Package ‘ggtree’

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Type Package

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

Version 1.6.4

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

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

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

Suggests Biostrings, colorspace, EBImage, emoji, font, knitr, rmarkdown, scales, testthat

VignetteBuilder knitr

ByteCompile true

License Artistic-2.0

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

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

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

RoxygenNote 5.0.1

NeedsCompilation no

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Description

capture name of variable

Usage

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

Arguments

* ...  expression
  * .env  environment

Value

expression

Examples

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

Description
add colorbar legend

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

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

Value
ggplot2 object

Author(s)
Guangchuang Yu

annotation_image

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

---

**Description**

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

**Usage**

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

**Arguments**

- `phylo` (phylo)
- `boot` (bootstrap values)

**Value**

an instance of `apeBootstrap`

**Author(s)**

Guangchuang Yu

---

**Description**

Class "apeBootstrap" This class stores ape bootstrapping analysis result

**Slots**

- `phylo` (phylo object of treetext)
- `fields` (available features)
- `bootstrap` (bootstrap value)
- `extraInfo` (extra information)

**Author(s)**

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)
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

Description
convert phylo to data.frame

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

Examples
require(ape)
tr <- read.tree(text="((A, B, C), D);")
is.data.frame.tr(tr)
tr2 <- as.data.frame(tr)
is.data.frame(tr2)
as.polytomy

Arguments

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

Value
data.frame

Author(s)
Yu Guangchuang

data.frame

as.polytomy

Description

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

Usage

as.polytomy(tree, feature, fun)

Arguments

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

Value

polytomy tree

Author(s)
Guangchuang
beast-class

Class "beast" This class stores information of beast output

Description

Class "beast" This class stores information of beast output

Slots

fields beast statistic variables
treetext tree text in beast file
phylo tree phylo object
translation tip number to name translation in beast file
stats beast statistics
file beast file, nexus formatextraInfo extra information

Author(s)

Guangchuang Yu http://guangchuangyu.github.io

See Also

show get.fields ggtree

codeml-class

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

Description

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

Slots

mlc A code_mlc object
rst A paml_rst objectextraInfo extra information

See Also

codeml_mlc paml_rst
### Description

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

### Slots

- **fields available features**
- **treetext** tree text
- **phylo** phylo object
- **dNdS** dN dS information
- **mlcfile** mlc file
- **extraInfo** extra information

### Author(s)

Guangchuang Yu

### See Also

- paml_rst codeml

---

### 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
Date2decimal

See Also
expand

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

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

Usage
decimal2Date(x)

Arguments
  x  numerical number, eg 2014.34

Value
Date

Author(s)
Guangchuang Yu
download.phylopic

download.phylopic

Description
download phylopic

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

Arguments
id phylopic id
size size of phylopic
color color
alpha alpha

Value
matrix

Author(s)
Guangchuang Yu

expand

expand

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

Description

plot tree associated data in an additional panel

Usage

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

Arguments

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

Value

ggplot object

Author(s)

Guangchuang Yu

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

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

modelphylo 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

**Description**

add horizontal align lines

**Usage**

```r
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

**Description**

highlights the two direct descendant clades of an internal node

**Usage**

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

**Arguments**

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

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

Value

ggplot2

Author(s)

Justin Silverman

References


---

**geom_cladelabel**

### Description

annotate a clade with bar and text label

### Usage

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

### Arguments

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

Value

ggplot layers

Author(s)

Guangchuang Yu

Description

layer of hilight clade with rectangle

Usage

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

Arguments

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

Value

ggplot2

Author(s)

Guangchuang Yu

---

**geom_label2**

Description

`geom_text2` support aes(subset) via setup_data

Usage

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

- **mapping**: the aesthetic mapping
- **data**: A layer specific dataset - only needed if you want to override the plot defaults.
- **...**: other arguments passed on to 'layer'
- **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**

Description

add node point

Usage

```r
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
- **...**: additional parameter
Value

point layer

Author(s)

Guangchuang Yu

Description

geom_point2 support aes(subset) via setup_data

Usage

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

Arguments

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

Value

point layer

Author(s)

Guangchuang Yu

See Also

geom_point
**geom_range**

Description

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

Usage

```r
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**

Description

Add root point.

Usage

```r
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
- `...`: additional parameter

Value

Root point layer
Author(s)

Guangchuang Yu

Description

`geom_segment2` support `aes(subset)` via `setup_data`

Usage

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

Arguments

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

Value

add segment layer

Author(s)

Guangchuang Yu

See Also

`geom_segment`
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, barexextend = 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
barexextend   extend bar vertically
fontsize       size of text
angle         angle of text
gem           one of 'text' or 'label'
hjust         hjust
fill           fill label background, only work with geom='label'
familly       sans by default, can be any supported font
parse         logical, whether parse label
...            additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu
**Description**

link between taxa

**Usage**

```r
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

---

**Description**

`geom_text2` support aes(subset) via setup_data

**Usage**

```r
geom_text2(mapping = NULL, data = NULL, position = "identity", parse = FALSE, na.rm = TRUE, show.legend = NA, inherit.aes = TRUE, ..., nudge_x = 0, nudge_y = 0, check_overlap = FALSE)
```
Arguments
  mapping  the aesthetic mapping
  data     A layer specific dataset - only needed if you want to override he plot defaults.
  position The position adjustment to use for overlapping points on this layer
  parse    if TRUE, the labels will be passed into expressions
  na.rm    logical
  show.legend logical
  inherit.aes logical
  ...      other arguments passed on to 'layer'
  nudge_x  horizontal adjustment
  nudge_y  vertical adjustment
  check_overlap if TRUE, text that overlaps previous text in the same layer will not be plotted

Value
text layer

Author(s)
Guangchuang Yu

See Also
  geom_text

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
**geom_tiplab2**

**Value**

- tip label layer

**Author(s)**

- Yu Guangchuang

**Examples**

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

**Description**

- add tip label for circular layout

**Usage**

```r
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/o3SPV3iHO-0](https://groups.google.com/forum/#!topic/bioc-ggtree/o3SPV3iHO-0)
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
- ...: additional parameter

Value

tip point layer

Author(s)

Guangchuang Yu

Description

add tree layer

Usage

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

Arguments

- mapping: aesthetic mapping
- data: data
- layout: one of 'rectangular', 'slanted', 'circular', 'radial' or 'unrooted'
- multiPhylo: logical
- ...: additional parameter
**geom_tree2**

**Value**

tree layer

**Author(s)**

Yu Guangchuang

---

**geom_tree2**

**Description**

add tree layer

**Usage**

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

**Arguments**

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

---

**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")

**Author(s)**

Yu Guangchuang

---

**geom_treescale**
get.fields

Arguments

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

Value

ggplot layers

Author(s)

Guangchuang Yu

get.fields get.fields method

Description

get.fields method

Usage

get.fields(object, ...)

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

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

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

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

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

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

## S4 method for signature 'hyphy'
g.get.fields(object, ...)
get.offspring.tip

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

**Arguments**

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

**Value**

available annotation variables

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

**Examples**

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

**Description**

extract offspring tips

**Usage**

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

**Arguments**

- **tr**
  - tree
- **node**
  - node

**Value**

- tip label

**Author(s)**

ygc
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 vector

**Author(s)**

Guangchuang Yu

---

get.phylopic

**Description**

download phylopic and convert to grob object

**Usage**

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

**Arguments**

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

**Value**

grob object

**Author(s)**

Guangchuang Yu
get.placements

Description
get.placement method

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

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

Value
data.frame

Author(s)
Guangchuang Yu http://ygc.name

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

get.subs

Description
get substitution information

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

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

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

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

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

### Arguments

- **object**: paml_rst object
- **type**: one of 'marginal_subs', 'marginal_AA_subs', 'joint_subs' or 'joint_AA_subs'.
- **...**: additional parameter

### Value

data.frame

### Examples

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

---

get.tipseq

### get.tipseq method

### Description

get tipseq

### Usage

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

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

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

### Arguments

- **object**: one of paml_rst or codeml object
- **...**: additional parameter

### Value

character
get.tree

Description
get.tree method

Usage
get.tree(object, ...)

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

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

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

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

get.tree(object, ...)

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

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

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

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

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

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

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

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

Arguments

object one of phylo, jplace, nhx, phangorn, beast, hyphy, codeml, codeml_mlc, paml_rst object

... additional parameter

by one of rst or mlc

Value

phylo object

Author(s)

Guangchuang Yu  http://guangchuangyu.github.io

Examples

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

get.treeinfo get.treeinfo method

Description

get.treeinfo method

Usage

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

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

Arguments

object jplace object

layout layout

ladderize ladderize, logical

right logical, parameter for ladderize

... additional parameter

Value

data.frame

Author(s)

Guangchuang Yu  http://ygc.name
`get.treetext` function

**Examples**

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

---

**get.treetext method**

**Description**

get.treetext method

**Usage**

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

**Arguments**

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

**Value**

phylo object

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

**Examples**

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

---

**getNodeNum**

**Description**

calculate total number of nodes

**Usage**

```r
getNodeNum(tr)
```

**Arguments**

- `tr`: phylo object
**getRoot**

**Description**
get the root number

**Usage**
```r
getRoot(tr)
```

**Arguments**
- `tr`: phylo object

**Value**
root number

**Author(s)**
Guangchuang Yu

---

**get_balance_position**

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

**Usage**
```r
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)**
Guangchuang Yu
**get_clade_position**

**Author(s)**
Justin Silverman

**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**

**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

Description
get taxa name of a selected node

Usage
get_taxa_name(tree_view = NULL, node)

Arguments
  tree_view  tree view
  node       node

Value
taxa name vector

Author(s)
Guangchuang Yu

ggtree

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

drawing phylogenetic tree from phylo object

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

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

**Value**

tree

**Author(s)**

Yu Guangchuang

**Examples**

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

---

**gheatmap**

**Description**

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

**Usage**

```r
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 method

description

Description

- group selected clade

Usage

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

### Arguments

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

### Value

- group index
Description

group tree based on selected OTU, will traceback to MRCA

Usage

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

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

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

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

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

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

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

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

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

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

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

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

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

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

## S4 method for signature 'phylo'
groupOTU.phylo

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

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

**Arguments**

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

**Value**

group index

---

**Description**

group OTU

**Usage**

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

**Arguments**

- **phy**: tree object
- **focus**: tip list
- **group_name**: name of the group

**Value**

phylo object

**Author(s)**

ygc
Description

zoom selected subtree

Usage

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

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

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

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

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

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

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

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

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

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

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

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

### Arguments

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

### Value

- **figure**

### Description

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

### Usage

```r
@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

```r
require(ape)
data(chiroptera)
gzoom(chiroptera, grep("Plecotus", chiroptera$tip.label))
```
Class "hyphy" This class stores information of HYPHY output

## Slots

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

### Author(s)

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

### See Also

- [paml_rst](http://guangchuangyu.github.io)

---

**identify.gg**

**identify**

## Description

identify node by interactive click

## Usage

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

## Arguments

- **x**: tree view
- **...**: additional parameters
inset

**Value**

node id

**Author(s)**

Guangchuang Yu

---

**Description**

add insets in a tree

**Usage**

```r
inset(tree_view, insets, width = 0.1, height = 0.1, hjust = 0,

vjust = 0, x = "node")
```

**Arguments**

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

**Value**

tree view with insets

**Author(s)**

Guangchuang Yu
jplace-class

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

Description

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

Slots

fields  colnames of first variable of placements

treetext  tree text

phylo  tree phylo object

placements  placement information

version  version

metadata  metadata

file  jplace file

extraInfo  extra information

Author(s)

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

See Also

show get.tree ggtree

mask

Description

site mask

Usage

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

Arguments

tree_object  tree object

field  selected field

site  site

mask_site  if TRUE, site will be masked. if FALSE, selected site will not be masked, while other sites will be masked.

Value

updated tree object
Author(s)

Guangchuang Yu

merge_tree

Description

merge two tree object

Usage

merge_tree(obj1, obj2)

Arguments

obj1           tree object 1
obj2           tree object 2

Value

tree object

Author(s)

Guangchuang Yu

MRCA

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
Description
multiple sequence alignment with phylogenetic tree

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

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

Value
tree view

Author(s)
Guangchuang Yu

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

---

**njx-class**

*Class "njx" This class stores njx tree*

**Description**
Class "njx" This class stores njx tree

**Slots**
- file: input file
- fields: available feature
- phylo: phylo object
- nhx_tags: tag information in njx file
- extraInfo: extra information

**Author(s)**
Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

**NJ**

*NJ*

**Description**
neighbor-joining method

**Usage**
NJ(X)

**Arguments**
- X: distance matrix

**Value**
phylo object

**Author(s)**
ygc
Examples

```r
## 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)
```

Description

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

Usage

```r
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

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

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**

**Description**

open tree with specific angle

**Usage**

open_tree(treeview, angle)

**Arguments**

- **treeview**: tree view
- **angle**: angle

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

---

**paml_rst-class**

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

**Description**

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

**Slots**

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

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

See Also

codeml codeml_mlc

---

### phangorn-class

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

#### Description

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

#### Slots

- fields available attributes
- phylo phylo object
- seq_type one of "NT" and "AA"
- tip_seq sequences of tips
- ancseq ancestral sequences
- subs sequence substitution
- AA_subs Amino acid sequence substitution
- extraInfo extra information

Author(s)

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

See Also

paml_rst

---

### phylip-class

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

#### Description

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

#### Slots

- file input file
- fields available feature
- phylo phylo or multiPhylo
- ntree number of trees
- sequence sequences
- extraInfo extra information
Author(s)

Guangchuang Yu

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tree_view</td>
<td>tree view</td>
</tr>
<tr>
<td>phylopic_id</td>
<td>phylopic id</td>
</tr>
<tr>
<td>size</td>
<td>size of phylopic to download</td>
</tr>
<tr>
<td>color</td>
<td>color</td>
</tr>
<tr>
<td>alpha</td>
<td>alpha</td>
</tr>
<tr>
<td>node</td>
<td>selected node</td>
</tr>
<tr>
<td>x</td>
<td>x position</td>
</tr>
<tr>
<td>y</td>
<td>y position</td>
</tr>
<tr>
<td>width</td>
<td>width of phylopic</td>
</tr>
</tbody>
</table>

Value

phylopic layer

Author(s)

Guangchuang Yu
Description

tree annotation of sequence substitution by comparing to parent node

Usage

phyPML(pmlTree, type = "ml")

Arguments

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

Value

phangorn object

Author(s)

Yu Guangchuang

plot

plot method

Description

plot method generics

Usage

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

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

## S4 method for signature 'r8s,ANY'
plot(x, layout = "rectangular", branch.length = "TREE",...
show.tip.label = TRUE, tip.label.size = 4, tip.label.hjust = 0, ...)

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

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

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

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

Arguments

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

Value

plot
### Examples

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

### Description

convert pml object to XStringSet object

### Usage

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

### Arguments

- `pml`: pml object
- `includeAncestor`: logical

### Value

XStringSet

### Author(s)

ygc

### Description

print information of a list of beast trees

### Usage

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

### Arguments

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

### Value

message
**r8s-class**

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

**Description**

Class "r8s" This class stores output info from r8s

**Slots**

- file: input file
- fields: available feature
- treetext: tree text
- phylo: multiPhylo, time tree, rate tree and absolute substitution tree
- extraInfo: extra information

**Author(s)**

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)

---

**raxml-class**

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

**Description**

Class "raxml" This class stores RAxML bootstrapping analysis result

**Slots**

- file: input file
- fields: available features
- treetext: tree text
- phylo: phylo object of treetext
- bootstrap: bootstrap value
- extraInfo: extra information

**Author(s)**

Guangchuang Yu [http://guangchuangyu.github.io](http://guangchuangyu.github.io)
**Description**

convert raxml bootstrap tree to newick format

**Usage**

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

**Arguments**

- `infile`: input file
- `outfile`: output file

**Value**

newick file

**Author(s)**

Guangchuang Yu

---

**Description**

read rst and mlb file from baseml output

**Usage**

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

**Arguments**

- `rstfile`: rst file
- `mlbfile`: mlb file

**Value**

A `paml_rst` object

**Author(s)**

Guangchuang Yu [http://ygc.name](http://ygc.name)

**Examples**

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

**Description**
read beast output

**Usage**
read.beast(file)

**Arguments**
- file: beast file

**Value**
beast object

**Author(s)**
Guangchuang Yu [http://ygc.name](http://ygc.name)

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

---

read.codeml

**Description**
read baseml output

**Usage**
read.codeml(rstfile, mlcfile)

**Arguments**
- rstfile: rst file
- mlcfile: mlc file

**Value**
A codeml object

**Author(s)**
ygc
Examples

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

Description

read mlc file of codeml output

Usage

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

Arguments

- `mlcfile` : mlc file

Value

A codeml_mlc object

Author(s)

ygc

Examples

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

Description

read HYPHY output

Usage

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

Arguments

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

A hyphy object

Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

Examples

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

read.jplace(file)

Arguments

file jplace file

Value

jplace instance

Author(s)

ygc

Examples

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

**Description**
read nhx tree file

**Usage**
```
read.nhx(file)
```

**Arguments**
- `file` nhx file

**Value**
nhx object

**Author(s)**
Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**read.paml_rst**

**Description**
read rst file from paml output

**Usage**
```
read.paml_rst(rstfile)
```

**Arguments**
- `rstfile` rst file

**Value**
A paml_rst object

**Author(s)**
Guangchuang Yu [http://ygc.name](http://ygc.name)

**Examples**
```r
rstfile <- system.file("extdata/PAML_BaseMl", "rst", package="ggtree")
read.paml_rst(rstfile)
```
**read.phyloT**

Description

parse output from phyloT

Usage

```r
read.phyloT(file, ...)  # Additional parameters to read.tree
```

Arguments

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

Value

phylo object

Author(s)

Guangchuang Yu

References

[http://phylot.biobyte.de/](http://phylot.biobyte.de/)
read.r8s

**Description**
parse output from r8s

**Usage**
```r
read.r8s(file)
```

**Arguments**
- **file**: r8s output log file

**Value**
r8s instance

**Author(s)**
Guangchuang Yu

---

read.raxml

**Description**
parse RAxML bootstrapping analysis output

**Usage**
```r
read.raxml(file)
```

**Arguments**
- **file**: RAxML bootstrapping analysis output

**Value**
raxml object

**Author(s)**
Guangchuang Yu
rerooot

Description
rerooot a tree

Usage
rerooot(object, node, ...)

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

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

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

Arguments

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

Value
tree object

rescale_tree

Description
rescale branch length of tree object

Usage
rescale_tree(tree_object, branch.length)

Arguments

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

Value
update tree object
**Description**
remove singleton

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

**Arguments**
- `nwk` newick file
- `outfile` output newick file

**Value**
tree text

**Author(s)**
Guangchuang Yu [http://ygc.name](http://ygc.name)

---

**Description**
rotate 180 degree of a selected branch

**Usage**
```r
rotate(tree_view = NULL, node)
```

**Arguments**
- `tree_view` tree view
- `node` selected node

**Value**
ggplot2 object

**Author(s)**
Guangchuang Yu
### rotate_tree

**Description**

rotate circular tree

**Usage**

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

**Arguments**

- `treeview`: tree view
- `angle`: angle

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

---

### rtree

**Description**

generate random tree

**Usage**

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

**Arguments**

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

**Source**

This is just the imported function from the ape package. The documentation you should read for the rtree function can be found here: [rtree](#)
scaleClade

Description
scale clade

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

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

Value
tree view

Author(s)
Guangchuang Yu

scale_color

Description
scale color by a numerical tree attribute

Usage
scale_color(object, by, ...)

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

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

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

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

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

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

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

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

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

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

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

### Arguments

- **object**:
  - supported objects, including phylo, paml_rst, codeml_mlc, codeml, jplace, beast, hyphy

- **by**:
  - one of numerical attributes

- **...**:
  - additional parameter

- **tree**:
  - which tree selected

### Value

color vector

---

`scale_x_ggtree` | `scale_x_ggtree`

### Description

scale x for tree with heatmap

### Usage

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

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

Value

- `tree_view`

Author(s)

Guangchuang Yu

Description

Show method for `jplace` instance

Usage

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

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

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

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

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

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

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

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

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

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

### Arguments

object 

one of jplace, beast, object

### Value

print info

### Author(s)

Guangchuang Yu [http://ygc.name](http://ygc.name)

### Examples

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

---

### Description

StatBalance

StatHilight

---

### Usage

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

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

**Description**

stat_hilight

**Usage**

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

**Arguments**

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

**Description**

Inset theme.

**Usage**

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

**Arguments**

- `...`: additional parameter

**Details**

Theme for inset function.
theme_transparent

Value

ggplot object

Author(s)

Guangchuang Yu

Description

transparent background theme

Usage

theme_transparent(...)

Arguments

... additional parameter to tweak the theme

Value

ggplot object

Author(s)

Guangchuang Yu

theme_tree

Description

tree theme

Usage

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

Arguments

bgcolor background color
fgcolor foreground color
... additional parameter

Value

updated ggplot object with new theme
Author(s)

Yu Guangchuang

Examples

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

Description

tree2 theme

Usage

```r
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

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

**Description**

view a clade of tree

**Usage**

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

**Arguments**

- tree_view: full tree view
- node: internal node number
- xmax_adjust: adjust xmax

**Value**

clade plot

**Author(s)**

Guangchuang Yu

---

**write.jplace**

**Description**

generate jplace file

**Usage**

write.jplace(nwk, data, outfile)

**Arguments**

- nwk: tree in newick format
- data: annotation data
- outfile: jplace output file

**Value**

jplace file

**Author(s)**

ygc
Examples

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

Description

add annotation data to a tree

Usage

pg %<+% data

Arguments

pg ggpplot2 object
data annotation data

Value

ggpplot 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
\texttt{p \%+\% data}

Arguments
\begin{itemize}
  \item \texttt{p} \hspace{1cm} tree view
  \item \texttt{data} \hspace{1cm} data.frame
\end{itemize}

Value
updated data.frame

Author(s)
Guangchuang Yu

Description
pipe

Usage
\texttt{lhs \%\% rhs}

Arguments
\begin{itemize}
  \item \texttt{lhs} \hspace{1cm} left hand side
  \item \texttt{rhs} \hspace{1cm} right hand side
\end{itemize}

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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