

Package ‘colorhplot’

July 22, 2025

Type Package

Title Colorful Hierarchical Clustering Dendrograms

Version 1.5.1

Date 2025-06-02

Encoding UTF-8

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Description

Build dendrograms with sample groups highlighted by different colors. Visualize results of hierarchical clustering analyses as dendrograms whose leaves and labels are colored according to sample grouping. Assess whether data point grouping aligns to naturally occurring clusters.

Depends R (>= 3.0)

Imports graphics, methods

Suggests stats, grDevices, rmarkdown, knitr

VignetteBuilder knitr

License GPL-3

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-06-04 12:00:11 UTC

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colorhplot-package *Introduction to the colorhplot Package*

Description

This is a simple one-function package. Please, refer to the colorhplot() function manual to check how the function works.

Details

This package contains the function colorhplot. This function generates simple colorful dendrograms and requires only 2 mandatory arguments: hc and fac. The argument hc is the result of a hclust() call, while fac is a factor defining the groups. Therefore, the number of leaves of the dendrogram has to be identical to the length of fac (i.e., length(hc\$labels) == length(fac) has to be TRUE). The function colorhplot() employs a custom color palette. However, users can specify a custom list of colors.

Author(s)

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See Also

[colorhplot](#)

colorhplot *Colorful Hierarchical Clustering Dendrograms*

Description

Build colorful dendrograms based on a "hclust-class" object and a factor describing the sample groups. Leaves belonging to different groups are identified by colors, and the resulting plot enables detection of pure clusters where all leaves belong to the same group.

Usage

```
colorhplot(  
  hc,  
  fac,  
  hang = 0.1,  
  main = "Cluster Dendrogram",  
  colors = NULL,  
  lab.cex = 1,  
  ylim = NULL,  
  lwd = 3,  
  las = 1,  
  lab.mar = 0.55  
)
```

Arguments

hc	hclust-class object, typically the result of a 'hclust()' function call.
fac	factor that defines the grouping.
hang	hang value, as in hclust. This is the fraction of the plot height by which labels should hang below the rest of the plot. A negative value will align all labels at the bottom of the plot.
main	string, title of the dendrogram plot.
colors	NULL or a character vector of length 1 or having the same length as the number of levels in fac. This argument defines the palette for the plot.
lab.cex	numeric value for adjusting the font size of the leaf labels (and legend text).
ylim	numeric, defines the minimum and maximum value of the y-axis of the plot.
lwd	numeric value that defines the width (in points) of the lines of the dendrogram.
las	numeric value, graphic parameter for the orientation of the y-axis tick labels.
lab.mar	numeric value, fraction of the plot area that is reserved for the labels (at the bottom of the plot).

Details

In order to generate a colorful dendrogram, the colorhplot() function requires 2 mandatory arguments: hc and fac. hc is the result of a hclust() call, while fac is a factor defining the groups. The number of leaves of the dendrogram has to be identical to the length of fac.

Value

Calling colorhplot() returns a colorful dendrogram plot.

Note

Online colorhplot() function reference at: <http://www.biotechworld.it/bioinf/2015/09/30/colorful-hierarchical-clustering-dendrograms-with-r/>

Author(s)

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See Also

[hclust](#)

Examples

```
### Example 1, using the USArrests dataset
data(USArrests)
hc <- hclust(dist(USArrests), "ave")
fac <- as.factor(c(rep("group 1", 10),
                  rep("group 2", 10),
                  rep("unknown", 30)))
```

```
plot(hc)
colorhcplot(hc, fac)
colorhcplot(hc, fac, hang = -1, lab.cex = 0.8)

### Example 2: use the "ward.D2" algorithm and
### the UScitiesD dataset
data(UScitiesD)
hcity.D2 <- hclust(UScitiesD, "ward.D2")
fac.D2 <- as.factor(c(rep("group1", 3),
                     rep("group2", 7)))
plot(hcity.D2, hang=-1)
colorhcplot(hcity.D2, fac.D2, color = c("chartreuse2", "orange2"))
colorhcplot(hcity.D2, fac.D2, color = "gray30",
            lab.cex = 1.2, lab.mar = 0.75)

### Example 3: use gene expression data
data(geneData, package="colorhcplot")
exprs <- geneData$exprs
fac <- geneData$fac
hc <- hclust(dist(t(exprs)))
colorhcplot(hc, fac, main = "default", col = "gray10")
colorhcplot(hc, fac, main="Control vs. Tumor Samples")
```

geneData

Example Gene Expression Dataset

Description

This is a gene expression dataset simulating information about 499 gene probes and 13 samples, from an Affymetrix U95v2 chip. Data are made up, as well as sample labels. This dataset is adapted from the Biobase-package, version 2.32.0.

Usage

```
data("geneData")
```

Format

A list with 2 elements:

exprs A matrix with 499 rows (genes) and 13 columns (samples) containing normalized gene expression values.

fac A factor including the grouping for each sample.

Source

Data were adapted from the Biobase package version 2.32.0, and prepared by the J. Ritz Laboratory (S. Chiaretti).

geneData

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Examples

```
data(geneData)
print(geneData[[1]][1:10, 1:6])
```

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