Package ‘ggtreeDendro’

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Title Drawing 'dendrogram' using 'ggtree'

Version 1.10.0

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

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biocViews Clustering, Classification, DecisionTree, Phylogenetics, Visualization

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`ggtreeDendro-package` *ggtreeDendro: Drawing 'dendrogram' using 'ggtree'*

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.

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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)

Guangchuang Yu

Examples

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

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