

# Package: ggtreeDendro (via r-universe)

June 30, 2024

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

**Version** 1.7.0

**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

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/ggtreeDendro>

**RemoteRef** HEAD

**RemoteSha** d2ae38fd01049261e05af994760272f346c05fc8

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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)
```

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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::hilight()'

**Value**

rect layer

**See Also**

[geom\\_highlight](#);

**Examples**

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

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

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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)**

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**Examples**

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

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