visDmatHeatmap

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visDmatHeatmap | *Function to visualise gene clusters/bases partitioned from a supra-hexagonal grid using heatmap*

Description

visDmatHeatmap is supposed to visualise gene clusters/bases partitioned from a supra-hexagonal grid using heatmap

Usage

```
visDmatHeatmap(sMap, data, sBase, base.color = "rainbow",
base.separated.arg = NULL, base.legend.location = c("none",
"bottomleft",
"bottomright", "bottom", "left", "topleft", "top", "topright", "right",
"center"), reorderRow = c("none", "hclust", "svd"), keep.data = F, ...)
```

Arguments

sMap | an object of class "sMap" or a codebook matrix

data | a data frame or matrix of input data

sBase | an object of class "sBase"

base.color | short name for the colormap used to encode bases (in row side bar). It can be one of "jet" (jet colormap), "bwr" (blue-white-red colormap), "gbr" (green-black-red colormap), "wyr" (white-yellow-red colormap), "br" (black-red colormap), "yr" (yellow-red colormap), "wb" (white-black colormap), and "rainbow" (rainbow colormap, that is, red-yellow-green-cyan-blue-magenta). Alternatively, any hyphen-separated HTML color names, e.g. "blue-black-yellow", "royalblue-white-sandybrown", "darkgreen-white-darkviolet". A list of standard color names can be found in http://html-color-codes.info/color-names

base.separated.arg
| a list of main parameters used for styling bar separated lines. See 'Note' below for details on the parameters

base.legend.location
| location of legend to describe bases. If "none", this legend will not be displayed

1

reorderRow	the way to reorder the rows within a base. It can be "none" for rows within a base being reorded by the hexagon indexes, "hclust" for rows within a base being reorded according to hierarchical clustering of patterns seen, "svd" for rows within a base being reorded according to svd of patterns seen
keep.data	logical to indicate whether or not to also write out the input data. By default, it sets to false for not keeping it. It is highly expensive to keep the large data sets
...	additional graphic parameters used in "visHeatmapAdv". For most parameters, please refer to http://www.inside-r.org/packages/cran/gplots/docs/heatmap.2

Value

a data frame with following components:

- ID: ID for data. It inherits the rownames of data (if exists). Otherwise, it is sequential integer values starting with 1 and ending with dlen, the total number of rows of the input data
- Hexagon_index: the index for best-matching hexagons
- Cluster_base: optional, it is only appended when sBase is given. It stores the cluster memberships/bases
- data: optional, it is only appended when keep.data is true

Note: the returned data has rows in the same order as visualised in the heatmap

Note

A list of parameters in "base.separated.arg":

- "lty": the line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "blank","solid","dashed","dotted","dotdash","longdash","twodash", where "blank" uses 'invisible lines' (i.e., does not draw them)
- "lwd": the line width
- "col": the line color

See Also

[sDmatCluster](), [visHeatmapAdv]()

Examples

```
# 1) generate an iid normal random matrix of 100x10
data <- matrix( rnorm(100*10,mean=0,sd=1), nrow=100, ncol=10)

# 2) get trained using by default setup
sMap <- sPipeline(data=data)

# 3) partition the grid map into clusters using region-growing algorithm
sBase <- sDmatCluster(sMap=sMap, which_neigh=1,
distMeasure="median", clusterLinkage="average")

# 4) heatmap visualisation
output <- visDmatHeatmap(sMap, data, sBase,
base.legend.location="bottomleft", labRow=NA)
```