Package 'proBatch'

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Type Package

Title Tools for Batch Effects Diagnostics and Correction

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Description The proBatch package contains functions for diagnosing and removing batch effects and other unwanted variation in high-thoughput experiment, primarily designed for DIA proteomics data.
The diagnostic part of the package can be broadly divided in (1) Genome-wide and (2) Gene-specific functions, explained in corresponding vignettes. Since the diagnostic part for batch effects does require batch effect removal, here we provide a few convenience wrappers for common batch-effect removal approaches, namely, ComBat (Johnson et al. 2007 Biostatistics) and mean/median centering. However, proteomics data may require more complicated technical artifact correction approaches like non-linear fitting, which is also found in ``normalization" section of this package.
The approaches are described in (Čuklina et al. 2019, MCP)

License What license is it under?

URL https://github.com/jelenachuklina/proBatch

BugReports https://github.com/jelenachuklina/proBatch/issues

Depends R (>= 3.4.0),
dplyr (>= 0.7.4),
ggplot2

Encoding UTF-8

LazyData true

Imports Biobase,
corrplot,
ggfortify,
data.table,
lazyeval,
lubridate,
magrittr,
pheatmap,
preprocessCore,
pvca,
RColorBrewer,

readr,
reshape2,
rlang,
scales,
sva,
tibble,
tidyverse (>= 1.2.1),
wesanderson,
WGCNA

Suggests knitr,
rmarkdown,
SWATH2stats

VignetteBuilder knitr

RoxygenNote 6.0.1

R topics documented:

`boxplot_all_steps` *Plot boxplots to compare various data normalization steps/approaches WARNING: extremely slow for big dataframes*

Description

Plot boxplots to compare various data normalization steps/approaches WARNING: extremely slow for big dataframes

Usage

```
boxplot_all_steps(list_of_dfs, sample_annotation, batch_col, step = NULL)
```

Arguments

`list_of_dfs`	list of data frames of format, specified in 'plot_boxplot'
`sample_annotation`	data matrix with 1) 'sample_id_col' (this can be repeated as row names) 2) biological and 3) technical covariates (batches etc)
`batch_col`	column in 'sample_annotation' that should be used for batch comparison
`step`	normalization step (e.g. 'Raw' or 'Quantile_normalized' or 'qNorm_ComBat'). Useful if consecutive steps are compared in plots. Note that in plots these are usually ordered alphabetically, so it's worth naming with numbers, e.g. '1_raw', '2_quantile'

Value

ggplot object

See Also

`plot_boxplot`

clean_requants *Remove requanted and sparse features*

Description

Cleans dataset df_long (proBatch) by removing requanted features and features not meeting user defined sparsness criterias.

Usage

```
clean_requants(df_long, sample_annotation, batch_col = "MS_batch.final",
  feature_id_col = "peptide_group_label", missing_frac_batch = 0.3,
  missing_frac_total = 0.3)
```

Arguments

df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
batch_col	column in sample_annotation that should be used for batch comparison
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
missing_frac_batch	maximally tolerated fraction of missing values for a feature in a batch
missing_frac_total	maximally tolerated fraction of globally missing values for a feature

Value

df_long (proBatch) like data frame filtered as follow:

- remove requant values
- remove features not meeting batch or global sparsness thresholds

See Also

Other dataset cleaning functions: remove_peptides_with_missing_batch, summarize_peptides

color_list_to_df *Color list to data frame*

Description

Turn color list to df (some plotting functions require the latter)

Usage

```
color_list_to_df(color_list, sample_annotation)
```

Arguments

color_list	list of colors
sample_annotation	factor-based configuration of the sample annotation

Value

a data frame representation of the input color list

convert_to_matrix *Long to wide conversion*

Description

Convert from a long data frame representation to a wide matrix representation

Usage

```
convert_to_matrix(df_long, feature_id_col = "peptide_group_label",
  measure_col = "Intensity", sample_id_col = "FullRunName")
```

Arguments

df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
measure_col	if df_long is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)

Value

data_matrix (proBatch) like matrix (features in rows, samples in columns)

See Also

Other matrix manipulation functions: join_data_matrices, matrix_to_long

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`create_peptide_annotation` *Create light-weight peptide annotation data frame for selection of illustrative proteins*

Description

Create light-weight peptide annotation data frame for selection of illustrative proteins

Usage

```
create_peptide_annotation(df_long, peptide_col = "peptide_group_label",
  protein_col = c("Uniprot_ID", "Gene"))
```

Arguments

peptide_col	column containing peptide ID
protein_col	one or more columns contatining protein ID

See Also

plot_peptides_of_one_protein, plot_corrplot_protein, plot_within_prot_distribution

Examples

```
\donotrun{
peptide_annotation = create_peptide_annotation(example_proteome)
peptide_summary =
}
```

`dates_to_posix` *Convert data/time to POSIXct*

Description

convert date/time column of sample_annotation to POSIX format required to keep number-like behaviour

Usage

```
dates_to_posix(sample_annotation, time_column = c("RunDate", "RunTime"),
  new_time_column = NULL, dateTimeFormat = c("%b_%d", "%H:%M:%S"))
```

Arguments

`sample_annotation`
: data matrix with:
  1. `sample_id_col` (this can be repeated as row names)
  2. biological covariates
  3. technical covariates (batches etc)

`time_column`
: name of the column(s) where run date & time are specified. These will be used to determine the run order

`new_time_column`
: name of the new column to which date&time will be converted to

`dateTimeFormat`
: POSIX format of the date and time. See `as.POSIXct` from base R for details

Value

sample annotation file with column names as 'new_time_column' with POSIX-formatted date

---

`date_to_sample_order` *Convert date/time to POSIXct and rank samples by it*

Description

Converts date/time columns fo sample_annotation to POSIXct format and calculates sample run rank in order column

Usage

```
date_to_sample_order(sample_annotation, time_column = c("RunDate", "RunTime"),
  new_time_column = "DateTime", dateTimeFormat = c("%b_%d",
  "%H:%M:%S"), order_col = "order", instrument_col = "instrument")
```

Arguments

`sample_annotation`
: data matrix with:
  1. `sample_id_col` (this can be repeated as row names)
  2. biological covariates
  3. technical covariates (batches etc)

`time_column`
: name of the column(s) where run date & time are specified. These will be used to determine the run order

`new_time_column`
: name of the new column to which date&time will be converted to

`dateTimeFormat`
: POSIX format of the date and time. See `as.POSIXct` from base R for details

Value

sample annotation file with column names as 'new_time_column' with POSIX-formatted date & `order_col` used in some diagnostic plots (e.g. `plot_iRTs`, `plot_sample_mean`)

`define_batches_by_MS_pauses` *Batch by date/time and instrument*

Description

Identify long stretches of time between samples on a per instrument basis and split them into batches.

Usage

```
define_batches_by_MS_pauses(sample_annotation, threshold,
  runtime_col = "RunDateTime", minimal_batch_size = 5,
  instrument_col = "instr", batch_name = "MS_batch")
```

Arguments

`sample_annotation`	data matrix with: 1. `sample_id_col` (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
`threshold`	time difference that would mean there was an interruption
`runtime_col`	POSIX or numeric-like column corresponding to the sample MS profile acquisition timepoint
`minimal_batch_size`	minimal number of samples in a batch
`instrument_col`	column specifying MS instrument used to acquired data (to account for the presence of multiple instruments in `sample_annotation`)
`batch_name`	string with a self-explanatory name for the batch (e.g. 'MS_batch' for MS-proteomics) to which batch number will be added

Value

`sample_annotation` data matrix with an additional column to indicate sample batching by MS run time and instrument.

`define_batches_by_MS_pauses_within_instrument` *Batch by date/time*

Description

Identify long stretches of time between samples and split them into batches. Most users are going to want to call define_batches_by_MS_pauses, rather then this function

Usage

```
define_batches_by_MS_pauses_within_instrument(date_vector, threshold,
  minimal_batch_size = 5, batch_name = "MS_batch")
```

Arguments

date_vector	POSIX or numeric-like vector corresponding to the sample MS profile acquisition timepoint
threshold	time difference that would mean there was an interruption
minimal_batch_size	minimal number of samples in a batch
batch_name	string with a self-explanatory name for the batch (e.g. 'MS_batch' for MS-proteomics) to which batch number will be added

Value

vector of batches for each sample

---

example_peptide_annotation

Peptide annotation data

Description

This is data from Evan's aging study annotated with gene names

Usage

```
example_peptide_annotation
```

Format

A data frame with 200625 rows and 8 variables:

Peptide peptide group label ID, identical to 'peptide_group_label' in 'example_proteome'

Gene HUGO gene ID

ProteinName protein group name as specified in 'example_proteome' ... other parameters determined by 'summarize_peptides' function

`example_proteome` *Example protein data*

Description

This is data from Evan's aging study with all iRT, spike-in peptides, few random peptides and QTL proteins for biological signal improvement demonstration

Usage

```
example_proteome
```

Format

A data frame with 200625 rows and 8 variables:

peptide_group_label peptide ID, which is regular feature level. This column is mostly used as 'feature_id_col'

RT retention time. Relevant to identify retention time related bias

Intensity peptide group intensity in given sample. Used in function as 'measure_col'

ProteinName Protein group ID, specified as N/UniProtID1|UniProtID2|..., where N is number of protein peptide group maps to. If 1/UniProtID, then this is proteotypic peptide

assay_rt retention time as in DIA library

m_score peptide group identification FDR as determined by pyProphet

FullRunName name of the file, in most functions used for 'sample_id_col' #' ...

Source

PRIDE ID will be added in future

`example_sample_annotation1` *Sample annotation data version 1*

Description

This is data from Evan's aging study with mock instruments to show how instrument-specific functionality works

Usage

```
example_sample_annotation1
```

Format

A data frame with 375 rows and 18 variables:

FullRunName name of the file, in most functions used for ‘sample_id_col‘

MS_batch.final mass-spectrometry batch: 7-level factor of manually annotated batches

EarTag mouse ID, i.e. ID of the biological object

Strain mouse strain ID - biological covariate #1

Diet diet - either ‘HFD‘ = ‘High Fat Diet‘ or ‘CD‘ = ‘Chow Diet‘. ‘Mix‘ stands for mixture of several samples

Sex mice sex - 3-level biological covariate. Possible values - ”

Age_Days mice age at sampling - numeric biological covariate

RunDate mass-spectrometry running date. In combination with ‘RunTime‘ used for running order determination

RunTime mass-spectrometry running time. In combination with ‘RunDate‘ used for running order determination

SacrificeDate date of mouse sacrifice - technical covariate

ProteinPrepDate date of protein preparation - technical covariate ...

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generate_colors_for_numeric

Generates color list

Description

Generates a list of colors for a vector of numeric, POSIXct (i.e. the (signed) number of seconds since the beginning of 1970 , or factors

Usage

```
generate_colors_for_numeric(num_col, palette_type = "brewer", i = 1,
  granularity = 10)
```

Arguments

num_col	a vector of type numeric of factor to generate colors for
palette_type	’brewer’ or ’viridis’
i	if palette_type is ’brewer’ the palette argument to brewer_pal. If palette_type is ’viridis’ the option argument to virids_pal ()
granularity	the breaks to use when generating colors for num_col

Value

list, containing the following items:

1. ‘color_vector‘ - string-like vector of colors
2. ‘new_annotation‘ - factor representation of numeric vector (factor with number of levels equal to "granularity")

get_peptide_corr_df *Transform square correlation matrix into long data frame of correlations*

Description

Transform square correlation matrix into long data frame of correlations

Usage

```
get_peptide_corr_df(peptide_cor, peptide_annotation,
  protein_col = "ProteinName", feature_id_col = "peptide_group_label")
```

Arguments

feature_id_col

get_sample_corr_distrib *Calculates correlation distribution for all pairs of the replicated samples*

Description

Calculates correlation distribution for all pairs of the replicated samples

Usage

```
get_sample_corr_distrib(cor_proteome, sample_annotation,
  sample_id_col = "sample_id", biospecimen_id_col = "EarTag",
  batch_col = "batch")
```

Arguments

cor_proteome	sample correlation matrix (square)
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
batch_col	column in ‘sample_annotation‘ that should be used for batch comparison

Value

dataframe with the following columns, that are suggested to use for plotting in `plot_sample_corr_distribution` as `plot_param`:

1. `replicate`
2. `batch_the_same`
3. `batch_replicate`
4. `batches`

other columns are:

1. `sample_id_1` & `sample_id_2`, both generated from `sample_id_col` variable
2. `correlation` - correlation of two corresponding samples
3. `batch_1` & `batch_2` or analogous, created the same as `sample_id_1`

`join_data_matrices` *Join data matrices*

Description

Joins 2 or more data matrices

Usage

```
join_data_matrices(matrices_list, step, sample_annotation,
  measure_col = "Intensity")
```

Arguments

`matrices_list`	list of matrices in `data_matrix` (proBatch) format to be joined
`step`	normalization step (e.g. 'Raw' or 'Quantile_normalized' or 'qNorm_ComBat'). Useful if consecutive steps are compared in plots. Note that in plots these are usually ordered alphabetically, so it's worth naming with numbers, e.g. '1_raw', '2_quantile'
`sample_annotation`	data matrix with: 1. `sample_id_col` (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
`measure_col`	if `df_long` is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency

Value

`df_long` (proBatch) like data frame with a row, having entries for:

1. `feature_id_col` (e.g. peptide name)
2. `sample_id_col` (e.g. filename)
3. `measure_col` (e.g. intensity/expression)
4. `step` (e.g. 'raw', 'quantile_norm')

See Also

Other matrix manipulation functions: convert_to_matrix, matrix_to_long

---

`matrix_to_long` *Wide to long conversion*

Description

Convert from wide matrix to a long data frame representation

Usage

```
matrix_to_long(data_matrix, sample_annotation,
  feature_id_col = "peptide_group_label", measure_col = "Intensity",
  sample_id_col = "FullRunName", step = NA)
```

Arguments

`data_matrix`	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. Usually the log transformed version of the original data
`sample_annotation`	data matrix with: 1. `sample_id_col` (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
`feature_id_col`	name of the column with feature/gene/peptide/protein ID used in the long format representation `df_long`. In the wide formatted representation `data_matrix` this corresponds to the row names.
`measure_col`	if `df_long` is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
`sample_id_col`	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
`step`	normalization step (e.g. 'Raw' or 'Quantile_normalized' or 'qNorm_ComBat'). Useful if consecutive steps are compared in plots. Note that in plots these are usually ordered alphabetically, so it's worth naming with numbers, e.g. '1_raw', '2_quantile'

Value

`df_long` (proBatch) like data frame

See Also

Other matrix manipulation functions: convert_to_matrix, join_data_matrices

merge_rare_levels *Replaces rare levels with other*

Description

Replaces levels with a maximal occurence of 1 with other

Usage

```
merge_rare_levels(column)
```

normalize *Data normalization and batch adjustment methods*

Description

Data normalization and batch adjustment methods

Median normalization of the data (per batch median)

Median normalization of the data (global)

normalize with the custom (continuous) fit

Standardized input-output ComBat normalization ComBat allows users to adjust for batch effects in datasets where the batch covariate is known, using methodology described in Johnson et al. 2007. It uses either parametric or non-parametric empirical Bayes frameworks for adjusting data for batch effects. Users are returned an expression matrix that has been corrected for batch effects. The input data are assumed to be cleaned and normalized before batch effect removal.

Usage

```
normalize_medians_batch(data_long, sample_annotation = NULL,
  sample_id_col = "FullRunName", batch_col = "MS_batch.final",
  feature_id_col = "peptide_group_label", measure_col = "Intensity")

normalize_medians_global(data_long, sample_id_col = "FullRunName",
  measure_col = "Intensity")

normalize_custom_fit(data_matrix, sample_annotation,
  batch_col = "MS_batch.final", feature_id_col = "peptide_group_label",
  sample_id_col = "FullRunName", measure_col = "Intensity",
  sample_order_col = "order", fit_func = fit_nonlinear, ...)

correct_with_ComBat(data_matrix, sample_annotation,
  batch_col = "MS_batch.final", par.prior = TRUE)
```

Arguments

sample_annotation	data matrix with 1) ‘sample_id_col‘ (this can be repeated as row names) 2) biological and 3) technical covariates (batches etc)
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
batch_col	column in ‘sample_annotation‘ that should be used for batch comparison
measure_col	if ‘df_long‘ is among the parameters, it is the column with expression/abundance/intensity, otherwise, it is used internally for consistency
data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. Usually the log transformed version of the original data
sample_order_col	column, determining the order of sample MS run, used as covariate to fit the non-linear fit
fit_func	function to fit the (non)-linear trend
...	other parameters, usually those of the ‘fit_func‘
par.prior	
return_long	whether the result should be the "long" data frame (as ‘df_long‘) or "wide" (as ‘data_matrix‘)

Value

‘data_matrix‘-size data matrix with batch-effect corrected by ‘ComBat‘

See Also

fit_nonlinear

---

plot_clustering *cluster the data matrix to visually inspect which confounder dominates*

Description

cluster the data matrix to visually inspect which confounder dominates

Usage

```
plot_clustering(data_matrix, color_df, distance = "euclidean",
  agglomeration = "complete", label_samples = T, label_font = 0.2,
  plot_title = NULL, ...)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. in most function, it is assumed that this is the log transformed version of the original data
color_df	data frame of colors, as created by 'sample_annotation_to_colors'
distance	distance metric used for clustering
agglomeration	agglomeration methods as used by 'hclust'
label_samples	if TRUE sample IDs (column names of data_matrix) will be printed
label_font	size of the font. Is active if label_samples is TRUE, ignored otherwise
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
...	other parameters of 'plotDendroAndColors' from 'WGCNA' package

See Also

hclust, sample_annotation_to_colors, plotDendroAndColors

---

plot_corr_matrix *Visualise correlation matrix*

Description

Plot correlation of selected samples or peptides

Usage

```
plot_corr_matrix(corr_matrix, flavor = "corrplot", filename = NULL,
  width = NA, height = NA, unit = c("cm", "in", "mm"), plot_title = "",
  ...)
```

Arguments

corr_matrix	square correlation matrix
flavor	either corrplot from 'corrplot' package or heatmap, as in 'pheatmap'
filename	path where the results are saved. If null the object is returned to the active window; otherwise, the object is save into the file. Currently only pdf and png format is supported
width	option determining the output image width
height	option determining the output image width
unit	units: 'cm', 'in' or 'mm'
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
...	parameters for the corrplot.mixed or pheatmap visualisation, for details see examples and help to corresponding functions

See Also

pheatmap, corrplot.mixed

plot_heatmap *Plot the heatmap of samples*

Description

Plot the heatmap of samples

Usage

```
plot_heatmap(data_matrix, sample_annotation = NULL, fill_the_missing = T,
  cluster_rows = T, cluster_cols = F, annotation_color_list = NA,
  heatmap_color = colorRampPalette(rev(RColorBrewer::brewer.pal(n = 7, name =
  "RdYlBu")))(100), color_for_missing = "black", filename = NA,
  plot_title = NA, ...)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. in most function, it is assumed that this is the log transformed version of the original data
sample_annotation	data matrix with 1. 'sample_id_col' (this can be repeated as row names) 2. biological and 3. technical covariates (batches etc) ; each column of sample annotation will get it's own row. If 'cluster_cols = T' this will indicate, whether sample proximity is driven by one of biolical or technical factors
fill_the_missing	boolean value determining if missing values should be substituted with -1 (and colored with black)
cluster_rows	boolean value determining if rows should be clustered
cluster_cols	boolean value determining if columns should be clustered
annotation_color_list	list specifying colors for columns (samples). Best created by 'sample_annotation_to_colors'
heatmap_color	vector of colors used in heatmap (typicall a gradient)
color_for_missing	special color to make missing values. Usually black or white, depending on 'heatmap_color'
filename	filepath where to save the image
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
...	other parameters of link[pheatmap]{pheatmap}

Value

object returned by link[pheatmap]{pheatmap}

See Also

sample_annotation_to_colors, pheatmap

---

plot_iRTs *Plot iRT measurements*

Description

Creates a iRT facetted ggplot2 plot of the value in measure_col vs order_col using plot_peptide_level. Additionally, the resulting plot can also be facetted by batch.

Usage

```
plot_iRTs(df_long, sample_annotation, order_col = NULL, irt_pattern = "iRT",
  batch_col = "MS_batch.final", sample_id_col = "FullRunName",
  feature_id_col = "peptide_group_label", measure_col = "Intensity",
  plot_title = "iRT peptide profile", ...)
```

Arguments

df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
order_col	column in sample_annotation that determines sample order. It is used for certain diagnostics and normalisations.
irt_pattern	substring used to identify irts proteins in the column 'ProteinName'
batch_col	column in sample_annotation that should be used for batch comparison
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
measure_col	if df_long is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
plot_title	the string indicating the source of the peptides
...	additional arguments to plot_peptide_level function

Value

ggplot2 type plot of measure_col vs order_col, faceted by irt_pattern containing proteins and (optionally) by batch_col

See Also

Other feature-level diagnostic functions: plot_peptide_level, plot_peptides_of_one_protein, plot_spike_ins, plot_with_fitting_curve

---

plot_pca *plot PCA plot*

Description

plot PCA plot

Usage

```
plot_pca(data_matrix, sample_annotation,
  feature_id_col = "peptide_group_label", color_by = "MS_batch",
  PC_to_plot = c(1, 2), fill_the_missing = 0, colors_for_factor = NULL,
  theme = "classic", plot_title = NULL)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. in most function, it is assumed that this is the log transformed version of the original data
sample_annotation	data matrix with 1) 'sample_id_col' (this can be repeated as row names) 2) biological and 3) technical covariates (batches etc)
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
color_by	column name (as in 'sample_annotation') to color by
PC_to_plot	principal component numbers for x and y axis
fill_the_missing	boolean value determining if missing values should be substituted with -1 (and colored with black)
colors_for_factor	named vector of colors for the 'color_by' variable
theme	ggplot theme, by default 'classic'. Can be easily overriden (see examples)
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))

Value

ggplot scatterplot colored by factor levels of column specified in 'factor_to_color'

See Also

autoplot.pca_common, ggplot

plot_peptides_of_one_protein *Plot peptides of one protein*

Description

Creates a spike-in facetted ggplot2 plot of the value in `measure_col` vs `order_col` using `plot_peptide_level`. Additionally, the resulting plot can also be facetted by batch.

Usage

```
plot_peptides_of_one_protein(proteinName, protein_col = "ProteinName",
  df_long, sample_annotation, peptide_annotation = NULL,
  order_col = "order", sample_id_col = "FullRunName",
  batch_col = "MS_batch", measure_col = "Intensity",
  feature_id_col = "peptide_group_label",
  plot_title = sprintf("Peptides of %s protein", proteinName), ...)
```

Arguments

`proteinName`	name of the protein as defined in `ProteinName`
`protein_col`	column where protein names are specified
`df_long`	data frame where each row is a single feature in a single sample. It minimally has a `sample_id_col`, a `feature_id_col` and a `measure_col`, but usually also an `m_score` (in OpenSWATH output result file)
`sample_annotation`	data matrix with: 1. `sample_id_col` (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
`order_col`	column in `sample_annotation` that determines sample order. It is used for certain diagnostics and normalisations.
`sample_id_col`	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
`batch_col`	column in `sample_annotation` that should be used for batch comparison
`measure_col`	if `df_long` is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
`feature_id_col`	name of the column with feature/gene/peptide/protein ID used in the long format representation `df_long`. In the wide formatted representation `data_matrix` this corresponds to the row names.
`plot_title`	the string indicating the source of the peptides
`...`	additional arguments to `plot_peptide_level` function

Value

ggplot2 type plot of `measure_col` vs `order_col`, faceted by `spike_ins` containing proteins and (optionally) by `batch_col`

See Also

Other feature-level diagnostic functions: plot_iRTs, plot_peptide_level, plot_spike_ins, plot_with_fitting_curve

---

`plot_peptide_correlation_distr_one_protein` *Plot distribution curves for each step to see if they shift by data normalization*

Description

Plot distribution curves for each step to see if they shift by data normalization

Usage

```
plot_peptide_correlation_distr_one_protein(data_matrix_list, protein_name,
  peptide_annotation, protein_col = "ProteinName",
  feature_id_col = "peptide_group_label",
  plot_title = sprintf("Distribution of peptide correlation at different correction steps,\n
  protein_name), theme = "classic")
```

Arguments

`protein_name`	name of the protein, as specified in `protein_col` of `peptide_annotation`
`theme`	

`plot_peptide_level` *Plot peptide measurements*

Description

Creates a peptide facetted ggplot2 plot of the value in `measure_col` vs `order_col`. Additionally, the resulting plot can also be facetted by batch.

Usage

```
plot_peptide_level(pep_name, df_long, sample_annotation, order_col = NULL,
  sample_id_col = "FullRunName", batch_col = "MS_batch.final",
  measure_col = "Intensity", feature_id_col = "peptide_group_label",
  geom = c("point", "line"), color_by_batch = F, facet_by_batch = F,
  plot_title = NULL, requant = NULL, theme = "classic")
```

Arguments

pep_name	name of the peptide for diagnostic profiling
df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
order_col	column in sample_annotation that determines sample order. It is used for certain diagnostics and normalisations.
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
batch_col	column in sample_annotation that should be used for batch comparison
measure_col	if df_long is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
geom	whether to show the feature as points and/or connect by lines
color_by_batch	(logical) whether to color points by batch
facet_by_batch	(logical) whether to plot each batch in its own facet
plot_title	the string indicating the source of the peptides
requant	if data frame: requant values; if logical: whether to indicate requant values (requires 'requant' or 'm_score' column in df_long)
theme	plot theme (default is 'classical'; other options not implemented)

Value

ggplot2 type plot of measure_col vs order_col, faceted by pep_name and (optionally) by batch_col

See Also

Other feature-level diagnostic functions: plot_iRTs, plot_peptides_of_one_protein, plot_spike_ins, plot_with_fitting_curve

---

plot_protein_corrplot *Peptide correlation matrix (heatmap)*

Description

Plots correlation plot of peptides from a single protein

Usage

```
plot_protein_corrplot(data_matrix, protein_name, peptide_annotation,
  protein_col = "ProteinName", peptide_col_name = "peptide_group_label",
  flavor = "corrplot", filename = NULL, width = NA, height = NA,
  unit = c("cm", "in", "mm"), plot_title = "peptide correlation matrix",
  ...)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. Usually the log transformed version of the original data
protein_name	the name of the protein
peptide_annotation	df with peptides and their corresponding proteins
protein_col	the column name in peptide_annotation with protein names
peptide_col_name	the column name in peptide_annotation with peptide names
flavor	either corrplot from 'corrplot' package or heatmap, as in 'pheatmap'
filename	path where the results are saved. If null the object is returned to the active window; otherwise, the object is save into the file. Currently only pdf and png format is supported
width	option determining the output image width
height	option determining the output image width
unit	units: 'cm', 'in' or 'mm'
plot_title	The title of the plot
...	parameters for the corrplot visualisation

Examples

```
\donotrun{plot_corr_plot(q_norm_proteome, protein_name = 'Haao',
               peptide_annotation = peptide_annotation, prot.column = 'Gene',
               title = 'Haao protein peptides after quantile norm',
               number.cex=0.75, tl.cex = .75
               mar=c(0,0,1,0))}
\donotrun{lower = "ellipse", upper = "number",
 tl.col = "black", diag = 'l', tl.pos = "lt", number.cex=0.75, tl.cex = .75}
```

---

plot_prot_corr_distribution

Plot distribution of peptide correlations within one protein and between proteins

---

Description

Plot distribution of peptide correlations within one protein and between proteins

Usage

```
plot_prot_corr_distribution(data_matrix, peptide_annotation,
  protein_col = "ProteinName", feature_id_col = "peptide_group_label",
  plot_title = "Distribution of peptide correlation", theme = "classic")
```

Arguments

theme

---

plot_pvca *Plot variance distribution by variable*

Description

Plot variance distribution by variable

Usage

```
plot_pvca(data_matrix, sample_annotation, sample_id_col = "FullRunName",
  feature_id_col = "peptide_group_label",
  technical_covariates = c("MS_batch", "instrument"),
  biological_covariates = c("cell_line", "drug_dose"), fill_the_missing = 0,
  threshold_pca = 0.6, threshold_var = 0.01, colors_for_bars = NULL,
  theme = "classic", plot_title = NULL)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. in most function, it is assumed that this is the log transformed version of the original data
sample_annotation	data matrix with 1) 'sample_id_col' (this can be repeated as row names) 2) biological and 3) technical covariates (batches etc)
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
technical_covariates	vector 'sample_annotation' column names that are technical covariates
biological_covariates	vector 'sample_annotation' column names, that are biologically meaningful covariates
threshold_pca	the percentile value of the minimum amount of the variabilities that the selected principal components need to explain
threshold_var	the percentile value of weight each of the covariates needs to explain (the rest will be lumped together)

colors_for_bars	four-item color vector, specifying colors for the following categories: c('residual', 'biological', 'biol:techn', 'technical')
theme	ggplot theme, by default 'classic'. Can be easily overriden (see examples)
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.

Value

list of two items: plot =gg, df = pvca_res

See Also

sample_annotation_to_colors, ggplot

---

plot_samples_corrplot *Sample correlation matrix (heatmap)*

Description

Plot correlation of selected samples

Usage

```
plot_samples_corrplot(data_matrix, samples_to_plot = NULL,
  flavor = "corrplot", filename = NULL, width = NA, height = NA,
  unit = c("cm", "in", "mm"), plot_title = "Correlation matrix of samples",
  ...)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. Usually the log transformed version of the original data
samples_to_plot	string vector of samples in data_matrix to be used in the plot
filename	path where the results are saved. If null the object is returned to the active window; otherwise, the object is save into the file. Currently only pdf and png format is supported
width	option determining the output image width
height	option determining the output image width
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
...	parameters for the corrplot.mixed or pheatmap visualisation, for details see examples and help to corresponding functions

See Also

pheatmap, corrplot.mixed

Examples

```
### Example 1: Plot heatmap of pre-specified samples
#'\dontrun{specified_samples = sample_annotation %>%
filter(RunID %in% paste('Run', 110:115, sep = '')) %>%
pull(FullRunName)
plot_samples_corr_heatmap(data_matrix, sample_to_plot = specified samples,
 flavor = 'pheatmap', cluster_rows = F, cluster_cols = F)

}
### Example 2: Plot corrplot of pre-specified samples
#' #'\dontrun{specified_samples = sample_annotation %>%
filter(RunID %in% paste('Run', 110:115, sep = '')) %>%
pull(FullRunName)
plot_samples_corr_heatmap(data_matrix, sample_to_plot = specified samples,
 flavor = 'corrplot', lower = "ellipse", upper = "number",
 tl.col = "black", diag = 'l', tl.pos = "lt", number.cex=0.75, tl.cex = .75)

}
```

`plot_sample_corr_distribution`

Create violin plot of correlation distribution

Description

Useful to visualize within batch vs within replicate vs non-related sample correlation

Usage

```
plot_sample_corr_distribution(data_matrix, sample_annotation,
  repeated_samples = NULL, sample_id_col = "sample_id",
  batch_col = "batch", biospecimen_id_col = "EarTag",
  plot_title = "Correlation distribution", plot_param = "batch_replicate")
```

Arguments

`repeated_samples`	if 'NULL', only repeated sample correlation is plotted
`sample_id_col`	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
`batch_col`	column in `sample_annotation` that should be used for batch comparison
`plot_title`	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
`plot_param`	columns, defined in correlation_df, which is output of `get_sample_corr_distrib`, specifically, #' 1. `replicate` 2. `batch_the_same`

3. batch_replicate
4. batches

;

Value

ggplot type object with violin plot for each plot_param

See Also

get_sample_corr_distrib, ggplot

---

plot_sample_means_or_boxplots *Plot per-sample average or boxplot (distribution) vs order (if the real running order available)*

Description

Plot per-sample average or boxplot (distribution) vs order (if the real running order available)

Usage

```
plot_sample_mean(data_matrix, sample_annotation = NULL,
  sample_id_col = "FullRunName", order_col = "order", batch_col = NULL,
  facet_col = "instrument", color_by_batch = F, color_scheme = "brewer",
  theme = "classic", plot_title = NULL, order_per_facet = F)

plot_boxplot(df_long, sample_annotation = NULL,
  sample_id_col = "FullRunName", measure_col = "Intensity",
  order_col = "order", batch_col = "MS_batch.final",
  facet_col = "instrument", color_by_batch = T, color_scheme = "brewer",
  theme = "classic", plot_title = NULL, order_per_facet = F)
```

Arguments

data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. in most function, it is assumed that this is the log transformed version of the original data
sample_annotation	data matrix with 1) 'sample_id_col' (this can be repeated as row names) 2) biological and 3) technical covariates (batches etc)
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
order_col	column where running order is specified.
batch_col	column in 'sample_annotation' that should be used for batch comparison
facet_col	recommended if more than one batch covariate is present. Faceting is most suited to examine instruments separately
color_by_batch	should the each batch be represented with its own color?

color_scheme	named vector, names corresponding to unique batch values as specified in 'sample_annotation'
theme	ggplot theme, by default 'classic'. Can be easily overriden (see examples)
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
order_per_facet	if order is defined ignoring facets (usually instrument), re-define order per-batch
df_long	data frame where each row is a single feature in a single sample, thus it has minimally, 'sample_id_col', 'feature_id_col' and 'measure_col', but usually also 'm_score' (in OpenSWATH output result file)
measure_col	if 'df_long' is among the parameters, it is the column with expression/abundance/intensity, otherwise, it is used internally for consistency

Details

functions for quick visual assessment of trends associated, overall or specific covariate-associated (see 'batch_col' and 'facet_col')

Value

ggplot2 class object. Thus, all aesthetics can be overriden

See Also

ggplot

---

plot_spike_ins *Plot spike-in measurements*

Description

Creates a spike-in facetted ggplot2 plot of the value in measure_col vs order_col using plot_peptide_level. Additionally, the resulting plot can also be facetted by batch.

Usage

```
plot_spike_ins(df_long, sample_annotation, order_col = "order",
  spike_ins = "BOVIN", sample_id_col = "FullRunName",
  batch_col = "MS_batch", measure_col = "Intensity",
  feature_id_col = "peptide_group_label",
  plot_title = "Spike-in BOVINE protein peptides", ...)
```

Arguments

df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names)

2. biological covariates
3. technical covariates (batches etc)

order_col	column in sample_annotation that determines sample order. It is used for certain diagnostics and normalisations.
spike_ins	substring used to identify spike-in proteins in the column 'ProteinName'
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
batch_col	column in sample_annotation that should be used for batch comparison
measure_col	if df_long is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
plot_title	the string indicating the source of the peptides
...	additional arguments to plot_peptide_level function

Value

ggplot2 type plot of measure_col vs order_col, faceted by spike_ins containing proteins and (optionally) by batch_col

See Also

Other feature-level diagnostic functions: plot_iRTs, plot_peptide_level, plot_peptides_of_one_protein, plot_with_fitting_curve

---

plot_within_prot_corr_distribution

Plot distribution of median correlations of peptides within same protein

---

Description

Plot distribution of median correlations of peptides within same protein

Usage

```
plot_within_prot_corr_distribution(data_matrix_list, peptide_annotation,
  protein_col = "ProteinName", feature_id_col = "peptide_group_label",
  plot_title = "Distribution of peptide correlation", theme = "classic")
```

Arguments

theme

`plot_with_fitting_curve` *Plot peptide measurements across multi-step analysis*

Description

Plot Intensity of a few representative peptides for each step of the analysis including the fitting curve

Usage

```
plot_with_fitting_curve(pep_name, data_df_all_steps, sample_annotation, fit_df,
  fit_value_var = "fit", fit_step = "3_loess_fit", order_col = NULL,
  sample_id_col = "FullRunName", batch_col = "MS_batch",
  measure_col = "Intensity", feature_id_col = "peptide_group_label",
  geom = c("point", "line"), color_by_batch = F, facet_by_batch = F,
  plot_title = NULL, requant = NULL, theme = "classic")
```

Arguments

`pep_name`	name of the peptide for diagnostic profiling
`data_df_all_steps`	data frame, similar to `df_long` proBatch, where each row is a single feature in a single sample, at a certain step of the analysis (minimally raw and after linear normalization) thus it has minimally the following columns: `sample_id_col`, `feature_id_col`, `measure_col`, and `fit_step`, but usually also `m_score`
`sample_annotation`	data matrix with: 1. `sample_id_col` (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
`order_col`	column in `sample_annotation` that determines sample order. It is used for certain diagnostics and normalisations.
`sample_id_col`	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
`batch_col`	column in `sample_annotation` that should be used for batch comparison
`measure_col`	if `df_long` is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
`feature_id_col`	name of the column with feature/gene/peptide/protein ID used in the long format representation `df_long`. In the wide formatted representation `data_matrix` this corresponds to the row names.
`geom`	for the intensity `measure_col` profile:
`color_by_batch`	(logical) whether to color points by batch
`facet_by_batch`	(logical) whether to plot each batch in its own facet
`plot_title`	the string indicating the source of the peptides
`requant`	if data frame: requant values; if logical: whether to indicate requant values (requires 'requant' or 'm_score' column in `df_long`)
`theme`	plot theme (default is 'classical'; other options not implemented)

Value

ggplot-class plot with minimally two facets (before and after non-linear fit) with measure_col (Intensity) vs order_col (injection order) for selected peptides (specified in pep_name)

See Also

Other feature-level diagnostic functions: plot_iRTs, plot_peptide_level, plot_peptides_of_one_protein, plot_spike_ins

---

proBatch *proBatch: A package for diagnostics and correction of batch effects, primarily in proteomics*

Description

It adresses the following needs:

- prepare the original data (e.g. OpenSWATH output matrix and sample annotation file) for analysis. However, you might need to use 'SWATH2stats' additionally
- Diagnose batch effects, sample-wide and feature-level
- Correct for batch effects (normalize the data). Other useful package for this purpose is 'Normalyzer'.

Arguments

df_long	data frame where each row is a single feature in a single sample. It minimally has a sample_id_col, a feature_id_col and a measure_col, but usually also an m_score (in OpenSWATH output result file)
data_matrix	features (in rows) vs samples (in columns) matrix, with feature IDs in rownames and file/sample names as colnames. Usually the log transformed version of the original data
sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
batch_col	column in sample_annotation that should be used for batch comparison
order_col	column in sample_annotation that determines sample order. It is used for certain diagnostics and normalisations.
measure_col	if df_long is among the parameters, it is the column with expression/abundance/intensity; otherwise, it is used internally for consistency
feature_id_col	name of the column with feature/gene/peptide/protein ID used in the long format representation df_long. In the wide formatted representation data_matrix this corresponds to the row names.
plot_title	Title of the plot (usually, processing step + representation level (fragments, transitions, proteins))
theme	ggplot theme, by default 'classic'. Can be easily overriden (see examples)

Details

To learn more about proBatch, start with the vignettes: ‘browseVignettes(package = "proBatch")‘

`quantile_normalize` *Quantile normalization of the data, ensuring that the row and column names are retained*

Description

Quantile normalization of the data, ensuring that the row and column names are retained

Usage

```
quantile_normalize(data_matrix)
```

Arguments

`data_matrix`	log transformed data matrix (features in rows and samples in columns)

Value

‘data_matrix‘-size matrix, with columns quantile-normalized

`remove_peptides_with_missing_batch` *Remove features missing in at least one batch*

Description

Cleans dataset `df_long` (proBatch) by removing all features that are not present in every batch

Usage

```
remove_peptides_with_missing_batch(df_long, batch_col = "MS_batch.final",
  feature_id_col = "peptide_group_label")
```

Arguments

`df_long`	data frame where each row is a single feature in a single sample. It minimally has a `sample_id_col`, a `feature_id_col` and a `measure_col`, but usually also an `m_score` (in OpenSWATH output result file)
`batch_col`	column in `sample_annotation` that should be used for batch comparison
`feature_id_col`	name of the column with feature/gene/peptide/protein ID used in the long format representation `df_long`. In the wide formatted representation `data_matrix` this corresponds to the row names.

Details

useful for some downstream functions as ComBat normalization, that would not work otherwise

Value

df_long (proBatch) like data frame freed of features that were not detected in each batch

See Also

Other dataset cleaning functions: clean_requants, summarize_peptides

---

sample_annotation_to_colors

Generate colors for sample annotation

Description

Convert the sample annotation data frame to list of colors the list is named as columns included to use in potting functions

Usage

```
sample_annotation_to_colors(sample_annotation, columns_for_plotting = NULL,
  sample_id_col = "FullRunName", factor_columns = c("subtype",
  "caseControl"), not_factor_columns = c("RunDate", "ProteinPrepDate"),
  rare_categories_to_other = T, numerics_to_log = F,
  numeric_palette_type = "brewer", granularity = 10)
```

Arguments

sample_annotation	data matrix with: 1. sample_id_col (this can be repeated as row names) 2. biological covariates 3. technical covariates (batches etc)
columns_for_plotting	only consider these columns from sample_annotation
sample_id_col	name of the column in sample_annotation file, where the filenames (colnames of the data matrix are found)
factor_columns	columns of sample_annotation to be treated as factors. Note that factor and character columns are treated as factors by default.
not_factor_columns	don't treat these columns as factors. This can be used to override the default behaviour of considering factors and character columns as factors.
rare_categories_to_other	if True rare categories will be merged as 'other'
numerics_to_log	NOT IMPLEMENTED!
numeric_palette_type	palette to be used for numeric values coloring
granularity	number of colors to map to the number vector (equally spaced between minimum and maximum)

Value

list of colors

`sample_random_peptides` *sample random peptides for diagnostics*

Description

sample random peptides for diagnostics

Usage

```
sample_random_peptides(proteome, seed = 1, pep_per_group = 3,
  groups_RT = 10, groups_intensity = 5)
```

Arguments

`proteome`	required columns: 1. `m_score` 2. `Intensity` 3. `peptide_group_label` 4. `RT`
`pep_per_group`	number of peptides to sample per group
`groups_intensity`	

`summarize_peptides` *Summarize run features*

Description

Summarizes various peptide properties on a per sample basis. By default will summarize RT, Intensity and m_score. If your feature does not have some of these set them to NULL when calling.

Usage

```
summarize_peptides(df_long, sample_id_col = "FullRunName",
  feature_id_col = "peptide_group_label", RT = "RT",
  measure_col = "Intensity", m_score = "m_score")
```

Details

summarize peptides by sample (ranking) and on the contrary, across peptide-wise across samples

Value

a data frame summarizing features in a dataset on a per sample basis. The following columns are returned: 'RT_mean', 'Int_mean', 'numb_requants', 'median_m_score', 'mean_m_score', 'median_good_m_score' (median of 'm_score' excluding requants)

See Also

Other dataset cleaning functions: `clean_requants`, `remove_peptides_with_missing_batch`

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