Package 'splots'

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Version 1.58.0

Title Visualization of high-throughput assays in microtitre plate or slide format

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Imports grid, RColorBrewer

Suggests BiocStyle, knitr, rmarkdown, assertthat, HD2013SGI

VignetteBuilder knitr

Description This package is provided to support legacy code and reverse dependencies, but it should not be used as a dependency for new code development. It provides a single function, plotScreen, for visualising data in microtitre plate or slide format. As a better alternative for such functionality, please consider the platetools package on CRAN (https://cran.r-project.org/package=platetools and https://github.com/Swarchal/platetools), or generic ggplot2 graphics functionality.

License LGPL

LazyLoad yes

biocViews Visualization, Sequencing, MicrotitrePlateAssay

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plotScreen   *Plot a false-color representation of screening data*

Description

plotScreen produces a false-color representation of screening data from multiple plates (typical use case: dozens of plates) in a single plot.

Usage

```
plotScreen(z,
           ncol = 6L,
           zrange,
           main = "",
           do.names = TRUE,
           do.legend = TRUE,
           legend.label = deparse(substitute(z)),
           nx = 24,
           ny = 16,
           fill,
           na.fill = "grey" ,
           do.grid.newpage = TRUE)
```

Arguments

z	A list of plate data. Each element provides data for a plate and is expected to be a vector of length at least nx*ny (only the first nx*ny elements will be displayed). The values are assumed to come in row-by-row order, e.g. A1, A2, A3, ..., B1, B2, ... Alternatively, the elements of z can be factors that represent well or spot classes (e.g. the different types of controls, empty wells, wells with reagent of interest).
ncol	Integer of length 1. Number of columns (plates in one row) for the plot.
zrange	If the elements of z are numeric, then this optional parameter can be used to specify the numeric range that is mapped to the color scale; by default, a symmetric interval around the median of unlist(z) is used. If the elements of z are factors, then this optional parameter can be used to specify the total ordered set of factor levels; by default, the union of the levels of the elements of z is used.
fill	If the elements of z are numeric, then this parameter can be used to specify a character vector of color names used to create a color ramp for the false color data representation. The default colors correspond to blue for low values, white for the middle of the range and red for high values. If the elements of z are factors, then this parameter can be used to define the corresponding color names; by default, a palette from RColorBrewer is used.
main	Character of length 1 or plotmath expression used for the plot title. To omit, set this argument to length 0, to the empty character "", to FALSE or to NULL.

do.names	Logical specifiying if plate captions should be plotted.
do.legend	Logical specifying if a legend for false color values should be output.
legend.label	Character of length 1 or plotmath expression that is printed next to the legend (see vignette for examples). To omit, set this argument to length 0, to the empty character `""`, to FALSE or to NULL.
nx	An integer for the number of columns in a plate. Default 24 for a 384-well plate.
ny	An integer for the number of rows in a plate. Default 16 for a 384-well plate.
na.fill	Color for NA values.
do.grid.newpage	
	Logical, if TRUE, then the function `grid.newpage` is called at the begin of this function.

Value

None. The function is called for its side effect.

Author(s)

Wolfgang Huber, based on an earlier version by Oleg Sklyar.

Examples

```
screen = lapply(1:12, function(i) cumsum(rnorm(384)))
plotScreen(screen, ncol=3, fill=c("white", "darkblue"))
```

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