

# Package ‘ggtreeDendro’

December 23, 2024

**Title** Drawing 'dendrogram' using 'ggtree'

**Version** 1.8.0

**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

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

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### 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.

### Author(s)

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autoplot	<i>autoplot</i>
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### 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*

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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)
```

---

geom\_rect\_subtree      *geom\_rect\_subtree*

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**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::highlight()'

**Value**

rect layer

**See Also**

[geom\\_highlight](#);

**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
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**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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