

Package ‘ggtreeDendro’

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Title Drawing 'dendrogram' using 'ggtree'

Version 1.0.0

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

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

License Artistic-2.0

VignetteBuilder knitr

ByteCompile true

Encoding UTF-8

biocViews Clustering, Classification, DecisionTree, Phylogenetics, Visualization

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

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geom_line_cutree	<i>geom_line_cutree</i>
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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)
```

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

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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