

# Package ‘ggtreeDendro’

April 15, 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, 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** 7.2.3

**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** 2024-04-15

**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](mailto:guangchuangyu@gmail.com)>

**R topics documented:**

|                               |   |
|-------------------------------|---|
| geom_line_cutree . . . . .    | 2 |
| geom_rect_subtree . . . . .   | 3 |
| ggtreeDendro . . . . .        | 3 |
| reexports . . . . .           | 4 |
| scale_color_subtree . . . . . | 6 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>7</b> |
|--------------|----------|

---

|                  |                         |
|------------------|-------------------------|
| geom_line_cutree | <i>geom_line_cutree</i> |
|------------------|-------------------------|

---

**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 | <i>geom_rect_subtree</i> |
|-------------------|--------------------------|

---

### 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)
```

---

|              |   |
|--------------|---|
| ggtreeDendro | <i>providing autoplot methods for many hierarchical clustering results based on ggtree.</i> |
|--------------|---|

---

### 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

```
## 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   |
| 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 paramters 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()
```

---

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)
```

# Index

## \* **internal**

reexports, 4

autoplot, 4

autoplot (reexports), 4

geom\_highlight, 3

geom\_line\_cutree, 2

geom\_rect\_subtree, 3

ggtreeDendro, 3

reexports, 4

scale\_color\_subtree, 6

scale\_colour\_subtree  
(scale\_color\_subtree), 6