

# Package: CMapViz (via r-universe)

November 3, 2024

**Type** Package

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

**Date** 2019-10-25

**Version** 0.1.0

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**Description** Automatically displays graphical visualization for  
exported data table (permuted results) from Connectivity Map  
(CMap) (2006) <[doi:10.1126/science.1132939](https://doi.org/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

**Repository** <https://peyronlab.r-universe.dev>

**RemoteUrl** <https://github.com/peyronlab/cmapviz>

**RemoteRef** HEAD

**RemoteSha** 7953886a5d8825a9c3940e9d4593946d50effa62

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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 (permuted 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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