Package 'MSstatsConvert'

November 20, 2024

Title Import Data from Various Mass Spectrometry Signal Processing Tools to MSstats Format

Version 1.16.0

Description
MSstatsConvert provides tools for importing reports of Mass Spectrometry data processing tools into R format suitable for statistical analysis using the MSstats and MSstatsTMT packages.

License Artistic-2.0

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

biocViews MassSpectrometry, Proteomics, Software, DataImport, QualityControl

Depends R (>= 4.0)

Imports data.table, log4r, methods, checkmate, utils, stringi

Suggests tinytest, covr, knitr, rmarkdown

Collate 'clean_ProteinProspector.R' 'clean_Metamorpheus.R' 'clean_DIANN.R' 'clean_Philosopher.R' 'clean_Spectronaut.R' 'clean_SpectroMine.R' 'clean_Skyline.R' 'clean_ProteomeDiscoverer.R' 'clean_Progenesis.R' 'clean_OpenSWATH.R' 'clean_OpenMS.R' 'clean_MaxQuant.R' 'clean_DIAUmpire.R' 'MSstatsConvert_core_functions.R' 'converters_DIANNtoMSstatsFormat.R' 'converters_DIAUmpiretoMSstatsFormat.R' 'converters_FragPipetoMSstatsFormat.R' 'converters_MaxQtoMSstatsFormat.R' 'converters_MetamorpheusToMSstatsFormat.R' 'converters_OpenMStoMSstatsFormat.R' 'converters_OpenSWATHtoMSstatsFormat.R' 'converters_PDtoMSstatsFormat.R' 'converters_ProgenesistoMSstatsFormat.R' 'converters_ProteinProspectortoMSstatsTMTFormat.R' 'converters_SkylinetoMSstatsFormat.R' 'converters_SpectronauttoMSstatsFormat.R' 'utils_MSstatsConvert.R' 'utils_annotation.R' 'utils_balanced_design.R' 'utils_checks.R' 'utils_classes.R'

'utils_clean_features.R' 'utils_documentation.R'
'utils_dt_operations.R' 'utils_filtering.R' 'utils_fractions.R'
'utils_logging.R' 'utils_shared_peptides.R'

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/MSstatsConvert

git_branch RELEASE_3_20

git_last_commit 0ee36b7

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-19

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Contents

`.addFractions` *Add a Fraction column to the output of* `MSstatsPreprocess`

Description

Add a Fraction column to the output of `MSstatsPreprocess`

Usage

```
.addFractions(input)
```

Arguments

`input`	output of `MSstatsPreprocess`

Value

data.table

`.adjustIntensities` *Fix invalid intensities: infinite to NA, between 0 and 1 to 0*

Description

Fix invalid intensities: infinite to NA, between 0 and 1 to 0

Usage

```
.adjustIntensities(input)
```

Arguments

`input`	data.table

Value

data.table

.aggregatePSMstoPeptideIons *Aggregate multiple PSMs to a single peptide ion.*

Description

Aggregate multiple PSMs to a single peptide ion.

Usage

```
.aggregatePSMstoPeptideIons(input, feature_columns, summary_function = sum)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
feature_columns	chr, names of columns that define features.
summary_function	function that will be used to aggregate intensities if needed.

Value

data.table

.checkAnnotation *Check if the annotation is valid*

Description

Check if the annotation is valid

Usage

```
.checkAnnotation(input, annotation)
```

Arguments

input	data processed by the MSstatsClean
annotation	annotation created by the MSstatsMakeAnnotation function

Value

TRUE invisibly if the annotation is correct, throws an error otherwise

.checkDDA *Check validity of DDA data*

Description

Check validity of DDA data

Usage

```
.checkDDA(input)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.

Value

logical

logical, TRUE means that the input dataset comes from a DDA experiment

.checkDuplicatedMeasurements *Check if there are duplicated measurements within run*

Description

Check if there are duplicated measurements within run

Usage

```
.checkDuplicatedMeasurements(input)
```

Arguments

input	output of MSstatsPreprocess

Value

character vector of feature labels

.checkMSstatsParams *Check validity of parameters to the* MSstatsImport *function.*

Description

Check validity of parameters to the MSstatsImport function.

Usage

```
.checkMSstatsParams(
  input,
  annotation,
  feature_columns,
  remove_shared_peptides,
  remove_single_feature_proteins,
  feature_cleaning
)
```

Value

none, throws an error if any of the assertions fail

.checkMultiRun *Check if fractionation exists*

Description

Check if fractionation exists

Usage

```
.checkMultiRun(input)
```

Arguments

input	output of MSstatsPreprocess

Value

list of two elements: has_fractions (logical) indicates if fractions was detected in the input dataset, is_risky (logical) indicates if there was a problem with detecting fractionation.

.checkOverlappedFeatures *Check if any features are measured in multiple fractions*

Description

Check if any features are measured in multiple fractions

Usage

```
.checkOverlappedFeatures(input)
```

Arguments

input	output of MSstatsPreprocess

Value

data.table

.cleanByFeature *Perform by-feature operations.*

Description

Perform by-feature operations.

Usage

```
.cleanByFeature(input, feature_columns, cleaning_control)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
feature_columns	character vector of names of columns that define features.
cleaning_control	named list of two or three elements. See the documentation for MSstatsImport for details.

Value

data.table

.cleanRawDIANN *Clean raw Diann files*

Description

Clean raw Diann files

Usage

```
.cleanRawDIANN(
  msstats_object,
  MBR = TRUE,
  quantificationColumn = "FragmentQuantCorrected"
)
```

Arguments

msstats_object	an object of class MSstatsDIANNFiles.
MBR	True if analysis was done with match between runs
quantificationColumn	Use 'FragmentQuantCorrected'(default) column for quantified intensities. 'FragmentQuantRaw' can be used instead.

Value

data.table

.cleanRawDIAUmpire *Clean raw DIAUmpire files*

Description

Clean raw DIAUmpire files

Usage

```
.cleanRawDIAUmpire(msstats_object, use_frag, use_pept)
```

Arguments

msstats_object	Object that inherits from MSstatsInputFiles class.
use_frag	TRUE will use the selected fragment for each peptide. 'Selected_fragments' column is required.
use_pept	TRUE will use the selected fragment for each protein 'Selected_peptides' column is required.

Value

data.table

.cleanRawMaxQuant *Clean raw output from MaxQuant*

Description

Clean raw output from MaxQuant

Usage

```
.cleanRawMaxQuant(
  msstats_object,
  protein_id_col,
  remove_by_site = FALSE,
  channel_columns = "Reporterintensitycorrected"
)
```

Arguments

msstats_object	object that inherits from MSstatsInputFiles class.
protein_id_col	character, name of a column with names of proteins.
remove_by_site	logical, if TRUE, proteins only identified by site will be removed.
channel_columns	character, regular expression that identifies channel columns in TMT data.

Value

data.table

.cleanRawMetamorpheus *Clean raw Metamorpheus files*

Description

Clean raw Metamorpheus files

Usage

```
.cleanRawMetamorpheus(msstats_object)
```

Arguments

msstats_object	an object of class MSstatsMetamorpheusFiles.

Value

data.table

.cleanRawOpenMS *Clean raw output from OpenMS*

Description

Clean raw output from OpenMS

Usage

```
.cleanRawOpenMS(msstats_object)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.

Value

data.table

.cleanRawOpenSWATH *Clean raw OpenSWATH files*

Description

Clean raw OpenSWATH files

Usage

```
.cleanRawOpenSWATH(msstats_object)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.

Value

data.table

.cleanRawPD *Clean raw Proteome Discoverer data*

Description

Clean raw Proteome Discoverer data

Usage

```
.cleanRawPD(
  msstats_object,
  quantification_column,
  protein_id_column,
  sequence_column,
  remove_shared,
  remove_protein_groups = TRUE,
  intensity_columns_regexp = "Abundance"
)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.
quantification_column	chr, name of a column used for quantification.
protein_id_column	chr, name of a column with protein IDs.
sequence_column	chr, name of a column with peptide sequences.
remove_shared	lgl, if TRUE, shared peptides will be removed.
remove_protein_groups	if TRUE, proteins with numProteins > 1 will be removed.
intensity_columns_regexp	regular expressions that defines intensity columns. Defaults to "Abundance", which means that columns that contain the word "Abundance" will be treated as corresponding to intensities for different channels.

Value

data.table

.cleanRawPDMSstats *Clean raw PD output*

Description

Clean raw PD output

Usage

```
.cleanRawPDMSstats(
  msstats_object,
  quantification_column,
  protein_id_column,
  sequence_column,
  remove_shared
)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.
quantification_column	chr, name of a column used for quantification.
protein_id_column	chr, name of a column with protein IDs.
sequence_column	chr, name of a column with peptide sequences.
remove_shared	lgl, if TRUE, shared peptides will be removed.

Value

data.table

.cleanRawPDTMT *Clean raw TMT data from Proteome Discoverer*

Description

Clean raw TMT data from Proteome Discoverer

Usage

```
.cleanRawPDTMT(
  msstats_object,
  remove_shared = TRUE,
  remove_protein_groups = TRUE,
  protein_id_column = "ProteinAccessions",
  intensity_columns_regexp = "Abundance"
)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.
remove_shared	lgl, if TRUE, shared peptides will be removed.
remove_protein_groups	if TRUE, proteins with numProteins > 1 will be removed.
protein_id_column	chr, name of a column with protein IDs.

`intensity_columns_regexp`
: regular expressions that defines intensity columns. Defaults to "Abundance", which means that columns that contain the word "Abundance" will be treated as corresponding to intensities for different channels.

Value

data.table

`.cleanRawPhilosopher` *Clean raw Philosopher files*

Description

Clean raw Philosopher files

Usage

```
.cleanRawPhilosopher(
  msstats_object,
  protein_id_col,
  peptide_id_col,
  channels,
  remove_shared_peptides
)
```

Arguments

`msstats_object` object of class MSstatsPhilosopherFiles

`protein_id_col` character name of a column that identifies proteins

`peptide_id_col` character name of a column that identifies peptides

`channels` character vector of channel labels

`remove_shared_peptides`
: logical, if TRUE, shared peptides will be removed based on the IsUnique column from Philosopher output

Value

data.table

.cleanRawProgenesis *Clean raw Progenesis output*

Description

Clean raw Progenesis output

Usage

```
.cleanRawProgenesis(msstats_object, runs, fix_colnames = TRUE)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.
runs	chr, vector of Run labels.
fix_colnames	lgl, if TRUE, one of the rows will be used as colnames.

Value

data.table

.cleanRawSkyline *Clean raw data from Skyline*

Description

Clean raw data from Skyline

Usage

```
.cleanRawSkyline(msstats_object)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.

Value

data.table

.cleanRawSpectroMineTMT *Clean raw SpectroMine TMT data*

Description

Clean raw SpectroMine TMT data

Usage

```
.cleanRawSpectroMineTMT(msstats_object)
```

Arguments

msstats_object	an object of class MSstatsSpectroMineFiles.

Value

data.table

.cleanRawSpectronaut *Clean raw Spectronaut output.*

Description

Clean raw Spectronaut output.

Usage

```
.cleanRawSpectronaut(msstats_object, intensity)
```

Arguments

msstats_object	an object of class MSstatsSpectronautFiles.
intensity	chr, specifies which column will be used for Intensity.

Value

data.table

.countCommonFeatures *Get common values from two vectors of features*

Description

Get common values from two vectors of features

Usage

```
.countCommonFeatures(features_1, features_2)
```

Arguments

features_1	vector of feature names
features_2	vector of feature_names

Value

character vector of common values of features_1 and features_2

.fillValues *Set column to a single value*

Description

Set column to a single value

Usage

```
.fillValues(input, fill_list)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
fill_list	named list, names correspond to column names, elements to values that will be used in the columns.

Value

data.table

.filterByPattern *Handle filtering by pattern*

Description

Handle filtering by pattern

Usage

```
.filterByPattern(input, col_name, patterns, filter, drop)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions.
col_name	chr, name of the column with peptide sequences.
filter	lgl, if TRUE, peptides will be actually filtered.
drop	lgl, if TRUE, the column will be dropped.
pattern	chr, regular expression - matching peptides will be removed from the data.

Value

data.table

.filterByScore *Filter PSMs / proteins by a given score column.*

Description

Filter PSMs / proteins by a given score column.

Usage

```
.filterByScore(
  input,
  score_column,
  score_threshold,
  direction,
  behavior,
  handle_na = "keep",
  fill_value = NA,
  filter = TRUE,
  drop = TRUE
)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions.
score_column	chr, name of the column that contains scores.
score_threshold	num, values below or above this threshold will be removed from the data.
direction	chr, if "greater" only values above the threshold will be retained, if "smaller" - below the threshold.
behavior	chr, if "remove", values below/above the threshold will be removed, if "replace", they will be set to fill_value.
fill_value	if behavior = "replace", values below/above the threshold will be replaced with fill_value. Defaults to NA.
filter	If TRUE, filtering will be performed.
drop	if TRUE, score_column will be removed.

Value

data.table

.filterExact *Filter out specified symbols.*

Description

Filter out specified symbols.

Usage

```
.filterExact(
  input,
  col_name,
  filter_symbols,
  behavior,
  fill_value,
  filter,
  drop
)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions.
col_name	chr, name of the column that will be the base for filtering
filter_symbols	character vector of symbols that will be removed
behavior	chr, if "remove", values below/above the threshold will be removed, if "replace", they will be set to fill_value.
fill_value	if behavior = "replace", values below/above the threshold will be replaced with fill_value. Defaults to NA.
filter	lgl, if TRUE, decoy proteins will be removed from the data.
drop	lgl, if TRUE, column that contains decoy proteins will be dropped.

Value

data.table

`.filterFewMeasurements` *Remove features with a small number of (non-missing) measurements across runs*

Description

Remove features with a small number of (non-missing) measurements across runs

Usage

```
.filterFewMeasurements(
  input,
  min_intensity,
  remove_few,
  feature_columns = NULL
)
```

Arguments

`input`	`data.table` pre-processed by one of the .cleanRaw* functions.
`min_intensity`	minimum intensity that will be considered non-missing.
`remove_few`	logical, if TRUE, features that have less than three measurements will be removed. If FALSE, only features with all missing runs will be removed.
`features_columns`	chr, vector of names of columns that define features.

Value

data.table

`.filterManyColumns` *Filter rows that contain specifed symbols in multiple columns.*

Description

Filter rows that contain specifed symbols in multiple columns.

Usage

```
.filterManyColumns(input, filter_columns, filter_symbols)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
filter_columns	chr, names of columns in which elements will be matched and removed.
filter_symbols	chr, vector of strings. Rows with corresponding elements in filter_columns will be removed.

Value

data.table

.filterOverlapped *Remove overlapped features*

Description

Remove overlapped features

Usage

```
.filterOverlapped(input, summary_function, overlapped_features)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions and merged with annotation.
summary_function	summary function (mean, sum, max) that will be used to pick one feature from multiple overlapping features
overlapped_features	features that overlap.

Value

data.table

.findAvailable *Select an available options from a set of possibilities*

Description

Select an available options from a set of possibilities

Usage

```
.findAvailable(possibilities, option_set, fall_back = NULL)
```

Arguments

possibilities	possible legal values of a variable
option_set	set of values that includes one of the possibilities
fall_back	if there is none of the possibilities in option_set, or there are multiple hits, default to fall_back

Value

same as option_set, usually character

.fixBasicColumns *Remove underscores from sequences and change intensity type to numeric*

Description

Remove underscores from sequences and change intensity type to numeric

Usage

```
.fixBasicColumns(input)
```

Arguments

input	data.table

Value

data.table

.fixColumnTypes *Change classes of multiple columns*

Description

Change classes of multiple columns

Usage

```
.fixColumnTypes(
  input,
  numeric_columns = NULL,
  character_columns = NULL,
  factor_columns = NULL
)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
numeric_columns	chr, vector of names of columns that will be converted to numeric.
character_columns	chr, vector of names of colums taht will be converted to character.
factor_columns	chr, vector of names of columns that will be converted to factor.

Value

data.table

.fixMissingValues *Change labels for missing values*

Description

Change labels for missing values

Usage

```
.fixMissingValues(input, fix_missing = NULL)
```

Arguments

input	output of MSstatsPreprocess
fix_missing	missing values can be labeled by NA, 0 or both. If NULL, data were processed by Skyline, so missing values will be denoted by both NA and 0. If "na_to_zero", NA values will be replaced by 0. If "zero_to_na", 0 values will be replaced by NA

Value

data.table

.getChannelColumns *Get intensity columns from wide-format data*

Description

Get intensity columns from wide-format data

Usage

```
.getChannelColumns(col_names, ...)
```

Arguments

col_names	names of columns, where some of the columns store intensity value for different channels
...	varying number of strings that define channel columns.

Value

character vector of column names that correspond to channel intensities

---

.getCorrectFraction *Get a name of fraction with the largest number of measurements or the largest average intensity*

Description

Get a name of fraction with the largest number of measurements or the largest average intensity

Usage

```
.getCorrectFraction(input)
```

Arguments

input	output of MSstatsPreprocess

Value

character - label of the fraction that has most measurements or highest mean intensity for a given feature

---

.getDataTable *Read file from a provided path or convert given data.frame to data.table*

Description

Read file from a provided path or convert given data.frame to data.table

Usage

```
.getDataTable(input, ...)
```

Arguments

input	report from a signal processing tool or a path to it
...	additional parameters for data.table::fread

Value

data.table

.getFullDesign *Create a data.frame of each combination of values for given variables*

Description

Create a data.frame of each combination of values for given variables

Usage

```
.getFullDesign(input, group_col, feature_col, measurement_col, is_tmt)
```

Arguments

input	output of MSstatsPreprocess
group_col	name of column in input. Combination of values of feature_col and measurement_col will be created within each unique value of this column
is_tmt	if TRUE, data will be treated as coming from TMT experiment.
‘feature_column‘	name of the column that labels features
‘measurement_col‘	name of a column with measurement labels - Runs in label-free case, Channels in TMT case.

Value

data.table

.getMissingRunsPerFeature *Get names of missing runs*

Description

Get names of missing runs

Usage

```
.getMissingRunsPerFeature(input)
```

Arguments

input	output of MSstatsPreprocess

Value

data.table

.getOverlappingFeatures *Get features that are overlapped among multiple runs*

Description

Get features that are overlapped among multiple runs

Usage

```
.getOverlappingFeatures(input)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions and merged with annotation.

Value

data.table

.handleFiltering *Handle PSM/proteins scores*

Description

Handle PSM/proteins scores

Usage

```
.handleFiltering(input, score_filtering, exact_filtering, pattern_filtering)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions.
score_filtering	list of by-score filtering controls.
exact_filtering	list of exact filtering controls.
pattern_filtering	list of by-pattern filtering controls.

Value

data.table

.handleFractions *Check if there are overlapping features and remove if needed*

Description

Check if there are overlapping features and remove if needed

Usage

```
.handleFractions(input)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions and merged with annotation.

Value

data.table

.handleFractionsLF *Handle overlapping features*

Description

Handle overlapping features

Usage

```
.handleFractionsLF(input)
```

Arguments

input	output of MSstatsPreprocess

Value

data.table

.handleFractionsTMT *Remove peptide ions overlapped among multiple fractions of the same biological mixture*

Description

Remove peptide ions overlapped among multiple fractions of the same biological mixture

Usage

```
.handleFractionsTMT(input)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions and merged with annotation.

Value

data.table

.handleIsotopicPeaks *Handle isotopic peaks*

Description

Handle isotopic peaks

Usage

```
.handleIsotopicPeaks(input, aggregate = FALSE)
```

Arguments

input	data.table preprocessed by one of the cleanRaw* functions.
aggregate	if TRUE, isotopic peaks will be summed.

Value

data.table

.handleSharedPeptides *Handle shared peptides.*

Description

Handle shared peptides.

Usage

```
.handleSharedPeptides(
  input,
  remove_shared = TRUE,
  protein_column = "ProteinName",
  peptide_column = "PeptideSequence"
)
```

Arguments

input	data.table pre-processed by one of the .cleanRaw* functions.
remove_shared	lgl, if TRUE, shared peptides will be removed
protein_column	chr, name of the column with names of proteins.
peptide_column	chr, name of the column with peptide sequences.

Value

data.table

.handleSingleFeaturePerProtein *Remove proteins only identified by a single feature*

Description

Remove proteins only identified by a single feature

Usage

```
.handleSingleFeaturePerProtein(input, remove_single_feature)
```

Arguments

input	data.table pre-processed by one of the .cleanRaw* functions.
remove_single_feature	lgl, if TRUE, proteins with a single feature will be removed.

Value

data.table

.logConverterOptions *Log information about converter options*

Description

Log information about converter options

Usage

```
.logConverterOptions(
  feature_columns,
  remove_shared_peptides,
  remove_single_feature_proteins,
  feature_cleaning,
  is_tmt = FALSE
)
```

Arguments

feature_columns	character vector of names of columns that define spectral features.
remove_shared_peptides	logical, if TRUE shared peptides will be removed.
remove_single_feature_proteins	logical, if TRUE, proteins that only have one feature will be removed.
feature_cleaning	named list with maximum two (for MSstats converters) or three (for MSstatsTMT converter) elements. If handle_few_measurements is set to "remove", feature with less than three measurements will be removed (otherwise it should be equal to "keep"). summarize_multiple_psms is a function that will be used to aggregate multiple feature measurements in a run. It should return a scalar and accept an na.rm parameter. For MSstatsTMT converters, setting remove_psms_with_any_missing will remove features which have missing values in a run from that run.
is_tmt	If TRUE, the dataset comes from a TMT experiment

Value

TRUE invisibly if message was logged

.logSuccess *Make a message about successful data cleaning/importing*

Description

Make a message about successful data cleaning/importing

Usage

```
.logSuccess(tool, event)
```

Arguments

tool	name of a signal processing tool

Value

TRUE invisibly if logging was sucessful

.makeBalancedDesign *Fill missing rows to create balanced design*

Description

Fill missing rows to create balanced design

Usage

```
.makeBalancedDesign(input, fill_missing)
```

Arguments

input	output of MSstatsPreprocess
fill_missing	if TRUE, missing Intensities values will be added to data and marked as NA

Value

data.table

.makeExactFilterMessage *Make a message about filtering based on fixed values*

Description

Make a message about filtering based on fixed values

Usage

```
.makeExactFilterMessage(col_name, filter_symbols, behavior, fill_value)
```

Arguments

col_name	chr, name of the column that will be the base for filtering
filter_symbols	character vector of symbols that will be removed
behavior	chr, if "remove", values below/above the threshold will be removed, if "replace", they will be set to fill_value.
fill_value	if behavior = "replace", values below/above the threshold will be replaced with fill_value. Defaults to NA.

Value

character - message

`.makeScoreFilterMessage` *Make a message about filtering based on a score*

Description

Make a message about filtering based on a score

Usage

```
.makeScoreFilterMessage(
  score_column,
  score_threshold,
  direction,
  behavior,
  fill_value
)
```

Arguments

`score_column`	chr, name of the column that contains scores.
`score_threshold`	num, values below or above this threshold will be removed from the data.
`direction`	chr, if "greater" only values above the threshold will be retained, if "smaller" - below the threshold.
`behavior`	chr, if "remove", values below/above the threshold will be removed, if "replace", they will be set to `fill_value`.
`fill_value`	if `behavior` = "replace", values below/above the threshold will be replaced with `fill_value`. Defaults to `NA`.

Value

character - message

`.mergeAnnotation` *Merge annotation with feature data*

Description

Merge annotation with feature data

Usage

```
.mergeAnnotation(input, annotation)
```

Arguments

annotation	data.table with annotation
data.table	preprocessed by one of the .cleanRaw* functions.

Value

data.table

.MSstatsFormat *Output format for further analysis by MSstats*

Description

Output format for further analysis by MSstats

Usage

```
.MSstatsFormat(input)
```

Arguments

input	data.table

Value

object of class MSstatsValidated that inherits from data.frame

---

.nullAppender *log4r appender used not to write messages*

Description

A convenience function written to save time on checking if messages should be printed or logs should be written to a file.

Usage

```
.nullAppender(level, ...)
```

Arguments

level	log level
...	messages - ignored

Value

NULL invisibly

.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

.removeOverlappingFeatures *Replace intensities of overlapped fractions with NA, keeping only one fraction*

Description

Replace intensities of overlapped fractions with NA, keeping only one fraction

Usage

```
.removeOverlappingFeatures(input)
```

Arguments

input	output of MSstatsPreprocess

Value

data.table

.removeSharedPeptides *Remove peptides assigned to more than one protein.*

Description

Remove peptides assigned to more than one protein.

Usage

```
.removeSharedPeptides(input, protein_column, peptide_column)
```

Arguments

input	data.table pre-processed by one of the .cleanRaw* functions.
protein_column	chr, name of the column with names of proteins.
peptide_column	chr, name of the column with peptide sequences.

Value

data.table

.selectMSstatsColumns *Select columns for MSstats format*

Description

Select columns for MSstats format

Usage

```
.selectMSstatsColumns(input)
```

Arguments

input	data.table

Value

data.table

`.sharedParametersAmongConverters` *A dummy function to store shared documentation items for converters.*

Description

A dummy function to store shared documentation items for converters.

Usage

```
.sharedParametersAmongConverters()
```

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 wil 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`.

.standardizeColnames *Change column names to match read.table/read.csv/read.delim conventions*

Description

Change column names to match read.table/read.csv/read.delim conventions

Usage

```
.standardizeColnames(col_names)
```

Arguments

col_names	chr, vector of column names

Value

character vector

.summarizeMultipleMeasurements *Summarize multiple measurements per feature in a single run*

Description

Summarize multiple measurements per feature in a single run

Usage

```
.summarizeMultipleMeasurements(input, aggregator, feature_columns)
```

Arguments

input	data.table pre-processed by one of the .cleanRaw* functions.
aggregator	function that will be used to aggregate duplicated values.
feature_columns	chr, vector of names of columns that define features.

Value

data.table

.summarizeMultiplePSMs

Pick one PSM from a data.table of several PSMs.

Description

Pick one PSM from a data.table of several PSMs.

Usage

```
.summarizeMultiplePSMs(input, summary_function)
```

Arguments

input	data.table preprocessed by one of the .cleanRaw* functions.
summary_function	function that will be used to aggregate intensities if needed.

Value

character - label of a chosen PSM

.validatePDTMTInputColumns

Helper method to validate input has necessary columns

Description

Helper method to validate input has necessary columns

Usage

```
.validatePDTMTInputColumns(
  pd_input,
  protein_id_column,
  num_proteins_column,
  channels
)
```

Arguments

pd_input	data.frame input
protein_id_column	column name for protein passed from user
num_proteins_column	column name for number of protein groups passed from user
channels	list of column names for channels

as.data.frame.MSstatsValidated

Convert output of converters to data.frame

Description

Convert output of converters to data.frame

Usage

```
## S3 method for class 'MSstatsValidated'
as.data.frame(x, ...)
```

Arguments

x	object of class MSstatsValidated
...	Additional arguments to be passed to or from other methods.

Value

data.frame

as.data.table.MSstatsValidated

Convert output of converters to data.table

Description

Convert output of converters to data.table

Usage

```
## S3 method for class 'MSstatsValidated'
as.data.table(x, ...)
```

Arguments

x	object of class MSstatsValidated
...	Additional arguments to be passed to or from other methods.

Value

data.tables

`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,
  quantificationColumn = "FragmentQuantCorrected",
  ...
)
```

Arguments

`input`	name of MSstats input report from Diann, which includes feature-level data.
`annotation`	name of 'annotation.txt' data which includes Condition, BioReplicate, Run.
`global_qvalue_cutoff`	The global qvalue cutoff
`qvalue_cutoff`	local qvalue cutoff for library
`pg_qvalue_cutoff`	local qvalue cutoff for protein groups Run should be the same as filename.
`useUniquePeptide`	should unique pepties be removed
`removeFewMeasurements`	should proteins with few measurements be removed
`removeOxidationMpeptides`	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 wil 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
quantificationColumn	Use 'FragmentQuantCorrected'(default) column for quantified intensities. 'FragmentQuantRaw' can be used instead.
...	additional parameters to data.table::fread.

Value

data.frame in the MSstats required format.

Author(s)

Elijah Willie

Examples

```
input_file_path = system.file("tinytest/raw_data/DIANN/diann_input.tsv",
                              package="MSstatsConvert")
annotation_file_path = system.file("tinytest/raw_data/DIANN/annotation.csv",
                              package = "MSstatsConvert")
input = data.table::fread(input_file_path)
annot = data.table::fread(annotation_file_path)
output = DIANNtoMSstatsFormat(input, annotation = annot, MBR = FALSE,
                              use_log_file = FALSE)
head(output)
```

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

raw.frag	name of FragSummary_date.xls data, which includes feature-level data.
raw.pep	name of PeptideSummary_date.xls data, which includes selected fragments information.
raw.pro	name of ProteinSummary_date.xls data, which includes selected peptides information.
annotation	name of annotation data which includes Condition, BioReplicate, Run information.
useSelectedFrag	TRUE will use the selected fragment for each peptide. 'Selected_fragments' column is required.
useSelectedPep	TRUE will use the selected peptide for each protein. 'Selected_peptides' column is required.
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 wil 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

```
diau_frag = system.file("tinytest/raw_data/DIAUmpire/dia_frag.csv",
                            package = "MSstatsConvert")
diau_pept = system.file("tinytest/raw_data/DIAUmpire/dia_pept.csv",
                            package = "MSstatsConvert")
diau_prot = system.file("tinytest/raw_data/DIAUmpire/dia_prot.csv",
                            package = "MSstatsConvert")
annot = system.file("tinytest/raw_data/DIAUmpire/annot_diau.csv",
                    package = "MSstatsConvert")
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)
```

`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 wil 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)
```

---

getDataType *Get type of dataset from an MSstatsInputFiles object.*

Description

Get type of dataset from an MSstatsInputFiles object.

Usage

```
getDataType(msstats_object)

## S4 method for signature 'MSstatsInputFiles'
getDataType(msstats_object)
```

Arguments

msstats_object	object that inherits from MSstatsInputFiles class.

Value

character - label of a data type. Currently, "MSstats" or "MSstatsTMT"

character "MSstats" or "MSstatsTMT".

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
class(imported)
getDataType(imported) # "MSstats"
```

---

getInputFile *Get one of files contained in an instance of* MSstatsInputFiles *class.*

Description

Get one of files contained in an instance of MSstatsInputFiles class.

Usage

```
getInputFile(msstats_object, file_type)

## S4 method for signature 'MSstatsInputFiles'
getInputFile(msstats_object, file_type = "input")

## S4 method for signature 'MSstatsPhilosopherFiles'
getInputFile(msstats_object, file_type = "input")
```

Arguments

msstats_object	object that inherits from MSstatsPhilosopherFiles class.
file_type	character name of a type file. Usually equal to "input".

Value

data.table

data.table

data.table

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
class(imported)
head(getInputFile(imported, "evidence"))
```

`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 wil 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)
```

`MetamorpheusToMSstatsFormat` *Import Metamorpheus files*

Description

Import Metamorpheus files

Usage

```
MetamorpheusToMSstatsFormat(
  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

`input`	name of Metamorpheus output file, which is tabular format. Use the AllQuantifiedPeaks.tsv file from the Metamorpheus output.
`annotation`	name of 'annotation.txt' data which includes Condition, BioReplicate.
`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 wil 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)

Anthony Wu

Examples

```
input = system.file("tinytest/raw_data/Metamorpheus/AllQuantifiedPeaks.tsv",
                                package = "MSstatsConvert")
input = data.table::fread(input)
annot = system.file("tinytest/raw_data/Metamorpheus/Annotation.tsv",
                                package = "MSstatsConvert")
annot = data.table::fread(annot)
metamorpheus_imported = MSstatsConvert:::MetamorpheusToMSstatsFormat(input, annotation = annot)
head(metamorpheus_imported)
```

MSstatsBalancedDesign *Creates balanced design by removing overlapping fractions and filling incomplete rows*

Description

Creates balanced design by removing overlapping fractions and filling incomplete rows

Usage

```
MSstatsBalancedDesign(
  input,
  feature_columns,
  fill_incomplete = TRUE,
  handle_fractions = TRUE,
  fix_missing = NULL,
  remove_few = TRUE
)
```

Arguments

input	data.table processed by the MSstatsPreprocess function
feature_columns	str, names of columns that define spectral features
fill_incomplete	if TRUE (default), Intensity values for missing runs will be added as NA
handle_fractions	if TRUE (default), overlapping fractions will be resolved
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.
remove_few	lgl, if TRUE, features with one or two measurements across runs will be removed.

Value

data.frame of class `MSstatsValidated`

Examples

```
unbalanced_data = system.file("tinytest/raw_data/unbalanced_data.csv",
                              package = "MSstatsConvert")
unbalanced_data = data.table::as.data.table(read.csv(unbalanced_data))
balanced = MSstatsBalancedDesign(unbalanced_data,
                                 c("PeptideSequence", "PrecursorCharge",
                                   "FragmentIon", "ProductCharge"))
dim(balanced) # Now balanced has additional rows (with Intensity = NA)
# for runs that were not included in the unbalanced_data table
```

MSstatsClean *Clean files generated by a signal processing tools.*

Description

Clean files generated by a signal processing tools.

Clean DIAUmpire files

Clean MaxQuant files

Clean OpenMS files

Clean OpenSWATH files

Clean Progenesis files

Clean ProteomeDiscoverer files

Clean Skyline files

Clean SpectroMine files

Clean Spectronaut files

Clean Philosopher files

Clean DIA-NN files

Clean Metamorpheus files

Clean Protein Prospector files

Usage

```
MSstatsClean(msstats_object, ...)

## S4 method for signature 'MSstatsDIAUmpireFiles'
MSstatsClean(msstats_object, use_frag, use_pept)

## S4 method for signature 'MSstatsMaxQuantFiles'
MSstatsClean(
  msstats_object,
  protein_id_col,
  remove_by_site = FALSE,
```

```
  channel_columns = "Reporterintensitycorrected"
)

## S4 method for signature 'MSstatsOpenMSFiles'
MSstatsClean(msstats_object)

## S4 method for signature 'MSstatsOpenSWATHFiles'
MSstatsClean(msstats_object)

## S4 method for signature 'MSstatsProgenesisFiles'
MSstatsClean(msstats_object, runs, fix_colnames = TRUE)

## S4 method for signature 'MSstatsProteomeDiscovererFiles'
MSstatsClean(
  msstats_object,
  quantification_column,
  protein_id_column,
  sequence_column,
  remove_shared,
  remove_protein_groups = TRUE,
  intensity_columns_regexp = "Abundance"
)

## S4 method for signature 'MSstatsSkylineFiles'
MSstatsClean(msstats_object)

## S4 method for signature 'MSstatsSpectroMineFiles'
MSstatsClean(msstats_object)

## S4 method for signature 'MSstatsSpectronautFiles'
MSstatsClean(msstats_object, intensity)

## S4 method for signature 'MSstatsPhilosopherFiles'
MSstatsClean(
  msstats_object,
  protein_id_col,
  peptide_id_col,
  channels,
  remove_shared_peptides
)

## S4 method for signature 'MSstatsDIANNFiles'
MSstatsClean(
  msstats_object,
  MBR = TRUE,
  quantificationColumn = "FragmentQuantCorrected"
)

## S4 method for signature 'MSstatsMetamorpheusFiles'
MSstatsClean(msstats_object)

## S4 method for signature 'MSstatsProteinProspectorFiles'
```

```
MSstatsClean(msstats_object)
```

Arguments

msstats_object	object that inherits from MSstatsInputFiles class.
...	additional parameter to specific cleaning functions.
use_frag	TRUE will use the selected fragment for each peptide. 'Selected_fragments' column is required.
use_pept	TRUE will use the selected fragment for each protein 'Selected_peptides' column is required.
protein_id_col	character, name of a column with names of proteins.
remove_by_site	logical, if TRUE, proteins only identified by site will be removed.
channel_columns	character, regular expression that identifies channel columns in TMT data.
runs	chr, vector of Run labels.
fix_colnames	lgl, if TRUE, one of the rows will be used as colnames.
quantification_column	chr, name of a column used for quantification.
protein_id_column	chr, name of a column with protein IDs.
sequence_column	chr, name of a column with peptide sequences.
remove_shared	lgl, if TRUE, shared peptides will be removed.
remove_protein_groups	if TRUE, proteins with numProteins > 1 will be removed.
intensity_columns_regexp	regular expressions that defines intensity columns. Defaults to "Abundance", which means that columns that contain the word "Abundance" will be treated as corresponding to intensities for different channels.
intensity	chr, specifies which column will be used for Intensity.
peptide_id_col	character name of a column that identifies peptides
channels	character vector of channel labels
remove_shared_peptides	logical, if TRUE, shared peptides will be removed based on the IsUnique column from Philosopher output
MBR	True if analysis was done with match between runs
quantificationColumn	Use 'FragmentQuantCorrected'(default) column for quantified intensities. 'FragmentQuantRaw' can be used instead.

Value

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

data.table

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
cleaned_data = MSstatsClean(imported, protein_id_col = "Proteins")
head(cleaned_data)
```

`MSstatsConvert` *MSstatsConvert: An R Package to Convert Data from Mass Spectrometry Signal Processing Tools to MSstats Format*

Description

MSstatsConvert helps convert data from different types of mass spectrometry experiments and signal processing tools to a format suitable for statistical analysis with the MSstats and MSstatsTMT packages.

Main functions

`MSstatsLogsSettings` for logs management, `MSstatsImport` for importing files created by signal processing tools, `MSstatsClean` for re-formatting imported files into a consistent format, `MSstatsPreprocess` for preprocessing cleaned files, `MSstatsBalancedDesign` for handling fractions and creating balanced data.

Author(s)

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`MSstatsImport` *Import files from signal processing tools.*

Description

Import files from signal processing tools.

Usage

```
MSstatsImport(input_files, type, tool, tool_version = NULL, ...)
```

Arguments

`input_files`	list of paths to input files or `data.frame` objects. Interpretation of this parameter depends on values of parameters `type` and `tool`.
`type`	chr, "MSstats" or "MSstatsTMT".
`tool`	chr, name of a signal processing tool that generated input files.
`tool_version`	not implemented yet. In the future, this parameter will allow handling different versions of each signal processing tools.
`...`	optional additional parameters to `data.table::fread`.

Value

an object of class `MSstatsInputFiles`.

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
class(imported)
head(getInputFile(imported, "evidence"))
```

`MSstatsInputFiles-class`
Class to model files that describe a single MS dataset.

Description

Class to model files that describe a single MS dataset.

MSstatsDIAUmpireFiles: class for DIAUmpire files.

MSstatsMaxQuantFiles: class for MaxQuant files.

MSstatsOpenMSFiles: class for OpenMS files.

MSstatsOpenSWATHFiles: class for OpenSWATH files.

MSstatsProgenesisFiles: class for Progenesis files.

MSstatsProteomeDiscovererFiles: class for ProteomeDiscoverer files.

MSstatsSkylineFiles: class for Skyline files.

MSstatsSkylineFiles: class for SpectroMine files.

MSstatsSpectronautFiles: class for Spectronaut files.

MSstatsPhilosopherFiles: class for Philosopher files.

MSstatsDIANNFiles: class for DIA-NN files.

MSstatsFragPipeFiles: class for FragPipe files.

MSstatsMetamorpheusFiles: class for Metamorpheus files.

MSstatsProteinProspectorFiles: class for ProteinProspector files.

Slots

`files` named list of files generated by a signal processing tools. In most cases, this will be a single file named `input`. In some cases, multiple files are used, for example `MaxQuant` outputs `evidence` and `proteinGroups` files.

`type` character: "MSstats" or "MSstatsTMT".

`tool` character: name of a signal processing tools that generated the output. Possible values are: DIAUmpire, MaxQuant, OpenMS, OpenSWATH, Progenesis, ProteomeDiscoverer, Skyline, SpectroMine, Spectronaut.

`version` description of a software version of the signal processing tool. Not implemented yet.

`MSstatsLogsSettings` *Set how MSstats will log information from data processing*

Description

Set how MSstats will log information from data processing

Usage

```
MSstatsLogsSettings(
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL,
  base = "MSstats_log_",
  pkg_name = "MSstats"
)
```

Arguments

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 wil 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.
base	start of the file name.
pkg_name	currently "MSstats", "MSstatsPTM" or "MSstatsTMT". Each package can use its own separate log settings.

Value

TRUE invisibly in case of successful logging setup.

Examples

```
# No logging and no messages
MSstatsLogsSettings(FALSE, FALSE, FALSE)
# Log, but do not display messages
MSstatsLogsSettings(TRUE, FALSE, FALSE)
# Log to an existing file
file.create("new_log.log")
MSstatsLogsSettings(TRUE, TRUE, log_file_path = "new_log.log")
# Do not log, but display messages
MSstatsLogsSettings(FALSE)
```

MSstatsMakeAnnotation *Create annotation*

Description

Create annotation

Usage

```
MSstatsMakeAnnotation(input, annotation, ...)
```

Arguments

input	data.table preprocessed by the MSstatsClean function
annotation	data.table
...	key-value pairs, where keys are names of columns of annotation

Value

data.table

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
cleaned_data = MSstatsClean(imported, protein_id_col = "Proteins")
annot_path = system.file("tinytest/raw_data/MaxQuant/annotation.csv",
                         package = "MSstatsConvert")
mq_annot = MSstatsMakeAnnotation(cleaned_data, read.csv(annot_path),
                                 Run = "Rawfile")
head(mq_annot)
```

MSstatsPreprocess *Preprocess outputs from MS signal processing tools for analysis with MSstats*

Description

Preprocess outputs from MS signal processing tools for analysis with MSstats

Usage

```
MSstatsPreprocess(
  input,
  annotation,
  feature_columns,
  remove_shared_peptides = TRUE,
  remove_single_feature_proteins = TRUE,
  feature_cleaning = list(remove_features_with_few_measurements = TRUE,
    summarize_multiple_psms = max),
  score_filtering = list(),
  exact_filtering = list(),
  pattern_filtering = list(),
  columns_to_fill = list(),
  aggregate_isotopic = FALSE,
  ...
)
```

Arguments

input	data.table processed by the MSstatsClean function.
annotation	annotation file generated by a signal processing tool.
feature_columns	character vector of names of columns that define spectral features.
remove_shared_peptides	logical, if TRUE shared peptides will be removed.

remove_single_feature_proteins
: logical, if TRUE, proteins that only have one feature will be removed.

feature_cleaning
: named list with maximum two (for MSstats converters) or three (for MSstatsTMT converter) elements. If handle_few_measurements is set to "remove", feature with less than three measurements will be removed (otherwise it should be equal to "keep"). summarize_multiple_psms is a function that will be used to aggregate multiple feature measurements in a run. It should return a scalar and accept an na.rm parameter. For MSstatsTMT converters, setting remove_psms_with_any_missing will remove features which have missing values in a run from that run.

score_filtering
: a list of named lists that specify filtering options. Details are provided in the vignette.

exact_filtering
: a list of named lists that specify filtering options. Details are provided in the vignette.

pattern_filtering
: a list of named lists that specify filtering options. Details are provided in the vignette.

columns_to_fill
: a named list of scalars. If provided, columns with names defined by the names of this list and values corresponding to its elements will be added to the output data.frame.

aggregate_isotopic
: logical. If TRUE, isotopic peaks will by summed.

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

Value

data.table

Examples

```
evidence_path = system.file("tinytest/raw_data/MaxQuant/mq_ev.csv",
                            package = "MSstatsConvert")
pg_path = system.file("tinytest/raw_data/MaxQuant/mq_pg.csv",
                      package = "MSstatsConvert")
evidence = read.csv(evidence_path)
pg = read.csv(pg_path)
imported = MSstatsImport(list(evidence = evidence, protein_groups = pg),
                         "MSstats", "MaxQuant")
cleaned_data = MSstatsClean(imported, protein_id_col = "Proteins")
annot_path = system.file("tinytest/raw_data/MaxQuant/annotation.csv",
                         package = "MSstatsConvert")
mq_annot = MSstatsMakeAnnotation(cleaned_data, read.csv(annot_path),
                                 Run = "Rawfile")

# To filter M-peptides and oxidatin peptides
m_filter = list(col_name = "PeptideSequence", pattern = "M",
                filter = TRUE, drop_column = FALSE)
oxidation_filter = list(col_name = "Modifications", pattern = "Oxidation",
                        filter = TRUE, drop_column = TRUE)
```

```
msstats_format = MSstatsPreprocess(
cleaned_data, mq_annot,
feature_columns = c("PeptideSequence", "PrecursorCharge"),
columns_to_fill = list(FragmentIon = NA, ProductCharge = NA),
pattern_filtering = list(oxidation = oxidation_filter, m = m_filter)
)
# Output in the standard MSstats format
head(msstats_format)
```

MSstatsSaveSessionInfo *Save session information*

Description

Save session information

Usage

```
MSstatsSaveSessionInfo(
  path = NULL,
  append = TRUE,
  base = "MSstats_session_info_"
)
```

Arguments

path	optional path to output file. If not provided, "MSstats_session_info" and current timestamp will be used as a file name
append	if TRUE and file given by the path parameter already exists, session info will be appended to the file
base	beginning of a file name

Value

TRUE invisibly after session info was saved

Examples

```
MSstatsSaveSessionInfo("session_info.txt")
MSstatsSaveSessionInfo("session_info.txt", base = "MSstatsTMT_session_info_")
```

`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

`input`	name of MSstats input report from OpenMS, which includes feature(peptide ion)-level data.
`annotation`	name of 'annotation.txt' data which includes Condition, BioReplicate, Run. Run should be the same as filename.
`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 wil 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

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

`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 wil 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

```
os_raw = system.file("tinytest/raw_data/OpenSWATH/openswath_input.csv",
                             package = "MSstatsConvert")
annot = system.file("tinytest/raw_data/OpenSWATH/annot_os.csv",
                    package = "MSstatsConvert")
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 wil 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/raw_data/PD/annot_pd.csv",
                    package = "MSstatsConvert")
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)
```

ProgenesistoMSstatsFormat

Import Progenesis files

Description

Import Progenesis files

Usage

```
ProgenesistoMSstatsFormat(
  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 wil 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)
```

`ProteinProspectortoMSstatsTMTFormat` *Generate MSstatsTMT required input format from Protein Prospector output*

Description

Generate MSstatsTMT required input format from Protein Prospector output

Usage

```
ProteinProspectortoMSstatsTMTFormat(
  input,
  annotation,
  useUniquePeptide = TRUE,
  removeFewMeasurements = TRUE,
  removeProtein_with1Feature = FALSE,
  summaryforMultipleRows = sum,
  use_log_file = TRUE,
  append = FALSE,
  verbose = TRUE,
  log_file_path = NULL
)
```

Arguments

`input`	txt report file from Protein Prospector with `Keep Replicates` option selected.
`annotation`	data frame which contains column Run, Fraction, TechRepMixture, Mixture, Channel, BioReplicate, Condition.
`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 wil 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

data.frame of class "MSstatsTMT"

Examples

```
input = system.file("tinytest/raw_data/ProteinProspector/Prospector_TotalTMT.txt",
    package = "MSstatsConvert")
input = data.table::fread(input)
annot = system.file("tinytest/raw_data/ProteinProspector/Annotation.csv",
                                package = "MSstatsConvert")
annot = data.table::fread(annot)
output <- ProteinProspectortoMSstatsTMTFormat(input, annot)
head(output)
```

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 wil 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 = FALSE,
  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	FALSE(default) will not perform any filtering. TRUE 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 wil 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)
```

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