

# Package ‘MSnbase’

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**Title** MSnbase: Base Functions and Classes for MS-based Proteomics

**Version** 1.6.2

**Description** Basic plotting, data manipulation and processing of MS-based Proteomics data

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**LazyData** yes

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## R topics documented:

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**Description**

MSnbase provides classes, methods and functions for visualisation, manipulation and processing of mass spectrometry data.

Important class are "[MSnExp](#)" (raw data file), "[MSnSet](#)" (quantitation data) and "[ReporterIons](#)" (reporter ions for labelled proteomics).

Other classes are "[Spectrum](#)" and the subclasses "[Spectrum1](#)" (for MS spectra) and "[Spectrum2](#)" (for MSMS spectra), "[MIAPE](#)" (Minimum Information about Proteomics Experiments) and "[MSnProcess](#)" (for processing information). These should however not be of direct utility to users.

**Author(s)**

Laurent Gatto

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**References**

Laurent Gatto and Kathryn S. Lilley, MSnbase - an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation, *Bioinformatics* 28(2), 288-289 (2012).

Gatto L. and Lilley K.S., Towards reproducible MSMS data preprocessing, quality control and quantification. BSPR/EBI Proteomics Meeting, Hinxton, United Kingdom, 13-15 July 2010, <http://dx.doi.org/10.1038/npre.2010.5010.1>.

**See Also**

Introductory information, use cases and details are available from the vignettes:

- The demo vignette describe an use-case using a dummy data set provided with the package. It can be accessed with `vignette("MSnbase-demo", package = "MSnbase")`.
- The development vignette describes the classes implemented in MSnbase and can be accessed with `vignette("MSnbase-development", package = "MSnbase")`.
- Details about input/output capabilities and formats can be found in `vignette("MSnbase-io", package = "MSnbase")`.

Complete listing of available documentation with `library(help = "MSnbase")`.

---

clean-methods

*Cleans 'MSnExp' or 'Spectrum' instances*

---

**Description**

This method cleans out individual spectra (Spectrum instances) or whole experiments (MSnExp instances) of 0-intensity peaks. Original 0-intensity values are retained only around peaks. If more than two 0's were separating two peaks, only the first and last ones, those directly adjacent to the peak ranges are kept. If two peaks are separated by only one 0-intensity value, it is retained. An illustrative example is shown below.

**Methods**

`signature(object = "MSnExp", verbose = "logical")` Cleans all spectra in MSnExp object. Displays a control bar if verbose set to TRUE (default). Returns a cleaned MSnExp instance.

`signature(object = "Spectrum")` Cleans the Spectrum object. Returns a cleaned Spectrum instance.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

[removePeaks](#) and [trimMz](#) for other spectra processing methods.

**Examples**

```
int <- c(1,0,0,0,0,0,0,1,1,1,0,0,0,0,0,1,1,0,0,0,0,0,0,0,0,0,0,1,0,0,0)
sp1 <- new("Spectrum2",
          intensity=int,
          mz=1:length(int))
sp2 <- clean(sp1)
intensity(sp1)
intensity(sp2)
```

```
data(itraqdata)
itraqdata2 <- clean(itraqdata)
sum(peaksCount(itraqdata))
sum(peaksCount(itraqdata2))
processingData(itraqdata2)
```

---

combineFeatures	<i>Combines features in an 'MSnSet' object</i>
-----------------	--

---

**Description**

This function combines the features in an "MSnSet" instance applying a summarisation function (see fun argument) to sets of features as defined by a factor (see groupBy argument).

Note that the feature names are automatically updated based on the groupBy parameter.

**Usage**

```
combineFeatures(object, groupBy, fun = c("mean", "median", "weighted.mean", "sum", "medpolish"), ..., verbose)
```

**Arguments**

object	An instance of class "MSnSet" whose features will be summerised.
groupBy	An object of class factor defining how to summerise the features.
fun	The summerising function. Currently, mean, median, weighted mean, sum and median polish are implemented, but user-defined functions can also be supplied.
...	Additional arguments for the fun function.
verbose	A logical indicating whether verbose output is to be printed out.

**Value**

A new "MSnSet" instance is returned with ncol (i.e. number of samples) is unchanged, but nrow (i.e. the number of features) is now equals to the number of levels in groupBy. The feature metadata (featureData slot) is updated accordingly and only the first occurrence of a feature in the original feature meta-data is kept.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

## Examples

```
data(itraqdata)
quant <- quantify(itraqdata[11:15], method = "max", reporters = iTRAQ4)
dim(quant)
## arbitrary grouping into two groups
grp <- as.factor(c(1, 1, 2, 2, 2))
quant.comb <- combineFeatures(quant, grp, "sum")
dim(quant.comb)
exprs(quant.comb)
```

---

extractPrecSpectra-methods

*Extracts precursor-specific spectra from an 'MSnExp' object*

---

## Description

Extracts the MSMS spectra that originate from the precursor(s) having the same MZ value as defined in the `prec` argument.

A warning will be issued if one or several of the precursor MZ values in `prec` are absent in the experiment precursor MZ values (i.e. in `precursorMz(object)`).

## Methods

`signature(object = "MSnExp", prec = "numeric")` Returns an "MSnExp" containing MSMS spectra whose precursor MZ values are in `prec`.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## Examples

```
file <- dir(system.file(package="MSnbase", dir="extdata"),
            full.name=TRUE, pattern="mzXML$")
aa <- readMSData(file, verbose=FALSE)
my.prec <- precursorMz(aa)[1]
my.prec
bb <- extractPrecSpectra(aa, my.prec)
precursorMz(bb)
processingData(bb)
```

fillUp

*Fills up a vector*

---

**Description**

This function replaces all the empty characters "" and/or NAs with the value of the closest preceding the preceding non-NA/"" element. The function is used to populate dataframe or matrix columns where only the cells of the first row in a set of partially identical rows are explicitly populated and the following are empty.

**Usage**

```
fillUp(x)
```

**Arguments**

x                    a vector.

**Value**

A vector as x with all empty characters "" and NA values replaced by the preceding non-NA/"" value.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
d <- data.frame(protein=c("Prot1","", "", "Prot2","", ""),
                peptide=c("pep11","", "pep12", "pep21", "pep22", ""),
                score=c(1:2, NA, 1:3))
d
e <- apply(d, 2, fillUp)
e
data.frame(e)
fillUp(d[,1])
```

---

formatRt*Format Retention Time*

---

**Description**

Converts seconds to min:sec format

**Usage**

```
formatRt(rt)
```

**Arguments**

rt                    retention in in seconds

**Details**

This function is used to convert retention times, expressed in seconds, in the more human friendly format mm:ss.

**Value**

A character string in mm:ss format

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
formatRt(1524)
```

---

getVariableName	<i>Return a variable name</i>
-----------------	-------------------------------

---

**Description**

Return the name of variable varname in call match\_call.

**Usage**

```
getVariableName(match_call, varname)
```

**Arguments**

match_call	An object of class call, as returned by match.call.
varname	An character of length 1 which is looked up in match_call.

**Value**

A character with the name of the variable passed as parameter varname in parent close of match\_call.

**Author(s)**

Laurent Gatto

**Examples**

```
a <- 1
f <- function(x, y)
  MSnbase::getVariableName(match.call(), "x")
f(x = a)
f(y = a)
```

---

iTRAQ4

*iTRAQ 4-plex set*

---

## Description

This instance of class "[ReporterIons](#)" corresponds to the iTRAQ 4-plex set, i.e the 114, 115, 116 and 117 isobaric tags. In the iTRAQ5 data set, an unfragmented tag, i.e reporter and attached isobaric tag, is also included at MZ 145. These objects are used to plot the reporter ions of interest in an MSMS spectra (see "[Spectrum2](#)") as well as for quantification (see [quantify](#)).

## Usage

```
iTRAQ4  
iTRAQ5  
iTRAQ8  
iTRAQ9
```

## References

Ross PL, Huang YN, Marchese JN, Williamson B, Parker K, Hattan S, Khainovski N, Pillai S, Dey S, Daniels S, Purkayastha S, Juhasz P, Martin S, Bartlet-Jones M, He F, Jacobson A, Pappin DJ. "Multiplexed protein quantitation in *Saccharomyces cerevisiae* using amine-reactive isobaric tagging reagents." *Mol Cell Proteomics*, 2004 Dec;3(12):1154-69. Epub 2004 Sep 22. PubMed PMID: 15385600.

## See Also

[TMT6](#).

## Examples

```
iTRAQ4  
iTRAQ4[1:2]  
  
newReporter <- new("ReporterIons",  
  description="an example",  
  name="my reporter ions",  
  reporterNames=c("myrep1","myrep2"),  
  mz=c(121,122),  
  col=c("red","blue"),  
  width=0.05)  
newReporter
```



---

itraqdata	<i>Example MSnExp data set</i>
-----------	--------------------------------

---

### Description

This example data sets is an iTRAQ 4-plex experiment that has been run on an Orbitrap Velos instrument. It includes identification data in the feature data slot obtain from the Mascot search engine.

itraqdata is a subset of an spike-in experiment where proteins have spiked in an *Erwinia* background, as described in Karp et al. (2010), *Addressing accuracy and precision issues in iTRAQ quantitation*, Mol Cell Proteomics. 2010 Sep;9(9):1885-97. Epub 2010 Apr 10. (PMID 20382981). The spiked-in proteins in itradata are BSA and ENO and are present in relative abundances 1, 2.5, 5, 10 and 10, 5, 2.5, 1 in the 114, 115, 116 and 117 reporter tags.

This example data set is used in the MSnbase-demo vignette, available with vignette("MSnbase-demo",package="MSnbase")

### Usage

```
itraqdata
```

### Examples

```
itraqdata
```

---

makeMTD	<i>Creates the mzTab metadata section</i>
---------	---

---

### Description

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general meta-data, protein, peptide and small molecule information (all of which are optional), including quantitation and identification. The metadata section (MTD) can be generated from an [MSnSet](#) instance using makeMTD. The detailed description of all the parameters can be found in the mzTab specification document (see references).

### Usage

```
makeMTD(x, unitId = NULL, title = NULL,
  mtdDescription = NULL, sampleProcessing = NULL,
  instrumentSource = NULL, instrumentAnalyzer = NULL,
  instrumentDetector = NULL, software = NULL, fdr = NULL,
  publication = NULL, contactName = NULL,
  contactAffiliation = NULL, contactEmail = NULL,
  mtdUri = NULL, mtdModifications = NULL,
  modProbabilityMethod = NULL, quantitationMethod = NULL,
  protQuantUnit = NULL, pepQuantUnit = NULL,
  msFileFormat = NULL, msFileLocation = NULL,
  msFileIdFormat = NULL, custom = NULL, species_ = NULL,
  tissue_ = NULL, cellType_ = NULL, disease_ = NULL,
  description_ = NULL, quantitationReagent_ = NULL,
  custom_ = NULL)
```

**Arguments**

x	An instance of class <a href="#">MSnSet</a> .
unitId	A character of length 1 or NULL (default), in which case x's variable name will be used. This identifier references the item under study all sections.
title	A character of length 1 or NULL (default), in which case <code>exptitle(x)</code> is used if available.
mtdDescription	A character of length 1 describing the unit or NULL (default) to ignore.
sampleProcessing	A list of (possibly multiple) valid CVPParam objects or NULL (default) to ignore.
instrumentSource	A list of valid CVPParam instances or NULL (default), in which case <code>ionSource(x)</code> is used to generate a CVPParam.
instrumentAnalyzer	A list of valid CVPParam instances or NULL (default), in which case <code>analyser(x)</code> is used to generate a CVPParam.
instrumentDetector	A list of valid CVPParam instances or NULL (default), in which case <code>detectorType(x)</code> is used to generate a CVPParam.
software	A list of valid CVPParam instances describing the ordered list of software used to process the data. NULL (default) to ignore.
fdR	A list of valid CVPParam instances describing the unit's false discovery rate or NULL (default) to ignore.
publication	A character (of length > 0) or NULL (default), in which case <code>pubMedIds(x)</code> is used.
contactName	A character (of length > 0) or NULL (default), in which case <code>expinfo(x)["name"]</code> is used.
contactAffiliation	A character (of length > 0) or NULL (default), in which case <code>expinfo(x)["lab"]</code> is used.
contactEmail	A character (of length > 0) or NULL (default), in which case <code>expemail(x)</code> is used.
mtdUri	A character (of length > 0) describing the unit's uniform resource identifier (a PRIDE experiment or a PeptideAtlas build for example). NULL (default) to ignore.
mtdModifications	A list of (possibly multipl) CVPParam instances describing all (distinct) PTMs reported in the unit. NULL (default) to ignore.
modProbabilityMethod	A user defined CVPParam reporting the modification (position) probabilities. NULL (default) to ignore.
quantitationMethod	A valid CVPParam, a <a href="#">ReporterIons</a> instance or NULL (default), in which case the isobaric tagging system is guessed from the number of columns in <code>exprs(x)</code> (4 or 8 for iTRAQ, 6 for TMT).
protQuantUnit	A valid CVPParam or NULL (default) to use PRIDE:0000330 (Arbitrary quantification unit).

pepQuantUnit	A valid CVPParam or NULL (default) to use PRIDE:0000330 (Arbitrary quantification unit).
msFileFormat	A list of valid CVPParam instances to NULL (default), in which case, the extension of fileNames(x)[1] is used to define the appropriate CVPParam. Recognised extensions are mzData, mzXML, mzML or mgf.
msFileLocation	A character (of length > 0) or NULL (default), in which case fileNames(x) is used.
msFileIdFormat	A list of CVPParam instances describing the original identification format used in the external data file. NULL (default) to ignore.
custom	A list of user defined CVPParam instances with additional parameters describing the unit. NULL (default) to ignore.
species_	A list of (possibly several) CVPParam instances with the respective (sub-)unit species. NULL (default) to ignore.
tissue_	A list of (possibly several) CVPParam instances describing the respective (sub-)unit tissue. NULL (default) to ignore.
cellType_	A list of (possibly several) CVPParam instances describing the respective (sub-)unit cell type. NULL (default) to ignore.
disease_	A list of (possibly several) CVPParam instances describing the respective (sub-)unit disease states. NULL (default) to ignore.
description_	A list of characters describing the (sub-)unit in human readable free text. NULL (default) to ignore.
quantitationReagent_	A list of CVPParam instances or NULL (default), in which case the reporter ions as defined by quantitationMethod as used.
custom_	A list of user defined CVPParam instances with additional (sub-)unit properties. NULL (default) to ignore.

**Value**

A character defining the mzTab metadata section.

**Author(s)**

Laurent Gatto

**References**

mzTab - Reporting Proteomics Results (<http://code.google.com/p/mztab/>)

**See Also**

[makePEP](#) and [makePRT](#) to generate mzTab peptide and protein sections.

---

makePEP	<i>Creates the mzTab peptide section</i>
---------	--

---

### Description

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general meta-data, protein, peptide and small molecule information (all of which are optional), including quantitation and identification. The peptide section (PEH header and PEP tabular data) can be generated from an [MSnSet](#) instance using makePEP. The detailed description of all the parameters can be found in the mzTab specification document (see references).

### Usage

```
makePEP(x, sequence = NA, pepAccession = NA,
        unitId = NULL, unique = NA, pepDatabase = NA,
        pepDatabaseVersion = NA, pepSearchEngine = NA,
        pepSearchEngineScore = NA, pepReliability = NA,
        pepModifications = NA, retentionTime = NA, charge = NA,
        massToCharge = NA, pepUri = NA, spectraRef = NA,
        pepAbundance = NULL, pepAbundanceStdev = NULL,
        pepAbundanceSterr = NULL, pepOpt_ = NULL)
```

### Arguments

x	An instance of class <a href="#">MSnSet</a> .
sequence	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the peptide sequence. Default is NA.
pepAccession	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the assigned protein accession. Default is NA.
unitId	A character of length 1 or NULL (default), in which case x's variable name will be used.
unique	A logical (converted to numeric to comply with format specification) of length( <code>nrow(x)</code> ) (will be recycled a whole number of times if of different length) specifying if peptide is proteotypic. Default is NA.
pepDatabase	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) describing the protein database used for peptide identification. Default is NA.
pepDatabaseVersion	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the database version. Default is NA.
pepSearchEngine	A list of length <code>nrow(x)</code> (of possibly multiple lists of) <code>CVPParam</code> instances identifying the search engine used for peptide identification. Default is NA.
pepSearchEngineScore	A list of length <code>nrow(x)</code> (of possibly multiple lists of) <code>CVPParam</code> instances specifying peptide identification scores. Default is NA.
pepReliability	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length). Values should be 1 (high reliability), 2 (medium reliability) or 3 (poor reliability). Default is NA.

pepModifications	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) describing the modifications and their position (see <code>mzTab</code> format specifications for details). Default is <code>NA</code> .
retentionTime	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length). Note that currently, unique retention times are expected, but could be extended to multiple times. Default is <code>NA</code> .
charge	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) indicating peptide charge state. Default is <code>NA</code> .
massToCharge	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the peptides precursor mass to charge ratio. Default is <code>NA</code> .
pepUri	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with peptide uniform resource identifiers (link to PRIDE database for instance). Default is <code>NA</code> .
spectraRef	A character in the format <code>ms_file[1-n]:{SPEC_REF}</code> (see <code>mzTab</code> specifications for details) of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length). Default is <code>NA</code> .
pepAbundance	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the peptides abundance. If <code>NULL</code> (default), ignored.
pepAbundanceStdev	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the standard deviation of peptides abundances. If <code>NULL</code> (default), ignored. If <code>pepAbundance</code> is not <code>NULL</code> , then <code>pepAbundanceStdev</code> is <code>NA</code> if not specified.
pepAbundanceSterr	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the standard error of peptides abundances. If <code>NULL</code> (default), ignored. If <code>pepAbundance</code> is not <code>NULL</code> , then <code>pepAbundanceSterr</code> is <code>NA</code> if not specified.
pepOpt_	An optional character of character matrix (possibly populated with text representations of <code>CVParam</code> instances) for any custom peptide annotation. Default is <code>NULL</code> to ignore.

**Value**

A `data.frame` defining the `mzTab` peptide section.

**Author(s)**

Laurent Gatto

**See Also**

[makeMTD](#) and [makePRT](#) to generate `mzTab` metadata and protein sections.

makePRT

*Creates the mzTab protein section***Description**

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general meta-data, protein, peptide and small molecule information (all of which are optional), including quantitation and identification. The proteome section (PRH header and PRT tabular data) can be generated from an [MSnSet](#) instance using makePRT. The detailed description of all the parameters can be found in the mzTab specification document (see references).

**Usage**

```
makePRT(x, protAccession = NA, unitId = NULL,
        protDescription = NA, taxId = NA, species = NA,
        protDatabase = NA, protDatabaseVersion = NA,
        protSearchEngine = NA, protSearchEngineScore = NA,
        protReliability = NA, numPep = NA, numPepDistinct = NA,
        numPepUnambiguous = NA, ambiguityMembers = NA,
        protModifications = NA, protUri = NA, goTerms = NA,
        protCoverage = NA, protAbundance = NULL,
        protAbundanceStdev = NULL, protAbundanceSterr = NULL,
        protOpt_ = NULL)
```

**Arguments**

x	An instance of class <a href="#">MSnSet</a> .
protAccession	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the protein accession. Default is NA.
unitId	A character of length 1 or NULL (default), in which case x's variable name will be used.
protDescription	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the protein name or description. Default is NA.
taxId	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) referencing the species NCBI/NEWT taxonomy id. Default is NA.
species	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) describing the species in human readable form. Default is NA.
protDatabase	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) describing the protein database. Default is NA.
protDatabaseVersion	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) describing the database version. Default is NA.
protSearchEngine	A list of length <code>nrow(x)</code> (of possibly several) <code>CVParam</code> instances describing the search engine used for protein identification. Default is NA.
protSearchEngineScore	A list of length <code>nrow(x)</code> (of possibly multiple lists of) <code>CVParam</code> instances specifying peptide identification scores. Default is NA.

protReliability	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length). Values should be 1 (high reliability), 2 (medium reliability) or 3 (poor reliability). Default is NA.
numPep	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) indicating the number of peptides identifying the proteins. Default is NA.
numPepDistinct	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) indicating the number of distinct peptides (sequence and modifications) identifying the proteins. Default is NA.
numPepUnambiguous	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) indicating the number of unambiguous distinct peptides identifying the proteins. Default is NA.
ambiguityMembers	A character of comma-separated protein accessions. See the <code>mzTab</code> specification document for details. Default is NA.
protModifications	A character of comma-delimited modifications/scores/positions describing the proteins. See the <code>mzTab</code> specification document for details. Default is NA.
protUri	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with peptide uniform resource identifiers (link to PRIDE database for instance). Default is NA.
goTerms	A character of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with comma-delimited GO terms describing the proteins. Default is NA.
protCoverage	A numeric of length <code>nrow(x)</code> (will be recycled a whole number of times if of different length) with the protein coverages ranging between 0 and 1. Default is NA.
protAbundance	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the protein abundance. If NULL (default), ignored.
protAbundanceStdev	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the standard deviation of protein abundances. If NULL (default), ignored. If <code>protAbundance</code> is not NULL, then <code>protAbundanceStdev</code> is NA if not specified.
protAbundanceSterr	A numeric of length <code>nrow(x)</code> or matrix with <code>nrow(x)</code> rows if multiple sub-samples are reported (see metadata section), specifying the standard error of protein abundances. If NULL (default), ignored. If <code>protAbundance</code> is not NULL, then <code>protAbundanceSterr</code> is NA if not specified.
protOpt_	An optional character of character matrix (possibly populated with text representations of <code>CVParam</code> instances) for any custom protein annotation. Default is NULL to ignore.

## Value

A `data.frame` defining the `mzTab` protein section.

**Author(s)**

Laurent Gatto

**References**

mzTab - Reporting Proteomics Results (<http://code.google.com/p/mztab/>)

**See Also**

[makeMTD](#) and [makePEP](#) to generate mzTab metadata and peptide sections.

---

MIAPE-class

*The "MIAPE" Class for Storing Proteomics Experiment Information*

---

**Description**

The Minimum Information About a Proteomics Experiment. The current implementation is based on the MIAPE-MS 2.4 document.

**Slots**

**title:** Object of class character containing a single-sentence experiment title.

**abstract:** Object of class character containing an abstract describing the experiment.

**url:** Object of class character containing a URL for the experiment.

**pubMedIds:** Object of class character listing strings of PubMed identifiers of papers relevant to the dataset.

**samples:** Object of class list containing information about the samples.

**preprocessing:** Object of class list containing information about the pre-processing steps used on the raw data from this experiment.

**other:** Object of class list containing other information for which none of the above slots does not apply.

**dateStamp:** Object of class character, giving the date on which the work described was initiated; given in the standard 'YYYY-MM-DD' format (with hyphens).

**name:** Object of class character containing the name of the (stable) primary contact person for this data set; this could be the experimenter, lab head, line manager, ...

**lab:** Object of class character containing the laboratory where the experiment was conducted.

**contact:** Object of class character containing contact information for lab and/or experimenter.

**email:** Object of class character containing email contact information for the primary contact person (see name above).

**instrumentModel:** Object of class character indicating the model of the mass spectrometer used to generate the data.

**instrumentManufacturer:** Object of class character indicating the manufacturing company of the mass spectrometer.

**instrumentCustomisations:** Object of class character describing any significant (i.e. affecting behaviour) deviations from the manufacturer's specification for the mass spectrometer.

**softwareName:** Object of class character with the instrument management and data analysis package(s) name(s).



- softwareVersion:** Object of class character with the instrument management and data analysis package(s) version(s).
- switchingCriteria:** Object of class character describing the list of conditions that cause the switch from survey or zoom mode (MS1) to or tandem mode (MSn where  $n > 1$ ); e.g. 'parent ion' mass lists, neutral loss criteria and so on [applied for tandem MS only].
- isolationWidth:** Object of class numeric describing, for tandem instruments, the total width (i.e. not half for plus-or-minus) of the gate applied around a selected precursor ion m/z, provided for all levels or by MS level.
- parameterFile:** Object of class character giving the location and name under which the mass spectrometer's parameter settings file for the run is stored, if available. Ideally this should be a URI+filename, or most preferably an LSID, where feasible.
- ionSource:** Object of class character describing the ion source (ESI, MALDI, ...).
- ionSourceDetails:** Object of class character describing the relevant details about the ion source. See MIAPE-MI document for more details.
- analyser:** Object of class character describing the analyser type (Quadrupole, time-of-flight, ion trap, ...).
- analyserDetails:** Object of class character describing the relevant details about the analyser. See MIAPE-MI document for more details.
- collisionGas:** Object of class character describing the composition of the gas used to fragment ions in the collision cell.
- collisionPressure:** Object of class numeric providing the pressure (in bars) of the collision gas.
- collisionEnergy:** Object of class character specifying for the process of imparting a particular impetus to ions with a given m/z value, as they travel into the collision cell for fragmentation. This could be a global figure (e.g. for tandem TOF's), or a complex function; for example a gradient (stepped or continuous) of m/z values (for quads) or activation frequencies (for traps) with associated collision energies (given in eV). Note that collision energies are also provided for individual "[Spectrum2](#)" instances, and is the preferred way of accessing this data.
- detectorType:** Object of class character describing the type of detector used in the machine (microchannel plate, channeltron, ...).
- detectorSensitivity:** Object of class character giving and appropriate measure of the sensitivity of the described detector (e.g. applied voltage).

## Methods

The following methods as in "[MIAME](#)":

- abstract(MIAPE):** An accessor function for abstract.
- expinfo(MIAPE):** An accessor function for name, lab, contact, title, and url.
- notes(MIAPE), notes(MIAPE) <- value:** Accessor functions for other. **notes(MIAME) <- character** *appends* character to notes; use **notes(MIAPE) <- list** to replace the notes entirely.
- otherInfo(MIAPE):** An accessor function for other.
- preproc(MIAPE):** An accessor function for preprocessing.
- pubMedIds(MIAPE), pubMedIds(MIAME) <- value:** Accessor function for pubMedIds.
- expemail(MIAPE):** An accessor function for email slot.
- exptitle(MIAPE):** An accessor function for title slot.

MIAPE-specific methods, including MIAPE-MS meta-data:

- show(MIAPE):** Displays the experiment data.
- msInfo(MIAPE):** Displays 'MIAPE-MS' information.

**Extends**

Class "MIAxE", directly. Class "Versioned", by class "MIAxE", distance 2.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**References**

About MIAPE: <http://www.psidev.info/index.php?q=node/91>, and references therein, especially 'Guidelines for reporting the use of mass spectrometry in proteomics', Nature Biotechnology 26, 860-861 (2008).

---

MSnExp-class

*The 'MSnExp' Class for MS Data And Meta-Data*


---

**Description**

The MSnExp class encapsulates data and meta-data for mass spectrometry experiments, as described in the slots section. Several data files (currently in mzXML) can be loaded together with the function [readMSData](#).

This class extends the virtual "pSet" class.

**Objects from the Class**

Objects can be created by calls of the form `new("MSnExp",...)`. However, it is preferred to use the [readMSData](#) function that will read raw mass spectrometry data to generate a valid "MSnExp" instance.

**Slots**

**assayData:** Object of class "environment" containing the MS spectra (see "[Spectrum1](#)" and "[Spectrum2](#)"). Slot is inherited from "pSet".

**phenoData:** Object of class "[AnnotatedDataFrame](#)" containing experimenter-supplied variables describing sample (i.e the individual tags for an labelled MS experiment) See [phenoData](#) for more details. Slot is inherited from "pSet".

**featureData:** Object of class "[AnnotatedDataFrame](#)" containing variables describing features (spectra in our case), e.g. identificaion data, peptide sequence, identification score,... (inherited from "eSet"). See [featureData](#) for more details. Slot is inherited from "pSet".

**experimentData:** Object of class "MIAPE", containing details of experimental methods. See [experimentData](#) for more details. Slot is inherited from "pSet".

**protocolData:** Object of class "[AnnotatedDataFrame](#)" containing equipment-generated variables (inherited from "eSet"). See [protocolData](#) for more details. Slot is inherited from "pSet".

**processingData:** Object of class "[MSnProcess](#)" that records all processing. Slot is inherited from "pSet".

**\_\_classVersion\_\_:** Object of class "[Versions](#)" describing the versions of R, the Biobase package, "pSet" and MSnExp of the current instance. Slot is inherited from "pSet". Intended for developer use and debugging (inherited from "eSet").

## Extends

Class "pSet", directly. Class "VersionedBiobase", by class "pSet", distance 2. Class "Versioned", by class "pSet", distance 3.

## Methods

See the "pSet" class for documentation on accessors inherited from pSet, subsetting and general attribute accession.

**clean** signature(object = "MSnExp"): Removes unused 0 intensity data points. See [clean](#) documentation for more details and examples.

**extractPrecSpectra** signature(object = "MSnExp", prec = "numeric"): extracts spectra with precursor MZ value equal to prec and returns an object of class 'MSnExp'. See [extractPrecSpectra](#) documentation for more details and examples.

**plot** signature(x = "MSnExp", y = "missing"): Plots all the spectra of the MSnExp instance. See [plot.MSnExp](#) documentation for more details.

**plot2d** signature(object = "MSnExp", ...): Plots retention time against precursor MZ for MSnExp instances. See [plot2d](#) documentation for more details.

**plotDensity** signature(object = "MSnExp", ...): Plots the density of parameters of interest. See [plotDensity](#) documentation for more details.

**plotMzDelta** signature(object = "MSnExp", ...): Plots a histogram of the m/z difference between all of the highest peaks of all MS2 spectra of an experiment. See [plotMzDelta](#) documentation for more details.

**quantify** signature(object = "MSnExp"): Performs quantification for all the MS2 spectra of the MSnExp instance. See [quantify](#) documentation for more details.

**removePeaks** signature(object = "MSnExp"): Removes peaks lower than a threshold t. See [removePeaks](#) documentation for more details and examples.

**removeReporters** signature(object = "MSnExp", ...): Removes reporter ion peaks from all MS2 spectra of an experiment. See [removeReporters](#) documentation for more details and examples.

**show** signature(object = "MSnExp"): Displays object content as text.

**trimMz** signature(object = "MSnExp"): Trims the MZ range of all the spectra of the MSnExp instance. See [trimMz](#) documentation for more details and examples.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## References

Information about the mzXML format as well converters from vendor specific formats to mzXML: <http://tools.proteomecenter.org/wiki/index.php?title=Formats:mzXML>.

## See Also

"pSet" and [readMSData](#) for loading mzXML, mzData or mzML files to generate an instance of MSnExp.

**Examples**

```
mzxmlfile <- dir(system.file("extdata",package="MSnbase"),
                 pattern="mzXML",full.names=TRUE)
msnexp <- readMSData(mzxmlfile)
msnexp
```

MSnProcess-class

*The "MSnProcess" Class***Description**

MSnProcess is a container for MSnExp and MSnSet processing information. It records data files, processing steps, thresholds, analysis methods and times that have been applied to MSnExp or MSnSet instances.

**Slots**

**files:** Object of class "character" storing the raw data files used in experiment described by the "MSnProcess" instance.

**processing:** Object of class "character" storing all the processing steps and times.

**merged:** Object of class "logical" indicating whether spectra have been merged.

**cleaned:** Object of class "logical" indicating whether spectra have been cleaned. See [clean](#) for more details and examples.

**removedPeaks:** Object of class "character" describing whether peaks have been removed and which threshold was used. See [removePeaks](#) for more details and examples.

**smoothed:** Object of class "logical" indicating whether spectra have been smoothed.

**trimmed:** Object of class "numeric" documenting if/how the data has been trimmed.

**normalised:** Object of class "logical" describing whether and how data have been normalised.

**MSnbaseVersion:** Object of class "character" indicating the version of MSnbase.

**.\_\_\_classVersion\_\_:** Object of class "Versions" indicating the version of the MSnProcess instance. Intended for developer use and debugging.

**Extends**

Class "[Versioned](#)", directly.

**Methods**

**fileNames** signature(object = "MSnProcess"): Returns the file names used in experiment described by the "MSnProcess" instance.

**show** signature(object = "MSnProcess"): Displays object content as text.

**combine** signature(x = "MSnProcess", y = "MSnProcess"): Combines multiple MSnProcess instances.

**Note**

This class is likely to be updated using an AnnotatedDataFrame.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

See the "[MSnExp](#)" and "[MSnSet](#)" classes that actually use MSnProcess as a slot.

**Examples**

```
showClass("MSnProcess")
```

---

MSnSet-class

*The "MSnSet" Class for MS Proteomics Expression Data and Meta-Data*

---

**Description**

The MSnSet holds quantified expression data for MS proteomics data and the experimental meta-data. The MSnSet class is derived from the "[eSet](#)" class and mimics the "[ExpressionSet](#)" class classically used for microarray data.

**Objects from the Class**

Objects can be created by calls of the form `new("MSnSet", exprs, ...)`. See also "[ExpressionSet](#)" for helpful information. Expression data produced from other softwares can thus make use of this standardized data container to benefit R and Bioconductor packages. Importer functions will be developed to stream-line the generation of "MSnSet" instances from third-party software.

In the frame of the MSnbase package, MSnSet instances are generated from "[MSnExp](#)" experiments when the "[ReporterIons](#)" using the "quantify" method).

**Slots**

**qual:** Object of class "data.frame" that records peaks data for each of the reporter ions to be used as quality metrics.

**processingData:** Object of class "[MSnProcess](#)" that records all processing.

**assayData:** Object of class "assayData" containing a matrix with equal with column number equal to `nrow(phenoData)`. assayData must contain a matrix exprs with rows representing features (e.g., reporters ions) and columns representing samples. See the "[AssayData](#)" class, [exprs](#) and [assayData](#) accessor for more details. This slot is indirectly inherited from "[eSet](#)".

**phenoData:** Object of class "AnnotatedDataFrame" containing experimenter-supplied variables describing sample (i.e the individual tags for an labelled MS experiment) (indirectly inherited from "[eSet](#)"). See [phenoData](#) and the "[eSet](#)" class for more details.

**featureData:** Object of class "AnnotatedDataFrame" containing variables describing features (spectra in our case), e.g. identification data, peptide sequence, identification score,... (inherited indirectly from "[eSet](#)"). See [featureData](#) and the "[eSet](#)" class for more details.

**experimentData:** Object of class "[MIAPE](#)", containing details of experimental methods (inherited from "[eSet](#)"). See [experimentData](#) and the "[eSet](#)" class for more details.

**annotation:** not used here.

**protocolData**: Object of class "[AnnotatedDataFrame](#)" containing equipment-generated variables (inherited indirectly from "[eSet](#)"). See [protocolData](#) and the "[eSet](#)" class for more details.

**.\_\_\_classVersion\_\_\_**: Object of class "[Versions](#)" describing the versions of R, the Biobase package, "[eSet](#)", "[pSet](#)" and MSnSet of the current instance. Intended for developer use and debugging (inherited indirectly from "[eSet](#)").

## Extends

Class "[eSet](#)", directly. Class "[VersionedBiobase](#)", by class "[eSet](#)", distance 2. Class "[Versioned](#)", by class "[eSet](#)", distance 3.

## Methods

MSnSet specific methods or over-riding it's super-class are described below. See also more "[eSet](#)" for inherited methods.

**dim** signature(x = "MSnSet"): Returns the dimensions of object's assay data, i.e the number of samples and the number of features.

**fileNames** signature(object = "MSnSet"): Access file names in the processingData slot.

**msInfo** signature(object = "MSnSet"): Prints the MIAPE-MS meta-data stored in the experimentData slot.

**processingData** signature(object = "MSnSet"): Access the processingData slot.

**show** signature(object = "MSnSet"): Displays object content as text.

**qual** signature(object = "MSnSet"): Access the reporter ion peaks description.

**purityCorrect** signature(object = "MSnSet", impurities = "matrix"): performs reporter ions purity correction. See [purityCorrect](#) documentation for more details.

**normalise** signature(object = "MSnSet"): Performs MSnSet normalisation. See [normalise](#) for more details.

**t** signature(x = "MSnSet"): Returns a transposed MSnSet object where features are now aligned along columns and samples along rows and the phenoData and featureData slots have been swapped. The protocolData slot is always dropped.

**as("ExpressionSet")** signature(x = "MSnSet"): Coerce object from MSnSet to [ExpressionSet-class](#). The experimentData slot is dropped.

**write.exprs** signature(x = "MSnSet") Writes expression values to a tab-separated file (default is tmp.txt). The fDataCols parameter can be used to specify which featureData columns (as column names, column number or logical) to append on the right of the expression matrix. The following arguments are the same as write.table.

**combine** signature(x = "MSnSet", y = "MSnSet", ...) Combines 2 or more MSnSet instances according to their feature names. Note that the qual slot and the processing information are silently dropped.

**topN** signature(object = "MSnSet", groupBy, n = 3, fun, ...) Selects the n most intense features (typically peptides or spectra) out of all available for each set defined by groupBy (typically proteins) and creates a new instance of class MSnSet. If less than n features are available, all are selected. The ncol(object) features are summerised using fun (default is sum) prior to be ordered in decreasing order. Additional parameters can be passed to fun through ..., for instance to control the behaviour of topN in case of NA values. Note that the qual slot and the processing information are silently dropped. (Works also with matrix instances.)

See also the [nQuants](#) function to retrieve the actual number of peptides out of n where retained.

**filterNA** signature(object = "MSnSet", pNA = "numeric") This methods subsets object by removing features that have more than pNA percent of NA values. Default pNA is 1/2. To remove any feature that exhibits missing data, use pNA = 0. This method also accepts matrix instances.

See also the [is.na.MSnSet](#) and [plotNA](#) methods for missing data exploration.

**log** signature(object = "MSnSet", base = "numeric") Log transforms `exprs(object)` using `base::log`. `base` (defaults is `e=exp(1)`) must be a positive or complex number, the base with respect to which logarithms are computed.

Additional accessors for the experimental metadata (`experimentData` slot) are defined. See "[MIAPE](#)" for details.

## Plotting

**meanSdPlot** signature(object = "MSnSet") Plots row standard deviations versus row means. See [meanSdPlot](#) (vsn package) for more details.

**image** signature(x = "MSnSet", yticks = "numeric", x.cex.axis = "numeric", y.cex.axis = "numeric", ...) Produces an image of expression values in the x object. `yticks` defines how many ticks should be used on the y axis. `x.cex.axis` and `y.cex.axis` are passed to calls to `axis` and defined the respective character expansion. ... is passed to `image`.

Plots missing data for an MSnSet instance. `pNA` is a numeric of length 1 that specifies the percentage of accepted missing data values per features. This value will be highlighted with a point on the figure, illustrating the overall percentage of NA values in the full data set and the number of proteins retained. Default is 1/2. See also [plotNA](#).

**MAplot** signature(object = "MSnSet", log.it = "logical", base = "numeric", ...) Produces MA plots (Ratio as a function of average intensity) for the samples in object. If `ncol(object) == 2`, then one MA plot is produced using the [ma.plot](#) function from the `affy` package. If object has more than 2 columns, then [mva.pairs](#). `log.it` specifies is the data should be log-transformed (default is TRUE) using `base`. Further ... arguments will be passed to the respective functions.

## Functions

**updateFvarLabels** signature(object, label, sep) This function updates object's featureData variable labels by appending label. By default, label is the variable name and the separator sep is ..

**updateSampleNames** signature(object, label, sep) This function updates object's sample names by appending label. By default, label is the variable name and the separator sep is ..

**updateFeatureNames** signature(object, label, sep) This function updates object's feature names by appending label. By default, label is the variable name and the separator sep is ..

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## See Also

"[eSet](#)" and "[ExpressionSet](#)". MSnSet quantitation values can be exported to a file with [write.exprs](#).

**Examples**

```
data(itraqdata)
itraqdata
msnset <- quantify(itraqdata[10:15], method = "trap", reporters = iTRAQ4, verbose = FALSE)
msnset
```

---

NAnnotatedDataFrame-class

*Class Containing Measured Variables and Their Meta-Data Description for Multiplexed Experiments.*

---

**Description**

An NAnnotatedDataFrame is an "[AnnotatedDataFrame](#)", as defined in the 'Biobase' package that includes additional labels for multiplexing annotation.

**Objects from the Class**

See "[AnnotatedDataFrame](#)" for object creation with new. Multiplexing data is defined by setting the multiplex and multiLabels paramters.

**Slots**

**multiplex:** Object of class "numeric" indicating the number of multiplexed samples described.

**multiLabels:** Object of class "character" describing the multiplexing.

**varMetadata:** Object of class "data.frame" with number of rows equal number of columns in data, and at least one column, named labelDescription, containing a textual description of each variable. Inherited from "[AnnotatedDataFrame](#)".

**data:** Object of class "data.frame" containing samples (rows) and measured variables (columns). Inherited from "[AnnotatedDataFrame](#)".

**dimLabels:** Object of class "character" of length 2 that provides labels for the rows and columns in the show method. Inherited from "[AnnotatedDataFrame](#)".

**.\_\_\_classVersion\_\_:** Object of class "Versions" describing the instance version. Intended for developer use. Inherited from "[AnnotatedDataFrame](#)".

**Extends**

Class "[AnnotatedDataFrame](#)", directly. Class "[Versioned](#)", by class "AnnotatedDataFrame", distance 2.

**Methods**

**dim** signature(object = "NAnnotatedDataFrame"): Returns the number of samples, variables and multiplex cardinality in the object.

**multiplex** signature(object = "NAnnotatedDataFrame"): Returns the number of multiplexed samples described by the object.

**multiLabels** signature(object = "NAnnotatedDataFrame"): Returns the multiplex labels.

**show** signature(object = "NAnnotatedDataFrame"): Textual description of the object.



**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

["AnnotatedDataFrame"](#).

**Examples**

```
df <- data.frame(x=1:3,
                y=LETTERS[1:3],
                row.names=paste("Sample",1:3,sep=""))
metaData <-
  data.frame(labelDescription=c(
    "Numbers",
    "Factor levels"))
mplx <- c("M1","M2")
new("NAnnotatedDataFrame",
    data=df,
    varMetadata=metaData,
    multiplex=length(mplx),
    multiLabels=mplx)
```

---

normalise-methods

*Normalisation of MSnExp, MSnSet and Spectrum objects*

---

**Description**

The `normalise` method performs basic normalisation on spectra intensities of single spectra ("[Spectrum](#)" objects), whole experiments ("[MSnExp](#)" objects) or quantified expression data ("[MSnSet](#)" objects).

Raw spectra and experiments are normalised using `max` or `sum` only. Each peak intensity is divided by the highest intensity in the spectrum or the sum of intensities. These methods aim at facilitating relative peaks heights between different spectra.

The method parameter for "[MSnSet](#)" can be one of `sum`, `max`, `quantiles`, `quantiles.robust` or `vsn`. For `sum` and `max`, each feature's reporter intensity is divided by the maximum of the sum respectively. Using `quantiles` or `quantiles.robust` uses (robust) quantile normalisation, as implemented in [normalize.quantiles](#) and [normalize.quantiles.robust](#) of the `preprocessCore` package. `vsn` uses the `vsn2` from the `vsn` package. Note that the latter also `glog`-transforms the intensities. See respective manuals for more details and function arguments.

**Arguments**

<code>object</code>	An object of class " <a href="#">Spectrum</a> ", " <a href="#">MSnExp</a> " or " <a href="#">MSnSet</a> ".
<code>method</code>	A character vector of length one that describes how to normalise the object. See description for details.
<code>...</code>	Additional arguments passed to the normalisation function.

**Methods**

signature(object = "MSnSet", method = "character") Normalises the object reporter ions intensities using method.

signature(object = "MSnExp", method = "character") Normalises the object peak intensities using method.

signature(object = "Spectrum", method = "character") Normalises the object peak intensities using method.

**Examples**

```
## quantifying full experiment
data(itraqdata)
qnt <- quantify(itraqdata,method="trap",reporters=iTRAQ4)
qnt.nrm <- normalise(qnt,"quantiles")
qnt.nrm
```

---

nQuants

---

*Count the number of quantified features.*


---

**Description**

This function counts the number of quantified features, i.e non NA quantitation values, for each group of features for all the samples in an "MSnSet" object. The group of features are defined by a feature variable names, i.e the name of a column of fData(object).

**Usage**

```
nQuants(object, fcol)
```

**Arguments**

object            An instance of class "MSnSet".  
fcol                The feature variable to consider when counting the number of quantified features.

**Details**

This function is typically used after [topN](#) and before [combineFeatures](#), when the summerising function is sum, or any function that does not normalise to the number of features aggregated. In the former case, sums of feautres might be the result of 0 (if no feature was quantified) to n (if all topN's n features were quantified) features, and one might want to rescale the sums based on the number of non-NA features effectively summed.

**Value**

A matrix of dimensions length(levels(factor(fData(object)[, fcol]))) by ncol(object) of integers.

**Author(s)**

Laurent Gatto

**Examples**

```

data(itraqdata)
x <- quantify(itraqdata, reporters = iTRAQ4)
n <- 2
x <- topN(x, groupBy = fData(x)$ProteinAccession, n)
m <- nQuants(x, fcol = "ProteinAccession")
y <- combineFeatures(x, groupBy = fData(x)$ProteinAccession, fun = sum)
stopifnot(dim(n) == dim(y))
head(exprs(y))
head(exprs(y) * (n/m))

```

plot-methods

*Plotting 'Spectrum' object(s)***Description**

These method plot mass spectra MZ values against the intensities as line plots. Full spectra (using the full parameter) or specific peaks of interest can be plotted using the reporters parameter. If reporters are specified and full is set to 'TRUE', a sub-figure of the reporter ions is inlaid inside the full spectrum.

If an "MSnExp" is provided as argument, all the spectra are aligned vertically. Experiments can be subset to extract spectra of interest using the `[` operator or `extractPrecSpectra` methods.

The methods make use the ggplot2 system. An object of class 'ggplot' is returned invisibly.

**Arguments**

x	Objects of class "Spectrum" or "MSnExp" to be plotted.
y	Not used in these methods.
reporters	An object of class "ReporterIons" that defines the peaks to be plotted. If not specified, full must be set to 'TRUE'.
full	Logical indicating whether full spectrum (respectively spectra) of only reporter ions of interest should be plotted. Default is 'FALSE', in which case reporters must be defined.
centroided	Logical indicating if spectrum or spectra are in centroided mode, in which case peaks are plotted as sticks, rather than curves.
plot	Logical specifying whether plot should be printed to current device. Default is 'TRUE'.
w1	Width of sticks for full centroided spectra. Default is to use maximum MZ value divided by 500.
w2	Width of sticks for centroided reporter ions plots. Default is 0.01.

**Methods**

```
signature(x = "MSnExp", y = "missing", reporters = "ReporterIons", full = "logical", plot = "logical")
```

Plots *\*all\** the spectra in the MSnExp object vertically. One of reporters must be defined or full set to 'TRUE'. In case of MSnExp objects, reporter ions are not inlaid when full is 'TRUE'.

```
signature(x = "Spectrum", y = "missing", reporters = "ReporterIons", full = "logical", centroided = "logical")
```

Displays the MZs against intensities of the Spectrum object as a line plot. At least one of reporters being defined or full set to 'TRUE' is required. reporters and full are used only for "Spectrum2" objects. Full "Spectrum1" spectra are plotted by default.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
data(itraqdata)
## plotting experiments
plot(itraqdata[1:2], reporters = iTRAQ4)
plot(itraqdata[1:2], full = TRUE)
## plotting spectra
plot(itraqdata[[1]],reporters = iTRAQ4, full = TRUE)
```

---

plot2d-methods

*The 'plot2d' method for 'MSnExp' quality assessment*

---

**Description**

These methods plot the retention time vs. precursor MZ for the whole "[MSnExp](#)" experiment. Individual dots will be colour-coded to describe individual spectra's peaks count, total ion count, precursor charge (MS2 only) or file of origin.

The methods make use the ggplot2 system. An object of class 'ggplot' is returned invisibly.

**Arguments**

object	An object of class " <a href="#">MSnExp</a> " or a data.frame. In the latter case, the data frame must have numerical columns named 'retention.time' and 'precursor.mz' and one of 'tic', 'file', 'peaks.count' or 'charge', depending on the z parameter. Such a data frame is typically generated using the header method on " <a href="#">MSnExp</a> " object.
z	A character indicating according to what variable to colour the dots. One of, possibly abbreviated, "ionCount" (total ion count), "file" (raw data file), "peaks.count" (peaks count) or "charge" (precursor charge).
alpha	Numeric [0,1] indicating transparence level of points.
plot	A logical indicating whether the plot should be printed (default is 'TRUE').

**Methods**

signature(object = "MSnExp", ...) Plots a 'MSnExp' summary.

signature(object = "data.frame", ...) Plots a summary of the 'MSnExp' experiment described by the data frame.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

The [plotDensity](#) and [plotMzDelta](#) methods for other QC plots.

## Examples

```
itraqdata
plot2d(itraqdata,z="ionCount")
plot2d(itraqdata,z="peaks.count")
plot2d(itraqdata,z="charge")
```

---

plotDensity-methods      *The 'plotDensity' method for 'MSnExp' quality assessment*

---

## Description

These methods plot the distribution of several parameters of interest for the different precursor charges for "MSnExp" experiment.

The methods make use the ggplot2 system. An object of class 'ggplot' is returned invisibly.

## Arguments

object	An object of class "MSnExp" or and 'data.frame'. In the latter case, the data frame must have numerical columns named 'charge' and one of 'precursor.mz', 'peaks.count' or 'ionCount', depending on the z parameter. Such a data frame is typically generated using the header method on "MSnExp" object.
z	A character indicating which parameter's density to plot. One of, possibly abbreviated, "ionCount" (total ion count), "peaks.count" (peaks count) or "precursor.mz" (precursor MZ).
log	Logical, whether to log transform the data (default is 'FALSE').
plot	A logical indicating whether the plot should be printed (default is 'TRUE').

## Methods

signature(object = "MSnExp", ...) Plots a 'MSnExp' summary.

signature(object = "data.frame", ...) Plots a summary of the 'MSnExp' experiment described by the data frame.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## See Also

The [plot2d](#) and [plotDensity](#) methods for other QC plots.

## Examples

```
itraqdata
plotDensity(itraqdata,z="ionCount")
plotDensity(itraqdata,z="peaks.count")
plotDensity(itraqdata,z="precursor.mz")
```

---

plotMzDelta-methods     *The delta m/z plot for 'MSnExp' quality assessment*

---

## Description

The m/z delta plot illustrates the suitability of MS2 spectra for identification by plotting the m/z differences of the most intense peaks. The resulting histogram should optimally show outstanding bars at amino acid residue masses. The plots have been described in Foster *et al* 2011.

Only a certain percentage of most intense MS2 peaks are taken into account to use the most significant signal. Default value is 10% (see percentage argument). The difference between peaks is then computed for all individual spectra and their distribution is plotted as a histogram where single bars represent 1 m/z differences. Delta m/z between 40 and 200 are plotted by default, to encompass the residue masses of all amino acids and several common contaminants, although this can be changed with the xlim argument.

In addition to the processing described above, isobaric reporter tag peaks (see the reporters argument) and the precursor peak (see the precMz argument) can also be removed from the MS2 spectrum, to avoid interference with the fragment peaks.

Note that figures in Foster *et al* 2011 have been produced and optimised for centroided data. Application of the plot as is for data in profile mode has not been tested thoroughly, although the example below suggests that it might work.

The methods make use of the ggplot2 system. An object of class 'ggplot' is returned invisibly.

Most of the code for plotMzDelta has kindly been contributed by Guangchuang Yu.

## Arguments

object	An object of class "MSnExp" containing MS2 spectra.
reporters	An object of class class "ReporterIons" that defines which reporter ion peaks to set to 0. The default value NULL leaves the spectra as they are.
percentage	The percentage of most intense peaks to be used for the plot. Default is 0.1.
precMz	A numeric of length one or NULL default. In the latter (and preferred) case, the precursor m/z values are extracted from the individual MS2 spectra using the <a href="#">precursorMz</a> method.
precMzWidth	A numeric of length 1 that specifies the width around the precursor m/z where peaks are set to 0. Default is 2.
bw	A numeric specifying the bandwidth to be used to bin the delta m/z value to plot the histogram. Default is 1. See <a href="#">geom_histogram</a> for more details.
xlim	A numeric of length 2 specifying the range of delta m/z to plot on the histogram. Default is c(40,200).
withLabels	A logical defining if amino acid residue labels are plotted on the figure. Default is TRUE.
size	A numeric of length 1 specifying the font size of amino acid labels. Default is 2.5.
plot	A logical of length 1 that defines whether the figure should be plotted on the active device. Default is TRUE. Note that the ggplot object is always returned invisibly.
verbose	A logical of length 1 specifying whether textual output and a progress bar illustrating the progress of data processing should be printed. Default is TRUE.

## Methods

signature(object = "MSnExp", ...) Plots and (invisibly) returns the m/z delta histogram.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## References

Foster JM, Degroevae S, Gatto L, Visser M, Wang R, Griss J, Apweiler R, Martens L. "A posteriori quality control for the curation and reuse of public proteomics data." *Proteomics*, 2011 Jun;11(11):2182-94. doi:10.1002/pmic.201000602. Epub 2011 May 2. PMID: 21538885

## See Also

The [plotDensity](#) and [plot2d](#) methods for other QC plots.

## Examples

```
mzdplot <- plotMzDelta(itraqdata,reporters=iTRAQ4,verbose=FALSE,plot=FALSE)
## let's retrieve peptide sequence information
## and get a table of amino acids
peps <- as.character(fData(itraqdata)$PeptideSequence)
aas <- unlist(strsplit(peps,""))
## table of aas
table(aas)
## mzDelta plot
print(mzdplot)
```

---

plotNA-methods

*Exploring missing data in 'MSnSet' instances*

---

## Description

These methods produce plots that illustrate missing data.

`is.na` returns the expression matrix of its `MSnSet` argument as a matrix of logicals referring whether the corresponding cells are NA or not. It is generally used in conjunction with `table` and `image` (see example below).

The `plotNA` method produces plots that illustrate missing data. The completeness of the full dataset or a set of proteins (ordered by increasing NA content along the x axis) is represented. The methods make use of the `ggplot2` system. An object of class `'ggplot'` is returned invisibly.

## Methods

**is.na** signature(x = "MSnSet") Returns the a matrix of logicals of dimensions `dim(x)` specifying if respective values are missing in the `MSnSet`'s expression matrix.

**plotNA** signature(object = "MSnSet", pNA = "numeric") Plots missing data for an `MSnSet` instance. `pNA` is a numeric of length 1 that specifies the percentage of accepted missing data values per features. This value will be highlighted with a point on the figure, illustrating the overall percentage of NA values in the full data set and the number of proteins retained. Default is 1/2.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

See also the [filterNA](#) method to filter out features with a specified proportion if missing values.

**Examples**

```
xx <- quantify(itraqdata, reporters = iTRAQ4, verbose = FALSE)
exprs(xx)[sample(prod(dim(xx)), 120)] <- NA

head(is.na(xx))
table(is.na(xx))
image(is.na(xx))

plotNA(xx, pNA = 1/4)
```

---

precSelection

*Number of precursor selection events*

---

**Description**

precSelection computes the number of selection events each precursor ions has undergone in a tandem MS experiment. This will be a function of amount of peptide loaded, chromatography efficiency, exclusion time,... and is useful when optimising and experimental setup. This function returns a named integer vector or length equal to the number of unique precursor MZ values in the original experiment. See `n` parameter to set the number of MZ significant decimals.

precSelectionTable is a wrapper around precSelection and returns a table with the number of single, 2-fold, ... selection events.

**Usage**

```
precSelection(object,n)
```

**Arguments**

object	An instance of class " <a href="#">MSnExp</a> ".
n	The number of decimal places to round the precursor MZ to. Is passed to the <a href="#">round</a> function.

**Value**

A named integer in case of precSelection and a table for precSelectionTable.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>



**Examples**

```

precSelection(itraqdata)
precSelection(itraqdata,n=2)
precSelectionTable(itraqdata)
## only single selection event in this reduced experiment

```

pSet-class

---

*Class to Contain Raw Mass-Spectrometry Assays and Experimental Metadata*

---

**Description**

Container for high-throughput mass-spectrometry assays and experimental metadata. This class is based on Biobase's "eSet" virtual class, with the notable exception that 'assayData' slot is an environment contain objects of class "Spectrum".

**Objects from the Class**

A virtual Class: No objects may be created from it. See "MSnExp" for instantiatable sub-classes.

**Slots**

**assayData:** Object of class "environment" containing the MS spectra (see "Spectrum1" and "Spectrum2"). Slot is inherited from "pSet".

**phenoData:** Object of class "AnnotatedDataFrame" containing experimenter-supplied variables describing sample (i.e the individual tags for an labelled MS experiment) See [phenoData](#) for more details. Slot is inherited from "pSet".

**featureData:** Object of class "AnnotatedDataFrame" containing variables describing features (spectra in our case), e.g. identificaion data, peptide sequence, identification score,... (inherited from "eSet"). See [featureData](#) for more details. Slot is inherited from "pSet".

**experimentData:** Object of class "MIAPE", containing details of experimental methods. See [experimentData](#) for more details. Slot is inherited from "pSet".

**protocolData:** Object of class "AnnotatedDataFrame" containing equipment-generated variables (inherited from "eSet"). See [protocolData](#) for more details. Slot is inherited from "pSet".

**processingData:** Object of class "MSnProcess" that records all processing. Slot is inherited from "pSet".

**.cache:** Object of class environment used to cache data. Under development.

**.\_\_\_classVersion\_\_:** Object of class "Versions" describing the versions of the class.

**Extends**

Class "VersionedBiobase", directly. Class "Versioned", by class "VersionedBiobase", distance 2.

## Methods

Methods defined in derived classes may override the methods described here.

[ signature(x = "pSet"): Subset current object and return object of same class.

[[] signature(x = "pSet"): Direct access to individual spectra.

**abstract** Access abstract in experimentData.

**assayData** signature(object = "pSet"): Access the assayData slot. Returns an environment.

**description** signature(x = "pSet"): Synonymous with experimentData.

**dim** signature(x = "pSet"): Returns the dimensions of the phenoData slot.

**experimentData** signature(x = "pSet"): Access details of experimental methods.

**featureData** signature(x = "pSet"): Access the featureData slot.

**fData** signature(x = "pSet"): Access feature data information.

**featureNames** signature(x = "pSet"): Coordinate access of feature names (e.g spectra, peptides or proteins) in assayData slot.

**fileNames** signature(object = "pSet"): Access file names in the processingData slot.

**fromFile** signature(object = "pSet"): Access raw data file indexes (to be found in the 'codeprocessingData' slot) from which the individual object's spectra were read from.

**centroided** signature(object = "pSet"): Indicates whether individual spectra are centroided ('TRUE') or uncentroided ('FALSE'). Use centroided(object) <- value to update a whole experiment, ensuring that object and value have the same length.

**fvarMetadata** signature(x = "pSet"): Access metadata describing features reported in fData.

**fvarLabels** signature(x = "pSet"): Access variable labels in featureData.

**length** signature(x = "pSet"): Returns the number of features in the assayData slot.

**notes** signature(x = "pSet"): Retrieve and unstructured notes associated with pSet in the experimentData slot.

**pData** signature(x = "pSet"): Access sample data information.

**phenoData** signature(x = "pSet"): Access the phenoData slot.

**processingData** signature(object = "pSet"): Access the processingData slot.

**protocolData** signature(x = "pSet"): Access the protocolData slot.

**pubMedIds** signature(x = "pSet"): Access PMIDs in experimentData.

**sampleNames** signature(x = "pSet"): Access sample names in phenoData.

**spectra** signature(x = "pSet"): Access the assayData slot, returning the features as a list.

**varMetadata** signature(x = "pSet"): Access metadata describing variables reported in pData.

**varLabels** signature(x = "pSet"): Access variable labels in phenoData.

**acquisitionNum** signature(object = "pSet"): Accessor for spectra acquisition numbers.

**collisionEnergy** signature(object = "pSet"): Accessor for MS2 spectra collision energies.

**intensity** signature(object = "pSet"): Accessor for spectra intensities, returned as named list.

**msInfo** signature(object = "pSet"): Prints the MIAPE-MS meta-data stored in the experimentData slot.

**msLevel** signature(object = "pSet"): Accessor for spectra MS levels.

**mz** signature(object = "pSet"): Accessor for spectra M/Z values, returned as a named list.

**peaksCount** signature(object = "pSet"): Accessor for spectra peak counts.

**peaksCount** signature(object = "pSet", scans = "numeric"): Accessor to scans spectra peak counts.

**polarity** signature(object = "pSet"): Accessor for MS1 spectra polarities.

**precursorCharge** signature(object = "pSet"): Accessor for MS2 precursor charges.

**precursorIntensity** signature(object = "pSet"): Accessor for MS2 precursor intensity.

**precursorMz** signature(object = "pSet"): Accessor for MS2 precursor M/Z values.

**precScanNum** signature(object = "pSet"): Accessor for MS2 precursor scan numbers.

**rttime** signature(object = "pSet"): Accessor for spectra retention times.

**tic** signature(object = "pSet"): Accessor for spectra total ion counts.

**ionCount** signature(object = "pSet"): Accessor for spectra total ion current.

**header** signature(object = "pSet"): Returns a data frame containing all available spectra parameters (MSn only).

**header** signature(object = "pSet", scans = "numeric"): Returns a data frame containing scans spectra parameters (MSn only).

Additional accessors for the experimental metadata (experimentData slot) are defined. See "[MIAPE](#)" for details.

#### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

#### References

The "[eSet](#)" class, on which pSet is based.

#### See Also

"[MSnExp](#)" for an instantiatable application of pSet.

#### Examples

```
showClass("pSet")
```

---

purityCorrect-methods    *Performs reporter ions purity correction*

---

#### Description

Manufacturers sometimes provide purity correction values indicating the percentages of each reporter ion that have masses differing by +/- n Da from the nominal reporter ion mass due to isotopic variants. This correction is generally applied after reporter peaks quantitation.

Purity correction here is applied using solve from the base package using the purity correction values as coefficient of the linear system and the reporter quantities as the right-hand side of the linear system. 'NA' values are ignored and negative intensities after correction are also set to 'NA'.

A more elaborated purity correction method is described in Shadforth *et al.*, i-Tracker: for quantitative proteomics using iTRAQ. BMC Genomics. 2005 Oct 20;6:145. (PMID 16242023).

Function `makeImpuritiesMatrix(x, edit = TRUE)` opens a simple graphical interface to guide the user in the creation of such a matrix. The function takes the dimension of the square matrix (i.e the number of reporter ions) as argument. When available, default values taken from manufacturer's certification sheets are provided, but batch specific values should be used whenever possible. `makeImpuritiesMatrix` returns the (possibly interactively updated) matrix to be used with `purityCorrect`. If `edit = FALSE`, the edition of the matrix is bypassed.

### Arguments

`object` An object of class "`MsnSet`".

`impurities` A square 'matrix' of dim equal to `ncol(object)` defining the correction coefficients to be applied. The reporter ions should be ordered along the columns and the relative percentages along the rows.

As an example, below is the correction factors as provided in an ABI iTRAQ 4-plex certificate of analysis:

reporter	% of -2	% of -1	% of +1	% of +2
114	0.0	1.0	5.9	0.2
115	0.0	2.0	5.6	0.1
116	0.0	3.0	4.5	0.1
117	0.1	4.0	3.5	0.1

The impurity table will be

0.929	0.059	0.002	0.000
0.020	0.923	0.056	0.001
0.000	0.030	0.924	0.045
0.000	0.001	0.040	0.923

where, the diagonal is computed as  $100 - \text{sum of rows of the original table}$  and subsequent cells are directly filled in.

Similarly, for TMT 6-plex tags, we observe

reporter	% of -3	% of -2	% of -1	% of +1	% of +2	% of +3
126	0	0	0	6.1	0	0
127	0	0	0.5	6.7	0	0
128	0	0	1.1	4.2	0	0
129	0	0	1.7	4.1	0	0
130	0	0	1.6	2.1	0	0
131	0	0.2	3.2	2.8	0	0

and obtain the following impurity correction matrix

0.939	0.061	0.000	0.000	0.000	0.000
0.005	0.928	0.067	0.000	0.000	0.000
0.000	0.011	0.947	0.042	0.000	0.000
0.000	0.000	0.017	0.942	0.041	0.000
0.000	0.000	0.000	0.016	0.963	0.021
0.000	0.000	0.000	0.002	0.032	0.938

These two examples above are provided as defaults impurity correction matrices in `makeImpuritiesMatrix`.

## Methods

```
signature(object = "MSnSet", impurities = "matrix")
```

## Examples

```
## quantifying full experiment
data(itraqdata)
msnset <- quantify(itraqdata, method = "trap", reporters = iTRAQ4)
impurities <- matrix(c(0.929,0.059,0.002,0.000,
                      0.020,0.923,0.056,0.001,
                      0.000,0.030,0.924,0.045,
                      0.000,0.001,0.040,0.923),
                    nrow=4, byrow = TRUE)
## or, using makeImpuritiesMatrix()
## Not run: impurities <- makeImpuritiesMatrix(4)
msnset.crct <- purityCorrect(msnset, impurities)
head(exprs(msnset))
head(exprs(msnset.crct))
processingData(msnset.crct)
```

---

quantify-methods

*Quantifies 'MSnExp' and 'Spectrum' objects*

---

## Description

This method quantifies individual "[Spectrum](#)" objects or full "[MSnExp](#)" experiments. Current implementation quantify specific peaks in individual spectra. The peaks of interest are defined by the `reporters` parameter using one of the possible method methods. This essentially qualifies for MSMS quantitation using isobaric tags, although any peak can be defined in reporters.

## Arguments

<code>object</code>	Objects of class " <a href="#">Spectrum</a> " or " <a href="#">MSnExp</a> ".
<code>method</code>	Peak quantitation method. One of, possibly abbreviated "trapezoidation", "max", or "sum". These methods return respectively the area under the peak(s), the maximum of the peak(s) or the sum of all intensities of the peak(s).
<code>reporters</code>	An object of class " <a href="#">ReporterIons</a> " that defines the peak(s) to be quantified.
<code>strict</code>	If <code>strict</code> is 'FALSE' (default), the quantitation is performed using data points along the entire width of a peak. If <code>strict</code> is set to 'TRUE', once the apex(es) is/are identified, only data points within apex +/- width of reporter (see " <a href="#">ReporterIons</a> ") are used for quantitation.
<code>parallel</code>	Logical defining if reporter peaks should be quantified in parallel (default is FALSE). Currently not supported on Windows.
<code>verbose</code>	Verbose of the output (only for <a href="#">MSnExp</a> objects).

## Details

"ReporterIons" define specific MZ at which peaks are expected and a window around that MZ value. A peak of interest is searched for in that window. Since version 1.1.2, warnings are not thrown anymore in case no data is found in that region or if the peak extends outside the window. This can be checked manually after quantitation, by inspecting the quantitation data (using the `exprs` accessor) for NA values or by comparing the `lowerMz` and `upperMz` columns in the "MSnSet" qual slot against the respective expected `mz(reporters) +/- width(reporters)`. This is illustrated in the example below.

Once the range of the curve is found, quantification is performed. If no data points are found in the expected region, 'NA' is returned for the reporter peak MZ.

## Methods

`signature(object = "MSnExp", method = "character", reporters = "ReporterIons", verbose = "logical")`

Quantifies peaks defined in reporters using method in all spectra of the MSnExp object. If verbose is set to TRUE, a progress bar will be displayed.

An object of class "MSnSet" is returned containing the quantified feature expression and all meta data inherited from the MSnExp argument.

`signature(object = "Spectrum", method = "character", reporters = "ReporterIons")` Quantifies peaks defined in reporters using method in the Spectrum object.

A list of length 2 will be returned. The first element, named `peakQuant`, is a 'numeric' of length equal to `length(reporters)` with quantitation of the reporter peaks using method.

The second element, named `curveStats`, is a 'data.frame' of dimension `length(reporters)` times 7 giving, for each reporter curve parameters: maximum intensity ('`maxInt`'), number of maxima ('`nMaxInt`'), number of data points defined the curve ('`baseLength`'), lower and upper MZ values for the curve ('`lowerMz`' and '`upperMz`'), reporter ('`reporter`') and precursor MZ value ('`precursor`') when available.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

## Examples

```
## quantifying full experiment
data(itraqdata)
msnset <- quantify(itraqdata ,method = "trap", reporters = iTRAQ4)
msnset
## checking for non-quantified peaks
sum(is.na(exprs(msnset)))
## quantifying single spectrum
qty <- quantify(itraqdata[[1]], method = "trap", iTRAQ4[1])
qty$peakQuant
qty$curveStats
```

---

readIspsyData

*Reads an ispy2 result spread sheet and creates a fully featured 'MSnSet' instance.*

---

**Description**

Reads an ispy2 tab-delimited spreadsheet and generates the corresponding [MSnSet](#) object.

**Usage**

```
readIspyData(file = "ispy_results.tsv", uniquePeps = TRUE, pep = 0.05,  
             na.rm = TRUE, min.int = 0, reporters = 19:23, keepAll = FALSE,  
             verbose = TRUE)
```

**Arguments**

file	A character, indicating the file name to be read in. Default is "ispy_results.tsv".
uniquePeps	A logical, indicating whether only unique peptides should be included. Default is TRUE.
pep	A numeric indicating the posterior error probability threshold for peptides to be considered correctly identified. Default is 0.05.
na.rm	A logical indicating whether reporter ions containing one or more NA values should be excluded. Default is TRUE.
min.int	A numeric indicating the minimal summed intensity threshold for reporter data to be imported. Default is 0. Note that 'NA' values are excluded when summing the values.
reporters	A numeric indicating column indices of reporter ions quantitation data. Default is 19:23 for iTRAQ 4-plex.
keepAll	A logical that defines whether all features of the ispy result should be imported. If 'TRUE', 'pep', 'na.rm' and 'min.int' are ignored. This is equivalent to 'pep=1', 'na.rm=FALSE' and 'min.int=0'. Default is 'FALSE'.
verbose	A logical indicating whether verbose output is to be printed out.

**Value**

An object of class "[MSnSet](#)".

**Author(s)**

Laurent Gatto

**References**

Ispy is a set of perl script to analyse SILAC, 15N and MSMS data developed by Phil D. Charles <pd35@cam.ac.uk> at CCP <http://www.bio.cam.ac.uk/proteomics/>. No ispy references published yet.

**See Also**

[readMSData](#) to import raw data.

**Examples**

```
## Not run: ispy <- readIspyData("ispy_results.tsv")
```

---

readMgfData                      *Import mgf files as 'MSnExp' instances.*

---

## Description

Reads an mgf file and generates an "MSnExp" object.

## Usage

```
readMgfData(file, pdata = NULL, centroided = TRUE, smoothed = FALSE,
  verbose = TRUE, cache = 1)
```

## Arguments

file	character vector with file name to be read.
pdata	an object of class "NAnnotatedDataFrame".
smoothed	Logical indicating whether spectra already smoothed or not. Default is 'FALSE'. Used to initialise "MSnProcess" object in processingData slot.
centroided	Logical indicating whether spectra are centroided or not. Default is 'TRUE'. Used to initialise "MSnProcess" object in processingData slot.
cache	Numeric indicating caching level. Default is 1. Under development.
verbose	verbosity flag.

## Details

Note that when reading an mgf file, the original order of the spectra is lost. Thus, if the data was originally written to mgf from an MSnExp object using writeMgfData, although the feature names will be identical, the spectra are not as a result of the reordering. See example below.

## Value

An instance of

## Author(s)

Guangchuang Yu <guangchuangyu@gmail.com> and Laurent Gatto <lg390@cam.ac.uk>

## See Also

[writeMgfData](#) method to write the content of "Spectrum" or "MSnExp" objects to mgf files. Raw data files can also be read with the [readMSData](#) function.

## Examples

```
## Not run:
data(itraqdata)
writeMgfData(itraqdata,file="itraqdata.mgf",COM="MSnbase itraqdata")
itraqdata2 <- readMgfData("itraqdata.mgf")
## note that the order of the spectra is altered
## and precision of some values (precursorMz for instance)
match(signif(precursorMz(itraqdata2),4),signif(precursorMz(itraqdata),4))
```



```

## [1] 1 10 11 12 13 14 15 16 17 18 ...
## ... but all the precursors are there
all.equal(sort(precursorMz(itraqdata2)),sort(precursorMz(itraqdata)),
          check.attributes=FALSE,
          tolerance=10e-5)
## is TRUE
all.equal(as.data.frame(itraqdata2[[1]]),as.data.frame(itraqdata[[1]]))
## is TRUE
all.equal(as.data.frame(itraqdata2[[3]]),as.data.frame(itraqdata[[11]]))
## is TRUE

## End(Not run)

```

---

readMSData                      *Imports mass-spectrometry raw data files as 'MSnExp' instances.*

---

## Description

Reads as set of XML-based mass-spectrometry data files and generates an "MSnExp" object. This function uses the functionality provided by the mzR package to access data and meta data in mzData, mzXML and mzML.

## Usage

```
readMSData(files, pdata = NULL, msLevel = 2, verbose = TRUE,
           centroided = FALSE, smoothed = FALSE, removePeaks = 0, clean = FALSE,
           cache = 1)
```

## Arguments

files	character vector with file names to be read.
pdata	an object of class "NAnnotatedDataFrame".
msLevel	MS level spectra to be read. Use '1' for MS1 spectra of any larger numeric for MSn spectra. Default is '2'.
centroided	Logical indicating whether spectra are centroided or not. Default is 'FALSE'. Used to initialise "MSnProcess" object in processingData slot.
smoothed	Logical indicating whether spectra already smoothed or not. Default is 'FALSE'. Used to initialise "MSnProcess" object in processingData slot.
removePeaks	If > 0 (default), all peaks less or equal then value will set to 0. See <a href="#">removePeaks</a> for more details and examples.
clean	Logical indicating whether 0 intensity peaks should be discarded from spectra. Useful is removePeaks is set. Default is 'FALSE'. See <a href="#">clean</a> for more details and examples.
cache	Numeric indicating caching level. Default is 0 for MS1 and 1 MS2 (or higher). Under development.
verbose	verbosity flag.

## Value

An "MSnExp" object.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

"[MSnExp](#)" or [readMgfData](#) to read mgf peak lists.

**Examples**

```
file <- dir(system.file(package="MSnbase",dir="extdata"),
           full.name=TRUE,
           pattern="mzXML$")
aa <- readMSData(file)
aa
```

---

readMSnSet

*Read 'MSnSet'*

---

**Description**

This function reads data files to generate an [MSnSet](#) instance. It is a wrapper around Biobase's [readExpressionSet](#) function with an additional `featureDataFile` parameter to include feature data. See also [readExpressionSet](#) for more details.

**Usage**

```
readMSnSet(exprsFile,
           phenoDataFile,
           featureDataFile,
           experimentDataFile,
           notesFile,
           path, annotation,
           exprsArgs = list(sep = sep, header = header, row.names = row.names, quote = quote, ...),
           phenoDataArgs = list(sep = sep, header = header, row.names = row.names, quote = quote, stringsAsFactors = FALSE),
           featureDataArgs = list(sep = sep, header = header, row.names = row.names, quote = quote, stringsAsFactors = FALSE),
           experimentDataArgs = list(sep = sep, header = header, row.names = row.names, quote = quote, stringsAsFactors = FALSE),
           sep = "\t",
           header = TRUE,
           quote = "",
           stringsAsFactors = FALSE,
           row.names = 1L,
           widget = getOption("BioC")$Base$use.widgets, ...)
```

**Arguments**

Arguments directly passed to [readExpressionSet](#). The description is from the [readExpressionSet](#) documentation page.

(character) File or connection from which to read expression values. The file should contain a matrix with rows as features and columns as samples. [read.table](#) is called with this as its file argument and further arguments given by `exprsArgs`.

phenoDataFile	(character) File or connection from which to read phenotypic data. <a href="#">read.AnnotatedDataFrame</a> is called with this as its file argument and further arguments given by phenoDataArgs.
experimentDataFile	(character) File or connection from which to read experiment data. <a href="#">read.MIAME</a> is called with this as its file argument and further arguments given by experimentDataArgs.
notesFile	(character) File or connection from which to read notes; <a href="#">readLines</a> is used to input the file.
path	(optional) directory in which to find all the above files.
annotation	(character) A single character string indicating the annotation associated with this ExpressionSet.
exprsArgs	A list of arguments to be used with <a href="#">read.table</a> when reading in the expression matrix.
phenoDataArgs	A list of arguments to be used (with <a href="#">read.AnnotatedDataFrame</a> ) when reading the phenotypic data.
experimentDataArgs	A list of arguments to be used (with <a href="#">read.MIAME</a> ) when reading the experiment data.
sep, header, quote, stringsAsFactors, row.names	arguments used by the <a href="#">read.table</a> -like functions.
widget	A boolean value indicating whether widgets can be used. Widgets are NOT yet implemented for <a href="#">read.AnnotatedDataFrame</a> .
...	Further arguments that can be passed on to the <a href="#">read.table</a> -like functions. Additional argument, specific to <a href="#">readMSnSet</a> :
featureDataFile	(character) File or connection from which to read feature data. <a href="#">read.AnnotatedDataFrame</a> is called with this as its file argument and further arguments given by phenoDataArgs.
featureDataArgs	A list of arguments to be used (with <a href="#">read.AnnotatedDataFrame</a> ) when reading the phenotypic data.

**Value**

An instance of the [MSnSet](#) class.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**Examples**

```
## Not run:
exprsFile <- "path_to_intensity_file.csv"
fdatafile <- "path_to_featuredata_file.csv"
pdatafile <- "path_to_sampledata_file.csv"
## Read ExpressionSet with appropriate parameters
res <- readMSnSet(exprsFile, pdataFile, fdataFile, sep = "\t", header=TRUE)

## End(Not run)
```

---

readMzTabData	<i>Read an 'mzTab' file</i>
---------------	-----------------------------

---

### Description

This function can be used to create a "MSnSet" by reading and parsing an mzTab file. The metadata section is always used to populate the MSnSet's experimentData slot.

### Usage

```
readMzTabData(file, what = c("PRT", "PEP"),  
              verbose = TRUE)
```

### Arguments

file	A character with the mzTab file to be read in.
what	One of "PRT" or "PEP", defining which of protein or peptide section should be parse. The metadata section, when available, is always used to populate the experimentData slot.
verbose	Produce verbose output.

### Value

An instance of class MSnSet.

### Author(s)

Laurent Gatto

### See Also

[writeMzTabData](#) to save an "MSnSet" as an mzTab file.

### Examples

```
## Not run:  
testfile <- "http://mztab.googlecode.com/svn/specification/trunk/examples/mztab_itraq_example.txt"  
prot <- readMzTabData(testfile, "PRT")  
prot  
pep <- readMzTabData(testfile, "PEP")  
pep  
  
## End(Not run)
```

---

removePeaks-methods      *Removes low intensity peaks*

---

### Description

This method sets low intensity peaks from individual spectra (Spectrum instances) or whole experiments (MSnExp instances) to 0. The intensity threshold is set with the `t` parameter. Default is the "min" character. The threshold is then set as the non-0 minimum intensity found in the spectrum. Any other numeric values is valid. All peaks with maximum intensity smaller or equal to `t` are set to 0.

Note that the number of peaks is not changed; the peaks below the threshold are set to 0 and the object is not cleaned out (see [clean](#)). An illustrative example is shown below.

### Methods

`signature(object = "MSnExp", t, verbose = "logical" )` Removes low intensity peaks of all spectra in MSnExp object. `t` sets the minimum peak intensity. Default is "min", i.e the smallest intensity in each spectrum. Other numeric values are valid. Displays a control bar if `verbose` set to TRUE (default). Returns a new MSnExp instance.

`signature(object = "Spectrum", t)` Removes low intensity peaks of Spectrum object. `t` sets the minimum peak intensity. Default is "min", i.e the smallest intensity in each spectrum. Other numeric values are valid. Returns a new Spectrum instance.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

### See Also

[clean](#) and [trimMz](#) for other spectra processing methods.

### Examples

```
int <- c(2,0,0,0,1,5,1,0,0,1,3,1,0,0,1,4,2,1)
sp1 <- new("Spectrum2",
          intensity=int,
          mz=1:length(int))
sp2 <- removePeaks(sp1) ## no peaks are removed here
                        ## as min intensity is 1 and
                        ## no peak has a max int <= 1
sp3 <- removePeaks(sp1,3)
intensity(sp1)
intensity(sp2)
intensity(sp3)

peaksCount(sp1) == peaksCount(sp2)
peaksCount(sp3) <= peaksCount(sp1)

data(itraqdata)
itraqdata2 <- removePeaks(itraqdata, t = 2.5e5)
table(unlist(intensity(itraqdata))) == 0)
table(unlist(intensity(itraqdata2))) == 0)
processingData(itraqdata2)
```

---

removeReporters-methods

*Removes reporter ion tag peaks*

---

### Description

This methods sets all the reporter tag ion peaks from one MS2 spectrum or all the MS2 spectra of an experiment to 0. Reporter data is specified using an "ReporterIons" instance. The peaks are selected around the expected reporter ion m/z value +/- the reporter width. Optionally, the spectrum/spectra can be cleaned to remove successive 0 intensity data points (see the [clean](#) function for details).

Note that this method only works for MS2 spectra or experiments that contain MS2 spectra. It will fail for MS1 spectrum.

### Methods

signature(object = "MSnExp", reporters = "ReporterIons", clean = "logical", verbose = "logical" )

The reporter ion peaks defined in the reporters instance of all the MS2 spectra of the "MSnExp" instance are set to 0 and, if clean is set to TRUE, cleaned. The default value of reporters is NULL, which leaves the spectra as unchanged. The verbose parameter (default is TRUE) defines whether a progress bar should be showed.

signature(object = "Spectrum", reporters = "ReporterIons", clean = "FALSE") The reporter ion peaks defined in the reporters instance of MS2 "Spectrum" instance are set to 0 and, if clean is set to TRUE, cleaned. The default value of reporters is NULL, which leaves the spectrum as unchanged.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

### See Also

[clean](#) and [removePeaks](#) for other spectra processing methods.

### Examples

```
sp1 <- itraqdata[[1]]
sp2 <- removeReporters(sp1,reporters=iTRAQ4)
sel <- mz(sp1) > 114 & mz(sp1) < 114.2
mz(sp1)[sel]
intensity(sp1)[sel]
plot(sp1,full=TRUE,reporters=iTRAQ4)
intensity(sp2)[sel]
plot(sp2,full=TRUE,reporters=iTRAQ4)
```

---

 ReporterIons-class      *The "ReporterIons" Class*


---

## Description

The ReporterIons class allows to define a set of isobaric reporter ions that are used for quantification in MSMS mode, e.g. iTRAQ (isobaric tag for relative and absolute quantitation) or TMT (tandem mass tags). ReporterIons instances can then be used when quantifying "MSnExp" data of plotting the reporters peaks based on in "Spectrum2" objects.

Some reporter ions are provided with MSnbase and can be loaded with the [data](#) function. These reporter ions data sets are:

iTRAQ4: ReporterIon object for the iTRAQ 4-plex set. Load with `data(iTRAQ4)`.

iTRAQ5: ReporterIon object for the iTRAQ 4-plex set plus the isobaric tag. Load with `data(iTRAQ5)`.

TMT6: ReporterIon object for the TMT 6-plex set. Load with `data(TMT6)`.

TMT7: ReporterIon object for the TMT 6-plex set plus the isobaric tag. Load with `data(TMT6)`.

## Objects from the Class

Objects can be created by calls of the form `new("ReporterIons", ...)`.

## Slots

**name:** Object of class "character" to identify the ReporterIons instance.

**reporterNames:** Object of class "character" naming each individual reporter of the ReporterIons instance. If not provided explicitly, they are names by concatenating the ReporterIons name and the respective MZ values.

**description:** Object of class "character" to describe the ReporterIons instance.

**mz:** Object of class "numeric" providing the MZ values of the reporter ions.

**col:** Object of class "character" providing colours to highlight the reporters on plots.

**width:** Object of class "numeric" indicating the width around the individual reporter ions MZ values were to search for peaks. This is dependent on the mass spectrometer's resolution and is used for peak picking when quantifying the reporters. See [quantify](#) for more details about quantification.

**.\_\_\_classVersion\_\_:** Object of class "Versions" indicating the version of the ReporterIons instance. Intended for developer use and debugging.

## Extends

Class "[Versioned](#)", directly.

## Methods

`show(object)` Displays object content as text.

`object[]` Subsets one or several reporter ions of the ReporterIons object and returns a new instance of the same class.

`length(object)` Returns the number of reporter ions in the instance.

`mz(object)` Returns the expected mz values of reporter ions.

reporterColours(object) **or** reporterColors(object) Returns the colours used to highlight the reporter ions.

reporterNames(object) Returns the name of the individual reporter ions. If not specified or is an incorrect number of names is provided at initialisation, the names are generated automatically by concatenating the instance name and the reporter's MZ values.

reporterNames(object) <- value Sets the reporter names to value, which must be a character of the same length as the number of reporter ions.

width(object) Returns the widths in which the reporter ion peaks are expected.

names(object) Returns the name of the ReporterIons object.

description(object) Returns the description of the ReporterIons object.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

### References

Ross PL, Huang YN, Marchese JN, Williamson B, Parker K, Hattan S, Khainovski N, Pillai S, Dey S, Daniels S, Purkayastha S, Juhasz P, Martin S, Bartlet-Jones M, He F, Jacobson A, Pappin DJ. "Multiplexed protein quantitation in *Saccharomyces cerevisiae* using amine-reactive isobaric tagging reagents." *Mol Cell Proteomics*, 2004 Dec;3(12):1154-69. Epub 2004 Sep 22. PubMed PMID: 15385600.

Thompson A, Sch\afner J, Kuhn K, Kienle S, Schwarz J, Schmidt G, Neumann T, Johnstone R, Mohammed AK, Hamon C. "Tandem mass tags: a novel quantification strategy for comparative analysis of complex protein mixtures by MS/MS." *Anal Chem*. 2003 Apr 15;75(8):1895-904. *Erratum in: Anal Chem*. 2006 Jun 15;78(12):4235. Mohammed, A Karim A [added] and *Anal Chem*. 2003 Sep 15;75(18):4942. Johnstone, R [added]. PubMed PMID: 12713048.

### See Also

[TMT6](#) or [iTRAQ4](#) for readily available examples.

### Examples

```
## Code used for the iTRAQ4 set
ri <- new("ReporterIons",
  description="4-plex iTRAQ",
  name="iTRAQ4",
  reporterNames=c("iTRAQ4.114","iTRAQ4.115",
    "iTRAQ4.116","iTRAQ4.117"),
  mz=c(114.1,115.1,116.1,117.1),
  col=c("red","green","blue","yellow"),
  width=0.05)
ri
reporterNames(ri)
ri[1:2]
```



---

Spectrum-class	<i>The "Spectrum" Class</i>
----------------	-----------------------------

---

**Description**

Virtual container for spectrum data common to all different types of spectra. A Spectrum object can not be directly instantiated. Use "[Spectrum1](#)" and "[Spectrum2](#)" instead.

**Slots**

**msLevel:** Object of class "integer" indicating the MS level: 1 for MS1 level Spectrum1 objects and 2 for MSMSM Spectrum2 objects. Levels > 2 have not been tested and will be handled as MS2 spectra.

**peaksCount:** Object of class "integer" indicating the number of MZ peaks.

**rt:** Object of class "numeric" indicating the retention time (in seconds) for the current ions.

**tic:** Object of class "numeric" indicating the total ion current.

**acquisitionNum:** Object of class "integer" corresponding to the acquisition number of the current spectrum.

**scanIndex:** Object of class "integer" indicating the scan index of the current spectrum.

**mz:** Object of class "numeric" of length equal to the peaks count (see peaksCount slot) indicating the MZ values that have been measured for the current ion.

**intensity:** Object of class "numeric" of same length as mz indicating the intensity at which each mz datum has been measured.

**centroided:** Object of class "logical" indicating if instance is centroided ('TRUE') or uncentroided ('FALSE').

**fromFile:** Object of class "integer" referencing the file the spectrum originates. The file names are stored in the processingData slot of the "[MSnExp](#)" or "[MSnSet](#)" instance that contains the current "Spectrum" instance.

**.\_\_\_classVersion\_\_:** Object of class "Versions" indicating the version of the Spectrum class. Intended for developer use and debugging.

**Extends**

Class "[Versioned](#)", directly.

**Methods**

**acquisitionNum(object)** Returns the acquisition number of the spectrum as an integer.

**centroided(object)** Indicates whether spectrum is centroided ('TRUE') or uncentroided ('FALSE').

**centroided(object) <- value** Sets the 'centroided' status of the spectrum object.

**fromFile(object)** Returns the index of the raw data file from which the current instances originates as an integer.

**intensity(object)** Returns an object of class "numeric" containing the intensities of the spectrum.

**msLevel(object)** Returns an MS level of the spectrum as an integer.

**mz(object)** Returns an object of class "numeric" containing the MZ value of the spectrum peaks.

**peaksCount(object)** Returns the number of peaks (possibly of 0 intensity) as an integer.

- `rtime(object)` Returns the retention time for the spectrum as an integer.
- `ionCount(object)` Returns the total ion count for the spectrum as a numeric.
- `tic(object)` Returns the total ion current for the spectrum as a numeric.
- clean** signature(object = "Spectrum"): Removes unused 0 intensity data points. See [clean](#) documentation for more details and examples.
- plot** signature(x = "Spectrum", y = "missing"): Plots intensity against mz. See [plot.Spectrum](#) documentation for more details.
- quantify** signature(object = "Spectrum"): Quantifies defined peaks in the spectrum. See [quantify](#) documentation for more details.
- removePeaks** signature(object = "Spectrum"): Remove peaks lower than a threshold t. See [removePeaks](#) documentation for more details and examples.
- show** signature(object = "Spectrum"): Displays object content as text.
- trimMz** signature(object = "Spectrum"): Trims the MZ range of all the spectra of the MSnExp instance. See [trimMz](#) documentation for more details and examples.
- as** signature(object = "Spectrum", "data.frame"): Coerces the Spectrum object to a two-column data.frame containing intensities and MZ values.

**Note**

This is a virtual class and can not be instantiated directly.

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

Instanciable sub-classes "[Spectrum1](#)" and "[Spectrum2](#)" for MS1 and MS2 spectra.

---

Spectrum1-class

*The "Spectrum1" Class for MS1 Spectra*

---

**Description**

Spectrum1 extends the "[Spectrum](#)" class and introduces an MS1 specific attribute in addition to the slots in "[Spectrum](#)". Spectrum1 instances are not created directly but are contained in the assayData slot of an "[MSnExp](#)".

**Slots**

- polarity:** Object of class "integer" indicating the polarity of the ion.
- msLevel:** Object of class "integer" indicating the MS level: always 1 in this case (inherited from "[Spectrum](#)").
- peaksCount:** Object of class "integer" indicating the number of MZ peaks (inherited from "[Spectrum](#)").
- rt:** Object of class "numeric" indicating the retention time (in seconds) for the current ions (inherited from "[Spectrum](#)").
- acquisitionNum:** Object of class "integer" corresponding to the acquisition number of the current spectrum (inherited from "[Spectrum](#)").

- scanIndex:** Object of class "integer" indicating the scan index of the current spectrum (inherited from "Spectrum").
- mz:** Object of class "numeric" of length equal to the peaks count (see peaksCount slot) indicating the MZ values that have been measured for the current ion (inherited from "Spectrum").
- intensity:** Object of class "numeric" of same length as mz indicating the intensity at which each mz datum has been measured "Spectrum").
- .\_\_\_classVersion\_\_:** Object of class "Versions" indicating the versions of the Spectrum and Spectrum1 classes of the instance. Intended for developer use and debugging.

### Extends

Class "Spectrum", directly. Class "Versioned", by class "Spectrum", distance 2.

### Methods

See "Spectrum" for additional accessors and methods to process Spectrum1 objects.

polarity(object) Returns the polarity of the spectrum as an integer.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

### See Also

Virtual super-class "Spectrum", "Spectrum2" for MS2 spectra and "MSnExp" for a full experiment container.

---

Spectrum2-class

*The "Spectrum2" Class for MSMS Spectra*

---

### Description

Spectrum2 extends the "Spectrum" class and introduces several MS2 specific attributes in addition to the slots in "Spectrum". Spectrum2 are not created directly but are contained in the assayData slot of an "MSnExp".

### Slots

- merged:** Object of class "numeric" indicating of how many combination the current spectrum is the result of.
- precScanNum:** Object of class "integer" indicating the precursor MS scan index in the original input file.
- precursorMz:** Object of class "numeric" providing the precursor ion MZ value.
- precursorIntensity:** Object of class "numeric" providing the precursor ion intensity.
- precursorCharge:** Object of class "integer" indicating the precursor ion charge.
- collisionEnergy:** Object of class "numeric" indicating the collision energy used to fragment the parent ion.
- msLevel:** Object of class "integer" indicating the MS level: 2 in this case (inherited from "Spectrum").

peaksCount: Object of class "integer" indicating the number of MZ peaks (inherited from "Spectrum").

rt: Object of class "numeric" indicating the retention time (in seconds) for the current ions (inherited from "Spectrum").

acquisitionNum: Object of class "integer" corresponding to the acquisition number of the current spectrum (inherited from "Spectrum").

scanIndex: Object of class "integer" indicating the scan index of the current spectrum (inherited from "Spectrum").

mz: Object of class "numeric" of length equal to the peaks count (see peaksCount slot) indicating the MZ values that have been measured for the current ion (inherited from "Spectrum").

intensity: Object of class "numeric" of same length as mz indicating the intensity at which each mz datum has been measured "Spectrum").

.\_\_\_classVersion\_\_\_.: Object of class "Versions" indicating the versions of the Spectrum and Spectrum2 classes of the instance. Intended for developer use and debugging.

### Extends

Class "Spectrum", directly. Class "Versioned", by class "Spectrum", distance 2.

### Methods

See "Spectrum" for additional accessors and methods for Spectrum2 objects.

precursorMz(object) Returns the precursor MZ value as a numeric.

precursorMz(object) Returns the precursor scan number in the original data file as an integer.

precursorIntensity(object) Returns the precursor intensity as a numeric.

precursorCharge(object) Returns the precursor intensity as a integer.

collisionEnergy(object) Returns the collision energy as an numeric.

removeReporters(object, ...) Removes all reporter ion peaks. See [removeReporters](#) documentation for more details and examples.

### Author(s)

Laurent Gatto <lg390@cam.ac.uk>

### See Also

Virtual super-class "Spectrum", "Spectrum1" for MS1 spectra and "MSnExp" for a full experiment container.

---

TMT6

*TMT 6-plex set*

---

### Description

This instance of class "ReporterIons" corresponds to the TMT 6-plex set, i.e the 126, 127, 128, 129, 130 and 131 isobaric tags. In the TMT7 data set, an unfragmented tag, i.e reporter and attached isobaric tag, is also included at MZ 229. These objects are used to plot the reporter ions of interest in an MSMS spectra (see "Spectrum2") as well as for quantification (see [quantify](#)).

## Usage

```
TMT6  
TMT7
```

## References

Thompson A, Sch\afner J, Kuhn K, Kienle S, Schwarz J, Schmidt G, Neumann T, Johnstone R, Mohammed AK, Hamon C. "Tandem mass tags: a novel quantification strategy for comparative analysis of complex protein mixtures by MS/MS." *Anal Chem*. 2003 Apr 15;75(8):1895-904. *Erratum in: Anal Chem*. 2006 Jun 15;78(12):4235. Mohammed, A Karim A [added] and *Anal Chem*. 2003 Sep 15;75(18):4942. Johnstone, R [added]. PubMed PMID: 12713048.

## See Also

[iTRAQ4](#).

## Examples

```
TMT6  
TMT6[1:2  
  
newReporter <- new("ReporterIons",  
  description="an example",  
  name="my reporter ions",  
  reporterNames=c("myrep1","myrep2"),  
  mz=c(121,122),  
  col=c("red","blue"),  
  width=0.05)  
newReporter
```

---

trimMz-methods

*Trims 'MSnExp' or 'Spectrum' instances*

---

## Description

This method selects a range of MZ values in a single spectrum (Spectrum instances) or all the spectra of an experiment (MSnExp instances). The regions to trim are defined by the range of mzlim argument, such that MZ values < min(mzlim) and MZ values > max(mzlim) are trimmed away.

## Methods

signature(object = "MSnExp", mzlim = "numeric") Trims all spectra in MSnExp object according to mzlim. Returns a cleaned MSnExp instance.

signature(object = "Spectrum", mzlim = "numeric") Trims the Spectrum object and retruns a new trimmed object.

## Author(s)

Laurent Gatto <lg390@cam.ac.uk>

**See Also**

[removePeaks](#) and [clean](#) for other spectra processing methods.

**Examples**

```
mz <- 1:100
sp1 <- new("Spectrum2",
          mz=mz,
          intensity=abs(rnorm(length(mz))))
sp2 <- trimMz(sp1,c(25,75))
range(mz(sp1))
range(mz(sp2))

data(itraqdata)
itraqdata2 <- trimMz(itraqdata,c(113,117))
range(mz(itraqdata))
range(mz(itraqdata2))
processingData(itraqdata2)
```

---

writeMgfData-methods    *Write an experiment or spectrum to an mgf file*

---

**Description**

Methods writeMgfData write individual "Spectrum" instances of whole "MSnExp" experiments to a file in Mascot Generic Format (mgf) (see [http://www.matrixscience.com/help/data\\_file\\_help.html](http://www.matrixscience.com/help/data_file_help.html) for more details). Function readMgfData read spectra from and mgf file and creates an "MSnExp" object.

**Arguments**

object	An instance of class "Spectrum" or "MSnExp".
con	A valid connection or a character string with the name of the file to save the object. In case of the latter, a file connection is created. If not specified, 'spectrum.mgf' or 'experiment.mgf' are used depending on the class of object. Note that existing files are overwritten.
COM	Optional character vector with the value for the 'COM' field.
TITLE	Optional character vector with the value for the spectrum 'TITLE' field. Not applicable for experiments.

**Details**

Note that when reading an mgf file, the original order of the spectra is lost. Thus, if the data was originally written to mgf from an MSnExp object using writeMgfData, although the feature names will be identical, the spectra are not as a result of the reordering. See example below.

**Methods**

signature(object = "MSnExp") Writes the full experiment to an mgf file.

signature(object = "Spectrum") Writes an individual spectrum to an mgf file.

**See Also**

[readMgfData](#) function to read data from and mgf file.

**Examples**

```
## Not run:
data(itraqdata)
writeMgfData(itraqdata,file="itraqdata.mgf",COM="MSnbase itraqdata")
itraqdata2 <- readMgfData("itraqdata.mgf")
## note that the order of the spectra
## and precision of some values (precursorMz for instance)
## are altered
match(signif(precursorMz(itraqdata2),4),signif(precursorMz(itraqdata),4))
## [1] 1 10 11 12 13 14 15 16 17 18 ...
## ... but all the precursors are there
all.equal(sort(precursorMz(itraqdata2)),sort(precursorMz(itraqdata)),
          check.attributes=FALSE,
          tolerance=10e-5)
## is TRUE
all.equal(as.data.frame(itraqdata2[[1]]),as.data.frame(itraqdata[[1]]))
## is TRUE
all.equal(as.data.frame(itraqdata2[[3]]),as.data.frame(itraqdata[[11]]))
## is TRUE
## But, beware that
all(featureNames(itraqdata2)==featureNames(itraqdata))
## is TRUE too!

## End(Not run)
```

---

writeMzTabData

*Writes an 'MSnSet' to an mzTab file*

---

**Description**

This function generates an mzTab file based on the data available in the x MSnSet instance and additional information passed by the user. It makes use of the respective section generators to create appropriate metadata, peptide and protein sections. If peptide and protein sections need to be generated, one has to first create the mzTab file with (metadata, optional, but recommended) and protein data and then append the peptide data, as per mzTab specification (<http://code.google.com/p/mztab/>). See the example section.

**Usage**

```
writeMzTabData(x, what = c("PEP", "PRT"), append = FALSE,
              MTD = TRUE, file, ...)
```

**Arguments**

x	An instance of class MSnSet.
what	One of "PEP" or "PRT" defining whether peptide or protein data is to be saved.
append	Logical. Should the data be appended to file. Default is FALSE.
MTD	Logical. Should the metadata section be generated. Default is TRUE.

file                    A character naming the file to print to.  
...                    Additional parameters passed to the respective section generators: [makeMTD](#) for metadata, [makePEP](#) for peptides and [makePRT](#) for proteins.

**Value**

None (invisible NULL).

**Author(s)**

Laurent Gatto

**References**

The mzTab specification document and example files: <http://code.google.com/p/mztab/>.

**See Also**

Functions to generate metadata ([makeMTD](#)), peptide data ([makePEP](#)) and proteins ([makePRT](#)). [readMzTabData](#) to create "MSnSet" instances from an mzTab file.

**Examples**

```
## Not run:
mzTabFile <- tempfile()
data(itraqdata)
pep <- quantify(itraqdata, reporters = iTRAQ4)
prot <- combineFeatures(pep, groupBy = fData(pep)$ProteinAccession)
fvarLabels(pep)
## First write metadata and protein data
writeMzTabData(prot, what = "PRT", file = mzTabFile,
              append = FALSE, MTD = TRUE,
              protAccession = fData(prot)$ProteinAccession,
              protDescription = fData(prot)$ProteinDescription,
              protAbundance = exprs(prot))
## append peptide data, without metadata section
writeMzTabData(pep, what = "PEP", file = mzTabFile,
              append = TRUE, MTD = FALSE,
              sequence = fData(pep)$PeptideSequence,
              charge = fData(pep)$charge,
              retentionTime = fData(pep)$retention.time,
              pepAbundance = exprs(pep))

## End(Not run)
```



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