

# Package ‘ggtreeDendro’

December 5, 2025

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

**Version** 1.13.0

**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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**Author** Guangchuang Yu [aut, cre, cph] (ORCID: <https://orcid.org/0000-0002-6485-8781>),  
Shuangbin Xu [ctb] (ORCID: <https://orcid.org/0000-0003-3513-5362>),  
Chuanjie Zhang [ctb]

**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

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|                      |                                                          |
|----------------------|----------------------------------------------------------|
| ggtreeDendro-package | <i>ggtreeDendro: Drawing 'dendrogram' using 'ggtree'</i> |
|----------------------|----------------------------------------------------------|

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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)

**Maintainer:** Guangchuang Yu <guangchuangyu@gmail.com> ([ORCID](#)) [copyright holder]

Other contributors:

- Shuangbin Xu <xshuangbin@163.com> ([ORCID](#)) [contributor]
- Chuanjie Zhang <959264868@qq.com> [contributor]

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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 parameters 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()
```

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

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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)
```

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

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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::hilight()' |

**Value**

rect layer

**See Also**

[geom\\_hilight](#);

**Examples**

```
d <- dist(USArrests)
hc <- hclust(d, "ave")
autoplot(hc) + geom_rect_subtree(4)
```

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|                     |                            |
|---------------------|----------------------------|
| scale_color_subtree | <i>scale_color_subtree</i> |
|---------------------|----------------------------|

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**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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