Package ‘ggtreeDendro’

April 3, 2024

Title Drawing ‘dendrogram’ using ‘ggtree’

Version 1.4.0

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, markdown, 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_18

git_last_commit 32d96cd

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-03

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>
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)
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

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

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

```r
## 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,
)```
reexports

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 parameters 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()
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

* internal
  * reexports, 4

autoplot, 4
autoplot (reexports), 4

gem_hilight, 3
gem_line_cutree, 2
gem_rect_subtree, 3
ggtreeDendro, 3

reexports, 4

scale_color_subtree, 6
scale_colour_subtree
  * (scale_color_subtree), 6