Package 'FlexDotPlot'

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Title Flexible Dot Plot

Version 0.2.2

Description Flexible Dotplot and Pacman plot for multimodal data.

Depends R (>= 3.6.0)

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Imports ggplot2, grDevices, stats, FactoMineR, scales, reshape2,
   ggdendro, grImport2, grid, gridExtra, sisal, dendextend, shiny,
   shinydashboard, shinyWidgets, ggforce, colourpicker, htmltools,
   bsplus, DT, magrittr

Suggests knitr, rmarkdown, markdown,

VignetteBuilder knitr

URL https://github.com/Simon-Leonard/FlexDotPlot

BugReports https://github.com/Simon-Leonard/FlexDotPlot/issues

NeedsCompilation no

Author Simon Leonard [aut, cre] (<https://orcid.org/0000-0002-6437-5800>)

Maintainer Simon Leonard <simon.leonard@univ-rennes1.fr>

Repository CRAN

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R topics documented:

CBMC8K_example_data   *CBMC 8K example dataset*

Description

A dataset containing expression informations of 12 genes in 11 celltypes. Original dataset from seurat-data package.

Usage

```
data(CBMC8K_example_data)
```

Format

A data frame with 132 rows and 12 variables

Details

- features.plot. Gene symbol
- id. Cell type
- RNA.pct.exp. RNA level : Percentage of cells expressing the gene in the cell type
- RNA.avg.exp. RNA level : Average expression of the gene in the cell type
- RNA.avg.exp.log2p1. RNA.avg.exp with log2(x+1) tranformation
- RNA.avg.exp.scaled. RNA level : Scaled average expression
- ADT.pct.exp.sup0. ADT level : Percentage of cells expressing the gene in the cell type (with expression >0)
- ADT.pct.exp.sup.cutoff. ADT level : Percentage of cells expressing the gene in the cell type (with expression > background)
- ADT.avg.exp. ADT level : Average expression of the gene in the cell type
- ADT.avg.exp.log2p1. ADT.avg.exp with log2(x+1) tranformation
- ADT.avg.exp.scaled. ADT level : Scaled average expression
- canonical_marker. If the gene is a canonical marker of the cell type (yes or no)

References

https://github.com/satijalab/seurat-data

CellphoneDB_example_data

CellphoneDB example dataset

Description

A dataset containing CellPhoneDB results of 11 gene pairs in 10 combinations of 2 cell types. Raw data obtained in doi: 10.1016/j.ccell.2021.02.015. Script used to generate this dataset from the raw data is available in the FlexDotPlot_cellphoneDB_dataset vignette.

Usage

```
data(CellphoneDB_example_data)
```

Format

A data frame with 55 rows and 11 variables

Details

- pair. Gene pair

- clusters. Cell type pair

- pvalue. pvalue from CellPhoneDB

- mean. Log2 mean (gene pair expressions) from CellPhoneDB

- mean1. Average expression of the first gene in the first cell type

- mean2. Average expression of the second gene in the second cell type

- pct1. Percentage of cells from the first cell type expressing the first gene

- pct2. Percentage of cells from the second cell type expressing the second gene

- log2mean1. mean1 with log2 transformation

- log2mean2. mean2 with log2 transformation

- log10pval. pvalue with -log10 transformation

References

doi: 10.1016/j.ccell.2021.02.015

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dot_plot   *Dot-plot - Pacman-plot function*

Description

Create dotplots to represent two discrete factors (x & y) described by several other factors. Each combination of the two discrete factors (x & y) can be described with : 1 continuous factor (setting shape size), 3 continuous or discrete factors (setting shape type, shape color and text on shape).

Usage

```
dot_plot(
  data.to.plot,
  size_var = NA,
  col_var = NA,
  text_var = NA,
  shape_var = 16,
  size_legend = "",
  col_legend = "",
  shape_legend = "",
  cols.use = "default",
  text.size = NA,
  text.vjust = 0,
  shape_use = "default",
  shape.scale = 12,
  scale.by = "radius",
  scale.min = NA,
  scale.max = NA,
  plot.legend = TRUE,
  do.return = FALSE,
  x.lab.pos = c("both", "top", "bottom", "none"),
  y.lab.pos = c("left", "right", "both", "none"),
  x.lab.size.factor = 1,
  y.lab.size.factor = 1,
  vertical_coloring = NA,
  horizontal_coloring = NA,
  size.breaks.number = 4,
  color.breaks.number = 5,
  shape.breaks.number = 5,
  size.breaks.values = NA,
  color.breaks.values = NA,
  shape.breaks.values = NA,
  display_max_sizes = TRUE,
  transpose = FALSE,
  dend_x_var = NULL,
  dend_y_var = NULL,
  dist_method = c("euclidean", "maximum", "manhattan", "canberra", "binary",
```

```
        "minkowski"),
    hclust_method = c("ward.D", "single", "complete", "average", "mcquitty", "median",
        "centroid", "ward.D2"),
     do.plot = TRUE
)
```

Arguments

data.to.plot	Input data. Can be a list or a data.frame. If data.frame : Column 1 = x axis (Factor); Col2= y axis (Factor). If list : x and y axis are fixed by row and col names of list elements.
size_var	If numeric : Column/List index which control shape sizes. This column/element has to be numeric. Can also be a column/element name or a vector of the same size than the input dataset. Set to NA if you don't want to control shape size.
col_var	If numeric : Column/List index which control shape colors. Can also be a column/element name or a vector of the same size than the input dataset. Set to NA if you don't want to control shape color.
text_var	If numeric : Column/List index which control text to add on shapes. Can also be a column/element name or a vector of the same size than the input dataset. Set to NA if you don't want to add text.
shape_var	If numeric = Similar to pch : square=15; circle=16; triangle=17. Can also be a column/element name or a vector of the same size than the input dataset.
size_legend	Custom name of shape legend.
col_legend	Custom name of shape color.
shape_legend	Name of the shape legend if shape_var is a vector.
cols.use	1 color or a vector containing multiple colors to color shapes. If coloring is continuous, default colors are taken from a "lightgrey" to "blue" gradient. If coloring is discrete, default colors are taken from the default ggplot2 palette.
text.size	Size of text to display on the shapes.
text.vjust	Vertical justification of text to display on the shapes. Default value = 0, which mean no justification. Recommended value is between -0.5 and 0.5.
shape_use	Shapes to uses (only when shape is controled by a discrete factor). Default shapes : \u25A0 \u25CF \u25C6 \u2BC8 \u2BC7 \u2BC6 \u2BC5 \u25D8 \u25D9 \u2726 \u2605 \u2736 \u2737.
shape.scale	Scale the size of the shapes, similar to cex.
scale.by	Scale the size by size or radius.
scale.min	Set lower limit for scaling, use NA for default values.
scale.max	Set upper limit for scaling, use NA for default values.
plot.legend	Plot the legends ?
do.return	Return ggplot2 object ?
x.lab.pos	Where to display x axis labels. This must be one of "bottom","top","both" or "none".

y.lab.pos   Where to display y axis labels. This must be one of "left","right","both"or
                   "none".

x.lab.size.factor
                   Factor resizing x-axis labels (default=1)

y.lab.size.factor
                   Factor resizing y-axis labels (default=1)

vertical_coloring
                   Which color use to color the plot vertically ? (colors are repeated untill the
                   end of the plot). Setting vertical and horizontal coloring at the same time is not
                   recommended !

horizontal_coloring
                   Which color use to color the plot horizontally ? (colors are repeated untill the
                   end of the plot). Setting vertical and horizontal coloring at the same time is not
                   recommended !

size.breaks.number
                   Number of shapes with different size to display in the legend. Not used if
                   size.breaks.values is not NA.

color.breaks.number
                   Number of labels for the color gradient legend. Not used if color.breaks.values
                   is not NA.

shape.breaks.number
                   Number of shapes to display in the legend. Used when shape is controled by a
                   continuous factor only. Not used if shape.breaks.values is not NA.

size.breaks.values
                   Vector containing numerical labels for the size legend.

color.breaks.values
                   Vector containing numerical labels for continuous color legend.

shape.breaks.values
                   Vector containing numerical labels for continuous shape legend.

display_max_sizes
                   Boolean : Display max shape size behind each shape ? (Default=TRUE)

transpose   Reverse x axis and y axis ?

dend_x_var   A vector containing Column/List indexes or Column/List names to compute the
                   x axis dendrogramm.

dend_y_var   A vector containing Column/List indexes or Column/List names to compute the
                   y axis dendrogramm.

dist_method   The distance measure to be used. This must be one of "euclidean", "maximum",
                   "manhattan", "canberra", "binary" or "minkowski".

hclust_method   The agglomeration method to be used. This must be one of "single", "complete",
                   "average", "mcquitty", "ward.D", "ward.D2", "centroid" or "median".

do.plot   Print the plot ? (default=TRUE)

Value

Print the plot (if do.plot=TRUE) and return a list containing input data, executed command, result-
ing dot plot and computed dendrograms (if do.return=TRUE)

Author(s)

Simon Leonard - simon.leonard@univ-rennes1.fr

Examples

```
library(FlexDotPlot)
data(CBMC8K_example_data)
dotplot = dot_plot(data.to.plot=CBMC8K_example_data, size_var="RNA.avg.exp.scaled",
col_var="ADT.avg.exp.scaled", text_var="ADT.pct.exp.sup.cutoff",
shape_var="canonical_marker", shape_use = c("\u25CF","\u2737"),x.lab.pos="bottom",
y.lab.pos="left", cols.use=c("lightgrey","orange","red", "darkred"),
size_legend="RNA", col_legend="ADT", shape_legend="Canonical marker ?",
shape.scale =12, text.size=3, plot.legend = TRUE,
size.breaks.number=4, color.breaks.number=4, shape.breaks.number=5,
dend_x_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
dend_y_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
dist_method="euclidean",hclust_method="ward.D", do.return = TRUE)
```

PBMC3K_example_data   *PBMC 3K example dataset*

Description

A dataset containing expression informations of 39 genes in 8 celltypes. Original dataset from seurat-data package.

Usage

```
data(PBMC3K_example_data)
```

Format

A data frame with 312 rows and 13 variables

Details

- genes.plot. Gene symbol
- id. Cell type
- pct.exp. Percentage of cells expressing the gene in the cell type
- pct.exp2. pct.exp with 2 decimal places
- pct.exp100. pct.exp.2 x 100
- avg.exp. Average expression of the gene in the cell type
- avg.exp.scale. Scaled average expression
- abs_avg_exp_scale Absolute value of avg.exp.scale
- avg_logFC. log fold-chage of the average expression of the gene between the cell type and the others

- avg_logFC2. avg_logFC with 2 decimal places
- p_val_adj. Adjusted p-value based on bonferroni correction
- p_val_adj2. p_val_adj with 2 decimal places
- pval_symb. Adjusted p-value classification ("<1e-100" or "<1e-50" or "<1e-10" or "<0.01" or ">0.01")

References

https://github.com/satijalab/seurat-data

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rotate_dot_plot_dendrogram

Interactively rotate dendrograms from dot_plot outputs

Description

Take a output from dot_plot function and allow interactive dendrogram rotation with dendextend package

Usage

```
rotate_dot_plot_dendrogram(dot_plot_output, axis_to_rotate = c("x", "y"))
```

Arguments

dot_plot_output

                Output from dot_plot function function

axis_to_rotate   Dendrogram to rotate "x" or "y"

Value

Print and return rotated dot plot

Author(s)

Simon Leonard - simon.leonard@univ-rennes1.fr

Examples

```
# Perform dot_plot
if(interactive()){
library(FlexDotPlot)
data(CBMC8K_example_data)

# Run dot_plot
dotplot_output = dot_plot(data.to.plot=CBMC8K_example_data, size_var="RNA.avg.exp.scaled",
dend_x_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
dend_y_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
```

```
dist_method="euclidean",hclust_method="ward.D", do.return = TRUE)

# The following command has to be run when the user
#is running example("rotate_dot_plot_dendrogram") only.
dotplot_output$command=call("dot_plot", data.to.plot=as.name("CBMC8K_example_data"),
size_var="RNA.avg.exp.scaled",
dend_x_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
dend_y_var=c("RNA.avg.exp.scaled","ADT.avg.exp.scaled"),
dist_method="euclidean",hclust_method="ward.D", do.return = TRUE)

# y  dendrogram rotation
r1=rotate_dot_plot_dendrogram(dotplot_output, axis_to_rotate = "y")
# add x dendrogram rotation to previous result
#r2=rotate_dot_plot_dendrogram(r1, axis_to_rotate = "x")
}
```

Shiny_dot_plot *Shiny dotplot*

Description

Shiny application to perform dot-plot pacman-plot

Usage

```
Shiny_dot_plot()
```

Author(s)

Simon Leonard - simon.leonard@univ-rennes1.fr

Examples

```
if(interactive()) Shiny_dot_plot()
```

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