

# Package ‘MSstats’

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**Title** Protein Significance Analysis in DDA, SRM and DIA for Label-free or Label-based Proteomics Experiments

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**Description** A set of tools for statistical relative protein significance analysis in DDA, SRM and DIA experiments.

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**Author** Meena Choi [aut, cre],  
 Mateusz Staniak [aut],  
 Tsung-Heng Tsai [aut],  
 Ting Huang [aut],  
 Olga Vitek [aut]

**Maintainer** Meena Choi <mnchoi67@gmail.com>

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---

.addCoverageInfo      *Add coverage information to a data.table*

---

**Description**

Add coverage information to a data.table

**Usage**

.addCoverageInfo(input)

**Arguments**

input                  data.table

**Value**

data.table

---

.addModelInformation      *Add model information*

---

**Description**

Add model information

**Usage**

.addModelInformation(input)

**Arguments**

input                  data.table

**Value**

data.table

---

`.addModelVariances`     *Add model variances*

---

**Description**

Add model variances

**Usage**

```
.addModelVariances(input)
```

**Arguments**

input             data.table

**Value**

data.table

---

`.addNInformativeInfo`     *Add information about number of informative features*

---

**Description**

Add information about number of informative features

**Usage**

```
.addNInformativeInfo(input, min_feature_count, column)
```

**Arguments**

input             data.table  
min\_feature\_count     minimum number of quality features to consider  
column             name of a column used for filtering

**Value**

data.table

---

`.addNoisyFlag`      *Add flag for noisy features*

---

### **Description**

Add flag for noisy features

### **Usage**

```
.addNoisyFlag(input)
```

### **Arguments**

input            data.table

### **Value**

data.table

---

`.addOutlierCutoff`      *Add outlier cutoff*

---

### **Description**

Add outlier cutoff

### **Usage**

```
.addOutlierCutoff(input, quantile_order = 0.01)
```

### **Arguments**

input            data.table  
quantile\_order    quantile used to label outliers

### **Value**

data.table

---

`.addOutlierInformation`*Add flag for outlier*

---

**Description**

Add flag for outlier

**Usage**

```
.addOutlierInformation(input, tol = 3, keep_run = FALSE)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>tol</code>	cutoff for outliers
<code>keep_run</code>	if TRUE, completely missing runs will be kept

**Value**

logical

---

`.addSurvivalPredictions`*Get predicted values from a survival model*

---

**Description**

Get predicted values from a survival model

**Usage**

```
.addSurvivalPredictions(input)
```

**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

**Value**

numeric vector of predictions



---

.adjustLRuns                      *Adjust summarized abundance based on the heavy channel*

---

**Description**

Adjust summarized abundance based on the heavy channel

**Usage**

```
.adjustLRuns(input, rename = FALSE)
```

**Arguments**

input	data.table
rename	if TRUE, rename the output column to LogIntensities

**Value**

data.table

---

.calculateOutlierCutoff  
*Calculate cutoff to label outliers*

---

**Description**

Calculate cutoff to label outliers

**Usage**

```
.calculateOutlierCutoff(input, quantile_order = 0.01)
```

**Arguments**

input	data.table
quantile_order	quantile used to label outliers

**Value**

numeric

---

`.calculatePower`      *Power calculation*

---

**Description**

Power calculation

**Usage**

```
.calculatePower(
  desiredFC,
  FDR,
  delta,
  median_sigma_error,
  median_sigma_subject,
  numSample
)
```

**Arguments**

<code>desiredFC</code>	the range of a desired fold change which includes the lower and upper values of the desired fold change.
<code>FDR</code>	a pre-specified false discovery ratio (FDR) to control the overall false positive rate. Default is 0.05
<code>delta</code>	difference between means (?)
<code>median_sigma_error</code>	median of error standard deviation
<code>median_sigma_subject</code>	median standard deviation per subject
<code>numSample</code>	minimal number of biological replicates per condition. TRUE represents you require to calculate the sample size for this category, else you should input the exact number of biological replicates.

---

`.calculateProteinVariance`  
*Calculate protein variances*

---

**Description**

Calculate protein variances

**Usage**

```
.calculateProteinVariance(input)
```

**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

**Value**

list of residuals, degrees of freedom and variances

---

.checkContrastMatrix *Check if contrast matrix includes all conditions*

---

**Description**

Check if contrast matrix includes all conditions

**Usage**

```
.checkContrastMatrix(contrast_matrix, input)
```

**Arguments**

contrast_matrix	contrast matrix
input	data.table of summarized data

---

.checkDataProcessParams  
*Check validity of parameters to dataProcess function*

---

**Description**

Check validity of parameters to dataProcess function

**Usage**

```
.checkDataProcessParams(  
  log_base,  
  normalization_method,  
  standards_names,  
  feature_selection,  
  summarization,  
  imputation  
)
```

**Arguments**

log_base	of logarithmic transformation
normalization_method	string: "quantile", "equalizemedians", "FALSE", "NONE" or "globalStandards"
feature_selection	list with elements: remove_uninformative
summarization	list with elements: method.
imputation	list with elements: cutoff, symbol.

---

```
.checkExperimentDesign
```

*Check if a given column exists in the data*

---

### **Description**

Check if a given column exists in the data

### **Usage**

```
.checkExperimentDesign(input, column_name)
```

### **Arguments**

input	data.table
column_name	chr, name of a column to check

---

```
.checkGCPlotsInput
```

*Check groupComparisonPlots parameters*

---

### **Description**

Check groupComparisonPlots parameters

### **Usage**

```
.checkGCPlotsInput(type, log_base, selected_labels, all_labels)
```

### **Arguments**

type	type of a plot: HEATMAP/VOLCANO PLOT/COMPARISON PLOT
log_base	2 or 10
selected_labels	character vector of contrast labels
all_labels	character vector of all contrast labels

---

`.checkGroupComparisonInput`

*Check if groupComparison input was processed by the dataProcess function*

---

### **Description**

Check if groupComparison input was processed by the dataProcess function

### **Usage**

`.checkGroupComparisonInput(input)`

### **Arguments**

input            data.table

---

`.checkSingleFeature`    *Check if data has less than two features*

---

### **Description**

Check if data has less than two features

### **Usage**

`.checkSingleFeature(input)`

### **Arguments**

input            data.table

### **Value**

logical

---

`.checkSingleLabelProteins`*Check if there are proteins with a single label in a labeled dataset*

---

**Description**

Check if there are proteins with a single label in a labeled dataset

**Usage**`.checkSingleLabelProteins(input)`**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

**Value**

TRUE invisibly

---

`.checkSingleSubject`*Check if there is only single subject*

---

**Description**

Check if there is only single subject

**Usage**`.checkSingleSubject(input)`**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

---

`.checkTechReplicate`*Check if there are technical replicates*

---

**Description**

Check if there are technical replicates

**Usage**`.checkTechReplicate(input)`**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

---

.checkUnProcessedDataValidity

*Check validity of data that were not processed by MSstats converter*

---

### **Description**

Check validity of data that were not processed by MSstats converter

### **Usage**

```
.checkUnProcessedDataValidity(input, fix_missing, fill_incomplete)
```

### **Arguments**

input	data.table
fix_missing	str, optional. Defaults to NULL, which means no action. If not NULL, must be one of the options: "zero_to_na" or "na_to_zero". If "zero_to_na", Intensity values equal exactly to 0 will be converted to NA. If "na_to_zero", missing values will be replaced by zeros.

---

.countInformative

*Count informative features*

---

### **Description**

Count informative features

### **Usage**

```
.countInformative(input, column)
```

### **Arguments**

input	data.table
column	name of a column used for filtering

### **Value**

numeric

---

```
.countMissingPercentage
```

*Count percentage of missing values in given conditions*

---

### Description

Count percentage of missing values in given conditions

### Usage

```
.countMissingPercentage(  
  contrast_matrix,  
  summarized,  
  result,  
  samples_info,  
  has_imputed  
)
```

### Arguments

contrast_matrix	contrast matrix
summarized	data.table summarized by the dataProcess function
result	result of groupComparison
samples_info	number of runs per group
has_imputed	if TRUE, missing values have been imputed by dataProcess

---

```
.documentFunction
```

*A dummy function to store shared documentation items.*

---

### Description

A dummy function to store shared documentation items.

### Usage

```
.documentFunction()
```

### Arguments

removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
summaryforMultipleRows	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.



removeProtein_with1Feature	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
removeProtein_with1Peptide	TRUE will remove the proteins which have only 1 peptide and charge. FALSE is default.
removeOxidationMpeptides	TRUE will remove the peptides including 'oxidation (M)' in modification. FALSE is default.
removeMpeptides	TRUE will remove the peptides including 'M' sequence. FALSE is default.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.

---

.finalizeInput	<i>Add summary statistics to dataProcess output</i>
----------------	---

---

### Description

Add summary statistics to dataProcess output

### Usage

```
.finalizeInput(input, summarized, method, impute, censored_symbol)
```

### Arguments

input	feature-level data
summarized	protein-level data (list)
method	summary method
impute	if TRUE, censored missing values were imputed
censored_symbol	censored missing value indicator

---

<code>.finalizeLinear</code>	<i>Summary statistics for linear model-based summarization</i>
------------------------------	--

---

**Description**

Summary statistics for linear model-based summarization

**Usage**

```
.finalizeLinear(input, censored_symbol)
```

**Arguments**

<code>input</code>	feature-level data
<code>censored_symbol</code>	censored missing value indicator

---

<code>.finalizeTMP</code>	<i>Summary statistics for output of TMP-based summarization</i>
---------------------------	---

---

**Description**

Summary statistics for output of TMP-based summarization

**Usage**

```
.finalizeTMP(input, censored_symbol, impute, summarized)
```

**Arguments**

<code>input</code>	feature-level data
<code>censored_symbol</code>	censored missing value indicator
<code>impute</code>	if TRUE, censored missing values were imputed
<code>summarized</code>	protein-level data (list)

---

<code>.fitHuber</code>	<i>Wrapper to fit robust linear model for one protein</i>
------------------------	---

---

**Description**

Wrapper to fit robust linear model for one protein

**Usage**

```
.fitHuber(input)
```

**Value**

rlm

---

.fitLinearModel      *Fit a linear model*

---

**Description**

Fit a linear model

**Usage**

```
.fitLinearModel(input, is_single_feature, is_labeled, equal_variances)
```

**Arguments**

input	data.table
is_single_feature	logical, if TRUE, data has single feature
is_labeled	logical, if TRUE, data comes from a labeled experiment
equal_variances	logical, if TRUE, equal variances are assumed

**Value**

lm or merMod

---

.fitModelForGroupComparison  
*Choose a model type (fixed/mixed effects) and fit it for a single protein*

---

**Description**

Choose a model type (fixed/mixed effects) and fit it for a single protein

**Usage**

```
.fitModelForGroupComparison(  
  input,  
  repeated,  
  is_single_subject,  
  has_tech_replicates  
)
```

**Arguments**

input	data.table of summarized data
repeated	if TRUE, experiment consists of repeated measurements
is_single_subject	if TRUE, experiment consists of a single subject
has_tech_replicates	if TRUE, there are technical replicates

---

```
.fitModelSingleProtein
```

*Fit model and perform group comparison for a single protein*

---

### Description

Fit model and perform group comparison for a single protein

### Usage

```
.fitModelSingleProtein(  
  input,  
  contrast_matrix,  
  has_tech_replicates,  
  is_single_subject,  
  repeated,  
  groups,  
  samples_info,  
  save_fitted_models,  
  has_imputed  
)
```

### Arguments

input	data.table of summarized data
contrast_matrix	contrast matrix
has_tech_replicates	if TRUE, there are technical replicates
is_single_subject	if TRUE, experiment consists of a single subject
repeated	if TRUE, experiment consists of repeated measurements
groups	unique labels for experimental conditions
samples_info	number of runs per group
save_fitted_models	if TRUE, fitted model will be saved. If FALSE, it will be replaced by NULL
has_imputed	if TRUE, missing values have been imputed by dataProcess

---

```
.fitTukey
```

*Fit tukey median polish for a data matrix*

---

### Description

Fit tukey median polish for a data matrix

### Usage

```
.fitTukey(input)
```

**Arguments**

input                    data.table with data for a single protein

**Value**

data.table

---

*.flagLowCoverage*            *Flag for low coverage features*

---

**Description**

Flag for low coverage features

**Usage**

```
.flagLowCoverage(input)
```

**Arguments**

input                    data.table

**Value**

logical

---

*.flagUninformativeSingleLabel*  
*Flag uninformative features*

---

**Description**

Flag uninformative features

**Usage**

```
.flagUninformativeSingleLabel(input, min_feature_count = 2)
```

**Arguments**

input                    data.table  
min\_feature\_count            minimum number of quality features to consider

**Value**

data.table

---

`.getAllComparisons`     *Get all comparisons for a single protein and a contrast matrix*

---

**Description**

Get all comparisons for a single protein and a contrast matrix

**Usage**

```
.getAllComparisons(input, fitted_model, contrast_matrix, groups, protein)
```

**Arguments**

<code>input</code>	summarized data
<code>fitted_model</code>	model fitted by the <code>.fitModelForGroupComparison</code> function
<code>contrast_matrix</code>	contrast matrix
<code>groups</code>	unique labels of experimental conditions
<code>protein</code>	name of a protein

---

`.getColorKeyGGPlot2`     *Create colorkey for ggplot2 heatmap*

---

**Description**

Create colorkey for ggplot2 heatmap

**Usage**

```
.getColorKeyGGPlot2(my.colors, blocks)
```

**Arguments**

<code>my.colors</code>	<code>blocks</code>
------------------------	---------------------

---

`.getColorKeyPlotly`     *Create colorkey for plotly heatmap*

---

**Description**

Create colorkey for plotly heatmap

**Usage**

```
.getColorKeyPlotly(my.colors, blocks)
```

**Arguments**

<code>my.colors</code>	<code>blocks</code>
------------------------	---------------------

---

.getContrast                      *Create a contrast for a model with only group as a fixed effect*

---

**Description**

Create a contrast for a model with only group as a fixed effect

**Usage**

.getContrast(input, contrast, coefs, groups)

**Arguments**

input                      summarized data for a single protein  
coefs                      coefficients of a linear model (named vector)  
groups                     unique group labels  
contrast\_matrix           row of a contrast\_matrix

---

.getContrastLabels              *Get labels for contrasts*

---

**Description**

Get labels for contrasts

**Usage**

.getContrastLabels(contrasts)

**Arguments**

contrasts                  list of lists of condition labels

---

.getEmptyComparison            *Comparison output when there are measurements only in a single condition*

---

**Description**

Comparison output when there are measurements only in a single condition

**Usage**

.getEmptyComparison(input, contrast\_matrix, groups, protein)

**Arguments**

input	summarized data
contrast_matrix	contrast matrix
groups	unique labels of experimental conditions
protein	name of a protein

---

.getFeatureVariances *Calculate variances of features*

---

**Description**

Calculate variances of features

**Usage**

```
.getFeatureVariances(input, tolerance = 3)
```

**Arguments**

input	data.table
tolerance	cutoff for outliers

**Value**

numeric

---

.getMedian *Get median of protein abundances for a given label*

---

**Description**

Get median of protein abundances for a given label

**Usage**

```
.getMedian(df, label)
```

**Arguments**

df	'data.table'
label	"L" for light isotopes, "H" for heavy isotopes.



---

`.getMedianSigmaSubject`  
*Get median per subject or group by subject*

---

**Description**

Get median per subject or group by subject

**Usage**

`.getMedianSigmaSubject(var_component)`

**Arguments**

`var_component` data.frame, output of `.getVarComponent`

---

`.getMin` *Utility function: get 0.99 \* minimum of non-missing values*

---

**Description**

Utility function: get 0.99 \* minimum of non-missing values

**Usage**

`.getMin(abundance, nonmissing)`

**Arguments**

`abundance` abundances values  
`nonmissing` logical vector

---

`.getModelParameters` *Get params (coefficients, covariance matrix, degrees of freedom) from a model*

---

**Description**

Get params (coefficients, covariance matrix, degrees of freedom) from a model

**Usage**

`.getModelParameters(fitted_model)`

**Arguments**

`fitted_model` object of class `lm` or `lmerMod`

---

`.getNonMissingFilter` *Identify non-missing values*

---

**Description**

Identify non-missing values

**Usage**

```
.getNonMissingFilter(input, impute, censored_symbol)
```

**Arguments**

`input`                    `'data.table'` in MSstats format  
`impute`                    if TRUE, missing values are supposed to be imputed  
`censored_symbol`            `'censoredInt'` parameter to `dataProcess`

---

`.getNonMissingFilterStats`

*Get a logical vector for non-missing values to calculate summary statistics*

---

**Description**

Get a logical vector for non-missing values to calculate summary statistics

**Usage**

```
.getNonMissingFilterStats(input, censored_symbol)
```

**Arguments**

`input`                    `data.table` with data for a single protein  
`censored_symbol`            Missing values are censored or at random. `'NA'` (default) assumes that all `'NA'`'s in `'Intensity'` column are censored. `'0'` uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use `'0'`. Null assumes that all NA intensities are randomly missing.

**Value**

`data.table`

---

.getNumSample                      *Get sample size*

---

**Description**

Get sample size

**Usage**

```
.getNumSample(  
  desiredFC,  
  power,  
  alpha,  
  delta,  
  median_sigma_error,  
  median_sigma_subject  
)
```

**Arguments**

desiredFC	the range of a desired fold change which includes the lower and upper values of the desired fold change.
power	a pre-specified statistical power which defined as the probability of detecting a true fold change. TRUE represent you require to calculate the power for this category, else you should input the average of power you expect. Default is 0.9
alpha	significance level
delta	difference between means (?)
median_sigma_error	median of error standard deviation
median_sigma_subject	median standard deviation per subject

---

.getSingleProteinForProfile  
                                    *Get data for a single protein to plot*

---

**Description**

Get data for a single protein to plot

**Usage**

```
.getSingleProteinForProfile(processed, all_proteins, i)
```

**Arguments**

all_proteins	character, set of protein names
i	integer, index of protein to use
dataProcess	output -> FeatureLevelData

---

`.getVarComponent`      *Get variances from models fitted by the groupComparison function*

---

**Description**

Get variances from models fitted by the groupComparison function

**Usage**

```
.getVarComponent(fitted_models)
```

**Arguments**

`fitted_models`    FittedModels element of groupComparison output

---

`.getWideTable`      *Utility function for quantile normalization - get table in wide format*

---

**Description**

Utility function for quantile normalization - get table in wide format

**Usage**

```
.getWideTable(input, runs, label = "L", remove_missing = TRUE)
```

**Arguments**

`input`                'data.table' in MSstats standard format  
`label`                "L" for light isotopes, "H" for heavy isotopes  
`remove_missing`    if TRUE, only non-missing values will be considered  
`vector`               of run labels

---

`.getYaxis`              *Get name for y-axis*

---

**Description**

Get name for y-axis

**Usage**

```
.getYaxis(temp)
```

**Arguments**

`temp`                 data.table

---

```
.groupComparisonWithMultipleCores
```

*Perform group comparison per protein in parallel*

---

**Description**

Perform group comparison per protein in parallel

**Usage**

```
.groupComparisonWithMultipleCores(  
  summarized_list,  
  contrast_matrix,  
  save_fitted_models,  
  repeated,  
  samples_info,  
  numberOfCores  
)
```

**Arguments**

<code>summarized_list</code>	output of <code>MSstatsPrepareForGroupComparison</code>
<code>contrast_matrix</code>	contrast matrix
<code>save_fitted_models</code>	if TRUE, fitted models will be included in the output
<code>repeated</code>	logical, output of <code>checkRepeatedDesign</code> function
<code>samples_info</code>	data.table, output of <code>getSamplesInfo</code> function
<code>numberOfCores</code>	Number of cores for parallel processing. A logfile named <code>'MSstats_groupComparison_log_progress.l</code> is created to track progress. Only works for Linux & Mac OS.

---

```
.groupComparisonWithSingleCore
```

*Perform group comparison per protein iteratively with a single loop*

---

**Description**

Perform group comparison per protein iteratively with a single loop

**Usage**

```
.groupComparisonWithSingleCore(  
  summarized_list,  
  contrast_matrix,  
  save_fitted_models,  
  repeated,  
  samples_info  
)
```

**Arguments**

summarized_list	output of MSstatsPrepareForGroupComparison
contrast_matrix	contrast matrix
save_fitted_models	if TRUE, fitted models will be included in the output
repeated	logical, output of checkRepeatedDesign function
samples_info	data.table, output of getSamplesInfo function

---

*.handleEmptyConditions*

*Handle contrast when some of the conditions are missing*

---

**Description**

Handle contrast when some of the conditions are missing

**Usage**

```
.handleEmptyConditions(
  input,
  fit,
  contrast,
  groups,
  parameters,
  protein,
  empty_conditions,
  coefs
)
```

**Arguments**

input	summarized data
contrast	single row of a contrast matrix
groups	unique labels of experimental conditions
parameters	parameters extracted from the model
protein	name of a protein
empty_conditions	labels of empty conditions
coefs	coefficient of the fitted model

---

.handleSingleContrast *Group comparison for a single contrast*

---

### Description

Group comparison for a single contrast

### Usage

```
.handleSingleContrast(input, fit, contrast, groups, parameters, protein, coefs)
```

### Arguments

input	summarized data
contrast	single row of a contrast matrix
groups	unique labels of experimental conditions
parameters	parameters extracted from the model
protein	name of a protein
coefs	coefficient of the fitted model

---

.isSummarizable *Check if a protein can be summarized with TMP*

---

### Description

Check if a protein can be summarized with TMP

### Usage

```
.isSummarizable(input, remove50missing)
```

### Arguments

input	data.table
remove50missing	if TRUE, proteins with more than 50 in all runs will not be summarized

### Value

data.table

---

`.logDatasetInformation`

*Log information about feature-level data*

---

**Description**

Log information about feature-level data

**Usage**

`.logDatasetInformation(input)`

**Arguments**

input            data.table

**Value**

TRUE invisibly after successful logging

---

`.logMissingness`

*Log information about missing data*

---

**Description**

Log information about missing data

**Usage**

`.logMissingness(input)`

**Arguments**

input            data.table

**Value**

TRUE invisibly



---

`.logSingleLabeledProteins`

*Print proteins with a single label to the log file*

---

**Description**

Print proteins with a single label to the log file

**Usage**

`.logSingleLabeledProteins(input, label)`

**Arguments**

<code>input</code>	<code>data.table</code>
<code>label</code>	label ("L" or "H")

**Value**

TRUE invisibly

---

`.logSummaryStatistics` *Print summary statistics to the log file*

---

**Description**

Print summary statistics to the log file

**Usage**

`.logSummaryStatistics(input)`

**Arguments**

<code>input</code>	<code>data.table</code>
--------------------	-------------------------

**Value**

TRUE invisibly

---

*.makeComparison*      *Create comparison plot*

---

### **Description**

Create comparison plot

### **Usage**

```
.makeComparison(
  input,
  log_base,
  dot.size,
  x.axis.size,
  y.axis.size,
  text.angle,
  hjust,
  vjust,
  y.limdown,
  y.limup
)
```

### **Arguments**

<code>input</code>	data.table
<code>log_base</code>	2 or 10
<code>dot.size</code>	size of dots in volcano plot and comparison plot. Default is 3.
<code>x.axis.size</code>	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
<code>y.axis.size</code>	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
<code>text.angle</code>	angle of x-axis labels represented each comparison at the bottom of graph in comparison plot. Default is 0.

---

*.makeConditionPlot*      *Make condition plot*

---

### **Description**

Make condition plot

### **Usage**

```
.makeConditionPlot(
  input,
  scale,
  single_protein,
  y.limdown,
  y.limup,
```

```
x.axis.size,  
y.axis.size,  
text.size,  
text.angle,  
legend.size,  
dot.size.condition,  
yaxis.name  
)
```

**Arguments**

input	data.table
scale	for "ConditionPlot" only, FALSE(default) means each conditional level is not scaled at x-axis according to its actual value (equal space at x-axis). TRUE means each conditional level is scaled at x-axis according to its actual value (unequal space at x-axis).
single_protein	data.table
x.axis.size	size of x-axis labeling for "Run" in Profile Plot and QC Plot, and "Condition" in Condition Plot. Default is 10.
y.axis.size	size of y-axis labels. Default is 10.
text.size	size of labels represented each condition at the top of graph in Profile Plot and QC plot. Default is 4.
text.angle	angle of labels represented each condition at the top of graph in Profile Plot and QC plot or x-axis labeling in Condition plot. Default is 0.
legend.size	size of feature legend (transition-level or peptide-level) above graph in Profile Plot. Default is 7.
dot.size.condition	size of dots in condition plot. Default is 3.

---

.makeFactorColumns     *Make factor columns where needed*

---

**Description**

Make factor columns where needed

**Usage**

```
.makeFactorColumns(input)
```

**Arguments**

input	data.table
-------	------------

---

`.makeHeatmapPlotly`      *Create heatmap*

---

### Description

Create heatmap

### Usage

```
.makeHeatmapPlotly(
  input,
  my.colors,
  my.breaks,
  x.axis.size,
  y.axis.size,
  height,
  numProtein
)
```

### Arguments

<code>input</code>	<code>data.table</code>
<code>x.axis.size</code>	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
<code>y.axis.size</code>	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
<code>height</code>	height of the saved file. Default is 10.
<code>numProtein</code>	For ggplot2: The number of proteins which will be presented in each heatmap. Default is 100. Maximum possible number of protein for one heatmap is 180. For Plotly: use this parameter to adjust the number of proteins to be displayed on the heatmap

---

`.makeProfilePlot`      *Create profile plot*

---

### Description

Create profile plot

### Usage

```
.makeProfilePlot(
  input,
  is_censored,
  featureName,
  y.limdown,
  y.limup,
  x.axis.size,
  y.axis.size,
```

```
text.size,  
text.angle,  
legend.size,  
dot.size.profile,  
ss,  
s,  
cumGroupAxis,  
yaxis.name,  
lineNameAxis,  
groupNametemp,  
dot_colors  
)
```

### Arguments

input	data.table
is_censored	TRUE if censored values were imputed
featureName	for "ProfilePlot" only, "Transition" (default) means printing feature legend in transition-level; "Peptide" means printing feature legend in peptide-level; "NA" means no feature legend printing.
x.axis.size	size of x-axis labeling for "Run" in Profile Plot and QC Plot, and "Condition" in Condition Plot. Default is 10.
y.axis.size	size of y-axis labels. Default is 10.
text.size	size of labels represented each condition at the top of graph in Profile Plot and QC plot. Default is 4.
text.angle	angle of labels represented each condition at the top of graph in Profile Plot and QC plot or x-axis labeling in Condition plot. Default is 0.
legend.size	size of feature legend (transition-level or peptide-level) above graph in Profile Plot. Default is 7.
dot.size.profile	size of dots in profile plot. Default is 2.

---

.makeQCPlot

*Make QC plot*

---

### Description

To illustrate the quantitative data after data-preprocessing and quality control of MS runs, `dataProcessPlots` takes the quantitative data from function (`dataProcess`) as input and automatically generate three types of figures in pdf files as output : (1) profile plot (specify "ProfilePlot" in option type), to identify the potential sources of variation for each protein; (2) quality control plot (specify "QCPlot" in option type), to evaluate the systematic bias between MS runs; (3) mean plot for conditions (specify "ConditionPlot" in option type), to illustrate mean and variability of each condition per protein.

**Usage**

```
.makeQCPlot(
  input,
  all_proteins,
  y.limdown,
  y.limup,
  x.axis.size,
  y.axis.size,
  text.size,
  text.angle,
  legend.size,
  label.color,
  cumGroupAxis,
  groupName,
  lineNameAxis,
  yaxis.name
)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>all_proteins</code>	character vector of protein names
<code>x.axis.size</code>	size of x-axis labeling for "Run" in Profile Plot and QC Plot, and "Condition" in Condition Plot. Default is 10.
<code>y.axis.size</code>	size of y-axis labels. Default is 10.
<code>text.size</code>	size of labels represented each condition at the top of graph in Profile Plot and QC plot. Default is 4.
<code>text.angle</code>	angle of labels represented each condition at the top of graph in Profile Plot and QC plot or x-axis labeling in Condition plot. Default is 0.
<code>legend.size</code>	size of feature legend (transition-level or peptide-level) above graph in Profile Plot. Default is 7.

**Details**

- Profile Plot : identify the potential sources of variation of each protein. `QuantData$FeatureLevelData` is used for plots. X-axis is run. Y-axis is log-intensities of transitions. Reference/endogenous signals are in the left/right panel. Line colors indicate peptides and line types indicate transitions. In summarization plots, gray dots and lines are the same as original profile plots with `QuantData$FeatureLevelData`. Dark dots and lines are for summarized intensities from `QuantData$ProteinLevelData`.
- QC Plot : illustrate the systematic bias between MS runs. After normalization, the reference signals for all proteins should be stable across MS runs. `QuantData$FeatureLevelData` is used for plots. X-axis is run. Y-axis is log-intensities of transition. Reference/endogenous signals are in the left/right panel. The pdf file contains (1) QC plot for all proteins and (2) QC plots for each protein separately.
- Condition Plot : illustrate the systematic difference between conditions. Summarized intensities from `QuantData$ProteinLevelData` are used for plots. X-axis is condition. Y-axis is summarized log transformed intensity. If scale is TRUE, the levels of conditions is scaled according to its actual values at x-axis. Red points indicate the mean for each condition. If interval is "CI", blue error bars indicate the confidence interval with 0.95 significant level for

each condition. If interval is "SD", blue error bars indicate the standard deviation for each condition. The interval is not related with model-based analysis.

The input of this function is the quantitative data from function `dataProcess`.

### Examples

```
# Consider quantitative data (i.e. QuantData) from a yeast study with ten time points of interests,
# three biological replicates, and no technical replicates which is a time-course experiment.
# The goal is to provide pre-analysis visualization by automatically generate two types of figures
# in two separate pdf files.
# Protein IDHC (gene name IDP2) is differentially expressed in time point 1 and time point 7,
# whereas, Protein PMG2 (gene name GPM2) is not.

QuantData<-dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
# Profile plot
dataProcessPlots(data=QuantData,type="ProfilePlot")
# Quality control plot
dataProcessPlots(data=QuantData,type="QCPlot")
# Quantification plot for conditions
dataProcessPlots(data=QuantData,type="ConditionPlot")
```

---

`.makeSummaryProfilePlot`

*Make summary profile plot*

---

### Description

Make summary profile plot

### Usage

```
.makeSummaryProfilePlot(
  input,
  is_censored,
  y.limdown,
  y.limup,
  x.axis.size,
  y.axis.size,
  text.size,
  text.angle,
  legend.size,
  dot.size.profile,
  cumGroupAxis,
  yaxis.name,
  lineNameAxis,
  groupNameTemp
)
```

**Arguments**

<code>input</code>	data.table
<code>is_censored</code>	TRUE if censored values were imputed
<code>x.axis.size</code>	size of x-axis labeling for "Run" in Profile Plot and QC Plot, and "Condition" in Condition Plot. Default is 10.
<code>y.axis.size</code>	size of y-axis labels. Default is 10.
<code>text.size</code>	size of labels represented each condition at the top of graph in Profile Plot and QC plot. Default is 4.
<code>text.angle</code>	angle of labels represented each condition at the top of graph in Profile Plot and QC plot or x-axis labeling in Condition plot. Default is 0.
<code>legend.size</code>	size of feature legend (transition-level or peptide-level) above graph in Profile Plot. Default is 7.
<code>dot.size.profile</code>	size of dots in profile plot. Default is 2.

---

<code>.makeVolcano</code>	<i>Create a volcano plot</i>
---------------------------	------------------------------

---

**Description**

Create a volcano plot

**Usage**

```
.makeVolcano(
  input,
  label_name,
  log_base_FC,
  log_base_pval,
  x.lim,
  ProteinName,
  dot.size,
  y.limdown,
  y.limup,
  text.size,
  FCcutoff,
  sig,
  x.axis.size,
  y.axis.size,
  legend.size,
  log_adjp
)
```

**Arguments**

<code>input</code>	data.table
<code>label_name</code>	contrast label
<code>log_base_FC</code>	2 or 10



log_base_pval	2 or 10
ProteinName	for volcano plot only, whether display protein names or not. TRUE (default) means protein names, which are significant, are displayed next to the points. FALSE means no protein names are displayed.
dot.size	size of dots in volcano plot and comparison plot. Default is 3.
text.size	size of ProteinName label in the graph for Volcano Plot. Default is 4.
FCcutoff	for volcano plot or heatmap, whether involve fold change cutoff or not. FALSE (default) means no fold change cutoff is applied for significance analysis. FC-cutoff = specific value means specific fold change cutoff is applied.
sig	FDR cutoff for the adjusted p-values in heatmap and volcano plot. level of significance for comparison plot. 100(1-sig)% confidence interval will be drawn. sig=0.05 is default.
x.axis.size	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
y.axis.size	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
legend.size	size of legend for color at the bottom of volcano plot. Default is 7.

---

.nicePrint                      *Print a table nicely*

---

**Description**

Print a table nicely

**Usage**

```
.nicePrint(string_vector)
```

**Arguments**

string\_vector    character

**Value**

character

---

.normalizeGlobalStandards  
*Normalization based on standards*

---

**Description**

Normalization based on standards

**Usage**

```
.normalizeGlobalStandards(input, peptides_dict, standards)
```

**Arguments**

input	data.table in MSstats format
peptides_dict	'data.table' of names of peptides and their corresponding features.
standards	character vector with names of standards, required if "GLOBALSTANDARDS" method was selected.

---

*.normalizeMedian*      *Median normalization*

---

**Description**

Median normalization

**Usage**

```
.normalizeMedian(input)
```

**Arguments**

input	'data.table' in standard MSstats format
-------	---

---

*.normalizeQuantile*      *Quantile normalization based on the 'preprocessCore' package*

---

**Description**

Quantile normalization based on the 'preprocessCore' package

**Usage**

```
.normalizeQuantile(input)
```

**Arguments**

input	'data.table' in MSstats standard format
-------	---

---

.onLoad                      *Set default logging object when package is loaded*

---

**Description**

Set default logging object when package is loaded

**Usage**

```
.onLoad(...)
```

**Arguments**

...                      ignored

**Value**

none, sets options called MSstatsLog and MSstatsMsg

---

.plotComparison              *Preprocess data for comparison plots and create them*

---

**Description**

Preprocess data for comparison plots and create them

**Usage**

```
.plotComparison(  
  input,  
  proteins,  
  address,  
  width,  
  height,  
  sig,  
  ylimUp,  
  ylimDown,  
  text.angle,  
  dot.size,  
  x.axis.size,  
  y.axis.size,  
  log_base_FC,  
  isPlotly  
)
```

**Arguments**

input	data.table
address	the name of folder that will store the results. Default folder is the current working directory. The other assigned folder has to be existed under the current working directory. An output pdf file is automatically created with the default name of "VolcanoPlot.pdf" or "Heatmap.pdf" or "ComparisonPlot.pdf". The command address can help to specify where to store the file as well as how to modify the beginning of the file name. If address=FALSE, plot will be not saved as pdf file but showed in window.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.
sig	FDR cutoff for the adjusted p-values in heatmap and volcano plot. level of significance for comparison plot. 100(1-sig)% confidence interval will be drawn. sig=0.05 is default.
ylimUp	for all three plots, upper limit for y-axis. FALSE (default) for volcano plot/heatmap use maximum of -log2 (adjusted p-value) or -log10 (adjusted p-value). FALSE (default) for comparison plot uses maximum of log-fold change + CI.
ylimDown	for all three plots, lower limit for y-axis. FALSE (default) for volcano plot/heatmap use minimum of -log2 (adjusted p-value) or -log10 (adjusted p-value). FALSE (default) for comparison plot uses minimum of log-fold change - CI.
text.angle	angle of x-axis labels represented each comparison at the bottom of graph in comparison plot. Default is 0.
dot.size	size of dots in volcano plot and comparison plot. Default is 3.
x.axis.size	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
y.axis.size	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
log_base_FC	log base for log-fold changes - 2 or 10
isPlotly	This parameter is for MSstatsShiny application for plotly render, this cannot be used for saving PDF files as plotly do not have support for PDFs currently. address and isPlotly cannot be set as TRUE at the same time.

---

.plotHeatmap

*Prepare data for heatmaps and plot them*

---

**Description**

Prepare data for heatmaps and plot them

**Usage**

```
.plotHeatmap(
  input,
  log_base_pval,
  ylimUp,
  FCcutoff,
  sig,
  clustering,
```

```
    numProtein,  
    colorkey,  
    width,  
    height,  
    log_base_FC,  
    x.axis.size,  
    y.axis.size,  
    address,  
    isPlotly  
  )
```

### Arguments

input	data.table
log_base_pval	log base for p-values
ylimUp	for all three plots, upper limit for y-axis. FALSE (default) for volcano plot/heatmap use maximum of $-\log_2$ (adjusted p-value) or $-\log_{10}$ (adjusted p-value). FALSE (default) for comparison plot uses maximum of log-fold change + CI.
FCcutoff	for volcano plot or heatmap, whether involve fold change cutoff or not. FALSE (default) means no fold change cutoff is applied for significance analysis. FC-cutoff = specific value means specific fold change cutoff is applied.
sig	FDR cutoff for the adjusted p-values in heatmap and volcano plot. level of significance for comparison plot. $100(1-\text{sig})\%$ confidence interval will be drawn. sig=0.05 is default.
clustering	Determines how to order proteins and comparisons. Hierarchical cluster analysis with Ward method(minimum variance) is performed. 'protein' means that protein dendrogram is computed and reordered based on protein means (the order of row is changed). 'comparison' means comparison dendrogram is computed and reordered based on comparison means (the order of comparison is changed). 'both' means to reorder both protein and comparison. Default is 'protein'.
numProtein	For ggplot2: The number of proteins which will be presented in each heatmap. Default is 100. Maximum possible number of protein for one heatmap is 180. For Plotly: use this parameter to adjust the number of proteins to be displayed on the heatmap
colorkey	TRUE(default) shows colorkey.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.
log_base_FC	log base for log-fold changes - 2 or 10
x.axis.size	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
y.axis.size	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
address	the name of folder that will store the results. Default folder is the current working directory. The other assigned folder has to be existed under the current working directory. An output pdf file is automatically created with the default name of "VolcanoPlot.pdf" or "Heatmap.pdf" or "ComparisonPlot.pdf". The command address can help to specify where to store the file as well as how to modify the beginning of the file name. If address=FALSE, plot will be not saved as pdf file but showed in window.

isPlotly This parameter is for MSstatsShiny application for plotly render, this cannot be used for saving PDF files as plotly do not have support for PDFs currently. address and isPlotly cannot be set as TRUE at the same time.

---

.plotVolcano *Preprocess data for volcano plots and create them*

---

### Description

Preprocess data for volcano plots and create them

### Usage

```
.plotVolcano(
  input,
  which.Comparison,
  address,
  width,
  height,
  log_base_pval,
  ylimUp,
  ylimDown,
  FCcutoff,
  sig,
  xlimUp,
  ProteinName,
  dot.size,
  text.size,
  legend.size,
  x.axis.size,
  y.axis.size,
  log_base_FC,
  isPlotly
)
```

### Arguments

which.Comparison	list of comparisons to draw plots. List can be labels of comparisons or order numbers of comparisons from levels(data\$Label), such as levels(testResultMultiComparisons\$Comparison). Default is "all", which generates all plots for each protein.
address	the name of folder that will store the results. Default folder is the current working directory. The other assigned folder has to be existed under the current working directory. An output pdf file is automatically created with the default name of "VolcanoPlot.pdf" or "Heatmap.pdf" or "ComparisonPlot.pdf". The command address can help to specify where to store the file as well as how to modify the beginning of the file name. If address=FALSE, plot will be not saved as pdf file but showed in window.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.

<code>ylimUp</code>	for all three plots, upper limit for y-axis. FALSE (default) for volcano plot/heatmap use maximum of $-\log_2$ (adjusted p-value) or $-\log_{10}$ (adjusted p-value). FALSE (default) for comparison plot uses maximum of log-fold change + CI.
<code>ylimDown</code>	for all three plots, lower limit for y-axis. FALSE (default) for volcano plot/heatmap use minimum of $-\log_2$ (adjusted p-value) or $-\log_{10}$ (adjusted p-value). FALSE (default) for comparison plot uses minimum of log-fold change - CI.
<code>FCcutoff</code>	for volcano plot or heatmap, whether involve fold change cutoff or not. FALSE (default) means no fold change cutoff is applied for significance analysis. FC-cutoff = specific value means specific fold change cutoff is applied.
<code>sig</code>	FDR cutoff for the adjusted p-values in heatmap and volcano plot. level of significance for comparison plot. $100(1-\text{sig})\%$ confidence interval will be drawn. <code>sig=0.05</code> is default.
<code>xlimUp</code>	for Volcano plot, the limit for x-axis. FALSE (default) for use maximum for absolute value of log-fold change or 3 as default if maximum for absolute value of log-fold change is less than 3.
<code>ProteinName</code>	for volcano plot only, whether display protein names or not. TRUE (default) means protein names, which are significant, are displayed next to the points. FALSE means no protein names are displayed.
<code>dot.size</code>	size of dots in volcano plot and comparison plot. Default is 3.
<code>text.size</code>	size of ProteinName label in the graph for Volcano Plot. Default is 4.
<code>legend.size</code>	size of legend for color at the bottom of volcano plot. Default is 7.
<code>x.axis.size</code>	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
<code>y.axis.size</code>	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
<code>isPlotly</code>	This parameter is for MSstatsShiny application for plotly render, this cannot be used for saving PDF files as plotly do not have support for PDFs currently. address and <code>isPlotly</code> cannot be set as TRUE at the same time.

---

`.prepareForDataProcess`

*Check validity of data already processed by MSstats converter*

---

### Description

Check validity of data already processed by MSstats converter

### Usage

```
.prepareForDataProcess(input, ...)
```

### Arguments

<code>input</code>	data.frame of class 'MSstatsValidated'
<code>..</code>	additional parameters, currently ignored

---

<code>.prepareLinear</code>	<i>Prepare feature-level data for linear summarization</i>
-----------------------------	--

---

**Description**

Prepare feature-level data for linear summarization

**Usage**

```
.prepareLinear(input, impute, censored_symbol)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>impute</code>	<code>logical</code>
<code>censored_symbol</code>	<code>"0"/"NA"</code>

**Value**

`data.table`

---

<code>.prepareSingleProteinForGC</code>	<i>Prepare data for a single protein for group comparison</i>
---	---

---

**Description**

Prepare data for a single protein for group comparison

**Usage**

```
.prepareSingleProteinForGC(single_protein)
```

**Arguments**

<code>single_protein</code>	<code>data.table</code>
-----------------------------	-------------------------



---

.prepareSummary      *Prepare feature-level data for summarization*

---

**Description**

Prepare feature-level data for summarization

**Usage**

```
.prepareSummary(input, method, impute, censored_symbol)
```

**Arguments**

input	data.table
method	"TMP" / "linear"
impute	logical
censored_symbol	"0"/"NA"

**Value**

data.table

---

.prepareTMP      *Prepare feature-level data for TMP summarization*

---

**Description**

Prepare feature-level data for TMP summarization

**Usage**

```
.prepareTMP(input, impute, censored_symbol)
```

**Arguments**

input	data.table
impute	logical
censored_symbol	"0"/"NA"

**Value**

data.table

---

```
.preProcessIntensities
```

*Create ABUNDANCE column and log-transform intensities*

---

**Description**

Create ABUNDANCE column and log-transform intensities

**Usage**

```
.preProcessIntensities(input, log_base)
```

**Arguments**

input	data.table
log_base	base of the logarithm

---

```
.quantileNormalizationSingleLabel
```

*Quantile normalization for a single label*

---

**Description**

Quantile normalization for a single label

**Usage**

```
.quantileNormalizationSingleLabel(input, runs, label = "L")
```

**Arguments**

input	'data.table' in MSstats standard format
runs	run labels
label	"L" for light isotopes, "H" for heavy isotopes

---

```
.replaceZerosWithNA
```

*Utility function for normalization: replace 0s by NA*

---

**Description**

Utility function for normalization: replace 0s by NA

**Usage**

```
.replaceZerosWithNA(vec)
```

**Arguments**

vec	vector
-----	--------

---

.runTukey *Fit Tukey median polish*

---

### Description

Fit Tukey median polish

### Usage

```
.runTukey(input, is_labeled, censored_symbol, remove50missing)
```

### Arguments

`input` data.table with data for a single protein

`is_labeled` logical, if TRUE, data is coming from an SRM experiment

`censored_symbol` Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.

`remove50missing` only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.

### Value

data.table

---

.saveSessionInfo *Save information about R session to sessionInfo.txt file.*

---

### Description

Save information about R session to sessionInfo.txt file.

### Usage

```
.saveSessionInfo()
```

---

<code>.saveTable</code>	<i>Save a data table to a file</i>
-------------------------	------------------------------------

---

**Description**

Save a data table to a file

**Usage**

```
.saveTable(input, name_base, file_name)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>name_base</code>	path to a folder (or "" for working directory)
<code>file_name</code>	name of a file to save. If this file already exists, an integer will be appended to this name

---

<code>.selectHighQualityFeatures</code>	<i>Select features of high quality</i>
---	--

---

**Description**

Select features of high quality

**Usage**

```
.selectHighQualityFeatures(input, min_feature_count)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>min_feature_count</code>	minimum number of quality features to consider

**Value**

`data.table`

---

`.selectTopFeatures`      *Select features with highest average abundance*

---

**Description**

Select features with highest average abundance

**Usage**

`.selectTopFeatures(input, top_n)`

**Arguments**

<code>input</code>	<code>data.table</code>
<code>top_n</code>	number of top features to select

**Value**

`data.table`

---

`.setCensoredByThreshold`  
*Set censored values based on minimum in run/feature/run or feature*

---

**Description**

Set censored values based on minimum in run/feature/run or feature

**Usage**

`.setCensoredByThreshold(input, censored_symbol, remove50missing)`

**Arguments**

<code>input</code>	'data.table' in MSstats format
<code>censored_symbol</code>	censoredInt parameter to 'dataProcess'
<code>remove50missing</code>	if TRUE, features with at least 50 will be removed

---

`.updateColumnsForProcessing`  
*Create columns for data processing*

---

**Description**

Create columns for data processing

**Usage**

```
.updateColumnsForProcessing(input)
```

**Arguments**

input	data.table
-------	------------

---

`.updateUnequalVariances`  
*Adjust model for unequal variances*

---

**Description**

Adjust model for unequal variances

**Usage**

```
.updateUnequalVariances(input, fit, num_iter)
```

**Arguments**

input	data.table
fit	lm
num_iter	number of iterations

**Value**

merMod

---

checkRepeatedDesign	<i>Check if data represents repeated measurements design</i>
---------------------	--

---

**Description**

Check if data represents repeated measurements design

**Usage**

```
checkRepeatedDesign(summarization_output)
```

**Arguments**

summarization\_output  
output of the dataProcess function

**Details**

This extracts information required by the group comparison workflow

**Value**

logical, TRUE if data represent repeated measurements design

**Examples**

```
QuantData1 <- dataProcess(SRMRawData, use_log_file = FALSE)
checkRepeatedDesign(QuantData1)
```

---

dataProcess	<i>Process MS data: clean, normalize and summarize before differential analysis</i>
-------------	---

---

**Description**

Process MS data: clean, normalize and summarize before differential analysis

**Usage**

```
dataProcess(  
  raw,  
  logTrans = 2,  
  normalization = "equalizeMedians",  
  nameStandards = NULL,  
  featureSubset = "all",  
  remove_uninformative_feature_outlier = FALSE,  
  min_feature_count = 2,  
  n_top_feature = 3,  
  summaryMethod = "TMP",
```

```

equalFeatureVar = TRUE,
censoredInt = "NA",
MBimpute = TRUE,
remove50missing = FALSE,
fix_missing = NULL,
maxQuantileforCensored = 0.999,
use_log_file = TRUE,
append = FALSE,
verbose = TRUE,
log_file_path = NULL,
numberOfCores = 1
)

```

### Arguments

raw	name of the raw (input) data set.
logTrans	base of logarithm transformation: 2 (default) or 10.
normalization	normalization to remove systematic bias between MS runs. There are three different normalizations supported: 'equalizeMedians' (default) represents constant normalization (equalizing the medians) based on reference signals is performed. 'quantile' represents quantile normalization based on reference signals 'globalStandards' represents normalization with global standards proteins. If FALSE, no normalization is performed.
nameStandards	optional vector of global standard peptide names. Required only for normalization with global standard peptides.
featureSubset	"all" (default) uses all features that the data set has. "top3" uses top 3 features which have highest average of log-intensity across runs. "topN" uses top N features which has highest average of log-intensity across runs. It needs the input for n_top_feature option. "highQuality" flags uninformative feature and outliers.
remove_uninformative_feature_outlier	optional. Only required if featureSubset = "highQuality". TRUE allows to remove 1) noisy features (flagged in the column feature_quality with "Uninformative"), 2) outliers (flagged in the column, is_outlier with TRUE, before run-level summarization. FALSE (default) uses all features and intensities for run-level summarization.
min_feature_count	optional. Only required if featureSubset = "highQuality". Defines a minimum number of informative features a protein needs to be considered in the feature selection algorithm.
n_top_feature	optional. Only required if featureSubset = 'topN'. It that case, it specifies number of top features that will be used. Default is 3, which means to use top 3 features.
summaryMethod	"TMP" (default) means Tukey's median polish, which is robust estimation method. "linear" uses linear mixed model.
equalFeatureVar	only for summaryMethod = "linear". default is TRUE. Logical variable for whether the model should account for heterogeneous variation among intensities from different features. Default is TRUE, which assume equal variance among intensities from features. FALSE means that we cannot assume equal variance among intensities from features, then we will account for heterogeneous variation from different features.



censoredInt	Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.
MBimpute	only for summaryMethod = "TMP" and censoredInt = 'NA' or '0'. TRUE (default) imputes 'NA' or '0' (depending on censoredInt option) by Accelerated failure model. FALSE uses the values assigned by cutoffCensored.
remove50missing	only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.
fix_missing	Optional, same as the 'fix_missing' parameter in MSstatsConvert::MSstatsBalancedDesign function
maxQuantileforCensored	Maximum quantile for deciding censored missing values, default is 0.999
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
numberOfCores	Number of cores for parallel processing. When > 1, a logfile named 'MSstats_dataProcess_log_progress' is created to track progress. Only works for Linux & Mac OS. Default is 1.

## Examples

```
# Consider a raw data (i.e. SRMRawData) for a label-based SRM experiment from a yeast study
# with ten time points (T1-T10) of interests and three biological replicates.
# It is a time course experiment. The goal is to detect protein abundance changes
# across time points.
head(SRMRawData)
# Log2 transformation and normalization are applied (default)
QuantData<-dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
# Log10 transformation and normalization are applied
QuantData1<-dataProcess(SRMRawData, logTrans=10, use_log_file = FALSE)
head(QuantData1$FeatureLevelData)
# Log2 transformation and no normalization are applied
QuantData2<-dataProcess(SRMRawData,normalization=FALSE, use_log_file = FALSE)
head(QuantData2$FeatureLevelData)
```

## Description

To illustrate the quantitative data after data-preprocessing and quality control of MS runs, `dataProcessPlots` takes the quantitative data from function (`dataProcess`) as input and automatically generate three types of figures in pdf files as output : (1) profile plot (specify "ProfilePlot" in option type), to identify the potential sources of variation for each protein; (2) quality control plot (specify "QCPlot" in option type), to evaluate the systematic bias between MS runs; (3) mean plot for conditions (specify "ConditionPlot" in option type), to illustrate mean and variability of each condition per protein.

## Usage

```
dataProcessPlots(
  data,
  type,
  featureName = "Transition",
  ylimUp = FALSE,
  ylimDown = FALSE,
  scale = FALSE,
  interval = "CI",
  x.axis.size = 10,
  y.axis.size = 10,
  text.size = 4,
  text.angle = 0,
  legend.size = 7,
  dot.size.profile = 2,
  dot.size.condition = 3,
  width = 800,
  height = 600,
  which.Protein = "all",
  originalPlot = TRUE,
  summaryPlot = TRUE,
  save_condition_plot_result = FALSE,
  remove_uninformative_feature_outlier = FALSE,
  address = "",
  isPlotly = FALSE
)
```

## Arguments

<code>data</code>	name of the (output of <code>dataProcess</code> function) data set.
<code>type</code>	choice of visualization. "ProfilePlot" represents profile plot of log intensities across MS runs. "QCPlot" represents quality control plot of log intensities across MS runs. "ConditionPlot" represents mean plot of log ratios (Light/Heavy) across conditions.
<code>featureName</code>	for "ProfilePlot" only, "Transition" (default) means printing feature legend in transition-level; "Peptide" means printing feature legend in peptide-level; "NA" means no feature legend printing.
<code>ylimUp</code>	upper limit for y-axis in the log scale. FALSE(Default) for Profile Plot and QC Plot use the upper limit as rounded off maximum of $\log_2(\text{intensities})$ after normalization + 3. FALSE(Default) for Condition Plot is maximum of log ratio + SD or CI.

ylimDown	lower limit for y-axis in the log scale. FALSE(Default) for Profile Plot and QC Plot is 0. FALSE(Default) for Condition Plot is minimum of log ratio - SD or CI.
scale	for "ConditionPlot" only, FALSE(default) means each conditional level is not scaled at x-axis according to its actual value (equal space at x-axis). TRUE means each conditional level is scaled at x-axis according to its actual value (unequal space at x-axis).
interval	for "ConditionPlot" only, "CI"(default) uses confidence interval with 0.95 significant level for the width of error bar. "SD" uses standard deviation for the width of error bar.
x.axis.size	size of x-axis labeling for "Run" in Profile Plot and QC Plot, and "Condition" in Condition Plot. Default is 10.
y.axis.size	size of y-axis labels. Default is 10.
text.size	size of labels represented each condition at the top of graph in Profile Plot and QC plot. Default is 4.
text.angle	angle of labels represented each condition at the top of graph in Profile Plot and QC plot or x-axis labeling in Condition plot. Default is 0.
legend.size	size of feature legend (transition-level or peptide-level) above graph in Profile Plot. Default is 7.
dot.size.profile	size of dots in profile plot. Default is 2.
dot.size.condition	size of dots in condition plot. Default is 3.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.
which.Protein	Protein list to draw plots. List can be names of Proteins or order numbers of Proteins from levels(data\$FeatureLevelData\$PROTEIN). Default is "all", which generates all plots for each protein. For QC plot, "allonly" will generate one QC plot with all proteins.
originalPlot	TRUE(default) draws original profile plots.
summaryPlot	TRUE(default) draws profile plots with summarization for run levels.
save_condition_plot_result	TRUE saves the table with values using condition plots. Default is FALSE.
remove_uninformative_feature_outlier	It only works after users used featureSubset="highQuality" in dataProcess. TRUE allows to remove 1) the features are flagged in the column, feature_quality="Uninformative" which are features with bad quality, 2) outliers that are flagged in the column, is_outlier=TRUE in Profile plots. FALSE (default) shows all features and intensities in profile plots.
address	prefix for the filename that will store the results.
isPlotly	Parameter to use Plotly or ggplot2. If set to TRUE, MSstats will save Plotly plots as HTML files. If set to FALSE MSstats will save ggplot2 plots as PDF files Default folder is the current working directory. The other assigned folder has to be existed under the current working directory. An output pdf file is automatically created with the default name of "ProfilePlot.pdf" or "QCplot.pdf" or "ConditionPlot.pdf" or "ConditionPlot_value.csv". The command address can help to specify where to store the file as well as how to modify the beginning of the file name. If address=FALSE, plot will be not saved as pdf file but showed in window.

## Details

- **Profile Plot** : identify the potential sources of variation of each protein. `QuantData$FeatureLevelData` is used for plots. X-axis is run. Y-axis is log-intensities of transitions. Reference/endogenous signals are in the left/right panel. Line colors indicate peptides and line types indicate transitions. In summarization plots, gray dots and lines are the same as original profile plots with `QuantData$FeatureLevelData`. Dark dots and lines are for summarized intensities from `QuantData$ProteinLevelData`.
- **QC Plot** : illustrate the systematic bias between MS runs. After normalization, the reference signals for all proteins should be stable across MS runs. `QuantData$FeatureLevelData` is used for plots. X-axis is run. Y-axis is log-intensities of transition. Reference/endogenous signals are in the left/right panel. The pdf file contains (1) QC plot for all proteins and (2) QC plots for each protein separately.
- **Condition Plot** : illustrate the systematic difference between conditions. Summarized intensities from `QuantData$ProteinLevelData` are used for plots. X-axis is condition. Y-axis is summarized log transformed intensity. If scale is TRUE, the levels of conditions is scaled according to its actual values at x-axis. Red points indicate the mean for each condition. If interval is "CI", blue error bars indicate the confidence interval with 0.95 significant level for each condition. If interval is "SD", blue error bars indicate the standard deviation for each condition. The interval is not related with model-based analysis.

The input of this function is the quantitative data from function [dataProcess](#).

## Examples

```
# Consider quantitative data (i.e. QuantData) from a yeast study with ten time points of interests,
# three biological replicates, and no technical replicates which is a time-course experiment.
# The goal is to provide pre-analysis visualization by automatically generate two types of figures
# in two separate pdf files.
# Protein IDHC (gene name IDP2) is differentially expressed in time point 1 and time point 7,
# whereas, Protein PMG2 (gene name GPM2) is not.
```

```
QuantData<-dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
# Profile plot
dataProcessPlots(data=QuantData,type="ProfilePlot")
# Quality control plot
dataProcessPlots(data=QuantData,type="QCPlot")
# Quantification plot for conditions
dataProcessPlots(data=QuantData,type="ConditionPlot")
```

---

DDARawData

*Example dataset from a label-free DDA, a controlled spike-in experiment.*

---

## Description

This is a data set obtained from a published study (Mueller, et. al, 2007). A controlled spike-in experiment, where 6 proteins, (horse myoglobin, bovine carbonic anhydrase, horse Cytochrome C, chicken lysozyme, yeast alcohol dehydrogenase, rabbit aldolase A) were spiked into a complex background in known concentrations in a latin square design. The experiment contained 6 mixtures, and each mixture was analyzed in label-free LC-MS mode with 3 technical replicates (resulting in the total of 18 runs). Each protein was represented by 7-21 peptides, and each peptide was represented by 1-5 transition.

**Usage**

```
DDARawData
```

**Format**

```
data.frame
```

**Details**

The raw data (input data for MSstats) is required to contain variable of ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity. The variable names should be fixed.

If the information of one or more columns is not available for the original raw data, please retain the column variables and type in fixed value. For example, the original raw data does not contain the information of PrecursorCharge and ProductCharge, we retain the column PrecursorCharge and ProductCharge and then type in NA for all transitions in RawData.

Variable Intensity is required to be original signal without any log transformation and can be specified as the peak of height or the peak of area under curve.

**Value**

data.frame with the required format of MSstats.

**Author(s)**

Meena Choi, Olga Vitek.

Maintainer: Meena Choi (<mnchoi67@gmail.com>)

**References**

Meena Choi, Ching-Yun Chang, Timothy Clough, Daniel Broudy, Trevor Killeen, Brendan MacLean and Olga Vitek. "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments" *Bioinformatics*, 30(17):1514-1526, 2014.

Timothy Clough, Safia Thaminy, Susanne Ragg, Ruedi Aebersold, Olga Vitek. "Statistical protein quantification and significance analysis in label-free LC-M experiments with complex designs" *BMC Bioinformatics*, 13:S16, 2012.

Mueller, L. N., Rinner, O., Schmidt, A., Letarte, S., Bodenmiller, B., Brusniak, M., Vitek, O., Aebersold, R., and Muller, M. (2007). SuperHirn - a novel tool for high resolution LC-MS based peptide/protein profiling. *Proteomics*, 7, 3470-3480. 3, 34

**Examples**

```
head(DDARawData)
```

---

DDARawData.Skyline	<i>Example dataset from a label-free DDA, a controlled spike-in experiment, processed by Skyline.</i>
--------------------	---

---

## Description

This is a data set obtained from a published study (Mueller, et. al, 2007). A controlled spike-in experiment, where 6 proteins, (horse myoglobin, bovine carbonic anhydrase, horse Cytochrome C, chicken lysozyme, yeast alcohol dehydrogenase, rabbit aldolase A) were spiked into a complex background in known concentrations in a latin square design. The experiment contained 6 mixtures, and each mixture was analyzed in label-free LC-MS mode with 3 technical replicates (resulting in the total of 18 runs). Each protein was represented by 7-21 peptides, and each peptide was represented by 1-5 transition. Skyline is used for processing.

## Usage

DDARawData.Skyline

## Format

data.frame

## Details

The raw data (input data for MSstats) is required to contain variable of ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity. The variable names should be fixed.

This is 'MSstats input' format from Skyline used by 'MSstats\_report.skyr'. The column names, 'FileName' and 'Area', should be changed to 'Run' and 'Intensity'. There are two extra columns called 'StandardType' and 'Truncated'. 'StandardType' column can be used for normalization='globalStandard' in [dataProcess](#). 'Truncated' columns can be used to remove the truncated peaks with skylineReport=TRUE in [dataProcess](#).

If the information of one or more columns is not available for the original raw data, please retain the column variables and type in fixed value. For example, the original raw data does not contain the information of PrecursorCharge and ProductCharge, we retain the column PrecursorCharge and ProductCharge and then type in NA for all transitions in RawData.

Variable Intensity is required to be original signal without any log transformation and can be specified as the peak of height or the peak of area under curve.

## Value

data.frame with the required format of MSstats.

## Author(s)

Meena Choi, Olga Vitek.

Maintainer: Meena Choi (<mnchoi67@gmail.com>)

## References

Meena Choi, Ching-Yun Chang, Timothy Clough, Daniel Broudy, Trevor Killeen, Brendan MacLean and Olga Vitek. "MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments" *Bioinformatics*, 30(17):1514-1526, 2014.

Timothy Clough, Safia Thaminy, Susanne Ragg, Ruedi Aebersold, Olga Vitek. "Statistical protein quantification and significance analysis in label-free LC-M experiments with complex designs" *BMC Bioinformatics*, 13:S16, 2012.

## Examples

```
head(DDARawData.Skyline)
```

---

designSampleSize	<i>Planning future experimental designs of Selected Reaction Monitoring (SRM), Data-Dependent Acquisition (DDA or shotgun), and Data-Independent Acquisition (DIA or SWATH-MS) experiments in sample size calculation</i>
------------------	---

---

## Description

Calculate sample size for future experiments of a Selected Reaction Monitoring (SRM), Data-Dependent Acquisition (DDA or shotgun), and Data-Independent Acquisition (DIA or SWATH-MS) experiment based on intensity-based linear model. Two options of the calculation: (1) number of biological replicates per condition, (2) power.

## Usage

```
designSampleSize(
  data,
  desiredFC,
  FDR = 0.05,
  numSample = TRUE,
  power = 0.9,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL
)
```

## Arguments

data	'FittedModel' in testing output from function groupComparison.
desiredFC	the range of a desired fold change which includes the lower and upper values of the desired fold change.
FDR	a pre-specified false discovery ratio (FDR) to control the overall false positive rate. Default is 0.05
numSample	minimal number of biological replicates per condition. TRUE represents you require to calculate the sample size for this category, else you should input the exact number of biological replicates.

power	a pre-specified statistical power which defined as the probability of detecting a true fold change. TRUE represent you require to calculate the power for this category, else you should input the average of power you expect. Default is 0.9
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.

### Details

The function fits the model and uses variance components to calculate sample size. The underlying model fitting with intensity-based linear model with technical MS run replication. Estimated sample size is rounded to 0 decimal. The function can only obtain either one of the categories of the sample size calculation (numSample, numPep, numTran, power) at the same time.

### Value

data.frame - sample size calculation results including variables: desiredFC, numSample, FDR, and power.

### Author(s)

Meena Choi, Ching-Yun Chang, Olga Vitek.

### Examples

```
# Consider quantitative data (i.e. QuantData) from yeast study.
# A time course study with ten time points of interests and three biological replicates.
QuantData <- dataProcess(SRMRawData)
head(QuantData$FeatureLevelData)
## based on multiple comparisons (T1 vs T3; T1 vs T7; T1 vs T9)
comparison1<-matrix(c(-1,0,1,0,0,0,0,0,0,0),nrow=1)
comparison2<-matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
comparison3<-matrix(c(-1,0,0,0,0,0,0,0,1,0),nrow=1)
comparison<-rbind(comparison1,comparison2, comparison3)
row.names(comparison)<-c("T3-T1", "T7-T1", "T9-T1")
colnames(comparison)<-unique(QuantData$ProteinLevelData$GROUP)

testResultMultiComparisons<-groupComparison(contrast.matrix=comparison,data=QuantData)

## Calculate sample size for future experiments:
#(1) Minimal number of biological replicates per condition
designSampleSize(data=testResultMultiComparisons$FittedModel, numSample=TRUE,
                 desiredFC=c(1.25,1.75), FDR=0.05, power=0.8)
#(2) Power calculation
designSampleSize(data=testResultMultiComparisons$FittedModel, numSample=2,
                 desiredFC=c(1.25,1.75), FDR=0.05, power=TRUE)
```



---

designSampleSizePlots *Visualization for sample size calculation*

---

## Description

To illustrate the relationship of desired fold change and the calculated minimal number sample size which are (1) number of biological replicates per condition, (2) number of peptides per protein, (3) number of transitions per peptide, and (4) power. The input is the result from function ([designSampleSize](#)).

## Usage

```
designSampleSizePlots(data, isPlotly = FALSE)
```

## Arguments

data	output from function <a href="#">designSampleSize</a> .
isPlotly	Parameter to use Plotly or ggplot2. If set to TRUE, MSstats will save Plotly plots as HTML files. If set to FALSE MSstats will save ggplot2 plots as PDF files

## Details

Data in the example is based on the results of sample size calculation from function [designSampleSize](#)

## Value

Plot for estimated sample size with assigned variable.

## Author(s)

Meena Choi, Ching-Yun Chang, Olga Vitek.

## Examples

```
# Based on the results of sample size calculation from function designSampleSize,
# we generate a series of sample size plots for number of biological replicates, or peptides,
# or transitions or power plot.
QuantData<-dataProcess(SRMRawData)
head(QuantData$ProcessedData)
## based on multiple comparisons (T1 vs T3; T1 vs T7; T1 vs T9)
comparison1<-matrix(c(-1,0,1,0,0,0,0,0,0,0),nrow=1)
comparison2<-matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
comparison3<-matrix(c(-1,0,0,0,0,0,0,0,1,0),nrow=1)
comparison<-rbind(comparison1,comparison2, comparison3)
row.names(comparison)<-c("T3-T1", "T7-T1", "T9-T1")
colnames(comparison)<-unique(QuantData$ProteinLevelData$GROUP)

testResultMultiComparisons<-groupComparison(contrast.matrix=comparison, data=QuantData)

# plot the calculated sample sizes for future experiments:
# (1) Minimal number of biological replicates per condition
result.sample<-designSampleSize(data=testResultMultiComparisons$FittedModel, numSample=TRUE,
```

```

                                desiredFC=c(1.25,1.75), FDR=0.05, power=0.8)
designSampleSizePlots(data=result.sample)
# (2) Power
result.power<-designSampleSize(data=testResultMultiComparisons$FittedModel, numSample=2,
                                desiredFC=c(1.25,1.75), FDR=0.05, power=TRUE)
designSampleSizePlots(data=result.power)

```

---

DIANNtoMSstatsFormat    *Import Diann files*

---

## Description

Import Diann files

## Usage

```

DIANNtoMSstatsFormat(
  input,
  annotation = NULL,
  global_qvalue_cutoff = 0.01,
  qvalue_cutoff = 0.01,
  pg_qvalue_cutoff = 0.01,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeOxidationMpeptides = TRUE,
  removeProtein_with1Feature = TRUE,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  MBR = TRUE,
  ...
)

```

## Arguments

<code>input</code>	name of MSstats input report from Diann, which includes feature-level data.
<code>annotation</code>	name of 'annotation.txt' data which includes Condition, BioReplicate, Run.
<code>global_qvalue_cutoff</code>	The global qvalue cutoff
<code>qvalue_cutoff</code>	local qvalue cutoff for library
<code>pg_qvalue_cutoff</code>	local qvalue cutoff for protein groups Run should be the same as filename.
<code>useUniquePeptide</code>	should unique peptides be removed
<code>removeFewMeasurements</code>	should proteins with few measurements be removed
<code>removeOxidationMpeptides</code>	should peptides with oxidation be removed

removeProtein_with1Feature	should proteins with a single feature be removed
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
MBR	True if analysis was done with match between runs
...	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Elijah Willie

**Examples**

```
## Not run:
input = fread('diann_pooled_report.tsv')
annot = fread('Annotation.csv')
colnames(annot) = c('Condition', 'Run', 'BioReplicate')
input = DIANNtoMSstatsFormat(input, annotation = annot, MBR = F)
head(input)

## End(Not run)
```

---

DIARawData

*Example dataset from a label-free DIA, a group comparison study of S. Pyogenes.*

---

**Description**

This example dataset was obtained from a group comparison study of *S. Pyogenes*. Two conditions, *S. Pyogenes* with 0% and 10% of human plasma added (denoted Strep 0% and Strep 10%), were profiled in two replicates, in the label-free mode, with a SWATH-MS-enabled AB SCIEX TripleTOF 5600 System. The identification and quantification of spectral peaks was assisted by a spectral library, and was performed using OpenSWATH software (<http://proteomics.ethz.ch/openswath.html>). For reasons of space, the example dataset only contains two proteins from this study. Protein FabG shows strong evidence of differential abundance, while protein Probable RNA helicase exp9 only shows moderate evidence of differential abundance between conditions.

**Usage**

DIARawData

**Format**

data.frame

**Details**

The raw data (input data for MSstats) is required to contain variable of ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity. The variable names should be fixed.

If the information of one or more columns is not available for the original raw data, please retain the column variables and type in fixed value. For example, the original raw data does not contain the information of PrecursorCharge and ProductCharge, we retain the column PrecursorCharge and ProductCharge and then type in NA for all transitions in RawData.

Variable Intensity is required to be original signal without any log transformation and can be specified as the peak of height or the peak of area under curve.

**Value**

data.frame with the required format of MSstats.

**Author(s)**

Meena Choi, Olga Vitek.

Maintainer: Meena Choi (<mnchoi67@gmail.com>)

**Examples**

```
head(DIARawData)
```

---

DIAUmpiretoMSstatsFormat

*Import DIA-Umpire files*

---

**Description**

Import DIA-Umpire files

**Usage**

```
DIAUmpiretoMSstatsFormat(  
  raw.frag,  
  raw.pep,  
  raw.pro,  
  annotation,  
  useSelectedFrag = TRUE,  
  useSelectedPep = TRUE,  
  removeFewMeasurements = TRUE,  
  removeProtein_with1Feature = FALSE,  
  summaryforMultipleRows = max,  
  use_log_file = TRUE,  
  append = FALSE,
```

```

    verbose = TRUE,
    log_file_path = NULL,
    ...
)

```

### Arguments

<code>raw.frag</code>	name of FragSummary_date.xls data, which includes feature-level data.
<code>raw.pep</code>	name of PeptideSummary_date.xls data, which includes selected fragments information.
<code>raw.pro</code>	name of ProteinSummary_date.xls data, which includes selected peptides information.
<code>annotation</code>	name of annotation data which includes Condition, BioReplicate, Run information.
<code>useSelectedFrag</code>	TRUE will use the selected fragment for each peptide. 'Selected_fragments' column is required.
<code>useSelectedPep</code>	TRUE will use the selected peptide for each protein. 'Selected_peptides' column is required.
<code>removeFewMeasurements</code>	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
<code>removeProtein_with1Feature</code>	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
<code>summaryforMultipleRows</code>	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
<code>use_log_file</code>	logical. If TRUE, information about data processing will be saved to a file.
<code>append</code>	logical. If TRUE, information about data processing will be added to an existing log file.
<code>verbose</code>	logical. If TRUE, information about data processing will be printed to the console.
<code>log_file_path</code>	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
<code>...</code>	additional parameters to 'data.table::fread'.

### Value

data.frame in the MSstats required format.

### Author(s)

Meena Choi, Olga Vitek

**Examples**

```
diau_frag = system.file("tinytest/raw_data/DIAUmpire/diau_frag.csv",
                        package = "MSstatsConvert")
diau_pept = system.file("tinytest/raw_data/DIAUmpire/diau_pept.csv",
                        package = "MSstatsConvert")
diau_prot = system.file("tinytest/raw_data/DIAUmpire/diau_prot.csv",
                        package = "MSstatsConvert")
annot = system.file("tinytest/annotations/annot_diau.csv",
                   package = "MSstats")
diau_frag = data.table::fread(diau_frag)
diau_pept = data.table::fread(diau_pept)
diau_prot = data.table::fread(diau_prot)
annot = data.table::fread(annot)
diau_frag = diau_frag[, lapply(.SD, function(x) if (is.integer(x)) as.numeric(x) else x)]
# In case numeric columns are not interpreted correctly

diau_imported = DIAUmpiretoMSstatsFormat(diau_frag, diau_pept, diau_prot,
                                         annot, use_log_file = FALSE)

head(diau_imported)
```

---

example\_SDRF

*Example SDRF.*

---

**Description**

An example SDRF file which is used to store metadata for MS-based proteomics experiments.

**Usage**

```
example_SDRF
```

**Format**

```
data.frame
```

**Details**

An example SDRF file which is used to store metadata for MS-based proteomics experiments.

**Value**

```
data.frame example of an SDRF file.
```

**Author(s)**

Mateusz Staniak, Devon Kohler, Olga Vitek.

**Examples**

```
head(example_SDRF)
```

---

 extractSDRF

*Extract experimental design from MSstats format into SDRF format*


---

## Description

Extract experimental design from MSstats format into SDRF format

## Usage

```
extractSDRF(
  data,
  run_name = "comment[data file]",
  condition_name = "characteristics[disease]",
  biological_replicate = "characteristics[biological replicate]",
  fraction = NULL,
  meta_data = NULL
)
```

## Arguments

data	MSstats formatted data that is the output of a dedicated converter, such as ‘MaxQ-toMSstatsFormat’, ‘SkylinetoMSstatsFormat’, ect.
run_name	Run column name in SDRF data
condition_name	Condition column name in SDRF data
biological_replicate	Biological replicate column name in SDRF data
fraction	Fraction column name in SDRF data (if applicable). Default is ‘NULL’. If there are no fractions keep ‘NULL’.
meta_data	A data.frame including any additional meta data for the SDRF file that is not included in MSstats. This meta data will be added into the final SDRF file. Please ensure the run names in the meta data matches the run names in the MSstats data.

## Examples

```
mq_ev = data.table::fread(system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                                     package = "MSstatsConvert"))
mq_pg = data.table::fread(system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                                     package = "MSstatsConvert"))
annot = data.table::fread(system.file("tinytest/raw_data/MaxQuant/annotation.csv",
                                     package = "MSstatsConvert"))
maxq_imported = MaxQtoMSstatsFormat(mq_ev, annot, mq_pg, use_log_file = FALSE)
head(maxq_imported)

SDRF_file = extractSDRF(maxq_imported)
```

---

 FragPipetoMSstatsFormat

*Import FragPipe files*


---

## Description

Import FragPipe files

## Usage

```
FragPipetoMSstatsFormat(
  input,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeProtein_with1Feature = FALSE,
  summaryforMultipleRows = max,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

## Arguments

input	name of FragPipe msstats.csv export. ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity are required.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
removeProtein_with1Feature	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
summaryforMultipleRows	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
...	additional parameters to 'data.table::fread'.



**Value**

data.frame in the MSstats required format.

**Author(s)**

Devon Kohler

**Examples**

```
fragpipe_raw = system.file("tinytest/raw_data/FragPipe/fragpipe_input.csv",
                           package = "MSstatsConvert")
fragpipe_raw = data.table::fread(fragpipe_raw)
fragpipe_imported = FragPipeToMSstatsFormat(fragpipe_raw, use_log_file = FALSE)
head(fragpipe_imported)
```

---

getProcessed	<i>Get feature-level data to be used in the MSstatsSummarizationOutput function</i>
--------------	---

---

**Description**

Get feature-level data to be used in the MSstatsSummarizationOutput function

**Usage**

```
getProcessed(input)
```

**Arguments**

input            data.table processed by dataProcess subfunctions

**Value**

data.table processed by dataProcess subfunctions

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input_all = MSstatsSelectFeatures(input, "all") # all features
input_5 = MSstatsSelectFeatures(data.table::copy(input),
"topN", top_n = 5) # top 5 features

proc1 = getProcessed(input_all)
proc2 = getProcessed(input_5)
```

```
proc1  
proc2
```

---

getSamplesInfo      *Get information about number of measurements for each group*

---

### Description

Get information about number of measurements for each group

### Usage

```
getSamplesInfo(summarization_output)
```

### Arguments

```
summarization_output  
                          output of the dataProcess function
```

### Details

This function extracts information required to compute percentages of missing and imputed values in group comparison.

### Value

data.table

### Examples

```
QuantData <- dataProcess(DDARawData, use_log_file = FALSE)  
samples_info <- getSamplesInfo(QuantData)  
samples_info
```

---

getSelectedProteins      *Get proteins based on names or integer IDs*

---

### Description

Get proteins based on names or integer IDs

### Usage

```
getSelectedProteins(chosen_proteins, all_proteins)
```

**Arguments**

chosen\_proteins      protein names or integers IDs  
 all\_proteins      all unique proteins

**Value**

character

---

groupComparison	<i>Whole plot testing</i>
-----------------	---------------------------

---

**Description**

Whole plot testing

**Usage**

```
groupComparison(
  contrast.matrix,
  data,
  save_fitted_models = TRUE,
  log_base = 2,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  numberOfCores = 1
)
```

**Arguments**

contrast.matrix      comparison between conditions of interests.

data      name of the (output of dataProcess function) data set.

save\_fitted\_models      logical, if TRUE, fitted models will be added to the output.

log\_base      base of the logarithm used in dataProcess.

use\_log\_file      logical. If TRUE, information about data processing will be saved to a file.

append      logical. If TRUE, information about data processing will be added to an existing log file.

verbose      logical. If TRUE, information about data processing will be printed to the console.

log\_file\_path      character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.

numberOfCores      Number of cores for parallel processing. When > 1, a logfile named 'MSstats\_groupComparison\_log\_' is created to track progress. Only works for Linux & Mac OS. Default is 1.

## Details

contrast.matrix : comparison of interest. Based on the levels of conditions, specify 1 or -1 to the conditions of interests and 0 otherwise. The levels of conditions are sorted alphabetically. Command levels(QuantData\$FeatureLevelData\$GROUP\_ORIGINAL) can illustrate the actual order of the levels of conditions. The underlying model fitting functions are lm and lmer for the fixed effects model and mixed effects model, respectively. The input of this function is the quantitative data from function (dataProcess).

## Value

list that consists of three elements: "ComparisonResult" - data.frame with results of statistical testing, "ModelQC" - data.frame with data used to fit models for group comparison and "FittedModel" - list of fitted models.

## Examples

```
# Consider quantitative data (i.e. QuantData) from yeast study with ten time points of interests,
# three biological replicates, and no technical replicates.
# It is a time-course experiment and we attempt to compare differential abundance
# between time 1 and 7 in a set of targeted proteins.
# In this label-based SRM experiment, MSstats uses the fitted model with expanded scope of
# Biological replication.
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
levels(QuantData$ProteinLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
groups = levels(QuantData$ProteinLevelData$GROUP)
colnames(comparison) <- groups[order(as.numeric(groups))]
# Tests for differentially abundant proteins with models:
# label-based SRM experiment with expanded scope of biological replication.
testResultOneComparison <- groupComparison(contrast.matrix=comparison, data=QuantData,
                                           use_log_file = FALSE)

# table for result
testResultOneComparison$ComparisonResult
```

---

groupComparisonPlots    *Visualization for model-based analysis and summarizing differentially abundant proteins*

---

## Description

To summarize the results of log-fold changes and adjusted p-values for differentially abundant proteins, groupComparisonPlots takes testing results from function ([groupComparison](#)) as input and automatically generate three types of figures in pdf files as output : (1) volcano plot (specify "VolcanoPlot" in option type) for each comparison separately; (2) heatmap (specify "Heatmap" in option type) for multiple comparisons ; (3) comparison plot (specify "ComparisonPlot" in option type) for multiple comparisons per protein.

**Usage**

```

groupComparisonPlots(
  data,
  type,
  sig = 0.05,
  FCcutoff = FALSE,
  logBase.pvalue = 10,
  ylimUp = FALSE,
  ylimDown = FALSE,
  xlimUp = FALSE,
  x.axis.size = 10,
  y.axis.size = 10,
  dot.size = 3,
  text.size = 4,
  text.angle = 0,
  legend.size = 13,
  ProteinName = TRUE,
  colorkey = TRUE,
  numProtein = 100,
  clustering = "both",
  width = 800,
  height = 600,
  which.Comparison = "all",
  which.Protein = "all",
  address = "",
  isPlotly = FALSE
)

```

**Arguments**

data	'ComparisonResult' in testing output from function groupComparison.
type	choice of visualization. "VolcanoPlot" represents volcano plot of log fold changes and adjusted p-values for each comparison separately. "Heatmap" represents heatmap of adjusted p-values for multiple comparisons. "ComparisonPlot" represents comparison plot of log fold changes for multiple comparisons per protein.
sig	FDR cutoff for the adjusted p-values in heatmap and volcano plot. level of significance for comparison plot. 100(1-sig)% confidence interval will be drawn. sig=0.05 is default.
FCcutoff	for volcano plot or heatmap, whether involve fold change cutoff or not. FALSE (default) means no fold change cutoff is applied for significance analysis. FC-cutoff = specific value means specific fold change cutoff is applied.
logBase.pvalue	for volcano plot or heatmap, (-) logarithm transformation of adjusted p-value with base 2 or 10(default).
ylimUp	for all three plots, upper limit for y-axis. FALSE (default) for volcano plot/heatmap use maximum of -log2 (adjusted p-value) or -log10 (adjusted p-value). FALSE (default) for comparison plot uses maximum of log-fold change + CI.
ylimDown	for all three plots, lower limit for y-axis. FALSE (default) for volcano plot/heatmap use minimum of -log2 (adjusted p-value) or -log10 (adjusted p-value). FALSE (default) for comparison plot uses minimum of log-fold change - CI.

<code>xlimUp</code>	for Volcano plot, the limit for x-axis. FALSE (default) for use maximum for absolute value of log-fold change or 3 as default if maximum for absolute value of log-fold change is less than 3.
<code>x.axis.size</code>	size of axes labels, e.g. name of the comparisons in heatmap, and in comparison plot. Default is 10.
<code>y.axis.size</code>	size of axes labels, e.g. name of targeted proteins in heatmap. Default is 10.
<code>dot.size</code>	size of dots in volcano plot and comparison plot. Default is 3.
<code>text.size</code>	size of ProteinName label in the graph for Volcano Plot. Default is 4.
<code>text.angle</code>	angle of x-axis labels represented each comparison at the bottom of graph in comparison plot. Default is 0.
<code>legend.size</code>	size of legend for color at the bottom of volcano plot. Default is 7.
<code>ProteinName</code>	for volcano plot only, whether display protein names or not. TRUE (default) means protein names, which are significant, are displayed next to the points. FALSE means no protein names are displayed.
<code>colorkey</code>	TRUE(default) shows colorkey.
<code>numProtein</code>	For ggplot2: The number of proteins which will be presented in each heatmap. Default is 100. Maximum possible number of protein for one heatmap is 180. For Plotly: use this parameter to adjust the number of proteins to be displayed on the heatmap
<code>clustering</code>	Determines how to order proteins and comparisons. Hierarchical cluster analysis with Ward method(minimum variance) is performed. 'protein' means that protein dendrogram is computed and reordered based on protein means (the order of row is changed). 'comparison' means comparison dendrogram is computed and reordered based on comparison means (the order of comparison is changed). 'both' means to reorder both protein and comparison. Default is 'protein'.
<code>width</code>	width of the saved file. Default is 10.
<code>height</code>	height of the saved file. Default is 10.
<code>which.Comparison</code>	list of comparisons to draw plots. List can be labels of comparisons or order numbers of comparisons from levels(data\$Label), such as levels(testResultMultiComparisons\$Comparison). Default is "all", which generates all plots for each protein.
<code>which.Protein</code>	Protein list to draw comparison plots. List can be names of Proteins or order numbers of Proteins from levels(testResultMultiComparisons\$ComparisonResult\$Protein). Default is "all", which generates all comparison plots for each protein.
<code>address</code>	the name of folder that will store the results. Default folder is the current working directory. The other assigned folder has to be existed under the current working directory. An output pdf file is automatically created with the default name of "VolcanoPlot.pdf" or "Heatmap.pdf" or "ComparisonPlot.pdf". The command address can help to specify where to store the file as well as how to modify the beginning of the file name. If address=FALSE, plot will be not saved as pdf file but showed in window.
<code>isPlotly</code>	This parameter is for MSstatsShiny application for plotly render, this cannot be used for saving PDF files as plotly do not have support for PDFs currently. address and isPlotly cannot be set as TRUE at the same time.

## Details

- Volcano plot : illustrate actual log-fold changes and adjusted p-values for each comparison separately with all proteins. The x-axis is the log fold change. The base of logarithm transformation is the same as specified in "logTrans" from [dataProcess](#). The y-axis is the negative log2 or log10 adjusted p-values. The horizontal dashed line represents the FDR cutoff. The points below the FDR cutoff line are non-significantly abundant proteins (colored in black). The points above the FDR cutoff line are significantly abundant proteins (colored in red/blue for up-/down-regulated). If fold change cutoff is specified (FCcutoff = specific value), the points above the FDR cutoff line but within the FC cutoff line are non-significantly abundant proteins (colored in black)/
- Heatmap : illustrate up-/down-regulated proteins for multiple comparisons with all proteins. Each column represents each comparison of interest. Each row represents each protein. Color red/blue represents proteins in that specific comparison are significantly up-regulated/down-regulated proteins with FDR cutoff and/or FC cutoff. The color scheme shows the evidences of significance. The darker color it is, the stronger evidence of significance it has. Color gold represents proteins are not significantly different in abundance.
- Comparison plot : illustrate log-fold change and its variation of multiple comparisons for single protein. X-axis is comparison of interest. Y-axis is the log fold change. The red points are the estimated log fold change from the model. The blue error bars are the confidence interval with 0.95 significant level for log fold change. This interval is only based on the standard error, which is estimated from the model.

## Examples

```

QuantData<-dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
## based on multiple comparisons (T1 vs T3; T1 vs T7; T1 vs T9)
comparison1<-matrix(c(-1,0,1,0,0,0,0,0,0),nrow=1)
comparison2<-matrix(c(-1,0,0,0,0,0,1,0,0),nrow=1)
comparison3<-matrix(c(-1,0,0,0,0,0,0,0,1),nrow=1)
comparison<-rbind(comparison1,comparison2, comparison3)
row.names(comparison)<-c("T3-T1","T7-T1","T9-T1")
groups = levels(QuantData$ProteinLevelData$GROUP)
colnames(comparison) <- groups[order(as.numeric(groups))]
testResultMultiComparisons<-groupComparison(contrast.matrix=comparison,
data=QuantData,
use_log_file = FALSE)
testResultMultiComparisons$ComparisonResult
# Volcano plot with FDR cutoff = 0.05 and no FC cutoff
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="VolcanoPlot",
logBase.pvalue=2, address="Ex1_")
# Volcano plot with FDR cutoff = 0.05, FC cutoff = 70, upper y-axis limit = 100,
# and no protein name displayed
# FCcutoff=70 is for demonstration purpose
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="VolcanoPlot",
FCcutoff=70, logBase.pvalue=2, ylimUp=100, ProteinName=FALSE,address="Ex2_")
# Heatmap with FDR cutoff = 0.05
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="Heatmap",
logBase.pvalue=2, address="Ex1_")
# Heatmap with FDR cutoff = 0.05 and FC cutoff = 70
# FCcutoff=70 is for demonstration purpose
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="Heatmap",
FCcutoff=70, logBase.pvalue=2, address="Ex2_")
# Comparison Plot

```

```
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="ComparisonPlot",
address="Ex1_")
# Comparison Plot
groupComparisonPlots(data=testResultMultiComparisons$ComparisonResult, type="ComparisonPlot",
ylimUp=8, ylimDown=-1, address="Ex2_")
```

---

groupComparisonQCPlots

*Visualization for model-based quality control in fitting model*

---

## Description

To check the assumption of linear model for whole plot inference, groupComparisonQCPlots takes the results after fitting models from function ([groupComparison](#)) as input and automatically generate two types of figures in pdf files as output: (1) normal quantile-quantile plot (specify "QQPlot" in option type) for checking normally distributed errors.; (2) residual plot (specify "ResidualPlot" in option type).

## Usage

```
groupComparisonQCPlots(
  data,
  type,
  axis.size = 10,
  dot.size = 3,
  width = 10,
  height = 10,
  which.Protein = "all",
  address = ""
)
```

## Arguments

data	output from function groupComparison.
type	choice of visualization. "QQPlots" represents normal quantile-quantile plot for each protein after fitting models. "ResidualPlots" represents a plot of residuals versus fitted values for each protein in the dataset.
axis.size	size of axes labels. Default is 10.
dot.size	size of points in the graph for residual plots and QQ plots. Default is 3.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.
which.Protein	Protein list to draw plots. List can be names of Proteins or order numbers of Proteins from levels(testResultOneComparison\$ComparisonResult\$Protein). Default is "all", which generates all plots for each protein.
address	name that will serve as a prefix to the name of output file.



**Details**

Results based on statistical models for whole plot level inference are accurate as long as the assumptions of the model are met. The model assumes that the measurement errors are normally distributed with mean 0 and constant variance. The assumption of a constant variance can be checked by examining the residuals from the model.

- **QQPlots** : a normal quantile-quantile plot for each protein is generated in order to check whether the errors are well approximated by a normal distribution. If points fall approximately along a straight line, then the assumption is appropriate for that protein. Only large deviations from the line are problematic.
- **ResidualPlots** : The plots of residuals against predicted(fitted) values. If it shows a random scatter, then the assumption is appropriate.

**Value**

produce a pdf file

**Examples**

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
levels(QuantData$FeatureLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
colnames(comparison) <- unique(QuantData$ProteinLevelData$GROUP)
# Tests for differentially abundant proteins with models:
# label-based SRM experiment with expanded scope of biological replication.
testResultOneComparison <- groupComparison(contrast.matrix=comparison, data=QuantData,
use_log_file = FALSE)
# normal quantile-quantile plots
groupComparisonQCPlots(data=testResultOneComparison, type="QQPlots", address="")
# residual plots
groupComparisonQCPlots(data=testResultOneComparison, type="ResidualPlots", address="")
```

---

makePeptidesDictionary

*Prepare a peptides dictionary for global standards normalization*

---

**Description**

Prepare a peptides dictionary for global standards normalization

**Usage**

```
makePeptidesDictionary(input, normalization)
```

**Arguments**

input                    'data.table' in MSstats standard format  
normalization        normalization method

**Details**

This function extracts information required to perform normalization with global standards. It is useful for running the summarization workflow outside of the dataProcess function.

**Examples**

```
input = data.table::as.data.table(DDARawData)
peptides_dict = makePeptidesDictionary(input, "GLOBALSTANDARDS")
head(peptides_dict) # ready to be passed to the MSstatsNormalize function
```

---

MaxQtoMSstatsFormat     *Import MaxQuant files*

---

**Description**

Import MaxQuant files

**Usage**

```
MaxQtoMSstatsFormat(
  evidence,
  annotation,
  proteinGroups,
  proteinID = "Proteins",
  useUniquePeptide = TRUE,
  summaryforMultipleRows = max,
  removeFewMeasurements = TRUE,
  removeMpeptides = FALSE,
  removeOxidationMpeptides = FALSE,
  removeProtein_with1Peptide = FALSE,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

**Arguments**

evidence	name of 'evidence.txt' data, which includes feature-level data.
annotation	name of 'annotation.txt' data which includes Raw.file, Condition, BioReplicate, Run, IsotopeLabelType information.
proteinGroups	name of 'proteinGroups.txt' data. It needs to matching protein group ID. If proteinGroups=NULL, use 'Proteins' column in 'evidence.txt'.
proteinID	'Proteins'(default) or 'Leading.razor.protein' for Protein ID.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.

summaryforMultipleRows	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
removeMpeptides	TRUE will remove the peptides including 'M' sequence. FALSE is default.
removeOxidationMpeptides	TRUE will remove the peptides including 'oxidation (M)' in modification. FALSE is default.
removeProtein_with1Peptide	TRUE will remove the proteins which have only 1 peptide and charge. FALSE is default.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
...	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Note**

Warning: MSstats does not support for metabolic labeling or iTRAQ experiments.

**Author(s)**

Meena Choi, Olga Vitek.

**Examples**

```
mq_ev = data.table::fread(system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                                     package = "MSstatsConvert"))
mq_pg = data.table::fread(system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                                     package = "MSstatsConvert"))
annot = data.table::fread(system.file("tinytest/raw_data/MaxQuant/annotation.csv",
                                     package = "MSstatsConvert"))
maxq_imported = MaxQtoMSstatsFormat(mq_ev, annot, mq_pg, use_log_file = FALSE)
head(maxq_imported)
```

**Description**

To check the assumption of linear model for whole plot inference, modelBasedQCPlots takes the results after fitting models from function ([groupComparison](#)) as input and automatically generate two types of figures in pdf files as output: (1) normal quantile-quantile plot (specify "QQPlot" in option type) for checking normally distributed errors.; (2) residual plot (specify "ResidualPlot" in option type).

**Usage**

```
modelBasedQCPlots(
  data,
  type,
  axis.size = 10,
  dot.size = 3,
  width = 10,
  height = 10,
  which.Protein = "all",
  address = "",
  displayDeprecationMessage = TRUE
)
```

**Arguments**

data	output from function groupComparison.
type	choice of visualization. "QQPlots" represents normal quantile-quantile plot for each protein after fitting models. "ResidualPlots" represents a plot of residuals versus fitted values for each protein in the dataset.
axis.size	size of axes labels. Default is 10.
dot.size	size of points in the graph for residual plots and QQ plots. Default is 3.
width	width of the saved file. Default is 10.
height	height of the saved file. Default is 10.
which.Protein	Protein list to draw plots. List can be names of Proteins or order numbers of Proteins from levels(testResultOneComparison\$ComparisonResult\$Protein). Default is "all", which generates all plots for each protein.
address	name that will serve as a prefix to the name of output file.

**Details**

Results based on statistical models for whole plot level inference are accurate as long as the assumptions of the model are met. The model assumes that the measurement errors are normally distributed with mean 0 and constant variance. The assumption of a constant variance can be checked by examining the residuals from the model.

- QQPlots : a normal quantile-quantile plot for each protein is generated in order to check whether the errors are well approximated by a normal distribution. If points fall approximately along a straight line, then the assumption is appropriate for that protein. Only large deviations from the line are problematic.

- **ResidualPlots** : The plots of residuals against predicted(fitted) values. If it shows a random scatter, then the assumption is appropriate.

## Value

produce a pdf file

## Examples

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
levels(QuantData$FeatureLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
colnames(comparison) <- unique(QuantData$ProteinLevelData$GROUP)
# Tests for differentially abundant proteins with models:
# label-based SRM experiment with expanded scope of biological replication.
testResultOneComparison <- groupComparison(contrast.matrix=comparison, data=QuantData,
use_log_file = FALSE)
# normal quantile-quantile plots
modelBasedQCPlots(data=testResultOneComparison, type="QQPlots", address="")
# residual plots
modelBasedQCPlots(data=testResultOneComparison, type="ResidualPlots", address="")
```

---

MSstatsContrastMatrix *Create a contrast matrix for groupComparison function*

---

## Description

Create a contrast matrix for groupComparison function

## Usage

```
MSstatsContrastMatrix(contrasts, conditions, labels = NULL)
```

## Arguments

contrasts	One of the following: i) list of lists. Each sub-list consists of two vectors that name conditions that will be compared. See the details section for more information ii) matrix. In this case, it's correctness will be checked iii) "pairwise". In this case, pairwise comparison matrix will be generated iv) data.frame. In this case, input will be converted to matrix
conditions	unique condition labels
labels	labels for contrasts (row.names of the contrast matrix)

---

MSstatsGroupComparison

*Group comparison*


---

## Description

Group comparison

## Usage

```
MSstatsGroupComparison(
  summarized_list,
  contrast_matrix,
  save_fitted_models,
  repeated,
  samples_info,
  numberOfCores = 1
)
```

## Arguments

summarized_list	output of MSstatsPrepareForGroupComparison
contrast_matrix	contrast matrix
save_fitted_models	if TRUE, fitted models will be included in the output
repeated	logical, output of checkRepeatedDesign function
samples_info	data.table, output of getSamplesInfo function
numberOfCores	Number of cores for parallel processing. When > 1, a logfile named 'MSstats_groupComparison_log_' is created to track progress. Only works for Linux & Mac OS.

## Examples

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
group_comparison_input = MSstatsPrepareForGroupComparison(QuantData)
levels(QuantData$ProteinLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
groups = levels(QuantData$ProteinLevelData$GROUP)
colnames(comparison) <- groups[order(as.numeric(groups))]
samples_info = getSamplesInfo(QuantData)
repeated = checkRepeatedDesign(QuantData)
group_comparison = MSstatsGroupComparison(group_comparison_input, comparison,
                                           FALSE, repeated, samples_info)
length(group_comparison) # list of length equal to number of proteins
group_comparison[[1]][[1]] # data used to fit linear model
group_comparison[[1]][[2]] # comparison result
group_comparison[[2]][[3]] # NULL, because we set save_fitted_models to FALSE
```

---

MSstatsGroupComparisonOutput

*Create output of group comparison based on results for individual proteins*

---

### Description

Create output of group comparison based on results for individual proteins

### Usage

```
MSstatsGroupComparisonOutput(input, summarization_output, log_base = 2)
```

### Arguments

input                    output of MSstatsGroupComparison function  
 summarization\_output                    output of dataProcess function  
 log\_base                base of the logarithm used in fold-change calculation

### Value

list, same as the output of ‘groupComparison‘

### Examples

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
group_comparison_input = MSstatsPrepareForGroupComparison(QuantData)
levels(QuantData$ProteinLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
groups = levels(QuantData$ProteinLevelData$GROUP)
colnames(comparison) <- groups[order(as.numeric(groups))]
samples_info = getSamplesInfo(QuantData)
repeated = checkRepeatedDesign(QuantData)
group_comparison = MSstatsGroupComparison(group_comparison_input, comparison,
                                           FALSE, repeated, samples_info)
group_comparison_final = MSstatsGroupComparisonOutput(group_comparison,
                                                       QuantData)
group_comparison_final[["ComparisonResult"]]
```

---

MSstatsGroupComparisonSingleProtein

*Group comparison for a single protein*

---

### Description

Group comparison for a single protein

**Usage**

```
MSstatsGroupComparisonSingleProtein(
  single_protein,
  contrast_matrix,
  repeated,
  groups,
  samples_info,
  save_fitted_models,
  has_imputed
)
```

**Arguments**

`single_protein` data.table with summarized data for a single protein

`contrast_matrix` contrast matrix

`repeated` if TRUE, repeated measurements will be modeled

`groups` unique labels of experimental conditions

`samples_info` number of runs per group

`save_fitted_models` if TRUE, fitted model will be saved. If not, it will be replaced with NULL

`has_imputed` TRUE if missing values have been imputed

**Examples**

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
group_comparison_input <- MSstatsPrepareForGroupComparison(QuantData)
levels(QuantData$ProteinLevelData$GROUP)
comparison <- matrix(c(-1,0,0,0,0,0,1,0,0,0),nrow=1)
row.names(comparison) <- "T7-T1"
groups = levels(QuantData$ProteinLevelData$GROUP)
colnames(comparison) <- groups[order(as.numeric(groups))]
samples_info <- getSamplesInfo(QuantData)
repeated <- checkRepeatedDesign(QuantData)
single_output <- MSstatsGroupComparisonSingleProtein(
  group_comparison_input[[1]], comparison, repeated, groups, samples_info,
  FALSE, TRUE)
single_output # same as a single element of MSstatsGroupComparison output
```

---

MSstatsHandleMissing *Handle censored missing values*

---

**Description**

Handle censored missing values



**Usage**

```
MSstatsHandleMissing(
  input,
  summary_method,
  impute,
  missing_symbol,
  censored_cutoff
)
```

**Arguments**

`input` 'data.table' in MSstats data format

`summary_method` summarization method ('summaryMethod' parameter to 'dataProcess')

`impute` if TRUE, missing values are supposed to be imputed ('MBimpute' parameter to 'dataProcess')

`missing_symbol` 'censoredInt' parameter to 'dataProcess'

`censored_cutoff` 'maxQuantileforCensored' parameter to 'dataProcess'

**Value**

data.table

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEDMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
head(input)
```

---

MSstatsMergeFractions *Re-format the data before feature selection*

---

**Description**

Re-format the data before feature selection

**Usage**

```
MSstatsMergeFractions(input)
```

**Arguments**

`input` 'data.table' in MSstats format

**Value**

data.table

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
head(input)
```

---

MSstatsNormalize	<i>Normalize MS data</i>
------------------	--------------------------

---

**Description**

Normalize MS data

**Usage**

```
MSstatsNormalize(
  input,
  normalization_method,
  peptides_dict = NULL,
  standards = NULL
)
```

**Arguments**

input	data.table in MSstats format
normalization_method	name of a chosen normalization method: "NONE" or "FALSE" for no normalization, "EQUALIZEMEDIANS" for median normalization, "QUANTILE" normalization for quantile normalization from 'preprocessCore' package, "GLOBALSTANDARDS" for normalization based on selected peptides or proteins.
peptides_dict	'data.table' of names of peptides and their corresponding features.
standards	character vector with names of standards, required if "GLOBALSTANDARDS" method was selected.

**Value**

data.table

**Examples**

```

raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS") # median normalization
head(input)

```

---

MSstatsPrepareForDataProcess

*Prepare data for processing by 'dataProcess' function*


---

**Description**

Prepare data for processing by 'dataProcess' function

**Usage**

```
MSstatsPrepareForDataProcess(input, log_base, fix_missing)
```

**Arguments**

input	'data.table' in MSstats format
log_base	base of the logarithm to transform intensities
fix_missing	str, optional. Defaults to NULL, which means no action. If not NULL, must be one of the options: "zero_to_na" or "na_to_zero". If "zero_to_na", Intensity values equal exactly to 0 will be converted to NA. If "na_to_zero", missing values will be replaced by zeros.

**Value**

data.table

**Examples**

```

raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
head(input)

```

---

MSstatsPrepareForGroupComparison

*Prepare output for dataProcess for group comparison*

---

### Description

Prepare output for dataProcess for group comparison

### Usage

```
MSstatsPrepareForGroupComparison(summarization_output)
```

### Arguments

```
summarization_output
      output of dataProcess
```

### Value

list of run-level data for each protein in the input. This list has a "has\_imputed" attribute that indicates if missing values were imputed in the input dataset.

### Examples

```
QuantData <- dataProcess(SRMRawData, use_log_file = FALSE)
group_comparison_input = MSstatsPrepareForGroupComparison(QuantData)
length(group_comparison_input) # list of length equal to number of proteins
# in protein-level data of QuantData
head(group_comparison_input[[1]])
```

---

MSstatsPrepareForSummarization

*Prepare feature-level data for protein-level summarization*

---

### Description

Prepare feature-level data for protein-level summarization

### Usage

```
MSstatsPrepareForSummarization(
  input,
  method,
  impute,
  censored_symbol,
  remove_uninformative_feature_outlier
)
```

**Arguments**

input	feature-level data processed by dataProcess subfunctions
method	summarization method - 'summaryMethod' parameter of the dataProcess function
impute	if TRUE, censored missing values will be imputed - 'MBimpute' parameter of the dataProcess function
censored_symbol	censored missing value indicator - 'censoredInt' parameter of the dataProcess function
remove_uninformative_feature_outlier	if TRUE, features labeled as outlier of uninformative by the MSstatsSelectFeatures function will not be used in summarization

**Value**

data.table

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
head(input)
```

---

MSstatsSelectFeatures *Feature selection before feature-level data summarization*

---

**Description**

Feature selection before feature-level data summarization

**Usage**

```
MSstatsSelectFeatures(input, method, top_n = 3, min_feature_count = 2)
```

**Arguments**

input	data.table
method	"all" / "highQuality", "topN"
top_n	number of features to use for "topN" method
min_feature_count	number of quality features for "highQuality" method

**Value**

data.table

**Examples**

```

raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input_all = MSstatsSelectFeatures(input, "all") # all features
input_5 = MSstatsSelectFeatures(data.table::copy(input), "topN", top_n = 5) # top 5 features
input_informative = MSstatsSelectFeatures(input, "highQuality") # feature selection

head(input_all)
head(input_5)
head(input_informative)

```

---

MSstatsSummarizationOutput

*Post-processing output from MSstats summarization*


---

**Description**

Post-processing output from MSstats summarization

**Usage**

```

MSstatsSummarizationOutput(
  input,
  summarized,
  processed,
  method,
  impute,
  censored_symbol
)

```

**Arguments**

input	‘data.table’ in MSstats format
summarized	output of the ‘MSstatsSummarizeWithSingleCore’ function
processed	output of MSstatsSelectFeatures
method	name of the summarization method (‘summaryMethod’ parameter to ‘dataProcess’)
impute	if TRUE, censored missing values were imputed (‘MBimpute’ parameter to ‘dataProcess’)
censored_symbol	censored missing value indicator (‘censoredInt’ parameter to ‘dataProcess’)

**Value**

list that consists of the following elements:

- FeatureLevelData - feature-level data after processing
- ProteinLevelData - protein-level (summarized) data
- SummaryMethod (string) - name of summarization method that was used

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input = MSstatsSelectFeatures(input, "all")
processed = getProcessed(input)
input = MSstatsPrepareForSummarization(input, method, impute, cens, FALSE)
summarized = MSstatsSummarizeWithSingleCore(input, method, impute, cens, FALSE, TRUE)
output = output = MSstatsSummarizationOutput(input, summarized, processed,
method, impute, cens)
```

---

MSstatsSummarize	<i>Feature-level data summarization</i>
------------------	---

---

**Description**

Feature-level data summarization

**Usage**

```
MSstatsSummarize(
  proteins_list,
  method,
  impute,
  censored_symbol,
  remove50missing,
  equal_variance
)
```

**Arguments**

proteins_list	list of processed feature-level data
method	summarization method: "linear" or "TMP"
impute	only for summaryMethod = "TMP" and censoredInt = 'NA' or '0'. TRUE (default) imputes 'NA' or '0' (depending on censoredInt option) by Accelerated failure model. FALSE uses the values assigned by cutoffCensored

censored_symbol	Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.
remove50missing	only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.
equal_variance	only for summaryMethod = "linear". Default is TRUE. Logical variable for whether the model should account for heterogeneous variation among intensities from different features. Default is TRUE, which assume equal variance among intensities from features. FALSE means that we cannot assume equal variance among intensities from features, then we will account for heterogeneous variation from different features.

**Value**

list of length one with run-level data.

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input = MSstatsSelectFeatures(input, "all")
processed = getProcessed(input)
input = MSstatsPrepareForSummarization(input, method, impute, cens, FALSE)
input_split = split(input, input$PROTEIN)
summarized = MSstatsSummarize(input_split, method, impute, cens, FALSE, TRUE)
length(summarized) # list of summarization outputs for each protein
head(summarized[[1]][[1]]) # run-level summary
```

---

MSstatsSummarizeSingleLinear

*Linear model-based summarization for a single protein*

---

**Description**

Linear model-based summarization for a single protein

**Usage**

```
MSstatsSummarizeSingleLinear(single_protein, equal_variances = TRUE)
```



**Arguments**

`single_protein` feature-level data for a single protein  
`equal_variances`  
 if TRUE, observation are assumed to be homoskedastic

**Value**

list with protein-level data

**Examples**

```
raw = DDARawData
method = "linear"
cens = NULL
impute = FALSE
# currently, MSstats only supports MBimpute = FALSE for linear summarization
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input = MSstatsSelectFeatures(input, "all")
input = MSstatsPrepareForSummarization(input, method, impute, cens, FALSE)
input_split = split(input, input$PROTEIN)
single_protein_summary = MSstatsSummarizeSingleLinear(input_split[[1]])
head(single_protein_summary[[1]])
```

---

MSstatsSummarizeSingleTMP

*Tukey Median Polish summarization for a single protein*

---

**Description**

Tukey Median Polish summarization for a single protein

**Usage**

```
MSstatsSummarizeSingleTMP(
  single_protein,
  impute,
  censored_symbol,
  remove50missing
)
```

**Arguments**

`single_protein` feature-level data for a single protein  
`impute` only for summaryMethod = "TMP" and censoredInt = 'NA' or '0'. TRUE (default) imputes 'NA' or '0' (depending on censoredInt option) by Accelerated failure model. FALSE uses the values assigned by cutoffCensored

censored\_symbol

Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.

remove50missing

only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.

### Value

list of two data.tables: one with fitted survival model, the other with protein-level data

### Examples

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
# currently, MSstats only supports MBimpute = FALSE for linear summarization
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input = MSstatsSelectFeatures(input, "all")
input = MSstatsPrepareForSummarization(input, method, impute, cens, FALSE)
input_split = split(input, input$PROTEIN)
single_protein_summary = MSstatsSummarizeSingleTMP(input_split[[1]],
                                                    impute, cens, FALSE)

head(single_protein_summary[[1]])
```

---

MSstatsSummarizeWithMultipleCores

*Feature-level data summarization with multiple cores*

---

### Description

Feature-level data summarization with multiple cores

### Usage

```
MSstatsSummarizeWithMultipleCores(
  input,
  method,
  impute,
  censored_symbol,
  remove50missing,
  equal_variance,
  numberOfCores = 1
)
```

**Arguments**

input	feature-level data processed by dataProcess subfunctions
method	summarization method: "linear" or "TMP"
impute	only for summaryMethod = "TMP" and censoredInt = 'NA' or '0'. TRUE (default) imputes 'NA' or '0' (depending on censoredInt option) by Accelerated failure model. FALSE uses the values assigned by cutoffCensored
censored_symbol	Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.
remove50missing	only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.
equal_variance	only for summaryMethod = "linear". Default is TRUE. Logical variable for whether the model should account for heterogeneous variation among intensities from different features. Default is TRUE, which assume equal variance among intensities from features. FALSE means that we cannot assume equal variance among intensities from features, then we will account for heterogeneous variation from different features.
numberOfCores	Number of cores for parallel processing. When > 1, a logfile named 'MSstats_dataProcess_log_progress' is created to track progress. Only works for Linux & Mac OS. Default is 1.

**Value**

list of length one with run-level data.

---

MSstatsSummarizeWithSingleCore

*Feature-level data summarization with 1 core*

---

**Description**

Feature-level data summarization with 1 core

**Usage**

```
MSstatsSummarizeWithSingleCore(
  input,
  method,
  impute,
  censored_symbol,
  remove50missing,
  equal_variance
)
```

**Arguments**

input	feature-level data processed by dataProcess subfunctions
method	summarization method: "linear" or "TMP"
impute	only for summaryMethod = "TMP" and censoredInt = 'NA' or '0'. TRUE (default) imputes 'NA' or '0' (depending on censoredInt option) by Accelerated failure model. FALSE uses the values assigned by cutoffCensored
censored_symbol	Missing values are censored or at random. 'NA' (default) assumes that all 'NA's in 'Intensity' column are censored. '0' uses zero intensities as censored intensity. In this case, NA intensities are missing at random. The output from Skyline should use '0'. Null assumes that all NA intensities are randomly missing.
remove50missing	only for summaryMethod = "TMP". TRUE removes the proteins where every run has at least 50% missing values for each peptide. FALSE is default.
equal_variance	only for summaryMethod = "linear". Default is TRUE. Logical variable for whether the model should account for heterogeneous variation among intensities from different features. Default is TRUE, which assume equal variance among intensities from features. FALSE means that we cannot assume equal variance among intensities from features, then we will account for heterogeneous variation from different features.

**Value**

list of length one with run-level data.

**Examples**

```
raw = DDARawData
method = "TMP"
cens = "NA"
impute = TRUE
MSstatsConvert::MSstatsLogsSettings(FALSE)
input = MSstatsPrepareForDataProcess(raw, 2, NULL)
input = MSstatsNormalize(input, "EQUALIZEMEDIANS")
input = MSstatsMergeFractions(input)
input = MSstatsHandleMissing(input, "TMP", TRUE, "NA", 0.999)
input = MSstatsSelectFeatures(input, "all")
processed = getProcessed(input)
input = MSstatsPrepareForSummarization(input, method, impute, cens, FALSE)
summarized = MSstatsSummarizeWithSingleCore(input, method, impute, cens, FALSE, TRUE)
length(summarized) # list of summarization outputs for each protein
head(summarized[[1]][[1]]) # run-level summary
```

---

OpenMStoMSstatsFormat *Import OpenMS files*

---

**Description**

Import OpenMS files

**Usage**

```

OpenMStoMSstatsFormat(
  input,
  annotation = NULL,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeProtein_with1Feature = FALSE,
  summaryforMultipleRows = max,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)

```

**Arguments**

<code>input</code>	name of MSstats input report from OpenMS, which includes feature(peptide ion)-level data.
<code>annotation</code>	name of 'annotation.txt' data which includes Condition, BioReplicate, Run. Run should be the same as filename.
<code>useUniquePeptide</code>	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
<code>removeFewMeasurements</code>	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
<code>removeProtein_with1Feature</code>	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
<code>summaryforMultipleRows</code>	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
<code>use_log_file</code>	logical. If TRUE, information about data processing will be saved to a file.
<code>append</code>	logical. If TRUE, information about data processing will be added to an existing log file.
<code>verbose</code>	logical. If TRUE, information about data processing will be printed to the console.
<code>log_file_path</code>	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
<code>...</code>	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Meena Choi, Olga Vitek.

**Examples**

```
openms_raw = data.table::fread(system.file("tinytest/raw_data/OpenMS/openms_input.csv",
                                           package = "MSstatsConvert"))
openms_imported = OpenMSstoMSstatsFormat(openms_raw, use_log_file = FALSE)
head(openms_imported)
```

---

OpenSWATHtoMSstatsFormat

*Import OpenSWATH files*


---

**Description**

Import OpenSWATH files

**Usage**

```
OpenSWATHtoMSstatsFormat(
  input,
  annotation,
  filter_with_mscore = TRUE,
  mscore_cutoff = 0.01,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeProtein_with1Feature = FALSE,
  summaryforMultipleRows = max,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

**Arguments**

input	name of MSstats input report from OpenSWATH, which includes feature-level data.
annotation	name of 'annotation.txt' data which includes Condition, BioReplicate, Run. Run should be the same as filename.
filter_with_mscore	TRUE(default) will filter out the features that have greater than mscore_cutoff in m_score column. Those features will be removed.
mscore_cutoff	Cutoff for m_score. Default is 0.01.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.

<code>removeProtein_with1Feature</code>	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
<code>summaryforMultipleRows</code>	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
<code>use_log_file</code>	logical. If TRUE, information about data processing will be saved to a file.
<code>append</code>	logical. If TRUE, information about data processing will be added to an existing log file.
<code>verbose</code>	logical. If TRUE, information about data processing will be printed to the console.
<code>log_file_path</code>	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
<code>...</code>	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Meena Choi, Olga Vitek.

**Examples**

```
os_raw = system.file("tinytest/raw_data/OpenSWATH/openswath_input.csv",
  package = "MSstatsConvert")
annot = system.file("tinytest/annotations/annot_os.csv",
  package = "MSstats")
os_raw = data.table::fread(os_raw)
annot = data.table::fread(annot)

os_imported = OpenSWATHtoMSstatsFormat(os_raw, annot, use_log_file = FALSE)
head(os_imported)
```

---

PDtoMSstatsFormat

*Import Proteome Discoverer files*

---

**Description**

Import Proteome Discoverer files

**Usage**

```
PDtoMSstatsFormat(
  input,
  annotation,
  useNumProteinsColumn = FALSE,
  useUniquePeptide = TRUE,
```

```

summaryforMultipleRows = max,
removeFewMeasurements = TRUE,
removeOxidationMpeptides = FALSE,
removeProtein_with1Peptide = FALSE,
which.quantification = "Precursor.Area",
which.proteinid = "Protein.Group.Accessions",
which.sequence = "Sequence",
use_log_file = TRUE,
append = FALSE,
verbose = TRUE,
log_file_path = NULL,
...
)

```

### Arguments

input	PD report or a path to it.
annotation	name of 'annotation.txt' or 'annotation.csv' data which includes Condition, BioReplicate, Run information. 'Run' will be matched with 'Spectrum.File'.
useNumProteinsColumn	TRUE removes peptides which have more than 1 in # Proteins column of PD output.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
summaryforMultipleRows	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
removeOxidationMpeptides	TRUE will remove the peptides including 'oxidation (M)' in modification. FALSE is default.
removeProtein_with1Peptide	TRUE will remove the proteins which have only 1 peptide and charge. FALSE is default.
which.quantification	Use 'Precursor.Area'(default) column for quantified intensities. 'Intensity' or 'Area' can be used instead.
which.proteinid	Use 'Protein.Accessions'(default) column for protein name. 'Master.Protein.Accessions' can be used instead.
which.sequence	Use 'Sequence'(default) column for peptide sequence. 'Annotated.Sequence' can be used instead.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.



`log_file_path` character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If `'append = TRUE'`, has to be a valid path to a file.

... additional parameters to `'data.table::fread'`.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Meena Choi, Olga Vitek

**Examples**

```
pd_raw = system.file("tinytest/raw_data/PD/pd_input.csv",
  package = "MSstatsConvert")
annot = system.file("tinytest/annotations/annot_pd.csv", package = "MSstats")
pd_raw = data.table::fread(pd_raw)
annot = data.table::fread(annot)

pd_imported = PDtoMSstatsFormat(pd_raw, annot, use_log_file = FALSE)
head(pd_imported)
```

---

ProgenesitoMSstatsFormat

*Import Progenesis files*

---

**Description**

Import Progenesis files

**Usage**

```
ProgenesitoMSstatsFormat(
  input,
  annotation,
  useUniquePeptide = TRUE,
  summaryforMultipleRows = max,
  removeFewMeasurements = TRUE,
  removeOxidationMpeptides = FALSE,
  removeProtein_with1Peptide = FALSE,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

**Arguments**

input	name of Progenesis output, which is wide-format. 'Accession', 'Sequence', 'Modification', 'Charge' and one column for each run are required.
annotation	name of 'annotation.txt' or 'annotation.csv' data which includes Condition, BioReplicate, Run information. It will be matched with the column name of input for MS runs.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
summaryforMultipleRows	max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
removeOxidationMpeptides	TRUE will remove the peptides including 'oxidation (M)' in modification. FALSE is default.
removeProtein_with1Peptide	TRUE will remove the proteins which have only 1 peptide and charge. FALSE is default.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
...	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Meena Choi, Olga Vitek, Ulrich Omasits

**Examples**

```
progenesis_raw = system.file("tinytest/raw_data/Progenesis/progenesis_input.csv",
                             package = "MSstatsConvert")
annot = system.file("tinytest/raw_data/Progenesis/progenesis_annot.csv",
                    package = "MSstatsConvert")
progenesis_raw = data.table::fread(progenesis_raw)
annot = data.table::fread(annot)

progenesis_imported = ProgenesistoMSstatsFormat(progenesis_raw, annot,
                                                  use_log_file = FALSE)
head(progenesis_imported)
```

---

quantification	<i>Protein sample quantification or group quantification</i>
----------------	--

---

### Description

Model-based quantification for each condition or for each biological sample per protein in a targeted Selected Reaction Monitoring (SRM), Data-Dependent Acquisition (DDA or shotgun), and Data-Independent Acquisition (DIA or SWATH-MS) experiment. Quantification takes the processed data set by [dataProcess](#) as input and automatically generate the quantification results (data.frame) in a long or matrix format.

### Usage

```
quantification(
  data,
  type = "Sample",
  format = "matrix",
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL
)
```

### Arguments

data	name of the (processed) data set.
type	choice of quantification. "Sample" or "Group" for protein sample quantification or group quantification.
format	choice of returned format. "long" for long format which has the columns named Protein, Condition, LogIntensities (and BioReplicate if it is subject quantification), NumFeature for number of transitions for a protein, and NumPeaks for number of observed peak intensities for a protein. "matrix" for data matrix format which has the rows for Protein and the columns, which are Groups(or Conditions) for group quantification or the combinations of BioReplicate and Condition (labeled by "BioReplicate_" "Condition") for sample quantification. Default is "matrix"
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.

### Details

- **Sample quantification** : individual biological sample quantification for each protein. The label of each biological sample is a combination of the corresponding group and the sample ID. If

there are no technical replicates or experimental replicates per sample, sample quantification is the same as run summarization from dataProcess. If there are technical replicates or experimental replicates, sample quantification is median among run quantification corresponding MS runs.

- Group quantification : quantification for individual group or individual condition per protein. It is median among sample quantification.
- The quantification for endogenous samples is based on run summarization from subplot model, with TMP robust estimation.

### Value

data.frame as described in details.

### Examples

```
# Consider quantitative data (i.e. QuantData) from a yeast study with ten time points of
# interests, three biological replicates, and no technical replicates which is
# a time-course experiment.
# Sample quantification shows model-based estimation of protein abundance in each biological
# replicate within each time point.
# Group quantification shows model-based estimation of protein abundance in each time point.
QuantData<-dataProcess(SRMRawData, use_log_file = FALSE)
head(QuantData$FeatureLevelData)
# Sample quantification
sampleQuant<-quantification(QuantData, use_log_file = FALSE)
head(sampleQuant)
# Group quantification
groupQuant<-quantification(QuantData, type="Group", use_log_file = FALSE)
head(groupQuant)
```

---

savePlot

*Save a plot to pdf file*

---

### Description

Save a plot to pdf file

### Usage

```
savePlot(name_base, file_name, width, height)
```

### Arguments

name_base	path to a folder (or "" for working directory)
file_name	name of a file to save. If this file already exists, an integer will be appended to this name
width	width of a plot
height	height of a plot

---

SDRFtoAnnotation	<i>Convert SDRF experimental design file into an MSstats annotation file</i>
------------------	--

---

## Description

Takes an SDRF file and outputs an MSstats annotation file. Note the information in the SDRF file must be correctly annotated for MSstats so that MSstats can identify the experimental design. In particular the biological replicates must be correctly annotated, with group comparison experiments having a unique ID for each BioReplicate. For more information on this please see the Supplementary of the most recent [MSstats paper](#)

## Usage

```
SDRFtoAnnotation(  
  data,  
  run_name = "comment[data file]",  
  condition_name = "characteristics[disease]",  
  biological_replicate = "characteristics[biological replicate]",  
  fraction = NULL  
)
```

## Arguments

data	SDRF annotation file
run_name	Column name in SDRF file which contains the name of the MS run. The information in this column must match exactly with the run names in the PSM file
condition_name	Column name in SDRF file which contains information on the conditions in the data.
biological_replicate	Column name in SDRF file which contains the identifier for the biological replicate. Note MSstats uses this column to determine if the experiment is a repeated measure design. BioReplicate IDs should only be reused if the replicate was measured multiple times.
fraction	Column name in SDFT file which contains information on the fractionation in the data. Only required if data contains fractions. Default is 'NULL'

## Examples

```
head(example_SDRF)  
  
msstats_annotation = SDRFtoAnnotation(example_SDRF)  
  
head(msstats_annotation)
```

---

 SkylinetoMSstatsFormat

*Import Skyline files*


---

## Description

Import Skyline files

## Usage

```
SkylinetoMSstatsFormat(
  input,
  annotation = NULL,
  removeiRT = TRUE,
  filter_with_Qvalue = TRUE,
  qvalue_cutoff = 0.01,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeOxidationMpeptides = FALSE,
  removeProtein_with1Feature = FALSE,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

## Arguments

input	name of MSstats input report from Skyline, which includes feature-level data.
annotation	name of 'annotation.txt' data which includes Condition, BioReplicate, Run. If annotation is already complete in Skyline, use annotation=NULL (default). It will use the annotation information from input.
removeiRT	TRUE (default) will remove the proteins or peptides which are labeled 'iRT' in 'StandardType' column. FALSE will keep them.
filter_with_Qvalue	TRUE(default) will filter out the intensities that have greater than qvalue_cutoff in DetectionQValue column. Those intensities will be replaced with zero and will be considered as censored missing values for imputation purpose.
qvalue_cutoff	Cutoff for DetectionQValue. default is 0.01.
useUniquePeptide	TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
removeFewMeasurements	TRUE (default) will remove the features that have 1 or 2 measurements across runs.
removeOxidationMpeptides	TRUE will remove the peptides including 'oxidation (M)' in modification. FALSE is default.

removeProtein_with1Feature	TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.
use_log_file	logical. If TRUE, information about data processing will be saved to a file.
append	logical. If TRUE, information about data processing will be added to an existing log file.
verbose	logical. If TRUE, information about data processing will be printed to the console.
log_file_path	character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.
...	additional parameters to 'data.table::fread'.

**Value**

data.frame in the MSstats required format.

**Author(s)**

Meena Choi, Olga Vitek

**Examples**

```
skyline_raw = system.file("tinytest/raw_data/Skyline/skyline_input.csv",
                          package = "MSstatsConvert")
skyline_raw = data.table::fread(skyline_raw)
skyline_imported = SkylinetoMSstatsFormat(skyline_raw)
head(skyline_imported)
```

---

SpectronauttoMSstatsFormat

*Import Spectronaut files*

---

**Description**

Import Spectronaut files

**Usage**

```
SpectronauttoMSstatsFormat(
  input,
  annotation = NULL,
  intensity = "PeakArea",
  filter_with_Qvalue = TRUE,
  qvalue_cutoff = 0.01,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeProtein_with1Feature = FALSE,
  summaryforMultipleRows = max,
  use_log_file = TRUE,
```

```

append = FALSE,
verbose = TRUE,
log_file_path = NULL,
...
)

```

### Arguments

**input** name of Spectronaut output, which is long-format. ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity, F.ExcludedFromQuantification are required. Rows with F.ExcludedFromQuantification=True will be removed.

**annotation** name of 'annotation.txt' data which includes Condition, BioReplicate, Run. If annotation is already complete in Spectronaut, use annotation=NULL (default). It will use the annotation information from input.

**intensity** 'PeakArea'(default) uses not normalized peak area. 'NormalizedPeakArea' uses peak area normalized by Spectronaut.

**filter\_with\_Qvalue** TRUE(default) will filter out the intensities that have greater than qvalue\_cutoff in EG.Qvalue column. Those intensities will be replaced with zero and will be considered as censored missing values for imputation purpose.

**qvalue\_cutoff** Cutoff for EG.Qvalue. default is 0.01.

**useUniquePeptide** TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.

**removeFewMeasurements** TRUE (default) will remove the features that have 1 or 2 measurements across runs.

**removeProtein\_with1Feature** TRUE will remove the proteins which have only 1 feature, which is the combination of peptide, precursor charge, fragment and charge. FALSE is default.

**summaryforMultipleRows** max(default) or sum - when there are multiple measurements for certain feature and certain run, use highest or sum of multiple intensities.

**use\_log\_file** logical. If TRUE, information about data processing will be saved to a file.

**append** logical. If TRUE, information about data processing will be added to an existing log file.

**verbose** logical. If TRUE, information about data processing will be printed to the console.

**log\_file\_path** character. Path to a file to which information about data processing will be saved. If not provided, such a file will be created automatically. If 'append = TRUE', has to be a valid path to a file.

**...** additional parameters to 'data.table::fread'.

### Value

data.frame in the MSstats required format.

### Author(s)

Meena Choi, Olga Vitek



**Examples**

```
spectronaut_raw = system.file("tinytest/raw_data/Spectronaut/spectronaut_input.csv",
                             package = "MSstatsConvert")
spectronaut_raw = data.table::fread(spectronaut_raw)
spectronaut_imported = SpectronauttoMSstatsFormat(spectronaut_raw, use_log_file = FALSE)
head(spectronaut_imported)
```

SRMRawData

*Example dataset from a SRM experiment with stable isotope labeled reference of a time course yeast study*

**Description**

This is a partial data set obtained from a published study (Picotti, et. al, 2009). The experiment targeted 45 proteins in the glycolysis/gluconeogenesis/TCA cycle/glyoxylate cycle network, which spans the range of protein abundance from less than 128 to 10E6 copies per cell. Three biological replicates were analyzed at ten time points (T1-T10), while yeasts transited through exponential growth in a glucose-rich medium (T1-T4), diauxic shift (T5-T6), post-diauxic phase (T7-T9), and stationary phase (T10). Prior to trypsinization, the samples were mixed with an equal amount of proteins from the same N15-labeled yeast sample, which was used as a reference. Each sample was profiled in a single mass spectrometry run, where each protein was represented by up to two peptides and each peptide by up to three transitions. The goal of this study is to detect significantly change in protein abundance across time points. Transcriptional activity under the same experimental conditions has been previously investigated by (DeRisi et. al., 1997). Genes coding for 29 of the proteins are differentially expressed between conditions similar to those represented by T7 and T1 and could be treated as external sources to validate the proteomics analysis. In this example data set, two of the targeted proteins are selected and validated with gene expression study: Protein IDHC (gene name IDP2) is differentially expressed in time point 1 and time point 7, whereas, Protein PMG2 (gene name GPM2) is not. The protein names are based on Swiss Prot Name.

**Usage**

```
SRMRawData
```

**Format**

```
data.frame
```

**Details**

The raw data (input data for MSstats) is required to contain variable of ProteinName, PeptideSequence, PrecursorCharge, FragmentIon, ProductCharge, IsotopeLabelType, Condition, BioReplicate, Run, Intensity. The variable names should be fixed.

If the information of one or more columns is not available for the original raw data, please retain the column variables and type in fixed value. For example, the original raw data does not contain the information of ProductCharge, we retain the column ProductCharge and type in NA for all transitions in RawData.

The column BioReplicate should label with unique patient ID (i.e., same patients should label with the same ID).

Variable Intensity is required to be original signal without any log transformation and can be specified as the peak of height or the peak of area under curve.

**Value**

data.frame with the required format of MSstats.

**Author(s)**

Meena Choi, Olga Vitek.

Maintainer: Meena Choi (<mnchoi67@gmail.com>)

**References**

Ching-Yun Chang, Paola Picotti, Ruth Huttenhain, Viola Heinzlmann-Schwarz, Marko Jovanovic, Ruedi Aebersold, Olga Vitek. Protein significance analysis in selected reaction monitoring (SRM) measurements. *Molecular & Cellular Proteomics*, 11:M111.014662, 2012.

**Examples**

```
head(SRMRawData)
```

---

theme\_msstats

*Theme for MSstats plots*

---

**Description**

Theme for MSstats plots

**Usage**

```
theme_msstats(
  type,
  x.axis.size = 10,
  y.axis.size = 10,
  legend_size = 13,
  strip_background = element_rect(fill = "gray95"),
  strip_text_x = element_text(colour = c("black"), size = 14),
  legend_position = "top",
  legend_box = "vertical",
  text_angle = 0,
  text_hjust = NULL,
  text_vjust = NULL,
  ...
)
```

**Arguments**

type	type of a plot
x.axis.size	size of text on the x axis
y.axis.size	size of text on the y axis
legend_size	size of the legend
strip_background	background of facet

strip_text_x	size of text on facets
legend_position	position of the legend
legend_box	legend.box
text_angle	angle of text on the x axis (for condition and comparison plots)
text_hjust	hjust parameter for x axis text (for condition and comparison plots)
text_vjust	vjust parameter for x axis text (for condition and comparison plots)
...	additional parameters passed on to ggplot2::theme()

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validateAnnotation	<i>Check if annotation matches intended experimental design</i>
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### Description

Check if annotation matches intended experimental design

### Usage

```
validateAnnotation(msstats_table, design_type = "group comparison")
```

### Arguments

msstats_table	output of a converter function
design_type	character, "group comparison" or "repeated measures"

### Value

TRUE if annotation file is consistent with intended experimental design. Otherwise, an error is thrown

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