

# Package ‘MSstatsTMT’

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**Title** Protein Significance Analysis in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling

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**Description** The package provides statistical tools for detecting differentially abundant proteins in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling. It provides multiple functionalities, including aata visualization, protein quantification and normalization, and statistical modeling and inference. Furthermore, it is inter-operable with other data processing tools, such as Proteome Discoverer, MaxQuant, OpenMS and SpectroMine.

**License** Artistic-2.0

**Depends** R (>= 4.2)

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**Author** Devon Kohler [aut, cre],  
Ting Huang [aut],  
Meena Choi [aut],  
Mateusz Staniak [aut],

Tony Wu [aut],  
 Deril Raju [aut],  
 Sicheng Hao [aut],  
 Olga Vitek [aut]

**Maintainer** Devon Kohler <kohler.d@northeastern.edu>

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---

<code>.calculatePower</code>	<i>Power calculation</i>
------------------------------	--------------------------

---

## Description

Power calculation

## Usage

```
.calculatePower(
  desiredFC,
  FDR,
  delta,
  median_sigma_error,
  median_sigma_subject,
  median_sigma_run,
  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

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.
-----------	---

---

.checkContrastMatrix	<i>check whether pairwise comparison. If pairwise, generate a contrast matrix.</i>
----------------------	--

---

### Description

check whether pairwise comparison. If pairwise, generate a contrast matrix.

### Usage

```
.checkContrastMatrix(contrast_matrix)
```

### Value

a contrast matrix

---

.checkSummarizationParams	<i>Check validity of parameters to proteinSummarization function</i>
---------------------------	--

---

### Description

Check validity of parameters to proteinSummarization function

### Usage

```
.checkSummarizationParams(
  data,
  method,
  global_norm,
  reference_norm,
  remove_norm_channel,
  remove_empty_channel,
  MBimpute,
  maxQuantileforCensored
)
```

### Arguments

data	Name of the output of PDtoMSstatsTMTFormat function or peptide-level quantified data from other tools. It should have columns ProteinName, PeptideSequence, Charge, PSM, Mixture, TechRepMixture, Run, Channel, Condition, BioReplicate, Intensity
method	Four different summarization methods to protein-level can be performed : "msstats"(default), "MedianPolish", "Median", "LogSum".

global_norm	Global median normalization on peptide level data (equalizing the medians across all the channels and MS runs). Default is TRUE. It will be performed before protein-level summarization.
reference_norm	Reference channel based normalization between MS runs on protein level data. TRUE(default) needs at least one reference channel in each MS run, annotated by 'Norm' in Condition column. It will be performed after protein-level summarization. FALSE will not perform this normalization step. If data only has one run, then reference_norm=FALSE.
remove_norm_channel	TRUE(default) removes 'Norm' channels from protein level data.
remove_empty_channel	TRUE(default) removes 'Empty' channels from protein level data.
MBimpute	only for method="msstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.
maxQuantileforCensored	We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.

**Value**

TRUE invisibly if all parameters are valid

---

.countRunsWithNorm      *Utility function: count runs with "Norm" channel*

---

**Description**

Utility function: count runs with "Norm" channel

**Usage**

```
.countRunsWithNorm(run, condition)
```

**Arguments**

run	vector of run labels
condition	vector of condition labels

**Value**

integer

---

.documentFunction      *A dummy function to store shared documentation items.*

---

## Description

A dummy function to store shared documentation items.

## Usage

```
.documentFunction(
    fewMeasurements,
    useUniquePeptide,
    summaryforMultipleRows,
    removeProtein_with1Feature,
    removeProtein_with1Protein,
    removeOxidationMpeptides,
    removeMpeptides
)
```

## Arguments

**fewMeasurements**      'remove'(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.

**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.

**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.

**Value**

NULL.

---

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

---

**Description**

Get median per subject or group by subject

**Usage**

`.getMedianSigmaRun(var_component)`

**Arguments**

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

---

`.getMedianSigmaSubject`  
*Get median per run or run by mix*

---

**Description**

Get median per run or run by mix

**Usage**

`.getMedianSigmaSubject(var_component)`

**Arguments**

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

---

`.getNormalizationAbundance`

*Utility function: get mean abundance for "Norm" channels*

---

### Description

Utility function: get mean abundance for "Norm" channels

### Usage

```
.getNormalizationAbundance(abundance, condition)
```

### Arguments

<code>abundance</code>	vector of abundances
<code>condition</code>	vector of condition labels

### Value

numeric

---

`.getNumSample`

*Get sample size*

---

### Description

Get sample size

### Usage

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

### Arguments

<code>desiredFC</code>	the range of a desired fold change which includes the lower and upper values of the desired fold change.
<code>power</code>	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
<code>alpha</code>	significance level

`delta`                    difference between means (?)  
`median_sigma_error`                    median of error standard deviation  
`median_sigma_subject`                    median standard deviation per subject

---

`.getPhilosopherInput`    *Convert Philosopher parameters to consistent format*

---

### **Description**

Convert Philosopher parameters to consistent format

### **Usage**

`.getPhilosopherInput(input, path, folder)`

### **Arguments**

`input`                    data.frame of 'msstats.csv' file produced by Philosopher

---

`.getRunsMedian`                    *Utility function: get median from unique values per run*

---

### **Description**

Utility function: get median from unique values per run

### **Usage**

`.getRunsMedian(input)`

### **Arguments**

`input`                    data.table / list

### **Value**

numeric

---

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

---

**Description**

Get variances from models fitted by the groupComparison function

**Usage**

```
.getVarComponentTMT(fitted_models)
```

**Arguments**

`fitted_models`    FittedModels element of groupComparison output

---

`.handleSingleContrastTMT`  
*perform statistical inference for single protein and single contrast*

---

**Description**

perform statistical inference for single protein and single contrast

**Usage**

```
.handleSingleContrastTMT(  
  contrast,  
  fit,  
  single_protein,  
  coefs,  
  protein,  
  groups,  
  s2_posterior,  
  rho,  
  vss,  
  df_prior,  
  s2_df  
)
```

---

.logSum                      *Utility function: compute log of sum of 2^x*

---

**Description**

Utility function: compute log of sum of 2^x

**Usage**

```
.logSum(x)
```

**Arguments**

x                      numeric

**Value**

numeric

---

.logSummarizationParams  
*Log parameters for proteinSummarization function*

---

**Description**

Log parameters for proteinSummarization function

**Usage**

```
.logSummarizationParams(  
  method,  
  global_norm,  
  reference_norm,  
  remove_norm_channel,  
  remove_empty_channel  
)
```

**Arguments**

method	Four different summarization methods to protein-level can be performed : "msstats"(default), "MedianPolish", "Median", "LogSum".
global_norm	Global median normalization on peptide level data (equalizing the medians across all the channels and MS runs). Default is TRUE. It will be performed before protein-level summarization.
reference_norm	Reference channel based normalization between MS runs on protein level data. TRUE(default) needs at least one reference channel in each MS run, annotated by 'Norm' in Condition column. It will be performed after protein-level summarization. FALSE will not perform this normalization step. If data only has one run, then reference_norm=FALSE.

`remove_norm_channel`

TRUE(default) removes 'Norm' channels from protein level data.

`remove_empty_channel`

TRUE(default) removes 'Empty' channels from protein level data.

### **Value**

TRUE invisibly after logging successfully

---

`.makeContrastSingleTMT`

*Make a contrast*

---

### **Description**

Make a contrast

### **Usage**

`.makeContrastSingleTMT(fit, contrast, single_protein, coefs)`

### **Value**

a contrast vector

---

`.makeFactorColumnsTMT` *Converts required columns to factor in summarization output*

---

### **Description**

Converts required columns to factor in summarization output

### **Usage**

`.makeFactorColumnsTMT(input)`

### **Arguments**

`input`            `data.table`

### **Value**

a data table with factored columns

---

.medianPolish      *Tukey median polish*

---

**Description**

Tukey median polish

**Usage**

```
.medianPolish(intensities, num_channels)
```

**Arguments**

intensities      vector of log-intensities per protein and run  
num\_channels    number of channels

**Value**

numeric vector with length 'num\_channels'

---

.normalizePeptides      *Normalization between channels (before summarization)*

---

**Description**

Normalization between channels (before summarization)

**Usage**

```
.normalizePeptides(input, normalize)
```

**Arguments**

input              data.table  
normalize          logical, if TRUE, 'input' data will be normalized

**Value**

data.table

---

<code>.normalizeProteins</code>	<i>Normalization between MS runs (after protein summarization)</i>
---------------------------------	--

---

**Description**

Normalization between MS runs (after protein summarization)

**Usage**

```
.normalizeProteins(input, normalize)
```

**Arguments**

<code>input</code>	<code>data.table</code>
<code>normalize</code>	logical, if TRUE, data will be normalized

**Value**

`data.table`

---

<code>.prepareForSummarization</code>	<i>Prepare TMT data for protein-level summarization</i>
---------------------------------------	---

---

**Description**

Prepare TMT data for protein-level summarization

**Usage**

```
.prepareForSummarization(input)
```

**Arguments**

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

**Value**

`data.table` with required column types

---

.removeRedundantChannels  
*Remove empty and normalization channels*

---

### Description

Remove empty and normalization channels

### Usage

```
.removeRedundantChannels(input, remove_empty_channel, remove_norm_channel)
```

### Arguments

input	data.table processed by the protein summarization function
remove_empty_channel	TRUE(default) removes 'Empty' channels from protein level data.
remove_norm_channel	TRUE(default) removes 'Norm' channels from protein level data.

### Value

data.table

---

.summarizeMSstats      *Summarization based on MSstats*

---

### Description

Summarization based on MSstats

### Usage

```
.summarizeMSstats(  
  input,  
  annotation,  
  impute,  
  max_quantile_censored = NULL,  
  log_file_path = NULL  
)
```

### Arguments

input	data.table
annotation	data.table with run and channel annotation
impute	only for method="msstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.

max\_quantile\_censored

We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.

log\_file\_path path to a MSstats log file

### Value

data.table

---

.summarizeSimpleStat *Summarize TMT data with a simple aggregate of log-intensities*

---

### Description

Summarize TMT data with a simple aggregate of log-intensities

### Usage

```
.summarizeSimpleStat(input, annotation, stat_aggregate)
```

### Arguments

input data.table

annotation data.table with run and channel annotation

stat\_aggregate function that will be used to compute protein-level summary

### Value

data.table

---

.summarizeTMP *Summarize TMT data with median polish*

---

### Description

Summarize TMT data with median polish

### Usage

```
.summarizeTMP(input, annotation)
```

### Arguments

input data.table

annotation data.table with run and channel annotation

### Value

data.table with summarized protein intensities

---

.summarizeTMT                      *Performs summarization for TMT data*

---

**Description**

Performs summarization for TMT data

**Usage**

```
.summarizeTMT(  
  input,  
  method,  
  annotation,  
  impute,  
  max_quantile_censored,  
  log_file_path  
)
```

**Arguments**

input	data.table
method	"mstats"/"MedianPolish"/"LogSum"/"Median"
annotation	data.table with run and channel annotation
impute	only for method="mstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.
max_quantile_censored	We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.
log_file_path	path to a MSstats log file

**Value**

data.table

---

annotation.mine                      *Example of annotation file for raw.mine, which is the output of SpectroMine.*

---

**Description**

Annotation of example data, raw.mine, in this package. It should be prepared by users. The variables are as follows:

**Usage**

annotation.mine

**Format**

A data frame with 72 rows and 7 variables.

**Details**

- Run : MS run ID. It should be the same as R.FileName info in raw.mine
- Channel : Labeling information (TMT6\_126, ..., TMT6\_131). The channels should be consistent with the channel columns in raw.mine.
- Condition : Condition (ex. Healthy, Cancer, Time0). If the channel doesn't have sample, please add 'Empty' under Condition.
- Mixture : Mixture of samples labeled with different TMT reagents, which can be analyzed in a single mass spectrometry experiment.
- TechRepMixture : Technical replicate of one mixture. One mixture may have multiple technical replicates. For example, if 'TechRepMixture' = 1, 2 are the two technical replicates of one mixture, then they should match with same 'Mixture' value.
- Fraction : Fraction ID. One technical replicate of one mixture may be fractionated into multiple fractions to increase the analytical depth. Then one technical replicate of one mixture should correspond to multiple fractions. For example, if 'Fraction' = 1, 2, 3 are three fractions of the first technical replicate of one TMT mixture of biological subjects, then they should have same 'TechRepMixture' and 'Mixture' value.
- BioReplicate : Unique ID for biological subject. If the channel doesn't have sample, please add 'Empty' under BioReplicate

**Examples**

```
head(annotation.mine)
```

---

annotation.mq	<i>Example of annotation file for evidence, which is the output of MaxQuant.</i>
---------------	--

---

**Description**

Annotation of example data, evidence, in this package. It should be prepared by users. The variables are as follows:

**Usage**

```
annotation.mq
```

**Format**

A data frame with 150 rows and 7 variables.

## Details

- Run : MS run ID. It should be the same as Raw.file info in raw.mq
- Channel : Labeling information (channel.0, ..., channel.9). The channel index should be consistent with the channel columns in raw.mq.
- Condition : Condition (ex. Healthy, Cancer, Time0)
- Mixture : Mixture of samples labeled with different TMT reagents, which can be analyzed in a single mass spectrometry experiment. If the channel doesn't have sample, please add 'Empty' under Condition.
- TechRepMixture : Technical replicate of one mixture. One mixture may have multiple technical replicates. For example, if 'TechRepMixture' = 1, 2 are the two technical replicates of one mixture, then they should match with same 'Mixture' value.
- Fraction : Fraction ID. One technical replicate of one mixture may be fractionated into multiple fractions to increase the analytical depth. Then one technical replicate of one mixture should correspond to multiple fractions. For example, if 'Fraction' = 1, 2, 3 are three fractions of the first technical replicate of one TMT mixture of biological subjects, then they should have same 'TechRepMixture' and 'Mixture' value.
- BioReplicate : Unique ID for biological subject. If the channel doesn't have sample, please add 'Empty' under BioReplicate.

## Examples

```
head(annotation.mq)
```

---

annotation.pd

*Example of annotation file for raw.pd, which is the PSM output of Proteome Discoverer*

---

## Description

Annotation of example data, raw.pd, in this package. It should be prepared by users. The variables are as follows:

## Usage

```
annotation.pd
```

## Format

A data frame with 150 rows and 7 variables.

## Details

- Run : MS run ID. It should be the same as Spectrum.File info in raw.pd.
- Channel : Labeling information (126, ... 131). It should be consistent with the channel columns in raw.pd.
- Condition : Condition (ex. Healthy, Cancer, Time0)

- **Mixture** : Mixture of samples labeled with different TMT reagents, which can be analyzed in a single mass spectrometry experiment. If the channel doesn't have sample, please add 'Empty' under Condition.
- **TechRepMixture** : Technical replicate of one mixture. One mixture may have multiple technical replicates. For example, if 'TechRepMixture' = 1, 2 are the two technical replicates of one mixture, then they should match with same 'Mixture' value.
- **Fraction** : Fraction ID. One technical replicate of one mixture may be fractionated into multiple fractions to increase the analytical depth. Then one technical replicate of one mixture should correspond to multiple fractions. For example, if 'Fraction' = 1, 2, 3 are three fractions of the first technical replicate of one TMT mixture of biological subjects, then they should have same 'TechRepMixture' and 'Mixture' value.
- **BioReplicate** : Unique ID for biological subject. If the channel doesn't have sample, please add 'Empty' under BioReplicate.

### Examples

```
head(annotation.pd)
```

---

dataProcessPlotsTMT      *Visualization for explanatory data analysis - TMT experiment*

---

### Description

To illustrate the quantitative data and quality control of MS runs, dataProcessPlotsTMT takes the quantitative data and summarized data from function 'proteinSummarization' as input and generate two 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 and channels.

### Usage

```
dataProcessPlotsTMT(
  data,
  type,
  featureName = "Transition",
  ylimUp = FALSE,
  ylimDown = FALSE,
  x.axis.size = 10,
  y.axis.size = 10,
  text.size = 2,
  text.angle = 90,
  legend.size = 7,
  dot.size.profile = 2,
  ncol.guide = 5,
  width = 10,
  height = 10,
  which.Protein = "all",
  originalPlot = TRUE,
  summaryPlot = TRUE,
```

```

    address = "",
    isPlotly = FALSE
)

```

### Arguments

data	the output of <code>proteinSummarization</code> function. It is a list with data frames 'FeatureLevelData' and 'ProteinLevelData'
type	choice of visualization. "ProfilePlot" represents profile plot of log intensities across MS runs. "QCPlot" represents box plots of log intensities across channels and MS runs.
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. FALSE(Default) for Profile Plot and QC Plot uses the upper limit as rounded off maximum of $\log_2(\text{intensities})$ after normalization + 3..
ylimUp	upper limit for y-axis in the log scale.
ylimDown	lower limit for y-axis in the log scale. FALSE(Default) for Profile Plot and QC Plot uses 0..
x.axis.size	size of x-axis labeling for "Run" and "channel in Profile Plot and QC Plot.
y.axis.size	size of y-axis labels. Default is 10.
text.size	size of labels represented each condition at the top of Profile plot and QC plot. Default is 4.
text.angle	angle of labels represented each condition at the top of Profile plot and QC plot. Default is 0.
legend.size	size of legend above Profile plot. Default is 7.
dot.size.profile	size of dots in Profile plot. Default is 2.
ncol.guide	number of columns for legends at the top of plot. Default is 5.
width	width of the saved pdf file. Default is 10.
height	height of the saved pdf file. Default is 10.
which.Protein	Protein list to draw plots. List can be names of Proteins or order numbers of Proteins. 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, without normalization.
summaryPlot	TRUE(default) draws profile plots with protein summarization for each channel and MS run.
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 "ProfilePlot.pdf" or "QCplot.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	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

**Value**

plot or pdf

**Examples**

```
data(input.pd)
quant.msstats = proteinSummarization(input.pd,
                                     method="msstats",
                                     global_norm=TRUE,
                                     reference_norm=TRUE)

## Profile plot
dataProcessPlotsTMT(data=quant.msstats,
                    type='ProfilePlot',
                    width = 21,
                    height = 7)

## NottoRun: QC plot
# dataProcessPlotsTMT(data=quant.msstats,
#                     # type='QCPlot',
#                     # width = 21,
#                     # height = 7)
```

---

designSampleSizeTMT	<i>Planning future experimental designs of Tandem Mass Tag (TMT) experiments acquired with Data-Dependent Acquisition (DDA or shotgun)</i>
---------------------	--

---

**Description**

Calculate sample size for future experiments of a TMT experiment based on intensity-based linear model. Two options of the calculation: (1) number of biological replicates per condition, (2) power.

**Usage**

```
designSampleSizeTMT(
  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 groupComparisonTMT.

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.

### Examples

```
data(input.pd)
# use protein.summarization() to get protein abundance data
quant.pd.msstats = proteinSummarization(input.pd,
                                       method="msstats",
                                       global_norm=TRUE,
                                       reference_norm=TRUE)

test.pairwise = groupComparisonTMT(quant.pd.msstats, save_fitted_models = TRUE)
head(test.pairwise$ComparisonResult)

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

---

evidence

*Example of output from MaxQuant for TMT-10plex experiments.*


---

### Description

Example of evidence.txt from MaxQuant. It is the input for MaxQtoMSstatsTMTFormat function, with proteinGroups.txt and annotation file. Annotation file should be made by users. It includes peak intensities for 10 proteins among 15 MS runs with TMT10. The important variables are as follows:

### Usage

```
evidence
```

### Format

A data frame with 1075 rows and 105 variables.

### Details

- Proteins
- Protein.group.IDs
- Modified.sequence
- Charge
- Raw.file
- Score
- Potential.contaminant
- Reverse
- Channels : Reporter.intensity.corrected.0, ..., Reporter.intensity.corrected.9

### Examples

```
head(evidence)
```

---

getProcessedTMT

*Get processed feature-level data*


---

### Description

Get processed feature-level data

### Usage

```
getProcessedTMT(summarized, input)
```

**Arguments**

summarized	output of the MSstatsSummarizeTMT function
input	output of MSstatsNormalizeTMT function

**Value**

data.table

---

getSummarizedTMT	<i>Get protein-level data from MSstatsSummarizeTMT output</i>
------------------	---

---

**Description**

Get protein-level data from MSstatsSummarizeTMT output

**Usage**

```
getSummarizedTMT(summarized)
```

**Arguments**

summarized	output of the MSstatsSummarizeTMT function
------------	--

**Value**

data.table

---

groupComparisonTMT	<i>Finding differentially abundant proteins across conditions in TMT experiment</i>
--------------------	---

---

**Description**

Tests for significant changes in protein abundance across conditions based on a family of linear mixed-effects models in TMT experiment. Experimental design of case-control study (patients are not repeatedly measured) is automatically determined based on proper statistical model.

**Usage**

```
groupComparisonTMT(
  data,
  contrast.matrix = "pairwise",
  moderated = FALSE,
  adj.method = "BH",
  remove_norm_channel = TRUE,
  remove_empty_channel = TRUE,
  save_fitted_models = FALSE,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL
)
```

**Arguments**

data	the output of <code>proteinSummarization</code> function. It is a list with data frames 'FeatureLevelData' and 'ProteinLevelData'
contrast.matrix	Comparison between conditions of interests. 1) default is "pairwise", which compare all possible pairs between two conditions. 2) Otherwise, users can specify the comparisons 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.
moderated	TRUE will moderate t statistic; FALSE (default) uses ordinary t statistic.
adj.method	adjusted method for multiple comparison. "BH" is default.
remove_norm_channel	TRUE(default) removes "Norm" channels from protein level data.
remove_empty_channel	TRUE(default) removes "Empty" channels from protein level data.
save_fitted_models	logical, if TRUE, fitted models will be added to
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.

**Value**

a list that consists of the following elements: (1) ComparisonResult: statistical testing results; (2) FittedModel: the fitted linear models

**Examples**

```
data(input.pd)
# use protein.summarization() to get protein abundance data
quant.pd.msstats = proteinSummarization(input.pd,
                                       method="msstats",
                                       global_norm=TRUE,
                                       reference_norm=TRUE)

test.pairwise = groupComparisonTMT(quant.pd.msstats, moderated = TRUE)
head(test.pairwise$ComparisonResult)

# Only compare condition 0.125 and 1
levels(quant.pd.msstats$ProteinLevelData$Condition)

# Compare condition 1 and 0.125
comparison=matrix(c(-1,0,0,1),nrow=1)

# Set the names of each row
row.names(comparison)="1-0.125"
```

```
# Set the column names
colnames(comparison)= c("0.125", "0.5", "0.667", "1")
test.contrast = groupComparisonTMT(data = quant.pd.msstats,
contrast.matrix = comparison,
moderated = TRUE)
head(test.contrast$ComparisonResult)
```

---

input.pd

*Example of output from PDtoMSstatsTMTFormat function*

---

## Description

It is made from [raw.pd](#) and [annotation.pd](#), which is the output of PDtoMSstatsTMTFormat function. It should include the required columns as below.

## Usage

```
input.pd
```

## Format

A data frame with 20110 rows and 11 variables.

## Details

- ProteinName : Protein ID
- PeptideSequence : peptide sequence
- Charge : peptide charge
- PSM : peptide ion and spectra match
- Channel : Labeling information (126, ... 131)
- Condition : Condition (ex. Healthy, Cancer, Time0)
- BioReplicate : Unique ID for biological subject.
- Run : MS run ID
- Mixture : Unique ID for TMT mixture.
- TechRepMixture : Unique ID for technical replicate of one TMT mixture.
- Intensity: Protein Abundance

## Examples

```
head(input.pd)
```

---

 MaxQtoMSstatsTMTFormat

*Generate MSstatsTMT required input format from MaxQuant output*


---

## Description

Generate MSstatsTMT required input format from MaxQuant output

## Usage

```
MaxQtoMSstatsTMTFormat(
  evidence,
  proteinGroups,
  annotation,
  which.proteinid = "Proteins",
  rmProt_Only.identified.by.site = FALSE,
  useUniquePeptide = TRUE,
  rmPSM_withfewMea_withinRun = TRUE,
  rmProtein_with1Feature = FALSE,
  summaryforMultipleRows = sum,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

## Arguments

evidence	name of 'evidence.txt' data, which includes feature-level data.
proteinGroups	name of 'proteinGroups.txt' data.
annotation	data frame which contains column Run, Fraction, TechRepMixture, Mixture, Channel, BioReplicate, Condition. Refer to the example 'annotation.mq' for the meaning of each column.
which.proteinid	Use 'Proteins' (default) column for protein name. 'Leading.proteins' or 'Leading.razor.proteins' or 'Gene.names' can be used instead to get the protein ID with single protein. However, those can potentially have the shared peptides.
rmProt_Only.identified.by.site	TRUE will remove proteins with '+' in 'Only.identified.by.site' column from proteinGroups.txt, which was identified only by a modification site. FALSE is the default.
useUniquePeptide	TRUE(default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
rmPSM_withfewMea_withinRun	TRUE (default) will remove the features that have 1 or 2 measurements within each Run.

rmProtein_with1Feature	TRUE will remove the proteins which have only 1 peptide and charge. Default is FALSE.
summaryforMultipleRows	sum(default) or max - when there are multiple measurements for certain feature in certain run, select the feature with the largest summation or maximal value.
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 of class "MSstatsTMT"

**Examples**

```
head(evidence)
head(proteinGroups)
head(annotation.mq)
input.mq <- MaxQtoMSstatsTMTFormat(evidence, proteinGroups, annotation.mq)
head(input.mq)
```

---

MSstatsComparisonModelSingleTMT

*Fit a linear model for group comparison for a single protein*

---

**Description**

Fit a linear model for group comparison for a single protein

**Usage**

```
MSstatsComparisonModelSingleTMT(single_protein, protein_name)
```

**Arguments**

`single_protein` protein-level data for a single protein (single element of list created by the `MSstatsPrepareForGroupComparisonTMT` function)

`protein_name` name of a protein from the `single_protein` data.table

**Value**

list

MSstatsFitComparisonModelsTMT

*Fit linear models for group comparison*

---

**Description**

Fit linear models for group comparison

**Usage**

```
MSstatsFitComparisonModelsTMT(input)
```

**Arguments**

input                      output of the MSstatsPrepareForGroupComparisonTMT function

**Value**

list

---

MSstatsGroupComparisonOutputTMT

*Combine testing results for individual proteins*

---

**Description**

Combine testing results for individual proteins

**Usage**

```
MSstatsGroupComparisonOutputTMT(testing_results, adj_method)
```

**Arguments**

testing\_results                      output of the MSstatsGroupComparisonTMT function

adj\_method                      method that will be used to adjust p-values for multiple comparisons

**Value**

data.table

---

MSstatsGroupComparisonTMT

*Group comparison for TMT data*

---

**Description**

Group comparison for TMT data

**Usage**

```
MSstatsGroupComparisonTMT(fitted_models, contrast_matrix)
```

**Arguments**

`fitted_models` output of the MSstatsModerateTTest function  
`contrast_matrix`  
contrast matrix

**Value**

data.table

---

MSstatsModerateTTest *Moderate T statistic for group comparison*

---

**Description**

Moderate T statistic for group comparison

**Usage**

```
MSstatsModerateTTest(summarized, fitted_models, moderated)
```

**Arguments**

`summarized` protein-level data produced by the proteinSummarization function  
`fitted_models` output of the MSstatsFitComparisonModelsTMT function  
`moderated` if TRUE, moderation will be performed

**Value**

list

---

MSstatsNormalizeTMT     *Normalization for TMT data*

---

**Description**

Normalization for TMT data

**Usage**

```
MSstatsNormalizeTMT(input, type, normalize)
```

**Arguments**

input	data.table
type	"peptides" for peptide normalization between channel and run, "proteins" for protein normalization
normalize	logical, if TRUE, data will be normalized

**Value**

data.table

---

MSstatsPrepareForGroupComparisonTMT  
*Prepare output of proteinSummarization for group comparison*

---

**Description**

Prepare output of proteinSummarization for group comparison

**Usage**

```
MSstatsPrepareForGroupComparisonTMT(
  input,
  remove_norm_channel,
  remove_empty_channel
)
```

**Arguments**

input	output of proteinSummarization
remove_norm_channel	if TRUE, "Norm" channel will be removed
remove_empty_channel	if TRUE, empty channel will be removed

**Value**

data.table

---

 MSstatsPrepareForSummarizationTMT

*Prepare output of MSstatsTMT converters for protein-level summarization*

---

## Description

Prepare output of MSstatsTMT converters for protein-level summarization

## Usage

```
MSstatsPrepareForSummarizationTMT(
  data,
  method,
  global_norm,
  reference_norm,
  remove_norm_channel,
  remove_empty_channel,
  MBimpute,
  maxQuantileforCensored
)
```

## Arguments

data	Name of the output of PDtoMSstatsTMTFormat function or peptide-level quantified data from other tools. It should have columns ProteinName, PeptideSequence, Charge, PSM, Mixture, TechRepMixture, Run, Channel, Condition, BioReplicate, Intensity
method	Four different summarization methods to protein-level can be performed : "msstats"(default), "MedianPolish", "Median", "LogSum".
global_norm	Global median normalization on peptide level data (equalizing the medians across all the channels and MS runs). Default is TRUE. It will be performed before protein-level summarization.
reference_norm	Reference channel based normalization between MS runs on protein level data. TRUE(default) needs at least one reference channel in each MS run, annotated by 'Norm' in Condition column. It will be performed after protein-level summarization. FALSE will not perform this normalization step. If data only has one run, then reference_norm=FALSE.
remove_norm_channel	TRUE(default) removes 'Norm' channels from protein level data.
remove_empty_channel	TRUE(default) removes 'Empty' channels from protein level data.
MBimpute	only for method="msstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.
maxQuantileforCensored	We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.

**Value**

data.table

---

MSstatsSummarizationOutputTMT

*Combine feature-level and protein-level data into single output*

---

**Description**

Combine feature-level and protein-level data into single output

**Usage**

```
MSstatsSummarizationOutputTMT(
  summarized,
  processed,
  remove_empty_channel,
  remove_norm_channel
)
```

**Arguments**

summarized      output of the getSummarizedTMT function  
 processed      output of the getProcessedTMT function  
 remove\_empty\_channel  
                  TRUE(default) removes 'Empty' channels from protein level data.  
 remove\_norm\_channel  
                  TRUE(default) removes 'Norm' channels from protein level data.

**Value**

list that consists of two data.frames with feature-level and protein-level data

---

MSstatsSummarizeTMT      *Protein summarization for TMT data*

---

**Description**

Protein summarization for TMT data

**Usage**

```
MSstatsSummarizeTMT(
  input,
  method,
  impute,
  max_quantile_censored = NULL,
  log_file_path = NULL
)
```

**Arguments**

input	data.table with TM quant data
method	Four different summarization methods to protein-level can be performed : "msstats"(default), "MedianPolish", "Median", "LogSum".
impute	only for method="msstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.
max_quantile_censored	We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.
log_file_path	path to a MSstats log file

**Value**

data.table

---

MSstatsTestSingleProteinTMT

*Hypothesis tests for a single protein in TMT data*

---

**Description**

Hypothesis tests for a single protein in TMT data

**Usage**

```
MSstatsTestSingleProteinTMT(fitted_model, contrast_matrix)
```

**Arguments**

fitted_model	single element of the MSstatsModerateTTest output
contrast_matrix	contrast matrix

**Value**

list

---

MSstatsTMT

*MSstatsTMT: A package for protein significance analysis in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling*

---

## Description

A set of tools for detecting differentially abundant peptides and proteins in shotgun mass spectrometry-based proteomic experiments with tandem mass tag (TMT) labeling.

## functions

- [PDtoMSstatsTMTFormat](#) : generates MSstatsTMT required input format for Proteome discoverer output.
- [MaxQtoMSstatsTMTFormat](#) : generates MSstatsTMT required input format for MaxQuant output.
- [SpectroMinetoMSstatsTMTFormat](#) : generates MSstatsTMT required input format for SpectroMine output.
- [OpenMStoMSstatsTMTFormat](#) : generates MSstatsTMT required input format for OpenMS output.
- [proteinSummarization](#) : summarizes PSM level quantification to protein level quantification.
- [dataProcessPlotsTMT](#) : visualizes for explanatory data analysis.
- [groupComparisonTMT](#) : tests for significant changes in protein abundance across conditions.

## Author(s)

**Maintainer:** Devon Kohler <kohler.d@northeastern.edu>

Authors:

- Ting Huang <thuang0703@gmail.com>
- Meena Choi <mnchoi67@gmail.com>
- Mateusz Staniak <mtst@mstaniak.pl>
- Sicheng Hao <hao.sic@husky.neu.edu>
- Olga Vitek <o.vitek@northeastern.edu>

## See Also

Useful links:

- <http://msstats.org/msstatstmt/>
- Report bugs at <https://groups.google.com/forum/#!forum/msstats>

---

 OpenMStoMSstatsTMTFormat

*Generate MSstatsTMT required input format for OpenMS output*


---

## Description

Generate MSstatsTMT required input format for OpenMS output

## Usage

```
OpenMStoMSstatsTMTFormat(
  input,
  useUniquePeptide = TRUE,
  rmPSM_withfewMea_withinRun = TRUE,
  rmProtein_with1Feature = FALSE,
  summaryforMultiplePSMs = sum,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

## Arguments

input	MSstatsTMT report from OpenMS
useUniquePeptide	TRUE(default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
rmPSM_withfewMea_withinRun	TRUE (default) will remove the features that have 1 or 2 measurements within each Run.
rmProtein_with1Feature	TRUE will remove the proteins which have only 1 peptide and charge. Default is FALSE.
summaryforMultiplePSMs	sum(default) or max - when there are multiple measurements for certain feature in certain run, select the feature with the largest summation or maximal value.
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' of class 'MSstatsTMT'.

**Examples**

```
head(raw.om)
input.om <- OpenMStoMSstatsTMTFormat(raw.om)
head(input.om)
```

---

PDtoMSstatsTMTFormat *Convert Proteome Discoverer output to MSstatsTMT format.*

---

**Description**

Convert Proteome Discoverer output to MSstatsTMT format.

**Usage**

```
PDtoMSstatsTMTFormat(
  input,
  annotation,
  which.proteinid = "Protein.Accessions",
  useNumProteinsColumn = TRUE,
  useUniquePeptide = TRUE,
  rmPSM_withfewMea_withinRun = TRUE,
  rmProtein_with1Feature = FALSE,
  summaryforMultipleRows = sum,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

**Arguments**

input	PD report or a path to it.
annotation	annotation with Run, Fraction, TechRepMixture, Mixture, Channel, BioReplicate, Condition columns or a path to file. Refer to the example 'annotation' for the meaning of each column.
which.proteinid	Use 'Protein.Accessions'(default) column for protein name. 'Master.Protein.Accessions' can be used instead to get the protein name with single protein.
useNumProteinsColumn	logical, TRUE(default) remove shared peptides by information of # Proteins column in PSM sheet.
useUniquePeptide	logical, if TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.

rmPSM_withfewMea_withinRun	TRUE (default) will remove the features that have 1 or 2 measurements within each Run.
rmProtein_with1Feature	TRUE will remove the proteins which have only 1 peptide and charge. Default is FALSE.
summaryforMultipleRows	sum (default) or max - when there are multiple measurements for certain feature in certain run, select the feature with the largest summation or maximal value.
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' of class 'MSstatsTMT'

**Examples**

```
head(raw.pd)
head(annotation.pd)
input.pd <- PDtoMSstatsTMTFormat(raw.pd, annotation.pd)
head(input.pd)
```

---

PhilosophertoMSstatsTMTFormat

*Convert Philosopher (Fragpipe) output to MSstatsTMT format.*

---

**Description**

Convert Philosopher (Fragpipe) output to MSstatsTMT format.

**Usage**

```
PhilosophertoMSstatsTMTFormat(
  input,
  annotation,
  protein_id_col = "Protein",
  peptide_id_col = "Peptide.Sequence",
  Purity_cutoff = 0.6,
  PeptideProphet_prob_cutoff = 0.7,
  useUniquePeptide = TRUE,
  rmPSM_withfewMea_withinRun = TRUE,
```

```

rmPeptide_OxidationM = TRUE,
rmProtein_with1Feature = FALSE,
summaryforMultipleRows = sum,
use_log_file = TRUE,
append = FALSE,
verbose = TRUE,
log_file_path = NULL,
...
)

```

## Arguments

input	data.frame of 'msstats.csv' file produced by Philosopher
annotation	annotation with Run, Fraction, TechRepMixture, Mixture, Channel, BioReplicate, Condition columns or a path to file. Refer to the example 'annotation' for the meaning of each column. Channel column should be consistent with the channel columns (Ignore the prefix "Channel ") in msstats.csv file. Run column should be consistent with the Spectrum.File columns in msstats.csv file.
protein_id_col	Use 'Protein'(default) column for protein name. 'Master.Protein.Accessions' can be used instead to get the protein ID with single protein.
peptide_id_col	Use 'Peptide.Sequence'(default) column for peptide sequence. 'Modified.Peptide.Sequence' can be used instead to get the modified peptide sequence.
Purity_cutoff	Cutoff for purity. Default is 0.6
PeptideProphet_prob_cutoff	Cutoff for the peptide identification probability. Default is 0.7. The probability is confidence score determined by PeptideProphet and higher values indicate greater confidence.
useUniquePeptide	logical, if TRUE (default) removes peptides that are assigned for more than one proteins. We assume to use unique peptide for each protein.
rmPSM_withfewMea_withinRun	TRUE (default) will remove the features that have 1 or 2 measurements within each Run.
rmPeptide_OxidationM	TRUE (default) will remove the peptides including oxidation (M) sequence.
rmProtein_with1Feature	TRUE will remove the proteins which have only 1 peptide and charge. Default is FALSE.
summaryforMultipleRows	sum (default) or max - when there are multiple measurements for certain feature in certain run, select the feature with the largest summation or maximal value.
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' of class 'MSstatsTMT'

---

proteinGroups	<i>Example of proteinGroups file from MaxQuant for TMT-10plex experiments.</i>
---------------	--

---

**Description**

Example of proteinGroup.txt file from MaxQuant, which is identified protein group information file. It is the input for MaxQtoMSstatsTMTFormat function, with evidence.txt and annotation file. It includes identified protein groups for 10 proteins among 15 MS runs with TMT10. The important variables are as follows:

**Usage**

```
proteinGroups
```

**Format**

A data frame with 1075 rows and 105 variables.

**Details**

- id
- Protein.IDs
- Only.identified.by.site
- Potential.contaminant
- Reverse

**Examples**

```
head(proteinGroups)
```

---

proteinSummarization	<i>Summarizing peptide level quantification to protein level quantification</i>
----------------------	---

---

**Description**

We assume missing values are censored and then impute the missing values. Protein-level summarization from peptide level quantification are performed. After all, global median normalization on peptide level data and normalization between MS runs using reference channels will be implemented.

**Usage**

```

proteinSummarization(
  data,
  method = "msstats",
  global_norm = TRUE,
  reference_norm = TRUE,
  remove_norm_channel = TRUE,
  remove_empty_channel = TRUE,
  MBimpute = TRUE,
  maxQuantileforCensored = NULL,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  msstats_log_path = NULL
)

```

**Arguments**

data	Name of the output of PDtoMSstatsTMTFormat function or peptide-level quantified data from other tools. It should have columns ProteinName, PeptideSequence, Charge, PSM, Mixture, TechRepMixture, Run, Channel, Condition, BioReplicate, Intensity
method	Four different summarization methods to protein-level can be performed : "msstats"(default), "MedianPolish", "Median", "LogSum".
global_norm	Global median normalization on peptide level data (equalizing the medians across all the channels and MS runs). Default is TRUE. It will be performed before protein-level summarization.
reference_norm	Reference channel based normalization between MS runs on protein level data. TRUE(default) needs at least one reference channel in each MS run, annotated by 'Norm' in Condition column. It will be performed after protein-level summarization. FALSE will not perform this normalization step. If data only has one run, then reference_norm=FALSE.
remove_norm_channel	TRUE(default) removes 'Norm' channels from protein level data.
remove_empty_channel	TRUE(default) removes 'Empty' channels from protein level data.
MBimpute	only for method="msstats". TRUE (default) imputes missing values by Accelerated failure model. FALSE uses minimum value to impute the missing value for each peptide precursor ion.
maxQuantileforCensored	We assume missing values are censored. maxQuantileforCensored is Maximum quantile for deciding censored missing value, for instance, 0.999. Default is Null.
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.

`msstats_log_path`  
path to a MSstats log file

**Value**

list that consists of two data.frames with feature-level (FeatureLevelData) and protein-level data (ProteinLevelData)

**Examples**

```
data(input.pd)
quant.pd.msstats <- proteinSummarization(input.pd,
                                         method = "msstats",
                                         global_norm = TRUE,
                                         reference_norm = TRUE)
head(quant.pd.msstats$ProteinLevelData)
```

---

`quant.pd.msstats`      *Example of output from proteinSummarization function*

---

**Description**

It is made from `input.pd`. It is the output of `proteinSummarization` function. It is a list that consists of two data.frames with feature-level (FeatureLevelData) and protein-level data (ProteinLevelData). ProteinLevelData should include the required columns as below.

**Usage**

```
quant.pd.msstats
```

**Format**

A data frame with 100 rows and 8 variables.

**Details**

- Run : MS run ID
- Protein : Protein ID
- Abundance: Protein-level summarized abundance
- Channel : Labeling information (126, ... 131)
- Condition : Condition (ex. Healthy, Cancer, Time0)
- BioReplicate : Unique ID for biological subject.
- TechRepMixture : Unique ID for technical replicate of one TMT mixture.
- Mixture : Unique ID for TMT mixture.

**Examples**

```
head(quant.pd.msstats$ProteinLevelData)
```

---

`raw.mine`*Example of output from SpectroMine for TMT-6plex experiments.*

---

**Description**

Example of SpectroMine PSM sheet. It is the output of SpectroMine and the input for SpectroMine-toMSstatsTMTFormat function, with annotation file. Annotation file should be made by users. It includes peak intensities for 10 proteins among 12 MS runs with TMT-6plex. The important variables are as follows:

**Usage**`raw.mine`**Format**

A data frame with 170 rows and 28 variables.

**Details**

- PG.ProteinAccessions
- P.MoleculeID
- PP.Charge
- R.FileName
- PG.QValue
- PSM.Qvalue
- Channels : PSM.TMT6\_126..Raw., ..., PSM.TMT6\_131..Raw.

**Examples**`head(raw.mine)`

---

`raw.om`*Example of MSstatsTMT report from OpenMS for TMT-10plex experiments.*

---

**Description**

Example of MSstatsTMT PSM sheet from MaxQuant. It is the input for OpenMStoMSstatsTMTFormat function. It includes peak intensities for 10 proteins among 27 MS runs from three TMT10 mixtures. The important variables are as follows:

**Usage**`raw.om`

**Format**

A data frame with 860 rows and 13 variables.

**Details**

- RetentionTime
- ProteinName
- PeptideSequence
- Charge
- Channel
- Condition
- BioReplicate
- Run
- Mixture
- TechRepMixture
- Fraction
- Intensity
- Reference

**Examples**

```
head(raw.om)
```

---

raw.pd

*Example of output from Proteome Discoverer 2.2 for TMT-10plex experiments.*

---

**Description**

Example of Proteome discover PSM sheet. It is the input for PDtoMSstatsTMTFormat function, with annotation file. Annotation file should be made by users. It includes peak intensities for 10 proteins among 15 MS runs with TMT-10plex. The variables are as follows:

**Usage**

```
raw.pd
```

**Format**

A data frame with 2858 rows and 50 variables.

**Details**

- Master.Protein.Accessions
- Protein.Accessions
- Annotated.Sequence
- Charge
- Ions.Score
- Spectrum.File
- Quan.Info
- Channels : 126, ..., 131

**Examples**

```
head(raw.pd)
```

---

SpectroMinetoMSstatsTMTFormat

*Import data from SpectroMine*

---

**Description**

Import data from SpectroMine

**Usage**

```
SpectroMinetoMSstatsTMTFormat(
  input,
  annotation,
  filter_with_Qvalue = TRUE,
  qvalue_cutoff = 0.01,
  useUniquePeptide = TRUE,
  rmPSM_withfewMea_withinRun = TRUE,
  rmProtein_with1Feature = FALSE,
  summaryforMultipleRows = sum,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  ...
)
```

**Arguments**

input	data name of SpectroMine PSM output. Read PSM sheet.
annotation	data frame which contains column Run, Fraction, TechRepMixture, Mixture, Channel, BioReplicate, Condition. Refer to the example 'annotation.mine' for the meaning of each column.

filter_with_Qvalue	TRUE(default) will filter out the intensities that have greater than <code>qvalue_cutoff</code> in EG.Qvalue column. Those intensities will be replaced with NA 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.
rmPSM_withfewMea_withinRun	TRUE (default) will remove the features that have 1 or 2 measurements within each Run.
rmProtein_with1Feature	TRUE will remove the proteins which have only 1 peptide and charge. Default is FALSE.
summaryforMultipleRows	sum(default) or max - when there are multiple measurements for certain feature in certain run, select the feature with the largest summation or maximal value.
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' of class 'MSstatsTMT'

**Examples**

```
head(raw.mine)
head(annotation.mine)
input.mine <- SpectroMinetoMSstatsTMTFormat(raw.mine, annotation.mine)
head(input.mine)
```

---

test.pairwise

*Example of output from groupComparisonTMT function*


---

**Description**

It is the output of `groupComparisonTMT` function, which is made from [quant.pd.msstats](https://www.bioconductor.org/packages/release/bioc/html/quant.pd.msstats/). It is a list that consists of the following elements: (1) `ComparisonResult`: statistical testing results; (2) `FittedModel`: the fitted linear models `ComparisonResult` should include the columns as below.

**Usage**

```
test.pairwise
```

**Format**

A data frame with 60 rows and 7 variables.

**Details**

- Protein : Protein ID
- Label: Label of the pairwise comparison or contrast
- log2FC: Log2 fold change
- SE: Standard error of the comparison of contrast results
- DF: Degree of freedom
- pvalue: Value of p statistic of the test
- adj.pvalue: adjusted p value
- issue: used for indicating the reason why a comparison is not testable. NA means the comparison is testable. 'oneConditionMissing' means the protein has no measurements in one condition of the comparison. Furthermore, when 'issue = oneConditionMissing', 'log2FC = Inf' means the negative condition (with coefficient -1 in the Label column) is missing and 'log2FC = -Inf' means the positive condition (with coefficient 1 in the Label column) is missing. 'completeMissing' means the protein has no measurements in all the conditions of the comparison. 'unfittableModel' means there is not enough measurements to fit the linear model. In other words, each condition has only one measurement.

**Examples**

```
head(test.pairwise$ComparisonResult)
```

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