Package ‘ggtreeDendro’

January 26, 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

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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)
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.
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 ob-
ject).

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)
Guangchuan Yu

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

* internal
  reexports, 4

autoplot, 4
autoplot (reexports), 4

geom_hilight, 3
gemm_line_cutree, 2
geom_rect_subtree, 3
ggtreeDendro, 3

reexports, 4

scale_color_subtree, 6
scale_colour_subtree
  (scale_color_subtree), 6