

Package ‘bioplots’

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Type Package

Title Visualization of Overlapping Results with Heatmap

Version 0.0.1

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Description Visualization of complex biological datasets is essential to understand complementary aspects of biology in big data era.

In addition, analyzing of multiple datasets enables to understand biological processes deeply and accurately. Multiple datasets produce multiple analysis results, and these overlappings are usually visualized in Venn diagram. bioplots is a tiny R package that generates a heatmap to visualize overlappings instead of using Venn diagram.

Depends R (>= 3.0.1)

Imports gplots, RColorBrewer, ggplot2, reshape2

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NeedsCompilation no

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heatmap.overlaps *Plot heatmap*

Description

Plot heatmap to visualize multiple Venn diagram.

Usage

```
heatmap.overlaps(x, legend = NA, xlab = NA, ylab = NA, col = NA,  
  lim = NA, x.axis.angle = 90)
```

Arguments

x	A matrix object or a list object with two-levels.
legend	A legend for colors.
xlab	A label for the x axis.
ylab	A label for the y axis.
col	A character vector of colors. Default is Spectral color palette in RColorBrewer package.
lim	A range of values.
x.axis.angle	A angle for labels in x axis. Default is 90 degrees.

Value

ggplot class object

Examples

```
mat <- matrix(rnbinom(135, size = 10, prob = 0.2), nrow = 15, ncol = 9)  
colnames(mat) <- paste0("Treat", 1:9)  
rownames(mat) <- c("a", "b", "c", "d", "ab", "ac", "ad", "bc", "bd", "cd",  
  "abc", "abd", "acd", "bcd", "abcd")  
head(mat)  
  
heatmap.overlaps(mat)
```

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