Package ‘ggtree’

Type Package
Title an R package for visualization of tree and annotation data
Version 3.10.1
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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 and other tree-like structures with their annotation data.
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(>= 0.4.5), treeio (>= 1.8.0), utils, scales, stats, cli
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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 and other tree-like structures with their annotation data.

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**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

**See Also**

Useful links:

- [https://www.amazon.com/Integration-Manipulation-Visualization-Phylogenetic-Computational-ebook/dp/B0B5NLZR1Z](https://www.amazon.com/Integration-Manipulation-Visualization-Phylogenetic-Computational-ebook/dp/B0B5NLZR1Z) (book)
- Report bugs at [https://github.com/YuLab-SMU/ggtree/issues](https://github.com/YuLab-SMU/ggtree/issues)
applyLayoutDaylight

Description

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

Usage

applyLayoutDaylight(df, node_id)

Arguments

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

Value

list with tree data.frame with updated layout using daylight algorithm and max_change angle.

as.polytomy

Description

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

Usage

as.polytomy(tree, feature, fun)

Arguments

tree: tree object, 'phylo' object only
feature: selected feature
fun: function to select nodes to collapse

Value

polytomy tree

Author(s)

Guangchuang Yu
Description

collapse a selected clade, which can later be expanded with the `expand()` function if necessary

Usage

## S3 method for class 'ggtree'
collapse(x = NULL, node, mode = "none", clade_name = NULL, ...)

Arguments

- **x**: tree view (i.e. the ggtree object). If `tree_view` is NULL, the last ggplot will be used.
- **node**: internal node number
- **mode**: one of 'none' (default), 'max', 'min' and 'mixed'. 'none' would simply collapse the clade as 'tip' and the rest will display a triangle, whose shape is determined by the farthest/closest tip of the collapsed clade to indicate it
- **clade_name**: set a name for the collapsed clade. If `clade_name` = NULL, do nothing
- **...**: additional parameters to set the color or transparency of the triangle

Value

tree view

Author(s)

Guangchuang Yu

See Also

expand

Examples

```r
x <- rtree(15)
p <- ggtree(x) + geom_tiplab()
p
p1 <- collapse(p, node = 17, mode = "mixed",
               clade_name = "cclade", alpha = 0.8,
               color = "grey", fill = "light blue")
```
**Date2decimal**

**Description**

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

**Usage**

Date2decimal(x)

**Arguments**

x  

**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  

**Value**

Date

**Author(s)**

Guangchuang Yu
**Description**

expand collapsed clade

**Usage**

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

**Arguments**

- `tree_view` : tree view (i.e. the ggtree object). If `tree_view` is NULL, the last ggplot object will be used.
- `node` : internal node number to specify a clade. If NULL, using the whole tree

**Value**

- `tree_view`

**Author(s)**

Guangchuang Yu

**See Also**

collapse

**Examples**

```r
x <- rtree(15)
p <- ggtree(x) + geom_tiplab()
p1 <- collapse(p, 17)
expand(p1, 17)
```

---

**Description**

extract data used in `facet_plot` or `geom_facet`

**Usage**

```r
facet_data(tree_view, panel)
```
Arguments

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

Value
data frame or a list of data frames

Author(s)
Guangchuang Yu

References

Description
function to relabel selected panels created by `geomfacet` or `facet_plot`

Usage
facet_labeller(p, label)

Arguments
p facet_plot output
label new labels of facet panels

Value
ggplot object

Author(s)
Guangchuang Yu
Description

plot tree associated data in an additional panel

Usage

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

gem_facet(mapping = NULL, data, geom, panel, ...)

Arguments

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

Details

'facet_plot()' automatically re-arranges the input 'data' according to the tree structure, visualizes the 'data' on specific 'panel' using the 'geom' function with aesthetic 'mapping' and other parameters, and align the graph with the tree 'p' side by side. 'geom_facet' is a 'ggplot2' layer version of 'facet_plot'

Value

ggplot object

Author(s)

Guangchuang Yu

References

Examples

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

---

**facet_widths**

Description

set relative widths (for column only) of facet plots

Usage

`facet_widths(p, widths)`

Arguments

- `p`: ggplot or ggtree object
- `widths`: relative widths of facet panels

Value

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

Author(s)

Guangchuang Yu

---

**flip**

Description

exchange the position of 2 clades

Usage

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

Arguments

- `tree_view`: tree view (i.e. the ggtree object). If `tree_view` is NULL, the last ggplot will be used.
- `node1`: node number of clade 1. It should share a same parent node with `node2`
- `node2`: node number of clade 2. It should share a same parent node with `node1`
**geom_aline**

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```r
set.seed(123)
x <- rtree(15)
p <- ggtree(x) + geom_tiplab() +
  geom_nodelab(aes(subset=!isTip, label=node), hjust = -.1, color = "red")
flip(p, 23, 24)  ## Depends on the condition of your tree
```

---

**Description**

add horizontal align lines layer to a tree

**Usage**

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

**Arguments**

- `mapping` : aes mapping
- `linetype` : set line type of the line, defaults to "dotted"
- `linewidth` : set width of the line, defaults to 1
- `...` : additional parameter

**Details**

'geom_aline' align all tips to the longest one by adding padding characters to the right side of the tip.

**Value**

aline layer

**Author(s)**

Yu Guangchuang
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 its two direct descendant
- **fill**: color to fill in the highlight rectangle, default to "steelblue"
- **color**: color to outline highlight rectangle and divide balance, defaults to "white"
- **alpha**: alpha (transparency) for the highlight rectangle, defaults to 0.5
- **extend**: extend xmax of the highlight rectangle by the value of extend
- **extendto**: extend xmax of the highlight rectangle to the value of 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 and modified by Guangchuang Yu

References


Examples

```r
library(ggtree)
set.seed(123)
tr <- rtree(15)
x <- ggtree(tr)
x + geom_balance(17)
```

Description

annotate a clade with bar and text label or (image)

Usage

```r
geom_cladelab(
  node = NULL,
  label = NULL,
  data = NULL,
  mapping = NULL,
  geom = "text",
  parse = FALSE,
  ...)
```

Arguments

- `node` selected node to annotate, when data and mapping is NULL, it is required.
- `label` character, character to be showed, when data and mapping is NULL, it is required.
- `data` data.frame, the data to be displayed in the annotation, defaults to NULL.
- `mapping` Set of aesthetic mappings, defaults to NULL. The detail see the following explanation.
- `geom` character, one of 'text', 'label', 'shadowtext', 'image' and 'phylopic', defaults to 'text', and the parameter see the Aesthetics For Specified Geom.
- `parse` logical, whether parse label to emoji font, defaults to FALSE.
- `...` additional parameters, see also following section.

additional parameters can refer the following parameters.

- `offset` distance bar and tree, offset of bar and text from the clade, defaults to 0.
- `offset.text` distance bar and text, offset of text from bar, defaults to 0.
- `align` logical, whether align clade lab, defaults to FALSE.
• extend numeric, extend the length of bar, defaults to 0.
• angle numeric or 'auto', if angle is auto, the angle of text will be calculated automatically, which is useful for the circular etc layout, defaults to 0.
• horizontal logical, whether set label to horizontal, defaults to TRUE.
• barsize the width of line, defaults to 0.5.
• barcolour the colour of line, defaults to 'black'.
• fontsize the size of text, defaults to 3.88.
• textcolour the colour of text, defaults to 'black'.
• imagesize the size of image, defaults to 0.05.
• imagecolor the colour of image, defaults to NULL, when geom="phylopic", it should be required.

The parameters also can be set in mapping, when data is provided. Note: the barsize, barcolour, fontsize, textcolour, imagesize and imagecolor should not be set in mapping (aesthetics). When the color and size are not be set in mapping, user can modify them to adjust the attributes of specified geom.

Aesthetics For Specified Geom

geom_cladelab() understands the following aesthetics for geom="text" (required aesthetics are in bold):

• node selected node to hight light, it is required.
• label labels to be shown, it is required.
• colour the colour of text, defaults to "black".
• size the size of text, defaults to 3.88.
• angle the angle of text, defaults to 0.
• hjust A numeric vector specifying horizontal justification, defaults to 0.
• vjust A numeric vector specifying vertical justification, defaults to 0.5.
• alpha the transparency of text, defaults to NA.
• family the family of text, defaults to 'sans'.
• fontface the font face of text, defaults to 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, defaults to 1.2 .

when the colour, size are not be set in mapping, and user want to modify the colour of text, they should use textcolour, fontsize to avoid the confusion with bar layer annotation.

geom_cladelab() understands the following aesthetics for geom="label" (required aesthetics are in bold):

• node selected node to hight light, it is required.
• label labels to be shown, it is required.
• colour the colour of text, defaults to "black".
• fill the background colour of the label, defaults to "white".
• size the size of text, defaults to 3.88.
• angle the angle of text, defaults to 0.
• hjust A numeric vector specifying horizontal justification, defaults to 0.
• vjust A numeric vector specifying vertical justification, defaults to 0.5.
• alpha the transparency of text, defaults to NA.
• family the family of text, defaults to 'sans'.
• fontface the font face of text, defaults to 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, defaults to 1.2.

when the colour, size are not be set in mapping, and user want to modify the colour of text, they should use textcolour, fontsize to avoid the confusion with bar layer annotation.

geom_cladelab() understands the following aesthetics for geom="shadowtext" (required aesthetics are in bold):

• node selected node to hight light, it is required.
• label labels to be shown, it is required.
• colour the colour of text, defaults to "black".
• bg.colour the background colour of text, defaults to 'black'.
• bg.r the width of background text, defaults to 0.1.
• size the size of text, defaults to 3.88.
• angle the angle of text, defaults to 0.
• hjust A numeric vector specifying horizontal justification, defaults to 0.
• vjust A numeric vector specifying vertical justification, defaults to 0.5.
• alpha the transparency of text, defaults to NA.
• family the family of text, defaults to 'sans'.
• fontface the font face of text, defaults to 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, defaults to 1.2.

when the colour, size are not be set in mapping, and user want to modify the colour of image, they should use imagecolour, imagesize to avoid the confusion with bar layer annotation.

geom_cladelab() understands the following aesthetics for geom="image" or geom="phylopic" (required aesthetics are in bold):

• node selected node to hight light, it is required.
• label labels to be shown, it is required.
• image the image to be annotated, when geom="phylopic", the uid of phylopic databases, it is required.
• colour the color of image, defaults to NULL.
• size the size of image, defaults to 0.05.
• alpha the alpha of image, defaults to 0.8.

when the colour, size are not be set in mapping, and user want to modify the colour of image, they should use imagecolour, imagesize to avoid the confusion with bar layer annotation.
Examples

```r
set.seed(2015-12-21)
tree <- rtree(30)
data <- data.frame(id=c(34, 56),
  annote=c("another clade", "long clade names"),
  image=c("7fb9bea8-e758-4986-afb2-95a2c3bf983d",
    "0174801d-15a6-4668-bfe0-4c421fbe51e8"),
  group=c("A", "B"),
  offset=c(0.1, 0.1),
  offset.text=c(0.1, 0.2))
p <- ggtree(tree) + xlim(NA, 6)
p + geom_cladelab(node=45, label="test label") +
  geom_cladelab(node=34, label="another clade")
p2 <- p + geom_cladelab(data=data,
  mapping=aes(
    node=id,
    label=annote,
    image=image,
    color=group,
    offset=offset
  ),
  geom="shadowtext",
  hjust=0.5,
  align=TRUE,
  horizontal=FALSE,
  angle=90,
  show.legend = FALSE
)
p2
```

Description

annotate a clade with bar and text label

Usage

```r
geom_cladelabel(
  node,
  label,
  offset = 0,
  offset.text = 0,
  extend = 0,
  align = FALSE,
  barsize = 0.5,
```
`geom_cladelabel`

```r
fontsize = 3.88,
angle = 0,
geom = "text",
hjust = 0,
color = NULL,
fill = NA,
family = "sans",
parse = FALSE,
horizontal = TRUE,
```

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**: justify text horizontally
- **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
- **horizontal**: logical, whether set label to horizontal, defaults to TRUE.
- **...**: additional parameter

Value

ggplot layers

Author(s)

Guangchuang Yu

See Also

`geom_cladelabel2`
Description

annotate a clade with bar and text label

Usage

```r
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,
  horizontal = TRUE,
  ...
)
```

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`: 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
- `horizontal`: logical, whether set label to horizontal, defaults to TRUE.
- `...`: additional parameter
Value

ggplot layers

Author(s)

JustGitting

See Also

gem_cladelabel

data.frame, The data to be displayed in this layer, defaults to NULL.
mapping Set of aesthetic mappings, defaults to NULL.
ode selected node toxilight, when data and mapping is NULL, it is required.
**geom_hilight**

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<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>type</strong></td>
<td>the type of layer, defaults to auto, meaning rectangular, circular, slanted, fan, inward_circular, radial, equal_angle, ape layout tree will use rectangular layer, unrooted and daylight layout tree use will use encircle layer. You can specify this parameter to rect (rectangular layer) or encircle (encircle layer), 'gradient' (gradient color), 'roundrect' (round rectangular layer).</td>
</tr>
<tr>
<td><strong>to.bottom</strong></td>
<td>logical, whether set the high light layer to the bottom in all layers of 'ggtree' object, default is FALSE.</td>
</tr>
</tbody>
</table>

... additional parameters, see also the below and Aesthetics section.

- **align** control the align direction of the edge of high light rectangular. Options is 'none' (default), 'left', 'right', 'both'. This argument only work when the 'geom_hilight' is plotting using geom_hilight(mapping=aes(...)).
- **gradient.direction** character, the direction of gradient color, defaults to 'rt' meaning the locations of gradient color is from root to tip, options are 'rt' and 'tr'.
- **gradient.length.out** integer, desired length of the sequence of gradient color, defaults to 2.
- **roundrect.r** numeric, the radius of the rounded corners, when roundrect=TRUE, defaults to 0.05.

**Details**

geom_hilight supports data.frame as input. And aesthetics of layer can be mapped. you can see the Aesthetics section to set parameters.

**Value**

a list object.

**Aesthetics**

geom_hilight() understands the following aesthetics for rectangular layer (required aesthetics are in bold):

- **node** selected node to highlight, it is required.
- **colour** the colour of margin, defaults to NA.
- **fill** the colour of fill, defaults to 'steelblue'.
- **alpha** the transparency of fill, defaults to 0.5.
- **extend** extend xmax of the rectangle, defaults to 0.
- **extendto** specify a value, meaning the rectangle extend to, defaults to NULL.
- **linetype** the line type of margin, defaults to 1.
- **linewidth** the width of line of margin, defaults to 0.5.

geom_hilight() understands the following aesthetics for encircle layer (required aesthetics are in bold):

- **node** selected node to highlight, it is required.
• `colour` the colour of margin, defaults to ‘black’.
• `fill` the colour of fill, defaults to ‘steelblue’.
• `alpha` the transparency of fill, defaults to 0.5.
• `expand` expands the xspline clade region, defaults to 0.
• `spread` control the size, when only one point.
• `linewidth` the width of line of margin, defaults to 0.5.
• `linetype` the line type of margin, defaults to 1.
• `s_shape` the shape of the spline relative to the control points, defaults to 0.5.
• `s_open` whether the spline is a line or a closed shape, defaults to FALSE.

Author(s)
Guangchuang Yu and Shuangbin Xu

References

Examples

```r
library(ggplot2)
set.seed(102)
tree <- rtree(60)
p <- ggtree(tree)
p1 <- p + geom_hilight(node=62) + geom_hilight(node=88, fill="red")
p1
dat <- data.frame(id=c(62, 88), type=c("A", "B"))
p2 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type))
p2
p3 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type), align="left")
p4 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type), align="right")
p5 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type), align="both")
# display the high light layer with gradiental color rectangular.
p6 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type), type = "gradient", alpha=0.68)
p7 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type),
                        type = "gradient", gradient.direction="tr", alpha=0.68)
# display the high light layer with round rectangular.
p8 <- p + geom_hilight(data=dat, mapping=aes(node=id, fill=type), type = "roundrect", alpha=0.68)
```
Description

gemo_inset can add subplots to tree by accepting a list of ggplot objects that are ancestral stats or data associated with selected nodes in the tree. These ggplot objects can be any kind of charts or hybrid of of these charts.
add subplots as insets in a tree

Usage

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

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

Arguments

insets         a list of ggplot objects, named by node number
width           width of the inset, relative to the range of x-axis, defaults to .1
height          height of the inset, relative to the range of y-axis, defaults to .1
hjust           adjust the horizontal position of the charts, charts will go left if hjust > 0
vjust           adjust the vertical position of the charts, charts will go down if vjust > 0
x                the position where users want to place the charts, one of 'node' (default) and 'branch'
Details

Users can also use

Value

inset layer
tree view with insets

Author(s)

Guangchuang Yu

References

For demonstration of this function, please refer to chapter 8.3 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* [http://yulab-smu.top/treedata-book/index.html](http://yulab-smu.top/treedata-book/index.html) by Guangchuang Yu.

Description

geom_label2 support aes(subset) via setup_data

Usage

```r
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  Set of aesthetic mappings, defaults to NULL.
data  A layer specific dataset - only needed if you want to override the plot defaults.
...  other arguments passed on to 'layer'.
stat  Name of the 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 parsed as expressions, defaults to 'FALSE'.
nudge_x  adjust the horizontal position of the labels.
nudge_y  adjust the vertical position of the labels.
label.padding  Amount of padding around label, defaults to unit(0.25, "lines").
label.r  Use to set the radius of rounded corners of the label, defaults to unit(0.15, "lines").
label.size  Size of label border, in mm, defaults to 0.25.
na.rm  If "FALSE" (default), missing values are removed with a warning. If "TRUE", missing values are silently removed, logical.
show.legend  Whether to show legend, logical, defaults to "NA".
inherit.aes  Whether to inherit aesthetic mappings, logical, defaults to "TRUE".

Details

'geom_label2' is a modified version of geom_label, with subset aesthetic supported

Value

label layer

Author(s)

Guangchuang Yu

References

For more detailed demonstration of this function, please refer to chapter A.4.5 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

See Also

geom_label
Examples

library(ggtree)
set.seed(123)
tr <- rtree(15)
x <- ggtree(tr)
x + geom_label2(aes(label = node, subset = isTip == FALSE))

Description

geom layer to draw aligned motif

Usage

geom_motif(mapping, data, on, label, align = "centre", ...)

Arguments

  mapping         aes mapping
  data            data
  on              gene to center (i.e. set middle position of the on gene to 0)
  label           specify a column to be used to label genes
  align           where to place gene label, default is 'centre' and can be set to 'left' and 'right'
  ...             additional parameters

Value

  geom layer

Author(s)

  Guangchuang Yu
geom_nodelab

Description

add node label layer for a tree

Usage

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

Arguments

- mapping: aesthetic mappings, defaults to NULL
- nudge_x: horizontal adjustment to nudge labels, defaults to 0
- nudge_y: vertical adjustment to nudge labels, defaults to 0
- geom: one of 'text', "shadowtext", 'label', 'image' and 'phylopic'
- hjust: horizontal alignment, defaults to 0.5
- node: a character indicating which node labels will be displayed, it should be one of 'internal', 'external' and 'all'. If it is set to 'internal' will display internal node labels, 'external' will display the tip labels, and 'all' will display internal node and tip labels.
- ... additional parameters, see also the additional parameters of geom_tiplab().

Value

geom layer

Author(s)

Guangchuang Yu

References

For demonstration of this function, please refer to chapter A.4.5 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.
See Also

geom_tiplab()

Description

add node label for circular layout

Usage

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

Arguments

mapping          aesthetic mappings, defaults to NULL
nudge_x          horizontal adjustment to nudge labels, defaults to 0
nudge_y          vertical adjustment to nudge labels, defaults to 0
geom             one of 'text', "shadowtext", 'label', 'image' and 'phylopic'
hjust            horizontal alignment, defaults to 0.5
...               additional parameters, see also the additional parameters of geom_tiplab()

Value

node label layer

Author(s)

Guangchuang Yu
geom_nodepoint

Description

add node point layer to a tree

Usage

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

Arguments

mapping Set of aesthetic mapping created by aes(). If inherit.aes = TRUE, the mapping can be inherited from the plot mapping as specified in the call to ggplot().
data The data to be displayed in this layer. If 'NULL' (the default), the data is inherited from the plot data as specified in the call to ggplot().
position Position adjustment.
na.rm logical. If 'FALSE' (default), missing values are removed with a warning. If 'TRUE', missing values are silently removed.
show.legend logical. Should this layer be included in the legends? 'NA', the default, includes if any aesthetics are mapped. 'FALSE' never includes, and 'TRUE' always includes.
inherit.aes logical (defaults to 'TRUE'). If 'FALSE', overrides the default aesthetics, rather then combining with them.
... additional parameters that passed on to this layer. These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3.

Value

node point layer

Author(s)

Guangchuang Yu library(ggtree) tr<- rtree(15) x <- ggtree(tr) x + geom_nodepoint()
References

For more detailed demonstration, please refer to chapter 4.3.2 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

Description

`geom_point2` is a modified version of `geom_point` that supports `aes(subset)`

Usage

```r
gem_point2(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

Arguments

- `mapping` Set of aesthetic mapping created by `aes()`. If `inherit.aes = TRUE`, the mapping can be inherited from the plot mapping as specified in the call to `ggplot()`.
- `data` The data to be displayed in this layer. If 'NULL' (the default), the data is inherited from the plot data as specified in the call to `ggplot()`.
- `stat` Name of the statistical transformation to be used on the data for this layer.
- `position` Position adjustment.
- `na.rm` logical. If 'FALSE' (default), missing values are removed with a warning. If 'TRUE', missing values are silently removed.
- `show.legend` logical. Should this layer be included in the legends? 'NA', the default, includes if any aesthetics are mapped. 'FALSE' never includes, and 'TRUE' always includes.
- `inherit.aes` logical (defaults to 'TRUE'). If 'FALSE', overrides the default aesthetics, rather then combining with them.
- `...` additional parameters that passed on to this layer. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. 
Details

`geom_point2` creates scatterplots, just similar to `ggplot2::geom_point`. It extends the `ggplot2::geom_point` to support filtering via the subset aesthetic mapping (see Aesthetics section).

Value

point layer

Aesthetics

`geom_point2()` understands the following aesthetics

- subset logical expression indicating elements or rows to keep: missing values are taken as false; should be in aes().
- colour the colour of point, defaults to "black".
- fill the colour of fill, defaults to "black".
- alpha the transparency of fill, defaults to 1.
- size the size of point, defaults to 1.5.
- shape specify a shape, defaults to 19.
- stroke control point border thickness of point, defaults to 0.5.

Author(s)

Guangchuang Yu

References


For more information about tree visualization, please refer to the online book https://yulab-smu.top/treedata-book/

See Also

`geom_point`; `geom_rootpoint` add point of root; `geom_nodepoint` add points of internal nodes; `geom_tippoint` add points of external nodes (also known as tips or leaves).
Examples

library(ggtree)
## add point by aes(subset)
tr <- rtree(10)
# group tip and node
ggtree(tr) + geom_point2(aes(shape=isTip, color=isTip), size=3)
# specify a node to display
ggtree(tr) + geom_point2(aes(subset=(node==15)), shape=21, size=5, fill='green')
# specify a tip to display
ggtree(tr) + geom_point2(aes(subset=(label %in% c("t1", "t3"))), shape=21, size=5, fill='green')

## color point with continuous variables
library(ggtree)
library(treeio)
library(ggplot2)
beast_file <- system.file("examples/MCC_FluA_H3.tree", package="ggtree")
beast_tree <- read.beast(beast_file)
p <- ggtree(beast_tree) +
  geom_tiplab(hjust = -.1)+
  geom_nodepoint(aes(fill = rate), shape = 21, size = 4) +
  scale_fill_continuous(low = 'blue', high = 'red') +
  theme_tree2() + theme(legend.position = 'right')
p

description

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

Usage

geom_range(range, center = "auto", ...)

Arguments

range range(interval) to be displayed, e.g. "height_0.95_HPD"
center center of the range, mean, median or auto (default, the center of the range)
... additional parameter, e.g. color, linewidth, alpha

Value

ggplot layer

Author(s)

Guangchuang Yu
References

For demonstration of this function, please refer to chapter 5.2.4 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* [http://yulab-smu.top/treedata-book/index.html](http://yulab-smu.top/treedata-book/index.html) by Guangchuang Yu.

---

**geom_rootedge**

**Description**

display root edge layer for a tree

**Usage**

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

**Arguments**

- `rootedge` length of rootedge; use phylo$root.edge if rootedge = NULL (default).
- `...` additional parameters

Additional parameters can be referred to the following parameters:
- `size` control the width of rootedge, defaults to 0.5.
- `colour` color of rootedge, defaults to black.
- `linetype` the type of line, defaults to 1.
- `alpha` modify colour transparency, defaults to 1.

**Details**

`geom_rootedge` is used to create a rootedge as ggtree doesn’t plot the root edge by default.

**Value**

ggtree rootedge layer

**Author(s)**

Guangchuang Yu

**References**

Examples

```r
library(ggtree)
set.seed(123)

## with root edge = 1
tree1 <- read.tree(text='((A:1,B:2):3,C:2):1;')
ggtree(tree1) + geom_tiplab() + geom_rootedge()

## without root edge
tree2 <- read.tree(text='((A:1,B:2):3,C:2);')
ggtree(tree2) + geom_tiplab() + geom_rootedge()

## setting root edge
.tree$root.edge <- 2
ggtree(tree2) + geom_tiplab() + geom_rootedge()

## specify length of root edge for just plotting
## this will ignore tree$root.edge
.gtree(tree2) + geom_tiplab() + geom_rootedge(rootedge = 3)
```

## For more detailed demonstration of this function, please refer to chapter A.4.5 of
## *Data Integration, Manipulation and Visualization of Phylogenetic Trees*

---

**Description**

`geom_rootpoint` is used to add root point layer to a tree

**Usage**

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

**Arguments**

- **mapping**: Set of aesthetic mapping created by `aes()`. If `inherit.aes = TRUE`, the mapping can be inherited from the plot mapping as specified in the call to `ggplot()`.
**data**
The data to be displayed in this layer. If 'NULL' (the default), the data is inherited from the plot data as specified in the call to `ggplot()`.

**position**
Position adjustment.

**na.rm**
logical. If 'FALSE' (default), missing values are removed with a warning. If 'TRUE', missing values are silently removed.

**show.legend**
logical. Should this layer be included in the legends? 'NA', the default, includes if any aesthetics are mapped. 'FALSE' never includes, and 'TRUE' always includes.

**inherit.aes**
logical (defaults to 'TRUE'). If 'FALSE', overrides the default aesthetics, rather then combining with them.

**...**
additional parameters that passed on to this layer. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`.

**Details**
`geom_rootpoint` inherit from `geom_point2`, and it is used to display and customize the points on the root.

**Value**
root point layer

**Author(s)**
Guangchuang Yu

**References**


**See Also**

`geom_point`; `geom_rootpoint` add point of root; `geom_nodepoint` add points of internal nodes; `geom_tippoint` add points of external nodes (also known as tips or leaves).
### Examples

```r
library(ggtree)
tr <- rtree(10)
## add root point
ggtree(tr) + geom_rootpoint()
```
```r
ggtree(tr) + geom_rootpoint(size=2, color="red", shape=2)
```

---

### Description

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

### Usage

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

### Arguments

- **mapping**: Set of aesthetic mappings, defaults to `NULL`
- **data**: A layer specific dataset - only needed if you want to override the plot defaults.
- **stat**: Name of stat to modify data.
- **position**: The position adjustment to use for overlapping points on this layer.
- **lineend**: Line end style, one of butt (default), round and square.
- **na.rm**: If "FALSE" (default), missing values are removed with a warning. If "TRUE", missing values are silently removed, logical.
- **show.legend**: Whether to show legend, logical.
- **inherit.aes**: Whether to inherit aesthetic mappings, logical, defaults to "TRUE".
- **nudge_x**: adjust the horizontal position of the segments.
- **arrow**: specification for arrow heads, as created by `arrow()`.
- **arrow.fill**: fill color to use for the arrow head (if closed). NULL means use `colour` aesthetic.
- **...**: additional parameter
Details

'geom_segment2' is a modified version of geom_segment, with subset aesthetic supported.

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,
  offset = 0,
  offset.text = 0,
  align = TRUE,
  barsize = 0.5,
  extend = 0,
  fontsize = 3.88,
  angle = 0,
  geom = "text",
  hjust = 0,
  color = "black",
  fill = NA,
  family = "sans",
  parse = FALSE,
  ...
)

**Arguments**

- `taxa1` (taxa2)
- `label`
- `offset`
- `offset.text`
- `align`
- `barsize`
- `extend`
- `fontsize`
- `angle`
- `geom`
- `hjust`
- `color`
- `fill`
- `family`
- `parse`
- `...`

**Value**

ggplot layers

**Author(s)**

Guangchuang Yu

**References**

For more detailed demonstration of this function, please refer to chapter 5.2.1 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* [http://yulab-smu.top/treedata-book/index.html](http://yulab-smu.top/treedata-book/index.html) by Guangchuang Yu.

**Examples**

```r
library(ggtree)
tr<- rtree(15)
x <- ggtree(tr)
x + geom_strip(13, 1, color = "red") + geom_strip(3, 7, color = "blue")
```
Description

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

Usage

```r
geom_striplab(
  taxa1 = NULL,
  taxa2 = NULL,
  label = NULL,
  data = NULL,
  mapping = NULL,
  geom = "text",
  parse = FALSE,
  ...
)
```

Arguments

taxa1 can be label or node number
taxa2 can be label or node number
label character, character to be showed, when data and mapping is NULL, it is required.
data data.frame, the data to be displayed in the annotation, default is NULL.
mapping Set of aesthetic mappings, default is NULL. The detail see the following explanation.
geom character, one of 'text', 'label', 'shadowtext', 'image' and 'phylopic', default is 'text', and the parameter see the Aesthetics For Specified Geom.
parse logical, whether parse label to emoji font, default is FALSE.
... additional parameters, see also following section.

additional parameters can refer the following parameters. ##'
  • offset distance bar and tree, offset of bar and text from the clade, default is 0.
  • offset.text distance bar and text, offset of text from bar, default is 0.
  • align logical, whether align clade lab, default is FALSE.
  • extend numeric, extend the length of bar, default is 0.
  • angle numeric or 'auto', if angle is auto, the angle of text will be calculated automatically, which is useful for the circular etc layout, default is 0.
  • horizontal logical, whether set label to horizontal, default is TRUE.
• barsize the width of line, default is 0.5.
• barcolour the colour of line, default is 'black'.
• fontsize the size of text, default is 3.88.
• textcolour the colour of text, default is 'black'.
• imagesize the size of image, default is 0.05.
• imagecolor the colour of image, default is NULL, when geom="phylopic", it should be required.

The parameters also can be set in mapping, when data is provided. Note: the barsize, barcolour, fontsize, textcolour, imagesize and imagecolor should not be set in mapping (aesthetics). When the color and size are not be set in mapping, user can modify them to adjust the attributes of specified geom.

Aesthetics For Specified Geom

gem_striplab() understands the following aesthetics for geom="text" (required aesthetics are in bold):

• taxa1 selected tip label or tip node, it is required.
• taxa2 selected another tip label or tip node, it is required.
• label labels to be shown, it is required.
• colour the colour of text, default is "black".
• size the size of text, default is 3.88.
• angle the angle of text, default is 0.
• hjust A numeric vector specifying horizontal justification, default is 0.
• vjust A numeric vector specifying vertical justification, default is 0.5.
• alpha the transparency of text, default is NA.
• family the family of text, default is 'sans'.
• fontface the font face of text, default is 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, default is 1.2.

when the colour, size are not be set in mapping, and user want to modify the colour of text, they should use textcolour, fontsize to avoid the confusion with bar layer annotation.

gem_striplab() understands the following aesthetics for geom="label" (required aesthetics are in bold):

• taxa1 selected node to hight light, it is required.
• taxa2 selected another tip label or tip node, it is required.
• label labels to be shown, it is required.
• colour the colour of text, default is "black".
• fill the background colour of the label, default is "white".
• size the size of text, default is 3.88.
• angle the angle of text, default is 0.
• hjust A numeric vector specifying horizontal justification, default is 0.
• vjust A numeric vector specifying vertical justification, default is 0.5.
• alpha the transparency of text, default is NA.
• family the family of text, default is 'sans'.
• fontface the font face of text, default is 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, default is 1.2.

When the colour, size are not be set in mapping, and user want to modify the colour of text, they should use textcolour, fontsize to avoid the confusion with bar layer annotation.

geom_striplab() understands the following aesthetics for geom="shadowtext" (required aesthetics are in bold):

• taxa1 selected node to highlight, it is required.
• taxa2 selected another tip label or tip node, it is required.
• label labels to be shown, it is required.
• colour the colour of text, default is "black".
• bg.colour the background colour of text, default is 'black'.
• bg.r the width of background text, default is 0.1.
• size the size of text, default is 3.88.
• angle the angle of text, default is 0.
• hjust A numeric vector specifying horizontal justification, default is 0.
• vjust A numeric vector specifying vertical justification, default is 0.5.
• alpha the transparency of text, default is NA.
• family the family of text, default is 'sans'.
• fontface the font face of text, default is 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
• lineheight The height of a line as a multiple of the size of text, default is 1.2.

When the colour, size are not be set in mapping, and user want to modify the colour of text, they should use textcolour, fontsize to avoid the confusion with bar layer annotation.

geom_striplab() understands the following aesthetics for geom="image" or geom="phylopic" (required aesthetics are in bold):

• taxa1 selected node to highlight, it is required.
• taxa2 selected another tip label or tip node, it is required.
• label labels to be shown, it is required.
• image the image to be annotated, when geom="phylopic", the uid of phylopic databases, it is required.
• colour the color of image, default is NULL.
• size the size of image, default is 0.05.
• alpha the alpha of image, default is 0.8.

When the colour, size are not be set in mapping, and user want to modify the colour of image, they should use imagecolour, imagesize to avoid the confusion with bar layer annotation.
Examples

```r
set.seed(123)
tr <- rtree(10)
dt <- data.frame(ta1=c("t5", "t1"), ta2=c("t6", "t3"), group=c("A", "B"))
p <- ggtree(tr) + geom_tiplab()
p2 <- p +
    geom_striplab(
      data = dt,
      mapping = aes(taxa1 = ta1, taxa2 = ta2,
                    label = group, color=group),
      align = TRUE,
      show.legend = FALSE
    )
p2
```

Description

`geom_taxalink` supports data.frame as input, the colour, linewidth, linetype and alpha can be mapped. When the data was provided, the mapping should be also provided, which `taxa1` and `taxa2` should be mapped created by `aes`, `aes_` or `aes_string`. In addition, the `hratio`, control the height of curve line, when tree layout is circular, default is 1. `ncp`, the number of control points used to draw the curve, more control points creates a smoother curve, default is 1. They also can be mapped to a column of data.

Usage

```r
gemom_taxalink(
  data = NULL,
  mapping = NULL,
  taxa1 = NULL,
  taxa2 = NULL,
  offset = NULL,
  outward = "auto",
  ...
)
```

Arguments

- **data**: data.frame, The data to be displayed in this layer, default is NULL.
- **mapping**: Set of aesthetic mappings, default is NULL.
- **taxa1**: can be label or node number.
- **taxa2**: can be label or node number.
- **offset**: numeric, control the shift of curve line (the ratio of axis value, range is "(0-1)") default is NULL.
outward logical, control the orientation of curve when the layout of tree is circular, fan or other layout in polar coordinate, default is "auto", meaning it will automatically.

..., additional parameter.

Value

a list object.

Aesthetics

`geom_taxalink()` understands the following aesthetics (required aesthetics are in bold):

- `taxa1` label or node number of tree.
- `taxa2` label or node number of tree.
- `group` group category of link.
- `colour` control the color of line, default is black.
- `linetype` control the type of line, default is 1 (solid).
- `linewidth` control the width of line, default is 0.5.
- `curvature` control the curvature of line, default is 0.5, it will be created automatically in polar coordinate.
- `hratio` control the height of curve line, default is 1.
- `ncp` control the smooth of curve line, default is 1.

Description

`geom_text2` support aes(subset) via setup_data

Usage

```r
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

Description

add tip label layer for a tree

Usage

gem_tiplab(
  mapping = NULL,
  hjust = 0,
  align = FALSE,
  linetype = "dotted",
  linesize = 0.5,
  geom = "text",
  offset = 0,
  as_ylab = FALSE,
  ...
)
Arguments

- **mapping**: aes mapping
- **hjust**: horizontal adjustment, defaults to 0
- **align**: if TRUE, align all tip labels to the longest tip by adding padding characters to the left side of tip labels, defaults to "FALSE" with a line connecting each tip and its corresponding label, defaults to "FALSE"
- **linetype**: set linetype of the line if align = TRUE, defaults to "dotted"
- **linesize**: set line width if align = TRUE, defaults to 0.5
- **geom**: one of 'text', 'label', 'shadowtext', 'image' and 'phylopic'
- **offset**: tiplabel offset, horizontal adjustment to nudge tip labels, defaults to 0
- **as_ylab**: display tip labels as y-axis label, only works for rectangular and dendrogram layouts, defaults to "FALSE"
- **...**: additional parameter

Additional parameters can refer the following parameters.

The following parameters for geom="text".

- **size**: control the size of tip labels, defaults to 3.88.
- **colour**: control the colour of tip labels, defaults to "black".
- **angle**: control the angle of tip labels, defaults to 0.
- **vjust**: A numeric vector specifying vertical justification, defaults to 0.5.
- **alpha**: the transparency of text, defaults to NA.
- **family**: the family of text, defaults to 'sans'.
- **fontface**: the font face of text, defaults to 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
- **lineheight**: The height of a line as a multiple of the size of text, defaults to 1.2.
- **nudge_x**: horizontal adjustment to nudge labels, defaults to 0.
- **nudge_y**: vertical adjustment to nudge labels, defaults to 0.
- **check.overlap**: if TRUE, text that overlaps previous text in the same layer will not be plotted.
- **parse**: if TRUE, the labels will be parsed into expressions, if it is 'emoji', the labels will be parsed into emojifont.

The following parameters for geom="label".

- **size**: the size of tip labels, defaults to 3.88.
- **colour**: the colour of tip labels, defaults to "black".
- **fill**: the colour of rectangular box of labels, defaults to "white".
- **vjust**: numeric vector specifying vertical justification, defaults to 0.5.
- **alpha**: the transparency of labels, defaults to NA.
- **family**: the family of text, defaults to 'sans'.
- **fontface**: the font face of text, defaults to 1 (plain), others are 2 (bold), 3 (italic), 4 (bold.italic).
- **lineheight**: The height of a line as a multiple of the size of text, defaults to 1.2.
**geom_tiplab**

- **nudge_x** horizontal adjustment to nudge labels, defaults to 0.
- **nudge_y** vertical adjustment, defaults to 0.
- **check.overlap** if TRUE, text that overlaps previous text in the same layer will not be plotted.
- **parse** if TRUE, the labels will be parsed into expressions, if it is 'emoji', the labels will be parsed into emojifont.
- **label.padding** Amount of padding around label, defaults to 'unit(0.25, "lines")'.
- **label.r** Radius of rounded corners, defaults to 'unit(0.15, "lines")'.
- **label.size** Size of label border, in mm, defaults to 0.25.

The following parameters for geom="shadowtext", some parameters are like to geom="text".
- **bg.colour** the background colour of text, defaults to "black".
- **bg.r** the width of background of text, defaults to 0.1.

The following parameters for geom="image" or geom="phylopic".
- **image** the image file path for geom='image', but when geom='phylopic', it should be the uid of phylopic databases.
- **size** the image size, defaults to 0.05.
- **colour** the color of image, defaults to NULL.
- **alpha** the transparency of image, defaults to 0.8.

The following parameters for the line when align = TRUE.
- **colour** the colour of line, defaults to 'black'.
- **alpha** the transparency of line, defaults to NA.
- **arrow** specification for arrow heads, as created by arrow(), defaults to NULL.
- **arrow.fill** fill color to use for the arrow head (if closed), defaults to 'NULL', meaning use 'colour' aesthetic.

**Details**

'geom_tiplab' not only supports using text or label geom to display tip labels, but also supports image geom to label tip with image files or phylopics.

For adding tip labels to a tree with circular layout, 'geom_tiplab' will automatically adjust the angle of the tip labels to the tree by internally calling 'geom_tiplab2'.

**Value**

tip label layer

**Author(s)**

Guangchuang Yu

**References**

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, defaults to 0
- `...`: additional parameter, see `geom_tiplab`

#### Details

'geom_tiplab2' will automatically adjust the angle of the tip labels to the tree with circular layout

#### Value

tip label layer

#### Author(s)

Guangchuang Yu

#### References

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

#### See Also

- `geom_tiplab`

#### Examples

```r
library(ggtree)
set.seed(123)
tr <- rtree(10)
ggtree(tr, layout = "circular") + geom_tiplab2()
```
**Description**

add tip point layer for a tree

**Usage**

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

**Arguments**

- `mapping`: Set of aesthetic mapping created by `aes()`. If `inherit.aes = TRUE`, the mapping can be inherited from the plot mapping as specified in the call to `ggplot()`.
- `data`: The data to be displayed in this layer. If 'NULL' (the default), the data is inherited from the plot data as specified in the call to `ggplot()`.
- `position`: Position adjustment.
- `na.rm`: logical. If 'FALSE' (default), missing values are removed with a warning. If 'TRUE', missing values are silently removed.
- `show.legend`: logical. Should this layer be included in the legends? 'NA', the default, includes if any aesthetics are mapped. 'FALSE' never includes, and 'TRUE' always includes.
- `inherit.aes`: logical (defaults to 'TRUE'). If 'FALSE', overrides the default aesthetics, rather than combining with them.
- `...`: additional parameters that passed on to this layer. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`.

**Value**

tip point layer

**Author(s)**

Guangchuang Yu
References


Examples

```r
library(ggtree)
tr <- rtree(15)
x <- ggtree(tr)
x + geom_tippoint()
```

Description

add tree layer

Usage

```r
gem_tree(
mapping = NULL,
data = NULL,
layout = "rectangular",
multiPhylo = FALSE,
continuous = "none",
position = "identity",
...
)
```

Arguments

- `mapping`: aesthetic mapping
- `data`: data of the tree
- `layout`: one of 'rectangular', 'dendrogram', 'slanted', 'ellipse', 'roundrect', 'fan', 'circular', 'inward_circular', 'radial', 'equal_angle', 'daylight' or 'ape'
- `multiPhylo`: logical, whether input data contains multiple phylo class, defaults to "FALSE".
- `continuous`: character, continuous transition for selected aesthetic ('size' or 'color'('colour')). It should be one of 'color' (or 'colour'), 'size', 'all' and 'none', default is 'none'
- `position`: Position adjustment, either as a string, or the result of a call to a position adjustment function, default is "identity".
- `...`: additional parameter

Some dot arguments:
- `nsplit` integer, the number of branch blocks divided when 'continuous' is not "none", default is 200.
Value
tree layer

Aesthetics
geom_tree() understands the following aesthetics:

- color character, control the color of line, default is black (continuous is "none").
- linetype control the type of line, default is 1 (solid).
- linewidth numeric, control the width of line, default is 0.5 (continuous is "none").

Author(s)
Yu Guangchuang

References
For demonstration of this function, please refer to chapter 4.2.1 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

Examples
tree <- rtree(10)
ggplot(tree) + geom_tree()

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
Description

add tree scale to a tree

Usage

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

Arguments

- `x`: set x position of the scale
- `y`: set y position of the scale
- `width`: set the length of the tree scale
- `offset`: set offset of text to line, defaults to NULL
- `offset.label`: set offset of the scale title to line.
- `label`: set the title of tree scale, defaults to NULL.
- `color`: set color of the scale
- `linesize`: set size of line
- `fontsize`: set size of text
- `family`: 'sans' by default, can be any supported font

Details

'geom_treescale' automatically adds a scale bar for evolutionary distance

Value

ggplot layers

Author(s)

Guangchuang Yu
**geom_zoom_clade**

**References**

For demonstration of this function, please refer to chapter 4.3.1 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* [http://yulab-smu.top/treedata-book/index.html](http://yulab-smu.top/treedata-book/index.html) by Guangchuang Yu.

---

**Description**

zoom selected clade of a tree

**Usage**

```r
geom_zoom_clade(node, xexpand = NULL)
```

**Arguments**

- `node` internal node number to zoom in its corresponding clade
- `xexpand` numeric, extend x, meaning the ratio of range of the xlim of the original tree, defaults to NULL.

**Details**

'geom_zoom_clade' zooms in on a selected clade of a tree, while showing its on the full view of tree as a seperated panel for reference

**Value**

updated tree view

**Author(s)**

Guangchuang Yu
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

getNodeAngle.df

Description
Get the angle between the two nodes specified.

Usage
getNodeAngle.df(df, origin_node_id, node_id)

Arguments
df tree data frame
origin_node_id origin node id number
node_id end node id number

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

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

Usage
getNodesBreadthFirst.df(df)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>df</td>
<td>tree data.frame</td>
</tr>
</tbody>
</table>

Value
list of node id’s in breadth-first order.

getSubtree

Description
Get all children of node from tree, including start_node.

Usage
getSubtree(tree, node)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tree</td>
<td>ape phylo tree object</td>
</tr>
<tr>
<td>node</td>
<td>is the tree node id from which the tree is derived.</td>
</tr>
</tbody>
</table>

Value
list of all child node id’s from starting node.
getSubtree.df

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

Usage
getSubtree.df(df, node)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>df</td>
<td>tree data.frame</td>
</tr>
<tr>
<td>node</td>
<td>id of starting node.</td>
</tr>
</tbody>
</table>

Value
list of all child node id’s from starting node.

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tree</td>
<td>ape phylo tree object</td>
</tr>
<tr>
<td>node</td>
<td>is the tree node id from which the subtrees are derived.</td>
</tr>
</tbody>
</table>

Value
named list of subtrees with the root id of subtree and list of node id’s making up subtree.
getSubtreeUnrooted.df

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

Usage
getSubtreeUnrooted.df(df, node)

Arguments
- df: tree data.frame
- node: is the tree node id from which the subtrees are derived.

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

getTreeArcAngles

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_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

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
**get_taxa_name**

**Author(s)**

Guangchuang Yu

---

**Description**

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

**Usage**

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

**Arguments**

- `tree_view` tree view (i.e. the ggtree object). If tree_view is NULL, the last ggplot object will be used.
- `node` internal node number to specify a clade. If NULL, using the whole tree

**Details**

This function extract an ordered vector of the tips from selected clade or the whole tree based on the ggtree() plot.

**Value**

ordered taxa name vector

**Author(s)**

Guangchuang Yu

**Examples**

```r
tree <- rtree(30)
p <- ggtree(tree)
get_taxa_name(p)
```
### ggdensitree

**Description**

drawing phylogenetic trees from list of phylo objects

**Usage**

```
ggdensitree(
  data = NULL,
  mapping = NULL,
  layout = "slanted",
  tip.order = "mode",
  align.tips = TRUE,
  jitter = 0,
  ...
)
```

**Arguments**

- `data`: a list of phylo objects or any object with an as.phylo and fortify method
- `mapping`: aesthetic mapping
- `tip.order`: the order of the tips by a character vector of taxa names; or an integer, N, to order the tips by the order of the tips in the Nth tree; ‘mode’ to order the tips by the most common order; ‘mds’ to order the tips based on MDS of the path length between the tips; or ‘mds_dist’ to order the tips based on MDS of the distance between the tips (default: ‘mode’)
- `align.tips`: TRUE (default) to align trees by their tips and FALSE to align trees by their root
- `jitter`: deviation to jitter tips
- `...`: additional parameters passed to fortify, ggtree and geom_tree

**Details**

The trees plotted by `ggdensitree()` will be stacked on top of each other and the structures of the trees will be rotated to ensure the consistency of the tip order.

**Value**

tree layer

**Author(s)**

Yu Guangchuang, Bradley R. Jones


References

For more detailed demonstration of this function, please refer to chapter 4.4.2 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

Examples

```r
require(ape)
require(dplyr)
require(tidyr)

# Plot multiple trees with aligned tips
trees <- list(read.tree(text="((a:1,b:1):1.5,c:2.5);"), read.tree(text="((a:1,c:1):1,b:2);"));
ggdensitree(trees) + geom_tiplab()

# Plot multiple trees with aligned tips with tip labels and separate tree colors
trees.fort <- list(trees[[1]] %>% fortify %>% mutate(tree="a"), trees[[2]] %>% fortify %>% mutate(tree="b"));
ggdensitree(trees.fort, aes(colour=tree)) + geom_tiplab(colour='black')

# Generate example data
set.seed(1)
random.trees <- rmrree(5, 10)
time.trees <- lapply(seq_along(random.trees), function(i) {
  tree <- random.trees[[i]]
  tree$tip.label <- paste0("t", 1:10)
  dates <- estimate.dates(tree, 1:10, mu=1, nsteps=1)
  tree$edge.length <- dates[tree$edge[, 2]] - dates[tree$edge[, 1]]
  fortify(tree) %>% mutate(tree=factor(i, levels=as.character(1:10)))
})

ggdensitree(time.trees, aes(colour=tree), tip.order=paste0("t", 1:10)) + geom_tiplab(colour='black')

# Read example data
eexample.trees <- read.tree(system.file("examples", "ggdensitree_example.tree", package="ggtree"))

# Compute OTU
grp <- list(A = c("a.t1", "a.t2", "a.t3", "a.t4"),
B = c("b.t1", "b.t2", "b.t3", "b.t4"),
C = c("c.t1", "c.t2", "c.t3", "c.t4"))

tree <- lapply(example.trees, groupOTU, grp)

ggdensitree(tree, aes(colour=group), alpha=1/6, tip.order='mds') +
  scale_colour_manual(values=c("black", "red", "green", "blue"))
```
ggtree

Description
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",
  root.position = 0,
  xlim = NULL,
  layout.params = list(),
  hang = 0.1,
  ...
)

Arguments

tr      phylo object
mapping aesthetic mapping
layout   one of 'rectangular', 'dendrogram', 'slanted', 'ellipse', 'roundrect', 'fan', 'circular', 'inward_circular', 'radial', 'equal_angle', 'daylight' or 'ape'
open.angle open angle, only for 'fan' layout
mrsd    most recent sampling date
as.Date logical whether using Date class in time tree
yscale  y scale
yscale_mapping yscale mapping for category variable
ladderize logical (default TRUE). Should the tree be re-organized to have a 'ladder' aspect?
right   logical. If ladderize = TRUE, should the ladder have the smallest clade on the right-hand side? See ape::ladderize() for more information.
branch.length variable for scaling branch, if 'none' draw cladogram
root.position position of the root node (default = 0)
xlim x limits, only works for 'inward_circular' layout
layout.params list, the parameters of layout, when layout is a function.
hang numeric The fraction of the tree plot height by which labels should hang below
the rest of the plot. A negative value will cause the labels to hang down from 0.
This parameter only work with the 'dendrogram' layout for 'hclust' like class,
default is 0.1.

additional parameter
some dot arguments:
• nsplit integer, the number of branch blocks divided when 'continuous' is
not "none", default is 200.

Value
tree

Author(s)
Yu Guangchuang

References
doi.org/10.1093/molbev/msy194
and annotation of phylogenetic trees with their covariates and other associated data. Methods

For more information, please refer to Data Integration, Manipulation and Visualization of Phylo-

See Also
geom_tree()

Examples
require(ape)
tr <- rtree(10)
ggtree(tr)
Description

append a heatmap of a matrix to the right side of a 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,
  family = "",
  hjust = 0.5,
  legend_title = "value",
  custom_column_labels = NULL
)

Arguments

  p  tree view
  data  matrix or data.frame
  offset  set offset of the heatmap to tree
  width  total width of heatmap, compare to width of tree, defaults to 1, which means
         they are of the same length
  low  set color of the lowest value, defaults to "green"
  high  set color of the highest value, defaults to "red"
  color  set color of heatmap cell border, defaults to "white"
  colnames  logical, whether to add matrix colnames, defaults to "TRUE"
  colnames_position  set the position of the colnames, one of 'bottom' (default) or 'top'
  colnames_angle  set the angle of colnames
colnames_level  set levels of colnames
colnames_offset_x  set x offset for colnames
colnames_offset_y  set y offset for colnames
font.size  set font size of matrix colnames
family  font of matrix colnames, can be any supported font
hjust  adjust horizontal position of column names (0: align left, 0.5: align center (default), 1: align right)
legend_title  title of fill legend
custom_column_labels  instead of using the colnames from the input matrix/data.frame, input a custom vector to be set as column labels

**Value**

tree view

**Author(s)**

Guangchuang Yu

**References**

For demonstration of this function, please refer to chapter 7.3 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

gzoom  gzoom method

**Description**

gzoom method
gzoom method
zoom selected subtree

**Usage**

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

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

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

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

**Arguments**

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

**Value**

figure

---

gzoom.phylo          gzoom

**Description**

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

**Usage**

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

**Arguments**

- **phy**: phylo object
- **focus**: selected tips
- **subtree**: logical
- **widths**: widths

**Value**

a list of ggplot object

**Author(s)**

ygc
**Description**

`hexexpand`

`vexpand`

expand `xlim` (`ylim`) by ratio of x (y) axis range

**Usage**

`hexexpand(ratio, direction = 1)`

`vexpand(ratio, direction = 1)`

`ggexpand(ratio, direction = 1, side = "hv")`

**Arguments**

`ratio`  
expand x (y) axis limits by amount of xrange (yrange) * ratio

`direction`  
expand x axis limit at right hand side if direction is 1 (default), or left hand side if direction is -1

`side`  
one of ‘h’ for horizontal and ‘v’ for vertical or ‘hv’ for both (default).

**Value**

`ggexpand` object

**Author(s)**

Guangchuang Yu

**Examples**

```r
x <- rtree(20)
x$tip.label <- paste0('RRRRREEEEEAAALLLLYYYY_Long_Lable_', x$tip.label)
p1 <- ggtree(x) + geom_tiplab()
p1 + ggexpand(1.5, side = "h")
```
label_pad

Padding taxa labels

Description
This function adds padding characters to the left side of taxa labels, adjust their length to the longest label.

Usage
label_pad(label, justify = "right", pad = "·")

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>label</td>
<td>taxa label</td>
</tr>
<tr>
<td>justify</td>
<td>should a character vector be right-justified (default), left-justified, centred or left alone.</td>
</tr>
<tr>
<td>pad</td>
<td>padding character (defaults to dots)</td>
</tr>
</tbody>
</table>

Value
Taxa labels with padding characters added

Author(s)
Guangchuang Yu and Yonghe Xia

References
https://groups.google.com/g/bioc-ggtree/c/INJ0Nfkq3b0/m/lXefnfV5AQAJ

Examples
library(ggtree)
set.seed(2015-12-21)
tree <- rtree(5)
tree$tip.label[2] <- "long string for test"
label_pad(tree$tip.label)
**layoutDaylight**

*Equal daylight layout method for unrooted trees.*

---

**Description**

```
#' @title
```

**Usage**

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

**Arguments**

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

**Value**

tree as data.frame with equal angle layout.

**References**

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

Leafs are subtrees with no children
Initialise tree using equal angle algorithm
```R
tree_df = equal_angle(tree)
```

nodes = get list of nodes in tree_df breadth-first
nodes = remove tip nodes.

---

**layoutEqualAngle**

*layoutEqualAngle*

---

**Description**

'Equal-angle layout algorithm for unrooted trees'

**Usage**

```R
layoutEqualAngle(model, branch.length = "branch.length")
```
Arguments

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

Value

tree as data.frame with equal angle layout.

References

"Inferring Phylogenies" by Joseph Felsenstein.

Description

transform circular/fan layout to rectangular layout
transform rectangular layout to circular layout
transform rectangular/circular layout to inward circular layout
transform rectangular/circular layout to fan layout
transform rectangular layout to dendrogram layout

Usage

layout_rectangular()
layout_circular()
layout_inward_circular(xlim = NULL)
layout_fan(angle = 180)
layout_dendrogram()

Arguments

xlim : setting x limits, which will affect the center space of the tree
angle : open tree at specific angle

Author(s)

Guangchuang Yu
**Examples**

```r
tree <- rtree(20)
p <- ggtree(tree, layout = "circular") + layout_rectangular()
tree <- rtree(20)
p <- ggtree(tree)
p + layout_circular()
tree <- rtree(20)
p <- ggtree(tree)
p + layout_inward_circular(xlim=4) + geom_tiplab(hjust=1)
tree <- rtree(20)
p <- ggtree(tree)
p + layout_fan(angle=90)
tree <- rtree(20)
p <- ggtree(tree)
p + p + layout_dendrogram()
```

---

**Description**

visualize phylogenetic tree with multiple sequence alignment

**Usage**

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

**Arguments**

- `p` tree view
- `fasta` fasta file that contains multiple sequence alignment information
- `offset` set the offset of MSA to tree
- `width` total width of alignment, compare to width of tree, defaults to 1, which means they are of the same length
- `color` set color of the tree
- `window` specific a slice of alignment to display
- `bg_line` whether to add background line in alignment, defaults to "TRUE"
- `height` height ratio of sequence, defaults to 0.8
multiplot

Value

tree view

Author(s)

Guangchuang Yu

References

For demonstration of this function, please refer to chapter 7.4 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

multiplot  multiplot

Description

plot multiple ggplot objects in one page

Usage

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

Arguments

  ...       plots
  plotlist  plot list
  ncol      set the number of column to display the plots
  widths    the width of each plot
  labels    set labels for labeling the plots
  label_size set font size of the label

Value

plot

Author(s)

Guangchuang Yu
nodebar

Description

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

Usage

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

Arguments

data a data.frame of stats with an additional column of node number named "node"
cols columns of the data.frame that store the stats
color set color of bars
alpha set transparency of the charts
position position of bars, if 'stack' (default) make bars stacked atop one another, 'dodge' make them dodged side-to-side

Value

list of ggplot objects

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,
    outline.color = "transparent",
    outline.size = 0
)

Arguments

data  a data.frame of stats with an additional column of node number named "node"
cols  columns of the data.frame that store the stats
color  set color of bars
alpha  set transparency of the charts
outline.color  color of outline
outline.size  size of outline

Value

list of ggplot objects

Author(s)

Guangchuang Yu

Description

transform a tree in either rectangular or circular layout into the fan layout that opens with a specific angle

Usage

open_tree(treeview, angle)

Arguments

treeview  tree view in rectangular/circular layout
angle  open the tree at a specific angle

Value

updated tree view

Author(s)

Guangchuang Yu

Examples

tree <- rtree(15)
p <- ggtree(tree) + geom_tiplab()
open_tree(p, 180)
Description
format a list of range (HPD, CI, etc that has length of 2)

Usage
range_format(x, trans = NULL)

Arguments
x input list
trans transformation function

Value
character vector of [lower, upper]

Author(s)
Guangchuang Yu

reexports
Objects exported from other packages

Description
These objects are imported from other packages. Follow the links below to see their documentation.

ape read.tree, rtree
aplot plot_list
dplyr collapse
ggfun identify
ggplot2 aes, fortify, geom_label, geom_point, geom_text, ggplot, ggsave, guide_legend,
        margin, scale_color_manual, scale_colour_manual, scale_fill_manual, scale_x_continuous,
        theme, xlim
grid arrow, unit
magrittr %>%
tidytree groupClade, groupOTU, MRCA, nodeid, nodelab
revts

Description
reverse timescale x-axis by setting the most recent tip to 0

Usage
revts(treeview)

Arguments
treeview original tree view

Details
'scale_x_continuous(labels=abs)' is required if users want to set the x-axis label to absolute value

Value
updated tree view

Author(s)
Guangchuang Yu

Examples
tr <- rtree(10)
p <- ggtree(tr) + theme_tree2()
p2 <- revts(p)
p2 + scale_x_continuous(labels=abs)

rotate

Description
rotate selected clade by 180 degree

Usage
rotate(tree_view = NULL, node)
rotateTreePoints.df

Arguments

- **tree_view**: tree view (i.e. the ggtree object). If tree_view is NULL, the last ggplot object will be used.
- **node**: internal node number to specify a clade. If NULL, using the whole tree

Value

ggplot2 object

Author(s)

Guangchuang Yu

Examples

```r
x <- rtree(15)
p <- ggtree(x) + geom_tiplab()
rotate(p, 17)
```

---

rotateTreePoints.df rotateTreePoints.data.frame

Description

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

Usage

```r
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 $[0, 2\pi]$, i.e. degrees/180, radians/pi

Value

updated tree data.frame with points rotated by angle
**rotate_tree**

**Description**

rotate circular tree in a certain angle

**Usage**

rotate_tree(treeview, angle)

**Arguments**

- treeview: tree view in circular layout
- angle: the angle of rotation

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

**Examples**

tree <- rtree(15)
p <- ggtree(tree) + geom_tiplab()
p2 <- open_tree(p, 180)
rotate_tree(p2, 180)

**scaleClade**

**Description**

zoom out/in a selected clade to emphasize or de-emphasize it

**Usage**

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

Arguments

- `tree_view`: tree view (i.e. the ggtree object). If `tree_view` is NULL, the last ggplot object will be used.
- `node`: internal node number to specify a clade. If NULL, using the whole tree
- `scale`: the scale of the selected clade. The clade will be zoom in when `scale > 1`, and will be zoom out when `scale < 1`
- `vertical_only`: logical. If TRUE (default), only vertical will be scaled. If FALSE, the clade will be scaled vertical and horizontally.

Value

tree view

Author(s)

Guangchuang Yu

Examples

```r
x <- rtree(15)
p <- ggtree(x) + geom_tiplab() +
  geom_nodelab(aes(subset=!isTip, label=node), hjust = -.1, color = "red")
scaleClade(p, 24, scale = .1)
```

scale_color

scale_color method

scale color by a numerical tree attribute

Usage

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

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

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

Arguments

- `object`: treedata object
- `by`: one of numerical attributes
- `...`: additional parameter
Value
color vector

scale_color_subtree  scale_color_subtree

Description
scale tree color by subtree (e.g., output of cutree, kmeans, or other clustering algorithm)

Usage
scale_color_subtree(group)
scale_colour_subtree(group)

Arguments
group  taxa group information

Value
updated tree view

Author(s)
Guangchuang Yu

scale_x_ggtree  scale_x_ggtree

Description
scale x for tree with gheatmap

Usage
scale_x_ggtree(breaks = waiver(), labels = waiver())

Arguments
breaks  set breaks for tree
labels  lables for corresponding breaks
**Details**
Since setting x-axis for tree with gheatmap by using 'theme_tree2()' is quite tricky, 'scale_x_ggtree' can help set the x-axis more reasonably.

**Value**
updated tree view

**Author(s)**
Guangchuang Yu

**References**
For more detailed demonstration of this function, please refer to chapter 7.3 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

---

**scale_x_range**

**Description**
add second x-axis for geom_range

**Usage**
scale_x_range()

**Details**
notice that the first axis is disabled in the default theme thus users need to enable it first before using scale_x_range

**Value**
ggtree object

**Author(s)**
Guangchuang Yu

**References**
For demonstration of this function ,please refer to chapter 5.2.4 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.
set_hilight_legend

**Description**

set legend for multiple geom_hilight layers

**Usage**

```r
set_hilight_legend(p, color, label, alpha = 1)
```

**Arguments**

- `p`: ggtree object
- `color`: color vector
- `label`: label vector
- `alpha`: transparency of color

**Value**

updated ggtree object

**Author(s)**

Guangchuang Yu

---

**StatBalance**

**Description**

StatBalance
Description

filter data for tree annotation layer

Usage

td_filter(..., .f = NULL)

Arguments

... Expressions that return a logical value.

.f a function (if any, defaults to NULL) that pre-operate the data

Details

The 'td_filter()' function returns another function that can be used to subset ggtree() plot data. The function can be passed to the 'data' parameter of geom layer to perform subsetting. All rows that satisfy your conditions will be retained.

Value

A function to filter ggtree plot data using conditions defined by '...'.

Author(s)

Guangchuang Yu

References

For more detailed demonstration of this function, please refer to chapter 12.5.1 of Data Integration, Manipulation and Visualization of Phylogenetic Trees http://yulab-smu.top/treedata-book/index.html by Guangchuang Yu.

See Also

filter

Examples

tree <- rtree(30)
## similar to 'ggtree(tree) + geom_tippoint()'
ggtree(tree) + geom_point(data = td_filter(isTip))
**td_mutate**  

**td-mutate**

**Description**

mutate data for tree annotation layer

**Usage**

```
td_mutate(..., .f = NULL)
```

**Arguments**

- `...`: additional parameters that pass to `dplyr::mutate`
- `.f`: a function (if any, defaults to NULL) that pre-operate the data

**Details**

The `td_mutate()` function returns another function that can be used to mutate `ggtree()` plot data. The function can be passed to the 'data' parameter of geom layer to perform adding new variables and preserving existing ones.

**Value**

A function to mutate `ggtree` plot data

**See Also**

- `mutate`

---

**td_unnest**

**td-unnest**

**Description**

flatterns a list-column of data frame

**Usage**

```
td_unnest(cols, ..., .f = NULL)
```

**Arguments**

- `cols`: columns to unnest
- `...`: additional parameters that pass to `tidyr::unnest`
- `.f`: a function (if any, defaults to NULL) that pre-operate the data
Details

The `td_unnest` function returns another function that can be used to unnest `ggtree()` plot data. The function can be passed to the 'data' parameter of a geom layer to flatten list-column tree data.

Value

A function to unnest `ggtree` plot data

Author(s)

Guangchuang Yu

References

For demonstration of this function, please refer to chapter 12.5.2 of *Data Integration, Manipulation and Visualization of Phylogenetic Trees* [http://yulab-smu.top/treedata-book/index.html](http://yulab-smu.top/treedata-book/index.html) by Guangchuang Yu.

See Also

`unnest`

---

**theme_dendrogram**

**theme_dendrogram**

Description
dendrogram theme

Usage
dtheme_dendrogram(bgcolor = "white", fgcolor = "black", ...)

Arguments

- `bgcolor`: set background color, defaults to "white"
- `fgcolor`: set color of axis
- `...`: additional parameter

Author(s)

Guangchuang Yu
theme_inset

Description
inset theme

Usage
theme_inset(legend.position = "none", ...)

Arguments
legend.position
  set the position of legend
...
  additional parameter

Details
theme for inset function

Value
ggplot object

Author(s)
Guangchuang Yu

theme_tree

Description
tree theme

Usage
theme_tree(bgcolor = "white", ...)

Arguments
bgcolor
  set background color, defaults to "white"
...
  additional parameter
'theme_tree' defines a blank background to display tree

updated ggplot object with new theme

Guangchuang Yu

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

---

```
theme_tree2  theme_tree2
```

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

```
bgcolor  set background color, defaults to "white"
fgcolor  set foreground color, defaults to "black"
...      additional parameter
```

'theme_tree2' supports displaying phylogenetic distance by setting x-axis

updated ggplot object with new theme

Guangchuang Yu
Examples

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

---

### Description

view a selected clade of tree, clade can be selected by specifying a node number or determined by the most recent common ancestor of selected tips

### Usage

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

### Arguments

- **tree_view**  
  tree view (i.e. the ggtree object). If `tree_view` is `NULL`, the last ggplot object will be used.
- **node**  
  internal node number to specify a clade. If `NULL`, using the whole tree
- **xmax_adjust**  
  adjust the max range of x axis

### Value

clade plot

### Author(s)

Guangchuang Yu

### Examples

```r
x <- rtree(15)
p <- ggtree(x) + geom_tiplab()
viewClade(p, 18, xmax_adjust = 0.)
```
**xlim_expand**

**Description**

expand x axis limits for specific panel

**Usage**

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

**Arguments**

- `xlim`: x axis limits
- `panel`: name of the panel to expand

**Value**

updated tree view

**Author(s)**

Guangchuang Yu

**Examples**

```r
x <- rtree(30)
p <- ggtree(x) + geom_tiplab()
d <- data.frame(label = x$tip.label,
                value = rnorm(30))
p2 <- p + geom_facet(panel = "Dot", data = d,
                    geom = geom_point, mapping = aes(x = value))
p2 + xlim_expand(c(-10, 10), 'Dot')
```

---

**xlim_tree**

**Description**

set x axis limits specially for Tree panel

**Usage**

```r
xlim_tree(xlim)
```
Arguments

\texttt{xlim} \quad \text{x axis limits}

Value

updated tree view

Author(s)

Guangchuang Yu

Examples

\begin{verbatim}
  x <- rtree(30)
p <- ggtree(x) + geom_tiplab()
d <- data.frame(label = x$tip.label,
                 value = rnorm(30))
p2 <- p + geom_facet(panel = "Dot", data = d,
                     geom = geom_point, mapping = aes(x = value))
p2 + xlim_tree(6)
\end{verbatim}

Description

zoom in on a selected clade of a tree, while showing its on the full view of tree as a seperated panel for reference

Usage

\begin{verbatim}
  zoomClade(tree_view = NULL, node, xexpand = NULL)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{tree_view} \quad \text{tree view (i.e. the ggtree object). If tree_view is NULL, the last ggplot object will be used.}
  \item \texttt{node} \quad \text{internal node number to specify a clade. If NULL, using the whole tree}
  \item \texttt{xexpand} \quad \text{numeric, expend the xlim of the zoom area. default is NULL.}
\end{itemize}

Value

full tree with zoom in clade

Author(s)

Guangchuang Yu
### Examples

```r
## Not run:
x <- rtree(15)
p <- ggtree(x) + geom_tiplab() +
   geom_nodelab(aes(subset=!isTip, label=node), hjust = -.1, color = "red")
   zoomClade(p, 21, xexpand = .2)

## End(Not run)
```

### Description

update data with tree info (y coordination and panel)

### Usage

```r
p %>% .data
```

### Arguments

- `p`  
  tree view
- `.data`  
  data.frame

### Details

add tree information to an input data. This function will setup y coordination and panel info for data used in facet_plot and geom_facett

### Value

updated data.frame

### Author(s)

Guangchuang Yu

### References

Description

add annotation data to a tree

Usage

pg %<+% data

Arguments

pg ggplot2 object
data annotation data that contains a column of “node”, or the first column of taxa labels

Details

This operator attaches annotation data to a ggtree graphic object

Value

ggplot object with annotation data added

Author(s)

Guangchuang Yu

References


See Also

geom_facet

Examples

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

Usage
pg %<% x

Arguments
pg ggtree object
x tree object

Details
This operator apply the visualization directives in ggtree object (lhs) to visualize another tree object (rhs), that is similar to Format Painter.

Value
updated ggplot object

Author(s)
Guangchuang Yu

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