Package 'CMapViz'

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Type Package

Title Representation Tool For Output Of Connectivity Map (CMap)
Analysis

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Description Automatically displays graphical visualization for exported data table (permutated re-
sults) from Connectivity Map (CMap) (2006) <doi:10.1126/science.1132939>.
It allows the representation of the statistics (p-
value and enrichment) according to each cell lines in the form of a bubble plot.

BugReports https://github.com/Peyronlab/CMapViz/issues

Imports readxl, ggplot2, dplyr, scales, reshape2, stringr

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests spelling

Language en-US

NeedsCompilation no

Repository CRAN

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bubble_plot   *Bubble plot of CMap output table*

Description

This function allows the user to represent the Connectivity Map (CMap) result table (broadinstitute) under the form of a bubble plot representing statistics and cell lines: - each drug is represented along the y axis according to its enrichment value - each drug is represented along the x axis according to the cell line tested and within the cell line according to batch specificity (0-50

Usage

```
bubble_plot(path, plot, enrichment, abs.enrich.cutoff=NULL, n.rep.cutoff=NULL ,
         jittering=FALSE, return.gg.table= FALSE, output_path = NULL)
```

Arguments

path	path of the excel file (permutated results)
plot	what data to plot: molecules only (plot="molecules") or molecules by cell lines batch (plot="cell.lines")
enrichment	whether to plot positive or negative enrichment
abs.enrich.cutoff	
	minimum value of enrichment to include a batch
n.rep.cutoff	minimum number of replicates to include a batch (default=NULL)
jittering	whether apply jittering to the values to avoid points overlap
return.gg.table	
	table prepared for ggplot, allows the user to customize the graphical representation
output_path	path for the experiment output folder, returns data table and figure (default=NULL)

Value

ggplot object - bubble plot

Examples

```
file.path <- system.file("extdata", "example.xls", package = "CMapViz")
#display results by cell lines, with negative enrichment (absolute cutoff: 0.5), and at least n=5.
#molecule position with respect of dotted line is the specificity of the molecule itself:
#left side of dotted line if specificity < 50 or right side of dotted line if specificity > 50 )
bubble_plot(file.path,
    plot = "cell.lines", enrichment = "negative", abs.enrich.cutoff = 0.5,
    n.rep.cutoff = 5, output_path = NULL
)
```

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