

Package ‘splots’

April 24, 2025

Version 1.74.0

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

Author Wolfgang Huber, Oleg Sklyar

Maintainer Wolfgang Huber <wolfgang.huber@embl.org>

Imports grid, RColorBrewer

Suggests BiocStyle, knitr, rmarkdown, assertthat, HD2013SGI, dplyr, ggplot2

VignetteBuilder knitr

Description This package is here to support legacy usages of it, but it should not be used 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 `ggplot2` (`geom_raster`, `facet_wrap`) as exemplified in the vignette of this package.

License LGPL

LazyLoad yes

biocViews Visualization, Sequencing, MicrotitrePlateAssay

git_url <https://git.bioconductor.org/packages/splots>

git_branch RELEASE_3_21

git_last_commit 8766bd8

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-04-23

Contents

plotScreen	2
Index	4

plotScreen

Plot a false-color representation of screening data

Description

This function is obsolete, please use ggplot with geom_raster and facet_wrap instead, as described in the vignette of the splots package.

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. |

<code>main</code>	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.
<code>do.names</code>	Logical specifying if plate captions should be plotted.
<code>do.legend</code>	Logical specifying if a legend for false color values should be output.
<code>legend.label</code>	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.
<code>nx</code>	An integer for the number of columns in a plate. Default 24 for a 384-well plate.
<code>ny</code>	An integer for the number of rows in a plate. Default 16 for a 384-well plate.
<code>na.fill</code>	Color for NA values.
<code>do.grid.newpage</code>	Logical, if TRUE, then the function <code>grid.newpage</code> 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"))
```

Index

- * **array**
 - plotScreen, [2](#)
- * **dplot**
 - plotScreen, [2](#)

plotScreen, [2](#)