

Package ‘ggtreeDendro’

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Title Drawing 'dendrogram' using 'ggtree'

Version 1.6.0

Description Offers a set of 'autoplot' methods to visualize tree-like structures (e.g., hierarchical clustering and classification/regression trees) using 'ggtree'. You can adjust graphical parameters using grammar of graphic syntax and integrate external data to the tree.

Depends ggtree (>= 3.5.3)

Imports ggplot2, stats, tidytree, utils

Suggests aplot, cluster, knitr, MASS, mdendro, prettydoc, pvclust, rmarkdown, testthat (>= 3.0.0), treeio, yulab.utils

License Artistic-2.0

VignetteBuilder knitr

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biocViews Clustering, Classification, DecisionTree, Phylogenetics, Visualization

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| | |
|------------------|-------------------------|
| geom_line_cutree | <i>geom_line_cutree</i> |
|------------------|-------------------------|

Description

geom_line_cutree

Usage

```
geom_line_cutree(group, linetype = "dashed", offset = 0, ...)
```

Arguments

| | |
|----------|-----------------------------------------------------------------|
| group | output of cutree or number of subtree |
| linetype | linetype |
| offset | offset of the line |
| ... | additional parameters to set the line (e.g., color, size, etc.) |

Value

line layer

Examples

```
d <- dist(USArrests)
hc <- hclust(d, "ave")
autoplot(hc) + geom_line_cutree(4)
```

| | |
|-------------------|--------------------------|
| geom_rect_subtree | <i>geom_rect_subtree</i> |
|-------------------|--------------------------|

Description

geom_rect_subtree

Usage

```
geom_rect_subtree(group = NULL, color = "red", ...)
```

Arguments

| | |
|-------|---------------------------------------------------|
| group | output of cutree or number of subtree |
| color | border color to highlight subtrees |
| ... | additional parameters pass to 'ggtree::highlight' |

Value

rect layer

See Also

[geom_highlight](#);

Examples

```
d <- dist(USArrests)
hc <- hclust(d, "ave")
autoplot(hc) + geom_rect_subtree(4)
```

| | |
|--------------|---------------------------------------------------------------------------------------------|
| ggtreeDendro | <i>providing autoplot methods for many hierarchical clustering results based on ggtree.</i> |
|--------------|---------------------------------------------------------------------------------------------|

Description

This package implements a set of 'autoplot()' methods to display tree structure. The output of it is a 'ggtree' object, which can be annotated by adding layers using 'ggplot2' syntax. Users also can integrate associated data to annotate the tree using 'ggtree' and 'ggtreeExtra' packages.

reexports

Objects exported from other packages

Description

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

ggplot2 [autoplot](#)

Usage

```
## S3 method for class 'hclust'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'linkage'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'dendrogram'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'agnes'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'diana'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'twins'  
autoplot(object, layout = "dendrogram", ladderize = FALSE, hang = 0.1, ...)
```

```
## S3 method for class 'bclust'  
autoplot(object, ...)
```

```
## S3 method for class 'hdbscan'  
autoplot(object, ...)
```

```
## S3 method for class 'hkmeans'  
autoplot(object, ...)
```

```
## S3 method for class 'dendro'  
autoplot(object, ...)
```

```
## S3 method for class 'pvclust'  
autoplot(  
  object,  
  layout = "dendrogram",  
  ladderize = FALSE,  
  label_edge = FALSE,
```

```

    pvrect = FALSE,
    alpha = 0.95,
    hang = 0.1,
    ...
)

## S3 method for class 'ClusterExperiment'
autoplot(object, layout = "rectangular", ...)

## S3 method for class 'genoMatrixeR'
autoplot(object, hctype = "rows", ...)

## S3 method for class 'multiLocalZScore'
autoplot(object, ...)

```

Arguments

| | |
|------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| object | input object |
| layout | layout for plotting the tree |
| ladderize | logical whether ladderize the tree (default FALSE) |
| 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. |
| ... | additional paramters that passed to ggtree |
| label_edge | logical whether display the label of edge (only for pvclust object), default is FALSE. |
| pvrect | logical whether display the clusters with relatively high/low p-values, default is FALSE. (only for pvclust object) |
| alpha | numeric the threshold value for p-values, default is 0.95 (only for pvclust object). |

Value

ggtree object

Examples

```

d <- dist(USArrests)
hc <- hclust(d, "ave")
autoplot(hc) + geom_tiplab()

```

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)

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Examples

```
d <- dist(USArrests)
hc <- hclust(d, "ave")
autoplot(hc) + scale_color_subtree(3)
```

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