

# Package ‘MACSQuantifyR’

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**Type** Package

**Title** Fast treatment of MACSQuantify FACS data

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**Description** Automatically process the metadata of MACSQuantify FACS sorter.  
It runs multiple modules: i) imports of raw file and graphical selection of duplicates in well plate,  
ii) computes statistics on data and iii) can compute combination index.

**Imports** readxl, graphics, tools, utils, grDevices, ggplot2, ggrepel, methods, stats, latticeExtra, lattice, rmarkdown, png, grid, gridExtra, prettydoc, rvest, xml2

**biocViews** DataImport, Preprocessing, Normalization, FlowCytometry, DataRepresentation, GUI

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.0

**Suggests** knitr, testthat, R.utils, spelling

**VignetteBuilder** knitr

**Language** en-US

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barplot_data	<i>Generate barplots</i>
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## Description

Uses the informations stored in the statistic tables of the MACSQuant object to generate barplots for the specified conditions. Plots can also be saved in the form of a png file in the output\_MQ directory.

## Usage

```
barplot_data(MACSQuant,plt.col=NULL,plt.conditions=NULL, plt.flavour=NULL,
plt.labels = NULL, plt.combo=FALSE,plt.3D.only = NULL,...)
```

## Arguments

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
plt.col	In case of manual run is used to define the bar colors. (must be the same for all conditions)
plt.conditions	user defined vector of conditions to plot (example: plt.conditions=c(1:9))
plt.flavour	Which barplot to produce, cell count or percentage of fluorochrome (i.e: "counts","percent")
plt.labels	xlabels of the plot
plt.combo	Does the experiment involves multiple variables (i.e some condition are a drug combination screening)
plt.3D.only	Whether to plot 3D barplot alone
...	params for lattice cloud namely z and x for parameter screen default for z and x are c(-110,-70) and argument xlab and ylab

## Value

returns a barplot of the data

**Examples**

```

drugs_R_image <- system.file("extdata",
  "drugs.RDS",
  package = "MACSQuantifyR")
MACSQuant <- readRDS(drugs_R_image)
flavour <- "counts"
number_of_conditions <-
  slot(MACSQuant, "param.experiment")$number_of_conditions
plt.col <- c(rep(2, number_of_conditions), 1)
barplot_data(MACSQuant,
  plt.col = plt.col,
  plt.conditions = NULL,
  plt.flavour = flavour,
  plt.labels = NULL,
  plt.combo = FALSE)

```

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combination_index	<i>compute combination index</i>
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**Description**

This function allows the user to compute combination index on the drug combinations. This function also generates intermediary plots and tables.

**Usage**

```
combination_index(MACSQuant, ...)
```

**Arguments**

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
...	params for lattice cloud namely z and x for parameter screen default for z and x are c(-110,-70) and argument xlab and ylab

**Value**

Several plots and combination index

**References**

Chou, T. C. (2006). Theoretical basis, experimental design, and computerized simulation of synergism and antagonism in drug combination studies. *Pharmacological reviews*, 58(3), 621-681.

**Examples**

```

filepath <- system.file("extdata", "drugs.Rdata",
  package = "MACSQuantifyR")
load(filepath)
combination_index(MACSQuant)

```

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generate_report	<i>Word report generation</i>
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**Description**

Allows the user to generate a report at every steps of the analysis  
 Also generates a complete report with the graphics

**Usage**

```
generate_report(MACSQuant)
```

**Arguments**

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
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**Value**

A formatted report

**Examples**

```
drugs_R_image <- system.file("extdata",
  "drugs.RDS",
  package = "MACSQuantifyR")
MACSQuant <- readRDS(drugs_R_image)
generate_report(MACSQuant)
```

---

load_MACSQuant	<i>Load xls file from maxQuant 96-well-plate device</i>
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**Description**

Load xls file from maxQuant 96-well-plate device

**Usage**

```
load_MACSQuant(filepath, sheet_name= NULL, MACSQuant.obj= NULL)
```

**Arguments**

filepath	path of the excel file
sheet_name	Name of the sheet to load (optional, first sheet is default)
MACSQuant.obj	object of class MACSQuant

**Value**

An object called MACSQuant of class MACSQuant containing variable my\_data that corresponds to the data of the excel file in R

**Examples**

```
filepath <- system.file("extdata", "SingleDrugs.xlsx",
  package = "MACSQuantifyR")
# load_MACSQuant(filepath)
```

MACSQuant

*The MACSQuant Class***Description**

MACSQuant object contains all the data and the user parameters

**Slots**

`my_data` Contains the raw data

`my_data_sorted` Contains the sorted data (according to replicates order)

`my_replicates_sorted` Contains the sorted matrix containing replicates names

`experiment_name` Contains the experiment name given by the user

`statistics` Contains the statistics for each condition

`combination.index.df` data.frame that contains the outputs of the `combination_index` function

`param.experiment` list that contains the parameters relative to the experiment (i.e, number of replicates, number of conditions...)

`param.output` List that contains the parameters relative to the report generation and outputs (i.e, save intermediary results, generate full report..)

new\_class\_MQ

*Create a new MACSQuant object***Description**

The user can create a new custom MACSQuant object This function is also used in internal code for MACSQuant initialization

**Usage**

```
#initialize empty MACSQuant object
new_class_MQ(my_data=NULL,my_data_sorted=NULL,my_replicates_sorted=NULL,
  experiment_name=NULL,statistics=NULL,combination.index.df=NULL,
  number_of_replicates=NULL,number_of_conditions=NULL,doses=NULL,
  doses.alt=NULL,c_names=NULL, control=NULL,plt.title=NULL,
  plt.labels=NULL,plt.col=NULL,save.files=NULL,path=tempdir())
#initialize custom MACSQuant object
new_class_MQ(my_data,my_data_sorted=NULL,my_replicates_sorted=NULL,
  experiment_name=NULL,statistics=NULL,combination.index.df=NULL,
  number_of_replicates=NULL,number_of_conditions=NULL,
  doses=NULL,doses.alt=NULL, c_names=NULL,control=NULL,plt.title=NULL,
  plt.labels=NULL,plt.col=NULL, save.files=NULL,path=tempdir())
```

**Arguments**

<code>my_data</code>	Contains the raw data
<code>my_data_sorted</code>	Contains the sorted data (according to replicates order)
<code>my_replicates_sorted</code>	Contains the sorted matrix containing replicates names
<code>experiment_name</code>	User defined experiment named. Used for the report generation
<code>statistics</code>	Contains the statistics for each condition
<code>combination.index.df</code>	data.frame that contains the outputs of the <code>combination_index</code> function
<code>number_of_replicates</code>	For each condition, the number of duplicates (must be the same for all conditions)
<code>number_of_conditions</code>	The number of conditions tested (eg: Drug 1 alone, Drug 2 alone)
<code>doses</code>	Numeric vector representing doses for each conditions
<code>doses.alt</code>	In case of interaction test second dose vector
<code>c_names</code>	Vector containing experiment names
<code>control</code>	logical: is there a control in this experiment (eg: Staurosporin)
<code>plt.title</code>	Title of the experiment to add to the barplot
<code>plt.labels</code>	legend labels for the bar plot
<code>plt.col</code>	color vector for the graphical representations
<code>save.files</code>	Used to save the image in the output folder
<code>path</code>	path of the experiment output folder (default '.')

**Value**

A formatted report file along with intermediates results

**Examples**

```
# initialize empty MACSQuant object
new_class_MQ()
# initialize custom MACSQuant object
my_data <- data.frame(character(length = 10), character(length = 10),
  numeric(length = 10), numeric(length = 10))
names(my_data) <- c("Full path", "WID", "%-#", "Count/mL")
new_class_MQ(my_data)
```

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on\_plate\_selection      *Sort experimental design on graphical 96-well-plate*

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### Description

Loads user's data, prompt a graphical representation of a 96 well plate and let the user select where the duplicates of each condition were placed. Use for reordering excel file. Plate image with selection can also be saved in the form of a png file in the "specified\_path/output\_MQ" directory.

### Usage

```
on_plate_selection(MACSQuant,number_of_replicates,number_of_conditions,
control=FALSE,save.files=FALSE)
```

### Arguments

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
number_of_replicates	For each condition, the number of duplicates (must be the same for all conditions)
number_of_conditions	The number of conditions tested (eg: Drug 1 alone, Drug 2 alone)
control	Is there a control in this experiment (eg: Staurosporin)
save.files	Used to save the image in the output folder

### Value

A formatted report file along with intermediates results

### Examples

```
print("run manually, requires user input")
# on_plate_selection(MACSQuant,3,5)
# let you select 5 conditions of 3 replicates each
```

---

pipeline      *pipeline with report generation*

---

### Description

Loads user's data, prompt a graphical representation of a 96 well plate and let the user select where the duplicates of each condition were placed. Use for reordering excel file. Plate image with selection can also be saved in the form of a png file in the output\_MQ directory.

Also generates a complete report with the graphics

### Usage

```
pipeline(filepath, sheet_name=NULL, number_of_replicates, number_of_conditions,
control=FALSE, save.files=TRUE, MACSQuant.obj=NULL)
```

**Arguments**

filepath	path of the excel file
sheet_name	Name of the sheet to load (optional, first sheet is default)
number_of_replicates	For each condition, the number of duplicates (must be the same for all conditions)
number_of_conditions	The number of conditions tested (eg: Drug 1 alone, Drug 2 alone)
control	Is there a control in this experiment (eg: Staurosporin)
save.files	Used to save the image in the output folder
MACSQuant.obj	object of class MACSQuant

**Value**

A formatted report file along with intermediates results

**Examples**

```
print("run manually, requires user input")
filepath <- system.file("extdata", "SingleDrugs.xlsx",
  package = "MACSQuantifyR")
# pipeline(filepath,3,5)
# let you select 5 conditions of 3 replicates each
```

---

rData	<i>accessor function to access raw data</i>
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---

**Description**

This function allows the user to access raw data table

**Usage**

```
rData(MACSQuant)
```

**Arguments**

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
-----------	---

**Value**

the raw data table

**Examples**

```
filepath <- system.file("extdata", "SingleDrugs.xlsx",
  package = "MACSQuantifyR")
#MACSQuant = load_MACSQuant(filepath)

#rData(MACSQuant)
```

---

setPath	<i>sets custom output path</i>
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---

**Description**

This function allows the user to set the output directory path

**Usage**

```
setPath(MACSQuant, path=NULL)
```

**Arguments**

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
path	user defined path, default is tempd

**Value**

object of class MACSQuant with updated path

**Examples**

```
filepath <- system.file("extdata", "SingleDrugs.xlsx",  
  package = "MACSQuantifyR")  
#MACSQuant = load_MACSQuant(filepath)  
user_path="."  
#MACSQuant = setPath(MACSQuant, path=user_path)
```

---

sorted	<i>accessor function to access sorted data</i>
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---

**Description**

This function allows the user to access sorted data table

**Usage**

```
sorted(MACSQuant)
```

**Arguments**

MACSQuant	object of class MACSQuant resulting of the function load_maxQuant(). Contains the original data table
-----------	---

**Value**

the raw data table

**Examples**

```
filepath <- system.file("extdata", "SingleDrugs.xlsx",  
  package = "MACSQuantifyR")  
#MACSQuant = load_MACSQuant(filepath)  
  
#sorted(MACSQuant)
```

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