Package: ggtreeDendro (via r-universe)

October 10, 2026

Title Drawing 'dendrogram' using 'ggtree'

Version 1.15.0

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

ByteCompile true

Encoding UTF-8

biocViews Clustering, Classification, DecisionTree, Phylogenetics, Visualization

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.0

Config/testthat/edition 3

Config/pak/sysreqs
libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev make libicu-dev libpng-dev libuv1-dev

Repository https://bioc.r-universe.dev

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`autoplot` *autoplot*

Description

autoplot

Usage

```
autoplot(object, ...)

## 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
...	additional paramters that passed to ggtree
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.
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()
```

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)
```

`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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