Package 'ggtreeDendro'

October 15, 2023

Title Drawing 'dendrogram' using 'ggtree'

Version 1.2.1

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

ByteCompile true

Encoding UTF-8

biocViews Clustering, Classification, DecisionTree, Phylogenetics, Visualization

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/ggtreeDendro

git_branch RELEASE_3_17

git_last_commit 0c52dc5

git_last_commit_date 2023-08-18

Date/Publication 2023-10-15

Author Guangchuang Yu [aut, cre, cph]
    (<https://orcid.org/0000-0002-6485-8781>),
    Shuangbin Xu [ctb] (<https://orcid.org/0000-0003-3513-5362>),
    Chuanjie Zhang [ctb]

Maintainer Guangchuang Yu <guangchuangyu@gmail.com>

R **topics documented:**

---

geom_line_cutree *geom_line_cutree*

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 *geom_rect_subtree*

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::hilight()'

Value

rect layer

See Also

geom_hilight;

Examples

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

---

ggtreeDendro *providing autoplot methods for many hierarchical clustering results based on ggtree.*

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 '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)

Guangchuang Yu

Examples

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

Index