

# Package ‘protGear’

April 18, 2025

**Type** Package

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

**Version** 1.13.0

**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), tidyr (>= 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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## Contents

|                                       |    |
|---------------------------------------|----|
| array_vars . . . . .                  | 3  |
| best_CV_estimation . . . . .          | 4  |
| bg_correct . . . . .                  | 5  |
| buffer_spots . . . . .                | 6  |
| check_sampleID_files . . . . .        | 6  |
| create_dir . . . . .                  | 7  |
| cv_by_sample_estimation . . . . .     | 7  |
| cv_estimation . . . . .               | 8  |
| error_replicates . . . . .            | 9  |
| extract_bg . . . . .                  | 10 |
| launch_protGear_interactive . . . . . | 11 |
| launch_select . . . . .               | 11 |
| matrix_normalise . . . . .            | 12 |
| merge_sampleID . . . . .              | 13 |
| minpositive . . . . .                 | 14 |
| name_of_files . . . . .               | 15 |
| output_trend_stats . . . . .          | 15 |
| plot_bg . . . . .                     | 16 |
| plot_buffer . . . . .                 | 16 |
| plot_FB . . . . .                     | 17 |
| plot_normalised . . . . .             | 18 |
| plot_normalised_antigen . . . . .     | 19 |
| read_array_files . . . . .            | 19 |
| read_array_visualize . . . . .        | 20 |
| rlm_normalise . . . . .               | 21 |
| rlm_normalise_matrix . . . . .        | 21 |
| tag_subtract . . . . .                | 22 |
| visualize_slide . . . . .             | 23 |
| visualize_slide_2d . . . . .          | 24 |

**Index**

**25**

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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 | <i>best CV estimation</i> |
|--------------------|---------------------------|

---

## 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 | <i>bg_correct</i> |
|------------|-------------------|

---

## 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 | <i>\\_End_Function_\\# Check existing sample ID names</i> |
|----------------------|-----------------------------------------------------------|

---

### 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

---

cv\_estimation

---

**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 | <i>\\_Start_Function_For Error\\_#</i> |
|------------------|----------------------------------------|

---

## 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 | <i>extract bg</i> |
|------------|-------------------|

---

## 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 <a href="#">array_vars</a> . |

## 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 appplication

### 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_cylic_log <- matrix_normalise(as.matrix(matrix_antigen),
method = "cyclic_loess_log",
return_plot = TRUE
)

```

---

|                |                                            |
|----------------|--------------------------------------------|
| merge_sampleID | <i>Merge sample ID with the array data</i> |
|----------------|--------------------------------------------|

---

**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 \code{\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 | <i>plot_FB</i> |
|---------|----------------|

---

**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> |
|---------------|--------------------------|

---

**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> |
|----------------------|-----------------------------|

---

**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 | <i>Visualize the slide mimicking the original scan image.</i> |
|-----------------|---------------------------------------------------------------|

---

**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 | <i>Visualize the slide mimicking the original scan image using a 2d plot.</i> |
|--------------------|-------------------------------------------------------------------------------|

---

**Description**

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

**Usage**

```
visualize_slide_2d(infile, MFI_var, 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>d_f</code>     | 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)
```

# Index

## \* **internal**

- error\_replicates, [9](#)
- rlm\_normalise, [21](#)

array\_vars, [3](#), [5](#), [6](#), [10](#), [13](#), [19](#)

backgroundCorrect, [5](#)  
best\_CV\_estimation, [4](#)  
bg\_correct, [5](#), [13](#)  
buffer\_spots, [6](#)

check\_sampleID\_files, [6](#)  
create\_dir, [7](#)  
cv\_by\_sample\_estimation, [7](#)  
cv\_estimation, [8](#)

error\_replicates, [9](#)  
extract\_bg, [10](#)

launch\_protGear\_interactive, [11](#)  
launch\_select, [11](#)

matrix\_normalise, [12](#), [21](#)  
merge\_sampleID, [13](#)  
minpositive, [14](#)

name\_of\_files, [15](#)

output\_trend\_stats, [15](#)

plot\_bg, [16](#)  
plot\_buffer, [16](#)  
plot\_FB, [17](#)  
plot\_normalised, [18](#)  
plot\_normalised\_antigen, [19](#)

read\_array\_files, [19](#)  
read\_array\_visualize, [20](#)  
rlm\_normalise, [21](#)  
rlm\_normalise\_matrix, [21](#), [21](#)

tag\_subtract, [22](#)

visualize\_slide, [23](#)  
visualize\_slide\_2d, [24](#)