

# Package ‘protGear’

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**Type** Package

**Title** Protein Micro Array Data Management and Interactive Visualization

**Version** 1.10.0

**Description** A generic three-step pre-processing package for protein microarray data. This package contains different data pre-processing procedures to allow comparison of their performance. These steps are background correction, the coefficient of variation (CV) based filtering, batch correction and normalization.

**License** GPL-3

**URL** <https://github.com/Keniajin/protGear>

**BugReports** <https://github.com/Keniajin/protGear/issues>

**Depends** R (>= 4.2), dplyr (>= 0.8.0), limma (>= 3.40.2), vsn (>= 3.54.0)

**Imports** magrittr (>= 1.5), stats (>= 3.6), ggplot2 (>= 3.3.0), tidyrr (>= 1.1.3), data.table (>= 1.14.0), ggpubr (>= 0.4.0), gtools (>= 3.8.2), tibble (>= 3.1.0), rmarkdown (>= 2.9), knitr (>= 1.33), utils (>= 3.6), genefilter (>= 1.74.0), readr (>= 2.0.1), Biobase (>= 2.52.0), plyr (>= 1.8.6), Kendall (>= 2.2), shiny (>= 1.0.0), purrr (>= 0.3.4), plotly (>= 4.9.0), MASS (>= 7.3), htmltools (>= 0.4.0), flexdashboard (>= 0.5.2), shinydashboard (>= 0.7.1), GGally (>= 2.1.2), pheatmap (>= 1.0.12), grid (>= 4.1.1), styler (>= 1.6.1), factoextra (>= 1.0.7), FactoMineR (>= 2.4), rlang (>= 0.4.11), remotes (>= 2.4.0)

**Suggests** gridExtra (>= 2.3), png (>= 0.1-7), magick (>= 2.7.3), ggplotify (>= 0.1.0), scales (>= 1.1.1), shinythemes (>= 1.2.0), shinyjs (>= 2.0.0), shinyWidgets (>= 0.6.2), shinycssloaders (>= 1.0.0), shinyalert (>= 3.0.0), shinyFiles (>= 0.9.1), shinyFeedback (>= 0.3.0)

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**Author** Kennedy Mwai [cre, aut],  
James Mburu [aut],  
Jacqueline Waeni [ctb]

**Maintainer** Kennedy Mwai <keniajin@gmail.com>

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---

array_vars	<i>List the array structure variables</i>
------------	---

---

### Description

A generic function returning a list with the data structure.

### Usage

```
array_vars(
  channel = "635",
  totsamples,
  FG = "",
  BG = "",
  FBG = "",
  blockspersample,
  chip_path = "data/array_data",
  sampleID_path = "data/array_sampleID/",
  mig_prefix = "_first",
  machine = "",
  date_process = ""
)
```

### Arguments

channel	A character indicating the channel that the data was scanned at. It is mostly included in the MFI variable names.
totsamples	A numeric value indicating the number of samples on a slide.
FG	Optional: A character indicating the name of the foreground variable name. if not specified its created as <code>paste0("F", channel, ".Median")</code>
BG	Optional: A character indicating the name of the background variable name. if not specified its created as <code>paste0("B", channel, ".Median")</code>
FBG	Optional: A character indicating the name of the foreground - background variable name. if not specified its created as <code>paste0("F", channel, ".Median...B", channel)</code>
blockspersample	A numeric value indicating the number of blocks in a mini-array. The ".gal" file can help in getting this
chip_path	A character indicating the path of the folder location with the array data.
sampleID_path	A character indicating the path of the folder location with the sample identifiers matching the array structure.
mig_prefix	Optional: A character indicating the identifier of an MIG dilution file
machine	Optional: A character indicating the machine used to process the data in the folder
date_process	Optional: A character indicating the date when the samples were processed.

### Value

a list of parameters required to process the data  
`genepix_vars`

## Examples

```
## specify the the parameters to process the data
genepix_vars <- array_vars(
## the channel the data was processed in
  channel = "635",
  ## folder where the array data is stored
  chip_path = "data/array_data",
  ## the number of samples per slide or in as single run
  totsamples = 21,
  ## How many blocks each sample occupies
  blockspersample = 2,
  ## folder where the array data samples id files are stored
  sampleID_path = "data/array_sampleID/",
  ## optional
  mig_prefix = "_first",
  machine = 1,
  date_process = "0520"
)
genepix_vars
```

---

best\_CV\_estimation      *best CV estimation*

---

## Description

A function to select the best CV by combining the replicates in duplicates. The function has been build for up to 3 replicates so far

## Usage

```
best_CV_estimation(dataCV, slide_id, lab_replicates, cv_cut_off)
```

## Arguments

dataCV	A data frame
slide_id	A character string containing the identifier of the data frame variable.
lab_replicates	A numeric value indicating the number of lab replicates.
cv_cut_off	a numeric value for the CV cut off. Should be between 0-100

## Details

Select set of replicates with the best CV

## Value

A data frame with the best CV's estimated

**Examples**

```
dataC <- readr::read_csv(system.file("extdata",
  "dataC.csv", package="protGear"))
## this file has 3 lab replicates and the default names
dataCV <- cv_estimation(dataC ,lab_replicates=3)
best_CV_estimation(dataCV,slide_id = "iden", lab_replicates = 3,
  cv_cut_off = 20)
```

---

 bg\_correct
 

---

*bg\_correct*


---

**Description**

A generic function to perform background correction.

**Usage**

```
bg_correct(iden, Data1, genepix_vars, method = "subtract_local")
```

**Arguments**

iden	A character indicating the name of the object to be used under Data1
Data1	A data frame with sample identifiers merged with micro array data.
genepix_vars	A list of specific definitions of the experiment design. See <a href="#">array_vars</a> .
method	a description of the background correction to be used. Possible values are "none", "subtract_local", "subtract_global", "movingmin_bg", "minimum_half", "edwards" or "normexp". The default is "subtract_local".

**Details****Background correction**

The function implements background correction methods developed by [backgroundCorrect](#). But the `minimum_half` and `movingmin_bg` uses the block of the protein array as the grid. If `method="movingmin_bg"` the minimum background value within a block is subtracted. If `method="minimum_half"` then any intensity which is negative after background subtraction is reset to be equal to half the minimum positive value in a block. If `method="movingmin_value"` then any intensity which is negative after background subtraction is reset to the minimum positive value in a block. For `edwards` we implement a similar algorithm with `limma::backgroundCorrect(method="edwards")` and for `'normexp'` we use the saddle-point approximation to maximum likelihood, [backgroundCorrect](#) for more details.

**Value**

A data frame with background corrected data

---

buffer_spots	<i>Extract buffer spots of data</i>
--------------	-------------------------------------

---

### Description

A function to extract the buffer spots data. A buffer spot only has the solution for proprietary ingredients for stabilizing protein and minimizing evaporation.

### Usage

```
buffer_spots(Data1, buffer_spot = "buffer")
```

### Arguments

Data1	An object of the class data frame
buffer_spot	A character string containing the name of the buffer spots.

### Value

A data frame of the buffer control spots

### Examples

```
bg_correct_df <- readr::read_csv(system.file("extdata", "Data1_sample.csv",
package="protGear"))
buffer_spots(Data1 = bg_correct_df)
```

---

check\_sampleID\_files *\\\_End\_Function\_\\# Check existing sample ID names*

---

### Description

A generic function to check if the file(s) with the MFI values have a corresponding sample ID file. Sample ID file is a file with the identifiers for the samples in array file.

### Usage

```
check_sampleID_files(genepix_vars)
```

### Arguments

genepix_vars	A list of specific definitions of the experiment design. See <a href="#">array_vars</a> .
--------------	---

### Value

A file with missing corresponding sample ID files

**Examples**

```
genepix_vars <- array_vars(  
  channel = "635",  
  chip_path = system.file("extdata", "array_data/machine1/",  
    package="protGear"),  
  totsamples = 21,  
  blockspersample = 2,  
  mig_prefix = "_first",  
  machine = 1,  
  date_process = "0520"  
)  
check_sampleID_files(genepix_vars)
```

---

create_dir	<i>Title Create directory function</i>
------------	--

---

**Description**

creating a directory

**Usage**

```
create_dir(path)
```

**Arguments**

path                    folder location to create a directory

**Value**

created directory

**Examples**

```
create_dir("data/sample_folder")
```

---

cv_by_sample_estimation	<i>cv by sample</i>
-------------------------	---------------------

---

**Description**

A function to give the summary of the CV's by the sampleID

**Usage**

```
cv_by_sample_estimation(  
  dataCV,  
  cv_variable,  
  lab_replicates,  
  sampleID_var = "sampleID"  
)
```

**Arguments**

dataCV	A dataframe
cv_variable	A character string containing the identifier of the variable with CV values.
lab_replicates	A numeric value indicating the number of lab replicates.
sampleID_var	A character string containing the name of the sample identifier variable. Default set to 'sampleID'

**Details**

Summarise CV by samples

**Value**

A data frame of CV calculated by sample

**Examples**

```
dataC <- readr::read_csv(system.file("extdata",
  "dataC.csv", package="protGear"))
## this file has 3 lab replicates and the default names
dataCV <- cv_estimation(dataC ,lab_replicates=3)
cv_by_sample_estimation(dataCV, cv_variable = "cvCat_all",
  lab_replicates = 3)
```

---

cv_estimation	<i>cv_estimation</i>
---------------	----------------------

---

**Description**

A function to calculate the CV for the technical lab replicates. The default values are set as per the object names generated by machine

**Usage**

```
cv_estimation(
  dataC,
  lab_replicates,
  sampleID_var = "sampleID",
  antigen_var = "antigen",
  replicate_var = "replicate",
  mfi_var = "FMedianBG_correct",
  cv_cut_off = 20
)
```

**Arguments**

dataC	A dataset a data frame with feature variables to be used
lab_replicates	A numeric value indicating the number of lab replicates
sampleID_var	A character string containing the name of the sample identifier variable. Default set to 'sampleID'



antigen_var	A character string containing the name of the features/protein variable. Default to 'antigen'
replicate_var	A character string containing the name of the replicate variable. Default to 'replicate'
mfi_var	A character string containing the name of the variable with MFI value. Assuming background correction is done already. Default to 'FMedianBG_correct'
cv_cut_off	Optional value indicating the cut off of flagging CV's. Default set at 20.

### Details

Coefficient of Variation

### Value

A data frame where CV's of the replicates have been calculated

### Examples

```
dataC <- readr::read_csv(system.file("extdata",
  "dataC.csv", package="protGear"))
## this file has 3 lab replicates and the default names
cv_estimation(dataC ,lab_replicates=3)
```

---

```
error_replicates      \\_Start_Function_For_Error\\#
```

---

### Description

A generic function to write into the log file with a replicate check error

### Usage

```
error_replicates(iden)
```

### Arguments

iden                    An id for the file with replicates error

### Value

a log file showing the replicate errors

---

 extract\_bg

*extract bg*


---

### Description

A generic function to extract the background data for micro array data.

### Usage

```
extract_bg(iden, data_files, genepix_vars = genepix_vars)
```

### Arguments

`iden` A character indicating the name of the object to be used under `data_files`.  
`data_files` A list of data objects with names utilised by `iden`.  
`genepix_vars` A list of specific definitions of the experiment design. See [array\\_vars](#).

### Details

Extract the background values

### Value

A data frame of background values

### Examples

```
## Not run:
genepix_vars <- array_vars(
  channel = "635",
  chip_path = system.file("extdata", "array_data/machine1/",
  package="protGear"),
  totsamples = 21,
  blockspersample = 2,
  mig_prefix = "_first",
  machine = 1,
  ## optional
  date_process = "0520"
)
#Define the data path
data_path <- paste0(genepix_vars$chip_path)
# List the file names to use
filenames <- list.files(genepix_vars$chip_path,
  pattern = '*.txt$|*.gpr$', full.names = FALSE
)
data_files <- purrr::map(
  .x = filenames,
  .f = read_array_files,
  data_path = data_path,
  genepix_vars = genepix_vars
)
data_files <- purrr::set_names(data_files,
  purrr::map(filenames, name_of_files))
```

```
names(data_files)
extract_bg(iden = "KK2-06" , data_files=data_files, genepix_vars=genepix_vars)
## End(Not run)
```

---

```
launch_protGear_interactive
      launch_protGear_interactive
```

---

**Description**

This is Function is to launch the shiny application

**Usage**

```
launch_protGear_interactive()
```

**Value**

launches the shiny interactive protGear app

**Examples**

```
app <- system.file("shiny-examples", "protGear_interactive",
"protGear_interactive.Rmd", package = "protGear")
if (app!=""){
## run this
#launch_protGear_interactive()
}
```

---

```
launch_select      launch_select
```

---

**Description**

This is Function is to launch mutiple shiny applications for protGear

**Usage**

```
launch_select(theApp)
```

**Arguments**

theApp            accepts one of the folders containing the shiny application

**Value**

launches the app defined under theApp

**Examples**

```
validExamples <-
list.files(system.file("shiny-examples", package = "protGear"))
#launch_select(validExamples[[1]])
```

---

matrix_normalise	<i>Normalize Arrays</i>
------------------	-------------------------

---

## Description

Normalize Arrays

## Usage

```
matrix_normalise(
  matrix_antigen,
  method = "log2",
  batch_correct = FALSE,
  batch_var1,
  batch_var2 = day_batches,
  return_plot = FALSE,
  plot_by_antigen = TRUE,
  control_antigens = NULL,
  array_matrix = NULL
)
```

## Arguments

matrix_antigen	An object of class matrix with features/proteins as columns and samples as the rows
method	character string specifying the normalization method. Choices are "none", "log2", "vsn", "cyclic_loess_log", "rlm"
batch_correct	A logical value indicating whether batch correction should be done or not
batch_var1	A character or factor vector of size similar to rows of matrix_antigen indicating the first batch.
batch_var2	A character or factor vector of size similar to rows of matrix_antigen indicating the second batch.
return_plot	A logical value indicating whether a plot is returned to show the results of normalisation.
plot_by_antigen	Logical to indicate whether to plot by antigen or not slide name for the matrix_antigen object.
control_antigens	logical vector specifying the subset of spots which are non-differentially-expressed control spots, for use with method="rlm"
array_matrix	An object of class dataframe or matrix used with method='rlm' indicating the sample index and

## Value

A data frame of normalised values

**Examples**

```

matrix_antigen <- readr::read_csv(system.file("extdata",
"matrix_antigen.csv", package="protGear"))
#VSN
normlise_vsn <- matrix_normalise(as.matrix(matrix_antigen),
method = "vsn",
return_plot = TRUE
)
## log
normlise_log <- matrix_normalise(as.matrix(matrix_antigen),
method = "log2",
return_plot = TRUE
)
## cyclic_loess_log
normlise_cyclic_log <- matrix_normalise(as.matrix(matrix_antigen),
method = "cyclic_loess_log",
return_plot = TRUE
)

```

---

merge\_sampleID

*Merge sample ID with the array data*


---

**Description**

A generic function that merges the protein data with the sample identifiers or sample names. If the file does not have sample identifiers the function generates it automatically.

**Usage**

```
merge_sampleID(iden, data_files, genepix_vars, method)
```

**Arguments**

iden	A character indicating the name of the object to be used under data_files.
data_files	A list of data objects with names utilised by iden.
genepix_vars	A list of specific definitions of the experiment design. See <a href="#">array_vars</a> .
method	A description of the background correction to be used. See <a href="#">bg_correct</a> .

**Value**

a data frame merged with corresponding sample ID's. The sample ID are specified in the sample ID files

**Examples**

```

## Not run:
### Define the genepix_vars
genepix_vars <- array_vars(
  channel = "635",
  chip_path = system.file("extdata", "array_data/machine1/",
  package="protGear"),
  totsamples = 21,

```

```

    blockspersample = 2,
    mig_prefix = "_first",
    machine = 1,
    ## optional
    date_process = "0520"
  )

  ## the path where the micro-array data is located
  data_path <- paste0(genepix_vars$chip_path)
  filenames <- list.files(genepix_vars$chip_path,
                        pattern = "*.txt$|*.gpr$", full.names = FALSE
  )
  ## create a list of all the files
  data_files <- purrr::map(
    .x = filenames,
    .f = read_array_files,
    data_path = data_path,
    genepix_vars = genepix_vars
  )
  data_files <- purrr::set_names(data_files,
                                purrr::map(filenames, name_of_files))
  ## merge the lab data with samples and perform bg correction
  merge_sampleID(iden = "KK2-06", data_files = data_files,
                genepix_vars = genepix_vars, method = "subtract_global" )
  ## End(Not run)

```

---

 minpositive

*Get the minimum positive value*


---

### Description

Get the minimum positive value

### Usage

```
minpositive(x)
```

### Arguments

x                    A numeric vector or variable

### Value

Returns the minimum positive value in an object

### Examples

```
minpositive(c(-1,-2,3,5,6,7,8,9,10))
```

---

name_of_files	<i>Object names of a list</i>
---------------	-------------------------------

---

**Description**

A generic function returning a vector with the names of files in the same directory. Removes the file extension

**Usage**

```
name_of_files(i)
```

**Arguments**

`i` - a list filenames with .txt or .gpr extension

**Value**

a list of file names  
name

**Examples**

```
name_of_files("KK2-06.txt")
```

---

output_trend_stats	<i>Trend test using Cox–Stuart (C–S) and Mann–Kendall (M–K) trend tests</i>
--------------------	---

---

**Description**

Trend test using Cox–Stuart (C–S) and Mann–Kendall (M–K) trend tests

**Usage**

```
output_trend_stats(name, p_val, z_val)
```

**Arguments**

`name` Name of the test  
`p_val` p value from the test  
`z_val` the Z value of the test

**Value**

A statistics of mean standard deviation trend

**Examples**

```
output_trend_stats(name="t.test", p_val=0.001, z_val=5)
```

---

plot_bg	<i>Plot background</i>
---------	------------------------

---

**Description**

A generic function for plotting of R objects.

**Usage**

```
plot_bg(df, x_axis = "antigen", bg_MFI = "BG_Median", log_mfi = TRUE)
```

**Arguments**

df	A default dataset to use for plot.
x_axis	The variable on the x axis
bg_MFI	A numeric variable describing which is the background MFI
log_mfi	a logical value indicating whether the MFI values should be log transformed or not.

**Value**

A ggplot of background values

**Examples**

```
## Not run:
##After extracting the background using \link{extract_bg}
##we plot the data using
allData_bg <- readr::read_csv(system.file("extdata", "bg_example.csv",
  package="protGear"))
plot_bg(allData_bg,
x_axis = "antigen",
bg_MFI = "BG_Median", log_mfi = TRUE
)
## End(Not run)
```

---

plot_buffer	<i>Plot the buffer values</i>
-------------	-------------------------------

---

**Description**

Plot the buffer values

**Usage**

```
plot_buffer(
  df = buffers,
  buffer_names = "antigen",
  buffer_mfi = "FMedianBG_correct",
  slide_id = ".id"
)
```



**Arguments**

df	A data frame to be used to plot
buffer_names	A character string containing the name of the variable with buffer spots. Default set to 'antigen'.
buffer_mfi	A character string containing the name of the variable with MFI value. Assuming background correction is done already. Default to 'FMedianBG_correct'
slide_id	A character string containing the name of the slide/array identifier variable.

**Value**

plot of buffer spots

**Examples**

```
buffers <- readr::read_csv(system.file("extdata", "buffers_sample2.csv",
package="protGear"))
plot_buffer(df=buffers,buffer_names = "sampleID")
```

---

plot\_FB

*plot\_FB*

---

**Description**

A generic function for plotting the background and foreground values.

**Usage**

```
plot_FB(
  df,
  antigen_name = "antigen",
  bg_MFI = "BG_Median",
  FG_MFI = "FBG_Median",
  log_mfi = FALSE
)
```

**Arguments**

df	An object containing the data to which the plot is done.
antigen_name	The variable describing which features/proteins/ antibodies in the data should be used to plot
bg_MFI	A numeric variable describing which is the background MFI
FG_MFI	A numeric variable describing which is the foreground MFI
log_mfi	a logical value indicating whether the MFI values should be log transformed or not.

**Details**

Plot foreground and background values

**Value**

a ggplot of foreground vs background MFI values

**Examples**

```
## Not run:
#After extracting the background using \code{\link{extract_bg}}
#we plot the data using
allData_bg <- readr::read_csv(system.file("extdata",
"bg_example.csv", package="protGear"))
plot_FB(allData_bg,
antigen_name = "antigen",
bg_MFI = "BG_Median", FG_MFI = "FBG_Median", log = FALSE
)
## End(Not run)
```

---

plot_normalised	<i>Comparison of normalised data by sample</i>
-----------------	--

---

**Description**

Comparison of normalised data by sample

**Usage**

```
plot_normalised(exprs_normalised_df, method, batch_correct)
```

**Arguments**

```
exprs_normalised_df
    a normalised data frame
method
    the method of normalisation used
batch_correct
    the batch correction
```

**Value**

A ggplot of normalised data

**Examples**

```
matrix_antigen <- readr::read_csv(system.file("extdata",
"matrix_antigen.csv", package="protGear"))
normlise_vsn <- matrix_normalise(as.matrix(matrix_antigen),
method = "vsn",
return_plot = FALSE
)
plot_normalised(normlise_vsn,method="vsn",batch_correct=FALSE)
```

---

 plot\_normalised\_antigen

*Comparison of normalised data by feature*


---

### Description

Comparison of normalised data by feature

### Usage

```
plot_normalised_antigen(exprs_normalised_df, method, batch_correct)
```

### Arguments

```
exprs_normalised_df
  a normalised data frame
method
  the method of normalisation used
batch_correct
  the batch correction
```

### Value

A ggplot of various normalisation approaches

### Examples

```
matrix_antigen <- readr::read_csv(system.file("extdata",
"matrix_antigen.csv", package="protGear"))
normlise_vsn <- matrix_normalise(as.matrix(matrix_antigen),
method = "vsn",
return_plot = FALSE
)
plot_normalised_antigen(normlise_vsn,method="vsn",batch_correct=FALSE)
```

---

 read\_array\_files

*Read array files*


---

### Description

This helps to read the chip file(s).

### Usage

```
read_array_files(i, data_path, genepix_vars)
```

### Arguments

```
i
  The name of the file which the data are to be read from.
data_path
  The path where the file with the data is located
genepix_vars
  A list of specific definitions of the experiment design. See array\_vars.
```

**Details**

Read multiple array files

**Value**

a number of data frames in the global environment

**Examples**

```
## Not run:
genepix_vars <- array_vars(
  channel = "635",
  chip_path = system.file("extdata", "array_data/machine1/",
    package="protGear"),
  totsamples = 21,
  blockspersample = 2,
  mig_prefix = "_first",
  machine = 1,
  date_process = "0520"
)
file_read <- "KK2-06.txt"
read_array_files(i=file_read,
  data_path=system.file("extdata", "array_data/machine1/",
    package="protGear"), genepix_vars=genepix_vars)
## End(Not run)
```

---

read\_array\_visualize *Read a gpr file to visualize*

---

**Description**

Read a gpr file to visualize

**Usage**

```
read_array_visualize(infile)
```

**Arguments**

infile            a .gpr file to be used to visualize the expression intensities of the slide spots

**Value**

a data frame to visualize the background or foreground values

**Examples**

```
## Not run:
read_array_visualize(infile = system.file("extdata",
  "/array_data/machine1/KK2-06.txt", package="protGear"))
## End(Not run)
```

---

rlm_normalise	<i>RLM normalisation</i>
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**Description**

A function for method='rlm' from [matrix\\_normalise](#).

**Usage**

```
rlm_normalise(rlm_normalise_df)
```

**Arguments**

```
rlm_normalise_df
      rlm normalised data frame
```

**Value**

an elist of RLM normalisation to be utilised by [rlm\\_normalise\\_matrix](#)

**Examples**

```
matrix_antigen <- readr::read_csv(system.file("extdata",
"matrix_antigen.csv", package="protGear"))
#rlm_normalise_df <- rlm_normalise_matrix(matrix_antigen=matrix_antigen,
#array_matrix=array_matrix,
# control_antigens=control_antigens)
# rlm_normalise(rlm_normalise_df)
```

---

rlm_normalise_matrix	<i>Nomrmalise using RLM</i>
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---

**Description**

A function for method='rlm' from [matrix\\_normalise](#).

**Usage**

```
rlm_normalise_matrix(matrix_antigen, array_matrix, control_antigens)
```

**Arguments**

```
matrix_antigen  A matrix with antigen data
array_matrix    A matrix with control antigen data
control_antigens
      the control antigens for RLM normalisation
```

**Value**

A RLM normalised data frame

**Examples**

```
matrix_antigen <- readr::read_csv(system.file("extdata",
  "matrix_antigen.csv", package="protGear"))
# rlm_normalise_matrix(matrix_antigen=matrix_antigen,
# array_matrix=array_matrix,
# control_antigens=control_antigens)
```

---

tag_subtract	<i>tag_subtract</i>
--------------	---------------------

---

**Description**

\\\_End\_Function\_\\#

**Usage**

```
tag_subtract(
  dataC_mfi,
  tag_antigens,
  mean_best_CV_var,
  tag_file,
  batch_vars,
  sampleID_var = "sampleID",
  antigen_var = "antigen"
)
```

**Arguments**

dataC_mfi	A dataframe
tag_antigens	A character vector with the names of proteins or antigens used as TAG.
mean_best_CV_var	A character string containing the identifier of the variable with the MFI values.
tag_file	A data frame with variables antigen, TAG, TAG_name to show the TAG for the different antigens or proteins in dataC_mfi
batch_vars	A list of characters identifying variables in dataC_mfi for indicating batch.
sampleID_var	A character string containing the name of the sample identifier variable. Default set to 'sampleID'
antigen_var	A character string containing the name of the features/protein variable. Default to 'antigen'

**Details**

Subtract the purification TAG data

**Value**

A data frame of TAG values subtracted

**Examples**

```

tag_file <- readr::read_csv(system.file("extdata", "TAG_antigens.csv",
package="protGear"))
tag_antigens <- c("CD4TAG", "GST", "MBP")
batch_vars <- list(machine = "m1", day = "0520")
dataC <- readr::read_csv(system.file("extdata", "dataC.csv",
package="protGear"))
## this file has 3 lab replicates and the default names
dataCV <- cv_estimation(dataC ,lab_replicates=3)
dataCV_best2 <- best_CV_estimation(dataCV,slide_id = "iden",
lab_replicates = 3, cv_cut_off = 20)
tag_subtract(dataCV_best2,tag_antigens=tag_antigens,
mean_best_CV_var="mean_best_CV",
tag_file = tag_file,antigen_var = "antigen", batch_vars = batch_vars)

```

---

visualize\_slide

*Visualize the slide mimicking the original scan image.*


---

**Description**

Visualize the slide mimicking the original scan image.

**Usage**

```
visualize_slide(infile, MFI_var, interactive = FALSE, d_f = NA)
```

**Arguments**

<code>infile</code>	a .gpr file to be used to visualize the expression intensities of the slide spots
<code>MFI_var</code>	the MFI variable to plot, can be either the background or foreground value
<code>interactive</code>	a logical to specify whether an interactive graph is returned or not
<code>d_f</code>	a data frame with array data

**Value**

A ggplot of slide foreground values

**Examples**

```

## Not run:
visualize_slide(
infile = system.file("extdata", "/array_data/machine1/KK2-06.txt",
package="protGear"),
MFI_var = "B635 Median"
)
## End(Not run)

```

---

visualize\_slide\_2d      *Visualize the slide mimicking the original scan image using a 2d plot.*

---

**Description**

Visualize the slide mimicking the original scan image using a 2d plot.

**Usage**

```
visualize_slide_2d(infile, MFI_var, d_f = NA)
```

**Arguments**

infile	- a .gpr file to be used to visualize the expression intensities of the slide spots
MFI_var	the MFI variable to plot, can be either the background or foreground value
d_f	a data frame with array data

**Value**

A 2d plot of either the background or foreground values

**Examples**

```
## Not run:  
visualize_slide_2d(  
  infile = system.file("extdata", "/array_data/machine1/KK2-06.txt",  
  package="protGear"),  
  MFI_var = "B635 Median"  
)  
## End(Not run)
```



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