# Package 'protGear'

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**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)

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# Contents

array_vars *List the array structure variables*

## 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 teh number of samples on a slide. |
| FG | Optional:A character indicating the name of the foreground variable name. if not specified its created as `paste0("F",channel,".Median")` |
| BG | Optional:A character indicating the name of the background variable name. if not specified its created as `paste0("B",channel,".Median")` |
| FBG | Optional:A character indicating the name of the foreground - background variable name. if not specified its created as `paste0("F",channel,".Median...B",channel)` |
| blockspersample | A numeric value indicating the numer 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 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 array_vars. |
| 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` *Extract buffer spots of data*

## 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 `array_vars`. |

## 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` *Title Create directory function*

---

## 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` *cv by sample*

---

## 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 _*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 appplication |

## Value

launches the app defined under theApp

## Examples

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

matrix_normalise *Normalize Arrays*

## 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_ "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` *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 `array_vars`. |
| `method` | A description of the background correction to be used. See `bg_correct`. |

## 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 *Object names of a list*

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

### 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 *Plot background*

### 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 *Plot the buffer values*

### 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 *Comparison of normalised data by sample*

---

## 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 *RLM normalisation*

### 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 *Nomrmalise using RLM*

### 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` *tag_subtract*

---

## 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

| | |
|---|---|
| `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 |
| `interactive` | a logical to specify whether an interactive graph is returned or not |
| `d_f` | 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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