justin Silverman

**References**

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

---

geom_cladelabel	<i>geom_cladelabel</i>
-----------------	------------------------

---

**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](#)

---

geom\_motif

*geom\_motif*

---

**Description**

geom layer to draw aligned motif

**Usage**

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

**Arguments**

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

**Value**

geom layer

**Author(s)**

guangchuang yu

---

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

---

**Description**

add node label layer

**Usage**

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

**Arguments**

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

**Value**

geom layer

**Author(s)**

guangchuang yu

---

geom_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

*geom\_point2*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

point layer

**Author(s)**

Guangchuang Yu

**See Also**

[geom\\_point](#)

---

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

---

**Description**

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

**Usage**

```
geom_range(range = "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	<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
...	addkktional parameter

**Value**

root point layer

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

**Usage**

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

**Arguments**

mapping	aes mapping
data	data
stat	Name of stat to modify data
position	position
arrow	arrow
lineend	lineend
na.rm	logical
show.legend	logical
inherit.aes	logical
nudge_x	horizontal adjustment of x
...	additional parameter

**Value**

add segment layer

**Author(s)**

Guangchuang Yu

**See Also**[geom\\_segment](#)

---

geom_strip	<i>geom_strip</i>
------------	-------------------

---

### 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, 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	<i>geom_taxalink</i>
---------------	----------------------

---

**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	<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

*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/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	<i>geom_tree</i>
-----------	------------------

---

**Description**

add tree layer

**Usage**

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

**Arguments**

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

**Value**

tree layer

**Author(s)**

Yu Guangchuang

---

geom\_tree2

*geom\_tree2*

---

**Description**

add tree layer

**Usage**

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

**Arguments**

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

**Value**

tree layer

**Author(s)**

Yu Guangchuang

---

geom\_treescale

*geom\_treescale*

---

**Description**

add tree scale

**Usage**

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

**Arguments**

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

**Value**

ggplot layers

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

extract offspring tips

**Usage**

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

**Arguments**

tr	tree
node	node

**Value**

tip label

**Author(s)**

ygc

get.path                      *get.path*

---

**Description**

path from start node to end node

**Usage**

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

**Arguments**

phylo	phylo object
from	start node
to	end node

**Value**

node vectot

**Author(s)**

Guangchuang Yu

---

get.phylopic                      *get.phylopic*

---

**Description**

download phylopic and convert to grob object

**Usage**

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

**Arguments**

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

**Value**

grob object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

Get list of child node id numbers of parent node

**Usage**

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

**Arguments**

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

**Value**

list of child node ids of parent

---

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

---

**Description**

Get the angle between the two nodes specified.

**Usage**

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

**Arguments**

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

**Value**

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

---

getNodeBreadthFirst.df  
*getNodeBreadthFirst.df*

---

**Description**

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

**Usage**

getNodeBreadthFirst.df(df)

**Arguments**

df                    tree data.frame

**Value**

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

---

getParent.df            *getParent.df*

---

**Description**

Get parent node id of child node.

**Usage**

getParent.df(df, node)

**Arguments**

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

**Value**

integer node id of parent



---

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

---

**Description**

Get all children of node from tree, including start\_node.

**Usage**

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

**Arguments**

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

**Value**

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

---

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

---

**Description**

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

**Usage**

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

**Arguments**

df	tree data.frame
node	id of starting node.

**Value**

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

---

`getSubtreeUnrooted`     *getSubtreeUnrooted*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

`getSubtreeUnrooted.df`     *getSubtreeUnrooted*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

getTreeArcAngles      *getTreeArcAngles*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

---

get\_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	<i>get_taxa_name</i>
---------------	----------------------

---

**Description**

get taxa name of a selected node (or tree if node=NULL) sorted by their position in plotting

**Usage**

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

**Arguments**

tree_view	tree view
node	node

**Value**

taxa name vector

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

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

drawing phylogenetic tree from phylo object

**Usage**

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

**Arguments**

tr	phylo object
mapping	aes mapping
layout	one of 'rectangular', 'slanted', 'fan', 'circular', 'radial', 'equal_angle' or '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
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 right)

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

groupClade	<i>groupClade method</i>
------------	--------------------------

---

**Description**

groupClade method for ggtree object

**Usage**

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

**Arguments**

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

---

groupOTU	<i>groupOTU method</i>
----------	------------------------

---

**Description**

groupOTU method for ggtree object

**Usage**

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

**Arguments**

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

---

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

---

**Description**

zoom selected subtree

**Usage**

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

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

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

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

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

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



```

    0.7))

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

```

**Arguments**

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

**Value**

figure

---

gzoom.phylo	<i>gzoom</i>
-------------	--------------

---

**Description**

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

**Usage**

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

**Arguments**

phy	phylo object
focus	selected tips
subtree	logical
widths	widths

**Value**

a list of ggplot object

**Author(s)**

ygc

**Examples**

```

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

```

---

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

---

**Description**

identify node by interactive click

**Usage**

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

**Arguments**

x	tree view
...	additional parameters

**Value**

node id

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

add insets in a tree

**Usage**

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

**Arguments**

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

**Value**

tree view with insets

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

#' @title

**Usage**

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

**Arguments**

tree            phylo object

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

**Value**

tree as data.frame with equal angle layout.

**References**

The following 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(tree, branch.length)
```

**Arguments**

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

**Value**

tree as data.frame with equal angle layout.

**References**

"Inferring Phylogenies" by Joseph Felsenstein.

---

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

---

**Description**

Find Most Recent Common Ancestor among a vector of tips

**Usage**

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

**Arguments**

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

**Value**

MRCA of two or more tips

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

multiple sequence alignment with phylogenetic tree

**Usage**

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

**Arguments**

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

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

plot multiple ggplot objects in one page

**Usage**

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

**Arguments**

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

**Value**

plot

**Author(s)**

Guangchuang Yu

---

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	<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

---

print.beastList	<i>print</i>
-----------------	--------------

---

**Description**

print information of a list of beast trees

**Usage**

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

**Arguments**

x	a list of beast object
...	no used

**Value**

message

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

reroot a tree

**Usage**

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

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

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

**Arguments**

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

**Value**

tree object

---

rescale_tree	<i>rescale_tree</i>
--------------	---------------------

---

**Description**

rescale branch length of tree object

**Usage**

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

**Arguments**

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

**Value**

update tree object

**Author(s)**

Guangchuang Yu

revts

*revts*

**Description**

reverse timescle x-axis

**Usage**

revts(treeview)

**Arguments**

treeview          treeview

**Value**

updated treeview

**Author(s)**

guangchuang yu

rm.singleton.newick

*rm.singleton.newick*

**Description**

remove singleton

**Usage**

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

**Arguments**

nwk                  newick file  
outfile              output newick file

**Value**

tree text

**Author(s)**

Guangchuang Yu <http://ygc.name>

---

rotate	<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 by a numerical tree attribute

**Usage**

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

```
## S4 method for signature 'beast'
```

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

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

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

```
## S4 method for signature 'paml_rst'
```

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

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

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

**Arguments**

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

**Value**

color vector

---

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

---

**Description**

scale x for tree with heatmap

**Usage**

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

**Arguments**

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

**Value**

tree view

**Author(s)**

Guangchuang Yu

---

set\_highlight\_legend      *set\_highlight\_legend*

---

**Description**

set legend for multiple geom\_highlight layers

**Usage**

```
set_highlight_legend(p, color, label)
```

**Arguments**

p	ggtree object
color	color vector
label	label vector

**Value**

updated ggtree object

**Author(s)**

guangchuang yu

---

StatBalance      *StatBalance*

---

**Description**

StatBalance  
StatHighlight  
GeomHighlight

---

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

---

**Description**

stat\_balance

**Usage**

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

**Arguments**

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

**Value**

layer

---

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

---

**Description**

stat\_highlight

**Usage**

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



**Arguments**

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

**Value**

layer

---

subview

*subview*

---

**Description**

add subview to mainview for ggplot2 objects

**Usage**

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

**Arguments**

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

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

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

---

**Description**

inset theme

**Usage**

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

**Arguments**

... additional parameter

**Details**

theme for inset function

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

---

theme_transparent	<i>theme_transparent</i>
-------------------	--------------------------

---

**Description**

transparent background theme

**Usage**

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

**Arguments**

... additional parameter to tweak the theme

**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

*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

---

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

---

**Description**

expand x axis limits for specific panel

**Usage**

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

**Arguments**

<code>xlim</code>	<code>xlim</code>
<code>panel</code>	<code>panel</code>

**Value**

updated tree view

**Author(s)**

guangchuang yu

---

<code>xlim_tree</code>	<i>xlim_tree</i>
------------------------	------------------

---

**Description**

set x axis limits for Tree panel

**Usage**

```
xlim_tree(xlim)
```

**Arguments**

<code>xlim</code>	<code>xlim</code>
-------------------	-------------------

**Value**

updated tree view

**Author(s)**

guangchuang yu

---

`%<+%``%<+% %`

---

**Description**

add annotation data to a tree

**Usage**

`pg %<+% data`

**Arguments**

<code>pg</code>	ggplot2 object
<code>data</code>	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**

<code>p</code>	tree view
<code>data</code>	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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