Package ‘MSnbase’

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Title Base Functions and Classes for MS-based Proteomics

Version 1.18.0

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

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Imports plyr, IRanges, preprocessCore, vsn, grid, reshape2, stats4, affy, impute, pcaMethods, mzID (>= 1.5.2), MALDIquant (>= 1.12), digest, lattice, ggplot2, S4Vectors, Rcpp

Suggests testthat, zoo, knitr (>= 1.1.0), rols, Rdisop, pRoloc, pRolocdata (>= 1.7.1), msdata, roxygen2, rgl, BiocStyle, imputeLCMD, norm, gplots

LinkingTo Rcpp

License Artistic-2.0

LazyData yes

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BugReports https://github.com/lgatto/MSnbase/issues

URL https://github.com/lgatto/MSnbase

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NeedsCompilation yes

R topics documented:

MSnbase-package .................................................. 3
addIdentificationData-methods ............................... 4
<table>
<thead>
<tr>
<th>R topics documented:</th>
</tr>
</thead>
<tbody>
<tr>
<td>averageMSnSet</td>
</tr>
<tr>
<td>bin-methods</td>
</tr>
<tr>
<td>calculateFragments-methods</td>
</tr>
<tr>
<td>chromatogram-methods</td>
</tr>
<tr>
<td>clean-methods</td>
</tr>
<tr>
<td>combineFeatures</td>
</tr>
<tr>
<td>commonFeatureNames</td>
</tr>
<tr>
<td>compareMSnSets</td>
</tr>
<tr>
<td>compareSpectra-methods</td>
</tr>
<tr>
<td>exprsToRatios-methods</td>
</tr>
<tr>
<td>extractPrecSpectra-methods</td>
</tr>
<tr>
<td>FeatComp-class</td>
</tr>
<tr>
<td>featureCV</td>
</tr>
<tr>
<td>FeaturesOfInterest-class</td>
</tr>
<tr>
<td>fillUp</td>
</tr>
<tr>
<td>formatRt</td>
</tr>
<tr>
<td>get.amino.acids</td>
</tr>
<tr>
<td>get.atomic.mass</td>
</tr>
<tr>
<td>getVariableName</td>
</tr>
<tr>
<td>grepEcols</td>
</tr>
<tr>
<td>imageNA2</td>
</tr>
<tr>
<td>impute-methods</td>
</tr>
<tr>
<td>iPQF</td>
</tr>
<tr>
<td>iTTRAQ4</td>
</tr>
<tr>
<td>itraqData</td>
</tr>
<tr>
<td>listOf</td>
</tr>
<tr>
<td>makeMTD</td>
</tr>
<tr>
<td>makePEP</td>
</tr>
<tr>
<td>makePRT</td>
</tr>
<tr>
<td>MIAPE-class</td>
</tr>
<tr>
<td>missing-data</td>
</tr>
<tr>
<td>MSmap-class</td>
</tr>
<tr>
<td>MSnExp-class</td>
</tr>
<tr>
<td>MSnProcess-class</td>
</tr>
<tr>
<td>MSnSet-class</td>
</tr>
<tr>
<td>MSnSetList-class</td>
</tr>
<tr>
<td>MzTab-class</td>
</tr>
<tr>
<td>NAnnotatedDataFrame-class</td>
</tr>
<tr>
<td>normalise-methods</td>
</tr>
<tr>
<td>npcv</td>
</tr>
<tr>
<td>nQuants</td>
</tr>
<tr>
<td>pickPeaks-methods</td>
</tr>
<tr>
<td>plot-methods</td>
</tr>
<tr>
<td>plot.Spectrum.Spectrum-methods</td>
</tr>
<tr>
<td>plot2d-methods</td>
</tr>
<tr>
<td>plotDensity-methods</td>
</tr>
<tr>
<td>plotMzDelta-methods</td>
</tr>
<tr>
<td>plotNA-methods</td>
</tr>
</tbody>
</table>
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.

If you have questions, want to report a bug or share suggestions, please file an issue at https://github.com/lgatto/MSnbase/issues, contact me directly or ask a question on the Bioconductor support forum https://support.bioconductor.org/.

Author(s)

Laurent Gatto

Maintainer: Laurent Gatto <lg390@cam.ac.uk>

See the DESCRIPTION file for a complete list of contributors.
addIdentificationData-methods

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).


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").

addIdentificationData-methods

Adds Identification Data

Description

This methods add identification data to an experiment "MSnExp" or to a "MSnSet".

Details

The featureData slots in an "MSnExp" or an "MSnSet" instance provides only one row per MS2 spectrum but the identification is not always bijective. If multiple possible matches are present only the highest ranked identification is added.

The column nprot contains the number of members in the protein group; the columns accession and description contain a semicolon separated list of all matches sorted by their rank values. The columns npsm.nprot and npep.nprot represent the number of PSMs and peptides that were matched to a particular protein group. The column npsm.pep indicates how many PSMs were attributed to a peptide (as defined by its sequence pepseq).

Methods

signature(object = "MSnExp", id = "character", fcol = "character", icol = "character", verbose = "logical")

Adds the identification data stored in mzIdentML files to a "MSnExp" instance. The method handles one or multiple mzIdentML files provided via id. id has to be a character vector of valid filenames. fcol and icol specify the columns in the featureData slot and the identification data.frame that are used to merge both data together as character vectors (defaults are fcol = c("spectrum.file", "acquisition.number") and icol = c("spectrumFile", "acquisitionNumber").

The verbose argument (default is TRUE) defines whether status messages should be showed.
signature(object = "MSnExp", id = "mzID", fcol = "character", icol = "character", verbose = "logical")
   Same as above but id could be an mzID object.
signature(object = "MSnExp", id = "mzIDCollection", fcol = "character", icol = "character", verbose = "logical")
   Same as above but id could be an mzIDCollection object.
signature(object = "MSnExp", id = "data.frame", fcol = "character", icol = "character", verbose = "logical")
   Same as above but id could be a data.frame.

signature(object = "MSnSet", id = "mzID", fcol = "character", icol = "character", verbose = "logical")
   Adds the identification data stored in mzIdentML files to an "MSnSet" instance. The method handles one or multiple mzIdentML files provided via id. id has to be a character vector of valid filenames.
   fcol and icol specify the columns in the featureData slot and the identification data.frame that are used to merge both data together as character vectors (defaults are fcol = c("spectrum.file", "acquisition.number") and icol = c("spectrumFile", "acquisitionnumber").
   The verbose argument (default is TRUE) defines whether status messages should be showed.
signature(object = "MSnSet", id = "mzIDCollection", fcol = "character", icol = "character", verbose = "logical")
   Same as above but id could be an mzIDCollection object.
signature(object = "MSnSet", id = "data.frame", fcol = "character", icol = "character", verbose = "logical")
   Same as above but id could be a data.frame.

Author(s)
Sebastian Gibb <mail@sebastiangibb.de>

See Also
   MSnExp and MSnSet.

Examples

   ## find path to a mzXML file
   quantFile <- dir(system.file(package = "MSnbase", dir = "extdata"),
                    full.name = TRUE, pattern = "mzXML$")

   ## find path to a mzIdentML file
   identFile <- dir(system.file(package = "MSnbase", dir = "extdata"),
                    full.name = TRUE, pattern = "dummyiTRAQ.mzid")

   ## create basic MSnExp
   msexp <- readMSData(quantFile)

   ## add identification information
   msexp <- addIdentificationData(msexp, identFile)

   ## access featureData; please note the multiple identification data
   ## for spectrum 1 (row 1)
   fData(msexp)

   idSummary(msexp)
**averageMSnSet**

Generate an average MSnSet

**Description**

Given a list of MSnSet instances, typically representing replicated experiments, the function returns an average MSnSet.

**Usage**

```r
averageMSnSet(x, avg = function(x) mean(x, na.rm = TRUE), disp = npcv)
```

**Arguments**

- `x` A list of valid MSnSet instances to be averaged.
- `avg` The averaging function. Default is the median after removing missing values, as computed by `function(x) median(x, na.rm = TRUE)`.
- `disp` The dispersion function. Default is a non-parametric coefficient of variation that replaces the standard deviation by the median absolute deviation as computed by `mad(x)/abs(mean(x))`. See `npcv` for details. Note that the mad of a single value is 0 (as opposed to NA for the standard deviation, see example below).

**Details**

This function is aimed at facilitating the visualisation of replicated experiments and should not be used as a replacement for a statistical analysis.

The samples of the instances to be averaged must be identical but can be in a different order (they will be reordered by default). The features names of the result will correspond to the union of the feature names of the input MSnSet instances. Each average value will be computed by the avg function and the dispersion of the replicated measurements will be estimated by the disp function. These dispersions will be stored as a data.frame in the feature metadata that can be accessed with `fData(.)$disp`. Similarly, the number of missing values that were present when average (and dispersion) were computed are available in `fData(.)$disp`.

Currently, the feature metadata of the returned object corresponds the the feature metadata of the first object in the list (augmented with the missing value and dispersion values); the metadata of the features that were missing in this first input are missing (i.e. populated with NAs). This may change in the future.

**Value**

A new average MSnSet.

**Author(s)**

Laurent Gatto
See Also

compfnames to compare MSnSet feature names.

Examples

```r
library("pRolocdata")
## 3 replicates from Tan et al. 2009
data(tan2009r1)
data(tan2009r2)
data(tan2009r3)
x <- MSnSetList(list(tan2009r1, tan2009r2, tan2009r3))
avg <- averageMSnSet(x)
dim(avg)
head(exprs(avg))
head(fData(avg)$nNA)
head(fData(avg)$disp)
## using the standard deviation as measure of dispersion
avg2 <- averageMSnSet(x, disp = sd)
head(fData(avg2)$disp)
## keep only complete observations, i.e proteins
## that had 0 missing values for all samples
sel <- apply(fData(avg)$nNA, 1, function(x) all(x == 0))
avg <- avg[sel, ]
disp <- rowMax(fData(avg)$disp)
library("pRoloc")
setStockcol(paste0(getStockcol(), "AA"))
plot2D(avg, cex = 7.7 * disp)
title(main = paste("Dispersion: non-parametric CV",
               paste(round(range(disp), 3), collapse = " - ")))
```

bin-methods

Bin `MSnExp` or `Spectrum` instances

Description

This method aggregates individual spectra (`Spectrum` instances) or whole experiments (`MSnExp` instances) into discrete bins. All intensity values which belong to the same bin are summed together.

Methods

signature(object = "MSnExp", binSize = "numeric", verbose = "logical") Bins all spectra in an MSnExp object. Use binSize to control the size of a bin (in Dalton, default is 1). Displays a control bar if verbose set to TRUE (default). Returns a binned MSnExp instance.

signature(object = "Spectrum", binSize = "numeric", breaks = "numeric") Bin the Spectrum object. Use binSize to control the size of a bin (in Dalton, default is 1). Similar to hist you could use breaks to specify the breakpoints between m/z bins. Returns a binned Spectrum instance.
calculateFragments-methods

Author(s)
Sebastian Gibb <mail@sebastiangibb.de>

See Also
clean, pickPeaks, smooth, removePeaks and trimMz for other spectra processing methods.

Examples
s <- new("Spectrum2", mz=1:10, intensity=1:10)
intensity(s)
intensity(bin(s, binSize=2))
data(itraqdata)
sum(peaksCount(itraqdata))
itraqdata2 <- bin(itraqdata, binSize=2)
sum(peaksCount(itraqdata2))
processingData(itraqdata2)

calculateFragments-methods
Calculate ions produced by fragmentation.

Description
These method calculates a-, b-, c-, x-, y- and z-ions produced by fragmentation.

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sequence</td>
<td>character, peptide sequence.</td>
</tr>
<tr>
<td>object</td>
<td>Object of class &quot;Spectrum2&quot; or &quot;missing&quot;.</td>
</tr>
<tr>
<td>tolerance</td>
<td>numeric tolerance between the theoretical and measured MZ values (only available if object is not missing).</td>
</tr>
<tr>
<td>method</td>
<td>method used for for duplicated matches. Choose &quot;highest&quot; or &quot;closest&quot; to select the peak with the highest intensity respectively the closest MZ in the tolerance range. If &quot;all&quot; is given all possible matches in the tolerance range are reported (only available if object is not missing).</td>
</tr>
<tr>
<td>type</td>
<td>character vector of target ions; possible values: c(&quot;a&quot;, &quot;b&quot;, &quot;c&quot;, &quot;x&quot;, &quot;y&quot;, &quot;z&quot;); default: type=c(&quot;b&quot;, &quot;y&quot;).</td>
</tr>
<tr>
<td>z</td>
<td>numeric desired charge state; default z=1.</td>
</tr>
<tr>
<td>modifications</td>
<td>named numeric vector of used modifications. The name must correspond to the one-letter-code of the modified amino acid and the numeric value must represent the mass that should be added to the original amino acid mass, default: Carbamidomethyl modifications=c(C=57.02146). Use Nterm or Cterm as names for modifications that should be added to the amino respectively carboxyl-terminus.</td>
</tr>
</tbody>
</table>
neutralLoss list, it has to have two named elements, namely water and ammonia that contain a character vector which type of neutral loss should be calculated. Currently neutral loss on the C terminal "Cterm", at the amino acids c("D", "E", "S", "T") for "water" (shown with an _) and c("K", "N", "Q", "R") for "ammonia" (shown with an *) are supported. There is a helper function defaultNeutralLoss that returns the correct list. It has two arguments disableWaterLoss and disableAmmoniaLoss to remove single neutral loss options. See the example section for use cases.

verbose logical if TRUE (default) the used modifications are printed.

Methods

signature(sequence = "character", object = "missing", ...) Calculates the theoretical fragments for a peptide sequence. Returns a data.frame with the columns c("mz", "ion", "type", "pos", "seqB").

signature(sequence = "character", object = "Spectrum2", ...) Calculates and matches the theoretical fragments for a peptide sequence and a "Spectrum2" object. The ... arguments are passed to the internal functions. Currently tolerance, method and relative are supported. You could change the tolerance (default 25e-6) and decide whether this tolerance should be applied relative (default relative = TRUE) or absolute (relative = FALSE) to match the theoretical fragment MZ with the MZ of the spectrum. In cases of multiple matches use method to select the peak with the highest intensity (method = "highest", default) respectively closest MZ (method = "closes"). If method = "all" is set all possible matches in the current tolerance range are reported. Returns the same data.frame as above but the mz column represents the matched MZ values of the spectrum. Additionally there is a column error that contains the difference between the observed MZ (from the spectrum) to the theoretical fragment MZ.

Author(s)

Sebastian Gibb <mailto@sebastiangibb.de>

Examples

```r
## find path to a mzXML file
file <- dir(system.file(package = "MSnbase", dir = "extdata"),
    full.name = TRUE, pattern = "mzXML")

## create basic MSnExp
msexp <- readMSData(file)

## centroid them
msexp <- pickPeaks(msexp)

## calculate fragments for ACE with default modification
calculateFragments("ACE", modifications=c(C=57.02146))

## calculate fragments for ACE with an addition N-terminal modification
calculateFragments("ACE", modifications=c(C=57.02146, Nterm=229.1629))

## calculate fragments for ACE without any modifications
```
calculateFragments("ACE", modifications=NULL)

calculateFragments("VESITARHGEVQLRPK",
    type=c("a", "b", "c", "x", "y", "z"),
    z=1:2)

calculateFragments("VESITARHGEVQLRPK", msexp[[1]])

## neutral loss
defaultNeutralLoss()

## disable water loss on the C terminal
defaultNeutralLoss(enableWaterLoss="Cterm")

## real example
calculateFragments("PQR")
calculateFragments("PQR",
    neutralLoss=defaultNeutralLoss(enableWaterLoss="Cterm"))
calculateFragments("PQR",
    neutralLoss=defaultNeutralLoss(enableAmmoniaLoss="Q"))

## disable neutral loss completely
calculateFragments("PQR", neutralLoss=NULL)

---

**chromatogram-methods**  
*Plots a chromatogram*

---

**Description**

The method plots the chromatogram for various types in inputs (see below). Additional arguments are

- **y**: One of "tic" (default) or "bpi" to plot the total ion current of base peak intensity chromatogram.
- **f**: Optional and only when the input is a data.frame. Otherwise, it is extracted automatically from object. f is used to print the filename on the figure.
- **legend**: A logical defining if the figure should be annotated.
- **plot**: A logical defining if the plot should be rendered.
- **ms**: A numeric defining what MS level spectra to use. Default is 1L.
- **...**: Additional arguments passed to the plot function.

xcms::plotChrom provides a similar functionality.

**Value**

The methods invisibly return the data.frame with the retention times (rt column) and intensities (either tic or bpi) used to generate the figure.
Methods

signature(object = "character") Plots the chromatogram for the mass-spectrometry data stored in the object file. The file format must be support by mzR. See mzR::openMSfile for details.

signature(object = "mzRamp") Plots the chromatogram for the mzRamp instance. See the mzR package for details.

signature(object = "data.frame") Plots the chromatogram using the relevant columns from the data.frame instance, i.e. retentionTime and totIonCurrent (for tic) and basePeakIntensity (for bpi). Such a data.frame would typically be generated by extracting the header from an mzRamp instance. See mzR::header for details.

Examples

```r
f <- system.file("lockmass/LockMass_test.mzXML", package = "msdata")
x <- chromatogram(f, main = "Source: mzXML file")
head(x)
dim(x)
x <- chromatogram(f, main = "Source: mzXML file",
ylim = c(0, 100))
## Not run:
library("mzR")
ms <- openMSfile(f)
chromatogram(ms, main = "Source: mzRamp",
             col = "red")
hd <- header(ms)
chromatogram(hd, main = "Source: mzRamp header",
             lty = "dashed")

library("RforProteomics")
f <- getPXD000001mzXML()
chromatogram(f)
grid()
## End(Not run)
```

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. Unless all is set to FALSE, 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", all = "logical" 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", all = "logical") 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

```r
int <- c(1,0,0,0,0,0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
sp1 <- new("Spectrum2",
    intensity=int,
    mz=1:length(int))
sp2 <- clean(sp1) ## default is all=FALSE
intensity(sp1)
intensity(sp2)
intensity(clean(sp1, all = TRUE))

mz(sp1)
mz(sp2)
mz(clean(sp1, all = TRUE))

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

combineFeatures

Combines features in an MSnSet object

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.

The coefficient of variations are automatically computed and collated to the featureData slot. See cv and cvNorm arguments for details.

NB: All the functions available as fun take a na.rm argument. This argument is FALSE by default. This will have as effect that NA get propagated at the higher level. It is generally advised to set na.rm = TRUE. See the example below.
Usage

combineFeatures(object, groupBy, fun = c("mean", "median", "weighted.mean", "sum", "medpolish", "iPQF"), redundancy.handler = c("unique", "multiple"), cv = TRUE, cv.norm = "sum", verbose = TRUE, ...)

Arguments

object
An instance of class "MSnSet" whose features will be summerised.

groupBy
A factor, character, numeric or a list of the above defining how to summarise the features. The list must be of length nrow(object). Each element of the list is a vector describing the feature mapping. If the list can be named, its names must match featureNames(object). See redundancy.handler for details about the latter.

fun
The summerising function. Currently, mean, median, weighted mean, sum and median polish and iPQF (see iPQF for details) are implemented, but user-defined functions can also be supplied.

redundancy.handler
If groupBy is a list, one of "unique" (default) or "multiple" (ignored otherwise) defining how to handle peptides that can be associated to multiple higher-level features (proteins) upon combination. Using "unique" will only consider uniquely matching features (features matching multiple proteins will be discarded). "multiple" will allow matching to multiple proteins and each feature will be repeatedly tallied for each possible matching protein.

cv
A logical defining if feature coefficients of variation should be computed and stored as feature meta-data. Default is TRUE.

cv.norm
A character defining how to normalise the feature intensities prior to CV calculation. Default is sum. Use none to keep intensities as is. See featureCV for more details.

verbose
A logical indicating whether verbose output is to be printed out.

... Additional arguments for the fun function. In particular, for the iPQF method, additional arguments are described in the details section.

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>
References

iPQF: A new peptide-to-protein summarization method using peptide characteristics to improve iTRAQ quantification Martina Fischer and Bernhard Y. Renard, in prep.

See Also

featureCV

Examples

data(msnset)
msnset <- msnset[11:15,]
exprs(msnset)

## arbitrary grouping into two groups
grp <- as.factor(c(1, 1, 2, 2, 2))
msnset.comb <- combineFeatures(msnset, grp, "sum")
dim(msnset.comb)
exprs(msnset.comb)
fvarLabels(msnset.comb)

## grouping with a list
grpl <- list(c("A", "B"), "A", "A", "C", c("C", "B"))
## optional naming
names(grpl) <- featureNames(msnset)
exprs(combineFeatures(msnset, grpl, fun = "sum", redundancy.handler = "unique"))
exprs(combineFeatures(msnset, grpl, fun = "sum", redundancy.handler = "multiple"))

## missing data
exprs(msnset)[4, 4] <-
  exprs(msnset)[2, 2] <- NA
exprs(msnset)
## NAs propagate in the 115 and 117 channels
exprs(combineFeatures(msnset, grp, "sum"))
## NAs are removed before summing
exprs(combineFeatures(msnset, grp, "sum", na.rm = TRUE))

## using iPQF
data(msnset2)
res <- combineFeatures(msnset2,
  groupBy = FData(msnset2)$accession,
  redundancy.handler = "unique",
  fun = "iPQF",
  low.support.filter = FALSE,
  ratio.calc = "sum",
  method.combine = FALSE)

head(exprs(res))
commonFeatureNames

Keep only common feature names

Description

Subsets MsnSet instances to their common feature names.

Usage

commonFeatureNames(x, y)

Arguments

x An instance of class MsnSet or a list of MsnSet instances of at least 2 MsnSet objects.

y An instance of class MsnSet. Ignored if x is a list of MsnSet instances.

Value

An linkS4class(MsnSetList) composed of the input MsnSet containing only common features in the same order. The names of the output are either the names of the x and y input variables or the names of x if a list is provided.

Author(s)

Laurent Gatto

Examples

library("pRolocdata")
data(tan2009r1)
data(tan2009r2)
cmn <- commonFeatureNames(tan2009r1, tan2009r2)
names(cmn)
## as a named list
names(commonFeatureNames(list(a = tan2009r1, b = tan2009r2)))
## without message
suppressMessages(cmn <- commonFeatureNames(tan2009r1, tan2009r2))
## more than 2 instance
data(tan2009r3)
cmn <- commonFeatureNames(list(tan2009r1, tan2009r2, tan2009r3))
length(cmn)
## compareMSnSets

**Compare two MSnSets**

**Description**

Compares two MSnSet instances. The qual and processingData slots are generally omitted.

**Usage**

```r
compareMSnSets(x, y, qual = FALSE, proc = FALSE)
```

**Arguments**

- `x`: First MSnSet
- `y`: Second MSnSet
- `qual`: Should the qual slots be compared? Default is FALSE.
- `proc`: Should the processingData slots be compared? Default is FALSE.

**Value**

A logical

**Author(s)**

Laurent Gatto

---

## compareSpectra-methods

**Compare Spectra of an 'MSnExp' or 'Spectrum' instances**

**Description**

This method compares spectra (Spectrum instances) pairwise or all spectra of an experiment (MSnExp instances). Currently the comparison is based on the number of common peaks `fun = "common"`, the Pearson correlation `fun = "cor"`, the dot product `fun = "dotproduct"` or a user-defined function.

For `fun = "common"` the tolerance (default 25e-6) can be set and the tolerance can be defined to be relative (default `relative = TRUE`) or absolute (`relative = FALSE`). To compare spectra with `fun = "cor"` and `fun = "dotproduct"`, the spectra need to be binned. The `binSize` argument (in Dalton) controls the binning precision. Please see `bin` for details.

Instead of these three predefined functions for `fun` a user-defined comparison function can be supplied. This function takes two Spectrum objects as the first two arguments and ... as third argument. The function must return a single numeric value. See the example section.
Methods

signature(object1 = "MSnExp", object2 = "missing", fun = "character", ...) Compares all spectra in an MSnExp object. The ... arguments are passed to the internal functions. Returns a matrix of dimension length(object1) by length(object1).

signature(object1 = "Spectrum", object2 = "Spectrum", fun = "character", ...) Compares two Spectrum objects. See the above explanation for fun and .... Returns a single numeric value.

Author(s)

Sebastian Gibb <mail@sebastiangibb.de>

References


See Also

bin, clean, pickPeaks, smooth, removePeaks and trimMz for other spectra processing methods.

Examples

s1 <- new("Spectrum2", mz=1:10, intensity=1:10)
s2 <- new("Spectrum2", mz=1:10, intensity=10:1)
compareSpectra(s1, s2)
compareSpectra(s1, s2, fun="cor", binsize=2)
compareSpectra(s1, s2, fun="dotproduct")

## define our own (useless) comparison function (it is just a basic example)
equalLength <- function(x, y, ...) {
  return(peaksCount(x)/(peaksCount(y)+.Machine$double.eps))
}
compareSpectra(s1, s2, fun=equalLength)
compareSpectra(s1, new("Spectrum2", mz=1:5, intensity=1:5), fun=equalLength)
compareSpectra(s1, new("Spectrum2"), fun=equalLength)

data(iTRAQData)
compareSpectra(iTRAQData[1:5], fun="cor")
exprsToRatios-methods  Calculate all ratio pairs

Description
Calculations all possible ratios for the assayData columns in an "MSnSet". The function `getRatios(x, log = FALSE)` takes a matrix x as input and is used by exprsToRatios.

Methods

signature(object = "MSnSet", log = "logical") If log is FALSE (default) the ratios for all the assayData columns are computed; otherwise, log ratios (differences) are calculated.

signature(object = "matrix", log = "logical") As above, but for a matrix instance.

Examples

data(msnset)
pData(msnset)
head(exprs(msnset))
r <- exprsToRatios(msnset)
head(exprs(r))
pData(r)

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 of 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

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

Description

Comparing feature names of two comparable MSnSet instances.

Objects from the Class

Objects can be created with compfnames. The method compares the feature names of two objects of class "MSnSet". It prints a summary matrix of common and unique feature names and invisibly returns a list of FeatComp instances.

The function will compute the common and unique features for all feature names of the two input objects (`featureNames(x)` and `featureNames(y)`) as well as distinct subsets as defined in the `fcoll` and `fcol2` feature variables.

Slots

- **name**: Object of class "character" defining the name of the compared features. By convention, "all" is used when all feature names are used; otherwise, the respective levels of the feature variables `fcoll1` and `fcol2`.
- **common**: Object of class "character" with the common feature names.
- **unique1**: Object of class "character" with the features unique to the first MSnSet (x in compfname).
- **unique2**: Object of class "character" with the features unique to the second MSnSet (y in compfname).
- **all**: Object of class "logical" defining if all features of only a subset were compared. One expects that name == "all" when all is TRUE.

Methods

Accessors `names`, `common`, `unique1` and `unique2` can be used to access the respective FeatComp slots.

### compfnames

- **signature**: (x = "MSnSet", y = "MSnSet", fcoll1 = "character", fcol2 = "character", simplify = FALSE)

  Creates the FeatComp comparison object for instances x and y. The feature variables to be considered to details feature comparison can be defined by `fcoll1` (default is "markers" and `fcol2` for x and y respectively). Setting either to NULL will only consider all feature names;
in such case, of simplify is TRUE (default), an FeatComp object is returned instead of a list of length 1. The verbose logical controls if a summary table needs to be printed (default is TRUE).

**comppfnames** signature(x = "list", y = "missing", ...): when x is a list of MSnSet instances, comppfnames is applied to all element pairs of x. Additional parameters fcol1, fcol2, simplify and verbose are passed to the pairwise comparison method.

**show** signature(object = "FeatComp"): prints a summary of the object.

**Author(s)**
Laurent Gatto <lg390@cam.ac.uk> and Thomas Naake

**See Also**

*averageMSnSet* to compute an average MSnSet.

**Examples**

```r
library("pRolocdata")
data(tan2009r1)
data(tan2009r2)
x <- comppfnames(tan2009r1, tan2009r2)
x[[1]]
x[2:3]
head(common(x[[1]]))

data(tan2009r3)
tan1 <- list(tan2009r1, tan2009r2, tan2009r3)
xx <- comppfnames(tan1, fcol1 = NULL)
length(xx)
tail(xx)

all.equal(xx[[15]],
          comppfnames(tan2009r2, tan2009r3, fcol1 = NULL))
str(sapply(xx, common))
```

---

**featureCV**

*Calculates coefficient of variation for features*

**Description**

This function calculates the column-wise coefficient of variation (CV), i.e. the ration between the standard deviation and the mean, for the features in an *MSnSet*. The CVs are calculated for the groups of features defined by groupBy. For groups defined by single features, NA is returned.

**Usage**

```r
featureCV(x, groupBy, na.rm = TRUE, norm = c("sum", "max", "none",
         "center.mean", "center.median", "quantiles", "quantiles.robust")
```


FeaturesOfInterest-class

Arguments

- **x**: An instance of class "MSnSet".
- **groupBy**: An object of class factor defining how to summarise the features.
- **na.rm**: A logical defining whether missing values should be removed.
- **norm**: One of 'none' (default), 'sum', 'max', 'center.mean', 'center.median', 'quantiles' or 'quantiles.robust' defining if and how the data should be normalised prior to CV calculation. See `normalise` for more details.

Value

A matrix of dimensions `length(levels(groupBy))` by `ncol(x)` with the respective CVs.

Author(s)

Laurent Gatto <lg390@cam.ac.uk>

See Also

- `combineFeatures`

Examples

```r
data(msnset)
msnset <- msnset[1:4]
gb <- factor(rep(1:2, each = 2))
featureCV(msnset, gb)
```

---

FeaturesOfInterest-class

*Features of Interest*

Description

The *Features of Interest* infrastructure allows to define a set of features of particular interest to be used/matched against existing data sets contained in "MSnSet". A specific set of features is stored as an `FeaturesOfInterest` object and a collection of such non-redundant instances (for example for a specific organism, project, ...) can be collected in a `FoICollection`.

Objects from the Class

Objects can be created with the respective `FeaturesOfInterest` and `FoICollection` constructors. `FeaturesOfInterest` instances can be generated in two different ways: the constructor takes either (1) a set of features names (a character vector) and a description (character of length 1 - any subsequent elements are silently ignored) or (2) feature names, a description and an instance of class "MSnSet". In the latter case, we call such `FeaturesOfInterest` objects traceable, because we can identify the origin of the feature names and thus their validity. This is done by inspecting the `MSnSet`
instance and recording its dimensions, its name and a unique md5 hash tag (these are stores as part of the optional objpar slot). In such cases, the feature names passed to the FeaturesOfInterest constructor must also be present in the MSnSet; if one or more are not, an error will be thrown. If your features of interest to be recorded stem for an existing experiment and have all been observed, it is advised to pass the 3 arguments to the constructor to ensure that the feature names as valid. Otherwise, only the third argument should be omitted.

FoICollection instances can be constructed by creating an empty collection and serial additions of FeaturesOfInterest using addFeaturesOfInterest or by passing a list of FeaturesOfInterest instance.

**Slots**

FeaturesOfInterest class:

- description: Object of class "character" describing the instance.
- objpar: Optional object of class "list" providing details about the MSnSet instance originally used to create the instance. See details section.
- fnames: Object of class "character" with the feature of interest names.
- date: Object of class "character" with the date the instance was first generated.
- .__classVersion__: Object of class "Versions" with the FeaturesOfInterest class version.
  Only relevant for development.

FoICollection class:

- foic: Object of class "list" with the FeaturesOfInterest.
- .__classVersion__: Object of class "Versions" with the FoICollection class version. Only relevant for development.

**Extends**

Class "Versioned", directly.

**Methods**

FeaturesOfInterest class:

- description signature(object = "FeaturesOfInterest"): returns the description of object.
- foi signature(object = "FeaturesOfInterest"): returns the features of interests.
- length signature(x = "FeaturesOfInterest"): returns the number of features of interest in x.
- show signature(object = "FeaturesOfInterest"): displays object.
- fnamesIn signature(x = "FeaturesOfInterst", y = "MSnSet", count = "logical"): if count is FALSE (default), return a logical indicating whether there is at least one feature of interest present in x? Otherwise, returns the number of such features. Works also with matrices and data.frames.

FoICollection class:

- description signature(object = "FoICollection"): returns the description of object.
FeaturesOfInterest-class

foi signature(object = "FoICollection"): returns a list of FeaturesOfInterest.

length signature(x = "FoICollection"): returns the number of FeaturesOfInterest in the collection.

lengths signature(x = "FoICollection"): returns the number of features of interest in each FeaturesOfInterest in the collection x.

addFeaturesOfInterest signature(x = "FeaturesOfInterest", y = "FoICollection"): add the FeaturesOfInterest instance x to FoICollection y. If x is already present, a message is printed and y is returned unchanged.

rmFeaturesOfInterest signature(object = "FoICollection", i = "numeric"): removes the ith FeatureOfInterest in the collection object.

show signature(object = "FoICollection"): displays object.

Author(s)
Laurent Gatto <lg390@cam.ac.uk>

Examples

library("pRolocdata")
data(tan2009r1)

x <- FeaturesOfInterest(description = "A traceable test set of features of interest",
                          fnames = featureNames(tan2009r1)[1:10],
                          object = tan2009r1)

x
description(x)
foi(x)

y <- FeaturesOfInterest(description = "Non-traceable features of interest",
                          fnames = featureNames(tan2009r1)[111:113])

y

## an illegal FeaturesOfInterest
try(FeaturesOfInterest(description = "Won't work",
                        fnames = c("A", "Z", featureNames(tan2009r1)),
                        object = tan2009r1))

FeaturesOfInterest(description = "This work, but not traceable",
                     fnames = c("A", "Z", featureNames(tan2009r1))))

xx <- FoICollection()
xx

xx <- addFeaturesOfInterest(x, xx)
xx <- addFeaturesOfInterest(y, xx)
xx
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 matrice 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**

```r
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/from 'min:sec' format

**Usage**
formatRt(rt)

**Arguments**
- *rt*: retention in seconds (numeric) or "mm:sec" (character).

**Details**
This function is used to convert retention times. Conversion is seconds to/from the more human friendly format "mm:sec".

**Value**
A vector of same length as *rt*.

**Author(s)**
Laurent Gatto <lg390@cam.ac.uk>

**Examples**
formatRt(1524)
formatRt("25:24")

get.amino.acids

**Amino acids**

**Description**

**Usage**
ge.get.amino.acids()
get.atomic.mass

**Value**

A data.frame

**Author(s)**

Laurent Gatto

**Examples**

get.amino.acids()

---

get.atomic.mass  
*Atomic mass.*

**Description**

Returns a double of used atomic mass.

**Usage**

get.atomic.mass()

**Value**

A named double.

**Author(s)**

Sebastian Gibb

**Examples**

get.atomic.mass()
getVariableName

Return a variable name

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)

grepEcols

Returns the matching column names of indices.

Description

Given a text spread sheet f and a pattern to be matched to its header (first line in the file), the function returns the matching columns names or indices of the corresponding data.frame.

Usage

grepEcols(f, pattern, ...)

gEcols(f, ...)
Arguments

- **f**: A connection object or a character string to be read in with `readLines(f, n = 1)`.
- **pattern**: A character string containing a regular expression to be matched to the file’s header.
- **...**: Additional parameters passed to `strsplit` to split the file header into individual column names.

Details

The function starts by reading the first line of the file (or connection) `f` with `readLines`, then splits it according to the optional `...` arguments (it is important to correctly specify `strsplit`’s split character vector here) and then matches `pattern` to the individual column names using `grep`.

Similarly, `getEcols` can be used to explore the column names and decide for the appropriate `pattern` value.

These functions are useful to check the parameters to be provided to `readMSnSet2`.

Value

Depending on `value`, the matching column names of indices. In case of `getEcols`, a character of column names.

Author(s)

Laurent Gatto

See Also

- `readMSnSet2`

---

### imageNA2

**NA heatmap visualisation for 2 groups**

**Description**

Produces a heatmap after reordering rows and columns to highlight missing value patterns.

**Usage**

```r
imageNA2(object, pcol, Rowv, Colv = TRUE, useGroupMean = FALSE, plot = TRUE, ...)
```
Arguments

- **object**: An instance of class MSnSet
- **pcol**: Either the name of a phenoData variable to be used to determine the group structure or a factor or any object that can be coerced as a factor of length equal to nrow(object). The resulting factor must have 2 levels. If missing (default) image(object) is called.
- **Rowv**: Determines if and how the rows/features are reordered. If missing (default), rows are reordered according to order((nNA1 + 1)^2/(nNA2 + 1)), where NA1 and NA2 are the number of missing values in each group. Use a vector of numerics of feature names to customise row order.
- **Colv**: A logical that determines if columns/samples are reordered. Default is TRUE.
- **useGroupMean**: Replace individual feature intensities by the group mean intensity. Default is FALSE.
- **plot**: A logical specifying of an image should be produced. Default is TRUE.
- **...**: Additional arguments passed to `image`.

Value

Used for its side effect of plotting. Invisibly returns Rowv and Colv.

Author(s)

Laurent Gatto, Samuel Wieczorek and Thomas Burger

Examples

```r
library("pRolocdata")
library("pRoloc")
data(dunkley2006)
pcol <- ifelse(dunkley2006$fraction <= 5, "A", "B")
nax <- makeNaData(dunkley2006, pNA = 0.10)
exprs(nax)[sample(nrow(nax), 30), pcol == "A"] <- NA
exprs(nax)[sample(nrow(nax), 50), pcol == "B"] <- NA
MSnbase:::imageNA2(nax, pcol)
MSnbase:::imageNA2(nax, pcol, useGroupMean = TRUE)
MSnbase:::imageNA2(nax, pcol, Colv = FALSE, useGroupMean = FALSE)
MSnbase:::imageNA2(nax, pcol, Colv = FALSE, useGroupMean = TRUE)
```
Description

The impute method performs data imputation on an MSnSet instance using a variety of methods (see below). The imputation and the parameters are logged into the processingData(object) slot.

Users should proceed with care when imputing data and take precautions to assure that the imputation produce valid results, in particular with naive imputations such as replacing missing values with 0.

Details

There are two types of mechanisms resulting in missing values in LC/MSMS experiments.

- Missing values resulting from absence of detection of a feature, despite ions being present at detectable concentrations. For example in the case of ion suppression or as a result from the stochastic, data-dependent nature of the MS acquisition method. These missing value are expected to be randomly distributed in the data and are defined as missing at random (MAR) or missing completely at random (MCAR).

- Biologically relevant missing values resulting from the absence of the low abundance of ions (below the limit of detection of the instrument). These missing values are not expected to be randomly distributed in the data and are defined as missing not at random (MNAR).

MNAR features should ideally be imputed with a left-censor method, such as QRILC below. Conversely, it is recommended to use host deck methods such nearest neighbours, Bayesian missing value imputation or maximum likelihood methods when values are missing at random.

Currently, the following imputation methods are available:

- **MLE** Maximum likelihood-based imputation method using the EM algorithm. Implemented in the norm::imp.norm function. See imp.norm for details and additional parameters. Note that here, ... are passed to the em.norm function, rather to the actual imputation function imp.norm.

- **bcpa** Bayesian missing value imputation are available, as implemented in the and pcaMethods::pca functions. See pca for details and additional parameters.

- **knn** Nearest neighbour averaging, as implemented in the impute::impute.knn function. See impute.knn for details and additional parameters.

- **QRILC** A missing data imputation method that performs the imputation of left-censored missing data using random draws from a truncated distribution with parameters estimated using quantile regression. Implemented in the imputeLCMD::impute.QRILC function. See impute.QRILC for details and additional parameters.

- **MinDet** Performs the imputation of left-censored missing data using a deterministic minimal value approach. Considering a expression data with \( n \) samples and \( p \) features, for each sample, the missing entries are replaced with a minimal value observed in that sample. The minimal value observed is estimated as being the \( q \)-th quantile (default \( q = 0.01 \)) of the observed values in that sample. Implemented in the imputeLCMD::impute.MinDet function. See impute.MinDet for details and additional parameters.

- **MinProb** Performs the imputation of left-censored missing data by random draws from a Gaussian distribution centred to a minimal value. Considering an expression data matrix with \( n \) samples
and $p$ features, for each sample, the mean value of the Gaussian distribution is set to a minimal observed value in that sample. The minimal value observed is estimated as being the $q$-th quantile (default $q = 0.01$) of the observed values in that sample. The standard deviation is estimated as the median of the feature standard deviations. Note that when estimating the standard deviation of the Gaussian distribution, only the peptides/proteins which present more than 50% recorded values are considered. Implemented in the `imputeLCMD::impute.MinProb` function. See `impute.MinProb` for details and additional parameters.

**min** Replaces the missing values by the smallest non-missing value in the data.

**zero** Replaces the missing values by 0.

**mixed** A mixed imputation applying two methods (to be defined by the user as `mar` for values missing at random and `mnar` for values missing not at random, see example) on two M[CA]R/MNAR subsets of the data (as defined by the user by a `randna` logical, of length equal to `nrow(object)`).

**nbavg** Average neighbour imputation for fractions collected along a fractionation/separation gradient, such as sub-cellular fractions. The method assumes that the fraction are ordered along the gradient and is invalid otherwise.

Continuous sets `NA` value at the beginning and the end of the quantitation vectors are set to the lowest observed value in the data or to a user defined value passed as argument $k$. Them, when a missing value is flanked by two non-missing neighbouring values, it is imputed by the mean of its direct neighbours. A stretch of 2 or more missing values will not be imputed. See the example below.

The `naset MSnSet` is an real quantitative data where quantitative values have been replaced by NAs. See script/naset.R for details.

**Methods**

```r
signature(object = "MSnSet", method, ...) This method performs data imputation on the object `MSnSet` instance using the method algorithm. ... is used to pass parameters to the imputation function. See the respective methods for details and additional parameters.
```

**Author(s)**

Laurent Gatto and Samuel Wieczorek

**References**


Examples

data(naset)
## table of missing values along the rows
table(fData(naset)$nNA)
## table of missing values along the columns
pData(naset)$nNA

## non-random missing values
notna <- which(!fData(naset)$randna)
length(notna)
notna

impute(naset, method = "min")

if (require("imputeLCMD")) {
impute(naset, method = "QRILC")
impute(naset, method = "MinDet")
}

if (require("norm"))
impute(naset, method = "MLE")
impute(naset, "mixed",
  randna = fData(naset)$randna,
  mar = "knn", mmar = "QRILC")

## neighbour averaging
x <- naset[1:4, 1:6]
exprs(x)[1, 1] <- NA ## min value
exprs(x)[2, 3] <- NA ## average
exprs(x)[3, 1:2] <- NA ## min value and average
## 4th row: no imputation
exprs(x)
exprs(impute(x, "nbavg"))

iPQF

iPQF: iTRAQ (and TMT) Protein Quantification based on Features

Description

The iPQF spectra-to-protein summarisation method integrates peptide spectra characteristics and quantitative values for protein quantitation estimation. Spectra features, such as charge state, sequence length, identification score and others, contain valuable information concerning quantification accuracy. The iPQF algorithm assigns weights to spectra according to their overall feature reliability and computes a weighted mean to estimate protein quantities. See also combineFeatures for a more general overview of feature aggregation and examples.
iPQF

Usage

iPQF(object, groupBy, low.support.filter = FALSE, ratio.calc = "sum", 
method.combine = FALSE, feature.weight = c(7, 6, 4, 3, 2, 1, 5)^2)

Arguments

object
An instance of class M5nSet containing absolute ion intensities.

groupBy
Vector defining spectra to protein matching. Generally, this is a feature variable
such as fData(object)$accession.

low.support.filter
A logical specifying if proteins being supported by only 1-2 peptide spectra
should be filtered out. Default is FALSE.

ratio.calc
Either "none" (don't calculate any ratios), "sum" (default), or a specific chan-
nel (one of sampleNames(object)) defining how to calculate relative peptides
intensities.

method.combine
A logical defining whether to further use median polish to combine features.

feature.weight
Vector "numeric" giving weight to the different features. Default is the squared
order of the features redundant -unique-distance metric, charge state, ion inten-
sity, sequence length, identification score, modification state, and mass based on
a robustness analysis.

Value

A matrix with estimated protein ratios.

Author(s)

Martina Fischer

References

iPQF: A new peptide-to-protein summarization method using peptide characteristics to improve
iTRAQ quantification Martina Fischer and Bernhard Y. Renard, in prep.

Examples

data(msnset2)
head(exprs(msnset2))
prot <- combineFeatures(msnset2, 
                      groupBy = fData(msnset2)$accession, 
                      fun = "iPQF")
head(exprs(prot))
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


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 is an example data set that is an iTRAQ 4-plex experiment that has been run on an Orbitrap Velos instrument. It includes identification data in the feature data slot obtained from the Mascot search engine. It 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 itraqdata 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. The msnset object is produced by running the quantify method on the itraqdata experimental data, as detailed in the quantify example. This example data set is used in the MSnbase-demo vignette, available with vignette("MSnbase-demo", package="MSnbase").

The msnset2 object is another example iTRAQ4 data that is used to demonstrate features of the package, in particular the iPQF feature aggregation method, described in iPQF. It corresponds to 11 proteins with spectra measurements from the original data set described by Breitwieser et al. (2011) *General statistical modeling of data from protein relative expression isobaric tags*. J. Proteome Res., 10, 2758-2766.

### Usage

```r
itraqdata
```

### Examples

```r
data(itraqdata)
itraqdata

## created by
## msnset <- quantify(itraqdata, method = "trap", reporters = iTRAQ4)
data(msnset)
msnset

data(msnset2)
msnset2
```

### listOf

*Tests equality of list elements class*

### Description

Compares equality of all members of a list.
Usage

```r
listOf(x, class, valid = TRUE)
```

Arguments

- `x`: A codelist.
- `class`: A character defining the expected class.
- `valid`: A logical defining if all elements should be tested for validity. Default is TRUE.

Value

TRUE is all elements of `x` inherit from `class`.

Author(s)

Laurent Gatto

Examples

```r
listOf(list(), "foo")
listOf(list("a", "b"), "character")
listOf(list("a", 1), "character")
```

```r
makeMTD("Creaes the mzTab metadata section")
```

Description

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general metadata, 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

```r
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 MSnSet.
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 expTitle(x) 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 CVParam objects or NULL (default) to ignore.
instrumentSource  A list of valid CVParam instances or NULL (default), in which case ionSource(x) is used to generate a CVParam.
instrumentAnalyzer  A list of valid CVParam instances or NULL (default), in which case analyzer(x) is used to generate a CVParam.
instrumentDetector  A list of valid CVParam instances or NULL (default), in which case detectorType(x) is used to generate a CVParam.
software  A list of valid CVParam instances describing the ordered list of software used to process the data. NULL (default) to ignore.
fdr  A list of valid CVParam 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 pubMedIds(x) is used.
contactName  A character (of length > 0) or NULL (default), in which case expInfo(x)["name"] is used.
contactAffiliation  A character (of length > 0) or NULL (default), in which case expInfo(x)["lab"] is used.
contactEmail  A character (of length > 0) or NULL (default), in which case expEmail(x) 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 multiple) CVParam instances describing all (distinct) PTMs reported in the unit. NULL (default) to ignore.
modProbabilityMethod  A user defined CVParam reporting the modification (position) probabilities. NULL (default) to ignore.
quantitationMethod  A valid CVParam, a ReporterIons instance or NULL (default), in which case the isobaric tagging system is guessed from the number of columns in exprs(x) (4 or 8 for iTRAQ, 6 for TMT).
protQuantUnit  A valid CVParsm or NULL (default) to use PRIDE:0000330 (Arbitrary quantification unit).

pepQuantUnit  A valid CVParsm or NULL (default) to use PRIDE:0000330 (Arbitrary quantification unit).

msFileFormat  A list of valid CVParsm instances to NULL (default), in which case, the extension of fileNames(x)[1] is used to define the appropriate CVParsm. 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 CVParsm instances describing the original identification format used in the external data file. NULL (default) to ignore.

custom  A list of user defined CVParsm instances with additional parameters describing the unit. NULL (default) to ignore.

species_  A list of (possibly several) CVParsm instances with the respective (sub-)unit species. NULL (default) to ignore.

tissue_  A list of (possibly several) CVParsm instances describing the respective (sub-)unit tissue. NULL (default) to ignore.

cellType_  A list of (possibly several) CVParsm instances describing the respective (sub-)unit cell type. NULL (default) to ignore.

disease_  A list of (possibly several) CVParsm 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 CVParsm instances or NULL (default), in which case the reporter ions as defined by quantitationMethod as used.

custom_  A list of user defined CVParsm 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**  
*Creates the mzTab peptide section*

**Description**

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general metadata, 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**

```r
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 **MSnSet**.
- **sequence**: A character of length `nrow(x)` (will be recycled a whole number of times if of different length) with the peptide sequence. Default is **NA**.
- **pepAccession**: A character of length `nrow(x)` (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 `nrow(x)` (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 `nrow(x)` (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 `nrow(x)` (will be recycled a whole number of times if of different length) with the database version. Default is **NA**.
- **pepSearchEngine**: A list of length `nrow(x)` (of possibly multiple lists of) **CVParm** instances identifying the search engine used for peptide identification. Default is **NA**.
- **pepSearchEngineScore**: A list of length `nrow(x)` (of possibly multiple lists of) **CVParm** instances specifying peptide identification scores. Default is **NA**.
pepReliability  A numeric of length nrow(x) (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 nrow(x) (will be recycled a whole number of times if of different length) describing the modifications and their position (see mzTab format specifications for details). Default is NA.

retentionTime  A numeric of length nrow(x) (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 NA.

charge  A numeric of length nrow(x) (will be recycled a whole number of times if of different length) indicating peptide charge state. Default is NA.

massToCharge  A numeric of length nrow(x) (will be recycled a whole number of times if of different length) with the peptides precursor mass to charge ratio. Default is NA.

pepUri  A character of length nrow(x) (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.

spectraRef  A character in the format ms_file[1-n]:{SPEC_REF} (see mzTab specifications for details) of length nrow(x) (will be recycled a whole number of times if of different length). Default is NA.

pepAbundance  A numeric of length nrow(x) or matrix with nrow(x) rows if multiple sub-samples are reported (see metadata section), specifying the peptides abundance. If NULL (default), ignored.

pepAbundanceStdev  A numeric of length nrow(x) or matrix with nrow(x) rows if multiple sub-samples are reported (see metadata section), specifying the standard deviation of peptides abundances. If NULL (default), ignored. If pepAbundance is not NULL, then pepAbundanceStdev is NA if not specified.

pepAbundanceSterr  A numeric of length nrow(x) or matrix with nrow(x) rows if multiple sub-samples are reported (see metadata section), specifying the standard error of peptides abundances. If NULL (default), ignored. If pepAbundance is not NULL, then pepAbundanceSterr is NA if not specified.

pepOpt_  An optional character of character matrix (possibly populated with text representations of CVParam instances) for any custom peptide annotation. Default is NULL 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

Create the mzTab protein section

Description

mzTab is a light-weight, tab-delimited file format for proteomics data. It describes general metadata, protein, peptide and small molecule information (all of which are optional), including quantitation and identification. The protein 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


Arguments

x An instance of class MSnSet.
protAccession A character of length nrow(x) (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 nrow(x) (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 nrow(x) (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 nrow(x) (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 nrow(x) (will be recycled a whole number of times if of different length) describing the protein database. Default is NA.
protDatabaseVersion A character of length nrow(x) (will be recycled a whole number of times if of different length) describing the database version. Default is NA.
makePRT

protSearchEngine
  A list of length nrow(x) (of possibly several) CVParam instances describing
  the search engine used for protein identification. Default is NA.

protSearchEngineScore
  A list of length nrow(x) (of possibly multiple lists of) CVParam instances specifying peptide identification scores. Default is NA.

protReliability
  A numeric of length nrow(x) (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 nrow(x) (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 nrow(x) (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 nrow(x) (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 mzTab specifi-
cation document for details. Default is NA.

protModifications
  A character of comma-delimited modifications/scores/positions describing the
proteins. See the mzTab specification document for details. Default is NA.

protUri
  A character of length nrow(x) (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 nrow(x) (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 nrow(x) (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 nrow(x) or matrix with nrow(x) rows if multiple sub-
samples are reported (see metadata section), specifying the protein abundance.
If NULL (default), ignored.

protAbundanceStdev
  A numeric of length nrow(x) or matrix with nrow(x) rows if multiple sub-
samples are reported (see metadata section), specifying the standard deviation
of protein abundances. If NULL (default), ignored. If protAbundance is not
NULL, then protAbundanceStdev is NA if not specified.

protAbundanceSterr
  A numeric of length nrow(x) or matrix with nrow(x) rows if multiple sub-
samples are reported (see metadata section), specifying the standard error of
protein abundances. If NULL (default), ignored. If protAbundance is not NULL, then protAbundanceSterr is NA if not specified.

protOpt_ An optional character of character matrix (possibly populated with text representations of CVParam 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 applies.
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 analyzer type (Quadrupole, time-of-flight, ion trap, ...).

analyserDetails: Object of class character describing the relevant details about the analyzer.

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(MIAPE) <- character
  append 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(MIAPE) <- value: Accessor function for pubMedIds.
- expemail(MIAPE): An accessor function for email slot.
- exptitle(MIAPE): An accessor function for title slot.
- analyzer(MIAPE): An accessor function for analyser slot. analyzer(MIAPE) is also available.
- analyzerDetails(MIAPE): An accessor function for analyserDetails slot. analyzerDetails is also available.
- detectorType(MIAPE): An accessor function for detectorType slot.
- ionSource(MIAPE): An accessor function for ionSource slot.
- ionSourceDetails(MIAPE): An accessor function for ionSourceDetails slot.
- instrumentModel(MIAPE): An accessor function for instrumentModel slot.
- instrumentManufacturer(MIAPE): An accessor function for instrumentManufacturer slot.
- instrumentCustomisations(MIAPE): An accessor function for instrumentCustomisations slot.

as("MIAME"): Coerce the object from MIAPE to MIAME class. Used when converting an MSnSet into an ExpressionSet.

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

Documenting missing data visualisation

Description

There is a need for adequate handling of missing value imputation in quantitative proteomics. Before developing a framework to handle missing data imputation optimally, we propose a set of visualisation tools. This document serves as an internal notebook for current progress and ideas that will eventually materialise in exported functionality in the MSnbase package.

Details

The explore the structure of missing values, we propose to

1. Explore missing values in the frame of the experimental design. The `imageNA2` function offers such a simple visualisation. It is currently limited to 2-group designs/comparisons. In case of time course experiments or sub-cellular fractionation along a density gradient, we propose to split the time/gradient into 2 groups (early/late, top/bottom) as a first approximation.

2. Explore the proportion of missing values in each group.

3. Explore the total and group-wise feature intensity distributions.

The existing `plotNA` function illustrates the completeness/missingness of the data.

Author(s)

Laurent Gatto <lg390@cam.ac.uk>, Samuel Wieczorek and Thomas Burger

See Also

`plotNA, imageNA2`.

Examples

```r
## Other suggestions
library("pRolocdata")
library("pRoloc")
data(dunkley2006)
set.seed(1)
nax <- makeNaData(dunkley2006, pNA = 0.10)
pcol <- factor(ifelse(dunkley2006$fraction <= 5, "A", "B"))
set1 <- pcol == "A"

## missing values in each sample
barplot(colSums(is.na(nax)), col = pcol)

## table of missing values in proteins
par(mfrow = c(3, 1))
barplot(table(rowSums(is.na(nax))), main = "All")
```
barplot(table(rowSums(is.na(nax)[sel1,])), main = "Group A")
barplot(table(rowSums(is.na(nax)[!sel1,])), main = "Group B")

fData(nax)$nNA1 <- rowSums(is.na(nax)[, sel1])
fData(nax)$nNA2 <- rowSums(is.na(nax)[, !sel1])
fData(nax)$nNA <- rowSums(is.na(nax))
o <- M5nbase:::imageNA2(nax, pcol)
plot((fData(nax)$nNA1 - fData(nax)$nNA2)[o], type = "l")
grid()

plot(sort(fData(nax)$nNA1 - fData(nax)$nNA2), type = "l")
grid()

o2 <- order(fData(nax)$nNA1 - fData(nax)$nNA2)
M5nbase:::imageNA2(nax, pcol, Rowv=o2)

layout(matrix(c(rep(1, 10), rep(2, 5)), nc = 3))
M5nbase:::imageNA2(nax, pcol, Rowv=o2)
plot((fData(nax)$nNA1 - fData(nax)$nNA2)[o2], type = "l", col = "red",
     ylim = c(-9, 9), ylab = "")
lines((fData(nax)$nNA - fData(nax)$nNA2)[o2], col = "steelblue")
lines((fData(nax)$nNA1 - fData(nax)$nNA2)[o2], type = "l",
     lwd = 2)

---

**MSmap-class**

**Class** MSmap

**Description**

A class to store mass spectrometry data maps, i.e intensities collected along the M/Z and retention time space during a mass spectrometry acquisition.

**Objects from the Class**

Objects can be created with the `MSmap` constructor. The constructor has the following arguments:

- **object** An object created by `mzR::openMSfile`.
- **scans** A numeric indicating the scan indices to be extracted from `object` to create the MS map. If missing, all MS1 spectra will be used.
- **lowMz** A numeric of length 1 defining the lower bound of the M/Z range of the MS map.
- **highMz** A numeric of length 1 defining the upper bound of the M/Z range of the MS map.
- **resMz** The resolution along the M/Z range.
- **hd** An optional `data.frame` as produced by `mzR::header(object)`. If missing, will be computed within the function.
- **zeroIsNA** Set 0 intensities to NA. This can be used to clarify the 3 dimensional plot produce by `plot3D`. 

```r
barplot(table(rowSums(is.na(nax)[sel1,])), main = "Group A")
barplot(table(rowSums(is.na(nax)[!sel1,])), main = "Group B")

fData(nax)$nNA1 <- rowSums(is.na(nax)[, sel1])
fData(nax)$nNA2 <- rowSums(is.na(nax)[, !sel1])
fData(nax)$nNA <- rowSums(is.na(nax))
o <- M5nbase:::imageNA2(nax, pcol)
plot((fData(nax)$nNA1 - fData(nax)$nNA2)[o], type = "l")
grid()

plot(sort(fData(nax)$nNA1 - fData(nax)$nNA2), type = "l")
grid()

o2 <- order(fData(nax)$nNA1 - fData(nax)$nNA2)
M5nbase:::imageNA2(nax, pcol, Rowv=o2)

layout(matrix(c(rep(1, 10), rep(2, 5)), nc = 3))
M5nbase:::imageNA2(nax, pcol, Rowv=o2)
plot((fData(nax)$nNA1 - fData(nax)$nNA2)[o2], type = "l", col = "red",
     ylim = c(-9, 9), ylab = "")
lines((fData(nax)$nNA - fData(nax)$nNA2)[o2], col = "steelblue")
lines((fData(nax)$nNA1 - fData(nax)$nNA2)[o2], type = "l",
     lwd = 2)
```
 Slots

call: Object of class "call" - the call used to generate the instance.
map: Object of class "matrix" containing the actual MS map.
mz: Object of class "numeric" with the M/Z sampling bins.
res: Object of class "numeric" storing the the M/Z resolution used to create the map.
rt: Object of class "numeric" with the retention times of the map spectra.
ms: Object of class "numeric" with the MS levels of the spectra.
t: Object of class "logical" indicating if the instance has been transposed.
filename: Object of class "character" specifying the filename of the original raw MS data.

 Methods

coerce signature(from = "MSmap", to = "data.frame"): convert the MSmap instance in a data.frame. Useful for plotting with lattice or ggplot2.

fileName signature(object = "MSmap"): returns the raw data filename.

msLevel signature(object = "MSmap"): returns the MS level of the map spectra.

msMap signature(object = "MSmap"): returns the actual map matrix.

mz signature(object = "MSmap", ...): returns the M/Z values of the map. Additional arguments are currently ignored.

rtime signature(object = "MSmap", ...): returns retention time values of the map. Additional arguments are currently ignored.

mzRes signature(object = "MSmap"): returns the resolution with which the sample along the M/Z range was done.

dim signature(x = "MSmap"): returns the dimensions of the map. ncol and nrow return the number of columns and rows respectively.

t signature(x = "MSmap"): transposes the map.

show signature(object = "MSmap"): prints a summary of the map.

plot signature(x = "MSmap", allTicks = "logical"): produces an image of the map using lattice::levelplot. By default, allTicks is TRUE and all M/Z and retention times ticks of drawn. If set to FALSE, only 10 ticks in each dimension are plotted.

plot3D signature(object = "MSmap", rgl = "logical"): produces an three dimensional view of the map using lattice::cloudes(..., type = "h"). If rgl is TRUE, the map is visualised on a rgl device and can be rotated with the mouse.

Author(s)

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Examples

```r
## Not run:
## downloads the data
library("rpX")
pxl <- PXDataset("PXD000001")
mzf <- pxget(pxl, 6)

## reads the data
ms <- openMSfile(mzf)
hd <- header(ms)

## a set of spectra of interest: MS1 spectra eluted
## between 30 and 35 minutes retention time
ms1 <- which(hd$msLevel == 1)
rtsel <- hd$retentionPolicy[ms1] / 60 > 30 &
        hd$retentionPolicy[ms1] / 60 < 35

## the map
M <- MSmap(ms, ms1[rtsel], 521, 523, .005, hd)

plot(M, aspect = 1, allTicks = FALSE)
plot3D(M)
if (require("rgl") & interactive())
    plot3D(M, rgl = TRUE)

## With some MS2 spectra
i <- ms1[which(rtsel)][1]
j <- ms1[which(rtsel)][2]
M2 <- MSmap(ms, i:j, 100, 1000, 1, hd)
plot3D(M2)

## End(Not run)
```

**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. identification 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.

bin signature(object = "MSnExp"): Bins spectra. See bin documentation for more details and examples.

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

compareSpectra signature(object1 = "Spectrum", object2 = "missing"): Compares spectra. See compareSpectra 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.

pickPeaks signature(object = "MSnExp"): Performs the peak picking to generate centroided spectra. See pickPeaks 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 that 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.

smooth signature(x = "MSnExp"): Smooths spectra. See smooth documentation for more details and examples.

addIdentificationData signature(object = "MSnExp", ...): Adds identification data to an experiment. See addIdentificationData documentation for more details and examples.

removeNoId signature(object = "MSnExp", fcol = "pepseq", keep = NULL): Removes non-identified features. See removeNoId documentation for more details and examples.

removeMultipleAssignment signature(object = "MSnExp", fcol = "nprot"): Removes protein groups with more than one member. The latter is defined by extracting a feature variable (default is "nprot").

idSummary signature(object = "MSnExp", ...): Prints a summary that lists the percentage of identified features per file (called coverage).

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.

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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.

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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 metadata. The MSnSet class is derived from the "eSet" class and mimics the "ExpressionSet" class classically used for microarray data.

Objects from the Class

The constructor MSnSet(exprs, fData, pData) can be used to create MSnSet instances. Argument exprs is a matrix and fData and pData must be of class data.frame or "AnnotatedDataFrame" and all must meet the dimensions and name validity constrains.

Objects can also 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.

A coercion method is also available to transform an IBSpectra object (names x) from the isobar package into an MSnSet: as(x, "MSnSet").

In the frame of the MSnbase package, MSnSet instances can be generated from "MSnExp" experiments 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 in 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 converted to a MIAME instance. It is also possible to coerce an ExpressionSet to and MSnSet, in which case the experimentData slot is newly initialised.

`as(,"data.frame")` signature(x = "MSnSet"): Coerce object from MSnSet to data.frame. The MSnSet is transposed and the PhenoData slot is appended. See also ms2df below.

`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 retained peptides out of n.

A complete use case using topN and nQuants is detailed in the synapter package vignette.

**filterNA** signature(object = "MSnSet", pNA = "numeric", pattern = "character", droplevels = "logical") This method subsets object by removing features that have (strictly) more than pNA percent of NA values. Default pNA is 0, which removes any feature that exhibits missing data. The method can also be used with a character pattern composed of P or Q characters only. A P represent a column/sample that is allowed a missing values, while columns/samples with and 1 must not have NAs.

This method also accepts matrix instances. droplevels defines whether unused levels in the feature meta-data ought to be lost. Default is TRUE. See the droplevels method below.

See also the is.na.MSnSet and plotNA methods for missing data exploration.

**filterZero** signature(object = "MSnSet", pNA = "numeric", pattern = "character", droplevels = "logical") As filterNA, but for zeros.

**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.

**droplevels** signature(x = "MSnSet", ...) Drops the unused factor levels in the featureData slot.

See droplevels for details.

**exprsToRatios** signature(object = "MSnSet", log = "logical") calculates all possible ratios between object's columns/samples. See exprsToRatios for more details.

**impute** signature(object = "MSnSet", ...) Performs data imputation on the MSnSet object.

See impute for more details.

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", facetBy = "character", sOrderBy = "character", legend = "character", low = "numeric") Produces an heatmap of expression values in the x object. Simple horizontal facetting is enabled by passing a single character as facetBy. Arbitrary facetting can be performed manually by saving the return value of the method (see example below). Re-ordering of the samples is possible by providing the name of a phenotypic variable to sOrderBy. The title of the legend can be set with legend and the colours with the low and high arguments.
If any negative value is detected in the data, the values are considered as log fold-changes and a divergent colour scale is used. Otherwise, a gradient from low to high is used. To scale the quantitative data in x prior to plotting, please see the scale method.

When there are more than nmax (default is 50) features/rows, these are not printed. This behaviour can be controlled by setting fnames to TRUE (always print) or FALSE (never print). See examples below.

The code is based on Vlad Petyuk's vp.misc::image_msnset. The previous version of this method is still available through the imageR function.

**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. 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.

**addIdentificationData** signature(object = "MSnSet", ...): Adds identification data to a MSnSet instance. See addIdentificationData documentation for more details and examples.

**removeNoId** signature(object = "MSnSet", fcol = "pepseq", keep = NULL): Removes non-identified features. See removeNoId documentation for more details and examples.

**removeMultipleAssignment** signature(object = "MSnSet", fcol = "nprot"): Removes protein groups with more than one member. The latter is defined by extracting a feature variable (default is "nprot").

**idSummary** signature(object = "MSnSet", ...): Prints a summary that lists the percentage of identified features per file (called coverage).

**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 ..
- **ms2df** signature(x, fcols) Coerces the MSnSet instance to a data.frame. The direction of the data is retained and the feature variable labels that match fcol are appended to the expression values. See also as(x, "data.frame") above.

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See Also

"eSet", "ExpressionSet" and quantify. MSnSet quantitation values can be exported to a file with write.exprs.

Examples

data(msnset)
msnset <- msnset[10:15]

exprs(msnset)[1, c(1, 4)] <- NA
exprs(msnset)[2, c(1, 2)] <- NA
is.na(msnset)

featureNames(filterNA(msnset, pNA = 1/4))
featureNames(filterNA(msnset, pattern = "0110"))

M <- matrix(rnorm(12, 4)
pd <- data.frame(otherpdata = letters[1:3])
fd <- data.frame(otherfdata = letters[1:4])
x0 <- MSnSet(M, fd, pd)
sampleNames(x0)

M <- matrix(rnorm(12, 4)
colnames(M) <- LETTERS[1:3]
rownames(M) <- paste0("id", LETTERS[1:4])
pd <- data.frame(otherpdata = letters[1:3])
rownames(pd) <- colnames(M)
fd <- data.frame(otherfdata = letters[1:4])
rownames(fd) <- rownames(M)
x <- MSnSet(M, fd, pd)
sampleNames(x)

## Visualisation

library(pRolocdata)
data(dunkley2006)
image(dunkley2006)

## Changing colours
image(dunkley2006, high = "darkgreen")
image(dunkley2006, high = "darkgreen", low = "yellow")

## Forcing feature names
image(dunkley2006, fnames = TRUE)

## Facetting
image(dunkley2006, facetBy = "replicate")
p <- image(dunkley2006)
library("ggplot2") ## for facet_grid
p + facet_grid(replicate ~ membrane.prep, scales = 'free', space = 'free')
p + facet_grid(markers ~ replicate)

## Fold-changes
dd <- dunkley2006
exprs(dd) <- exprs(dd) - 0.25
image(dd)
MSnSetList-class

Storing multiple related MSnSets

Description

A class for storing lists of MSnSet instances.

Details

There are two ways to store different sets of measurements pertaining an experimental unit, such as replicated measures of different conditions that were recorded over more than one MS acquisition. Without focusing on any proteomics technology in particular, these multiple assays can be recorded as

- A single combined MSnSet (see the section Combining MSnSet instances in the MSnbase-demo section). In such cases, the different experimental (phenotypical) conditions are recorded as an AnnotatedDataFrame in the phenoData slots. Quantitative data for features that were missing in an assay are generally encode as missing with NA values. Alternatively, only features observed in all assays could be selected. See the commonFeatureNames functions to select only common features among two or more MSnSet instance.
- Each set of measurements is stored in an MSnSet which are combined into one MSnSetList. Each MSnSet elements can have identical or different samples and features. Unless compiled directly manually by the user, one would expect at least one of these dimensions (features/rows or samples/columns) are conserved (i.e. all feature or samples names are identical). See split/unsplit below.

Objects from the Class

Objects can be created and manipulated with:

MSnSetList(x) The class constructor that takes a list of valid MSnSet instances as input x.

split(x, f) An MSnSetList can be created from an MSnSet instance. x is a single MSnSet and f is a factor or a character of length 1. In the latter case, f will be matched to the feature- and phenodata variable names (in that order). If a match is found, the respective variable is extracted, converted to a factor if it is not one already, and used to split x along the features/rows (f was a feature variable name) or samples/columns (f was a phenotypic variable name). If f is passed as a factor, its length will be matched to nrow(x) or ncol(x) (in that order) to determine if x will be split along the features (rows) or sample (columns). Hence, the length of f must match exactly to either dimension.
unsplit(value, f) The unsplit method reverses the effect of splitting the value MSnSet along the groups f.

as(x, "MSnSetList") Where x is an instance of class MzTab. See the class documentation for details.

Slots

x: Object of class list containing valid MSnSet instances. Can be extracted with the msnsets() accessor.

log: Object of class list containing an object creation log, containing among other elements the call that generated the object. Can be accessed with objlog().

__classVersion__: The version of the instance. For development purposes only.

Methods

"[[" Extracts a single MSnSet at position.

"[" Extracts one or more MSnSets as MSnSetList.

length: Returns the number of MSnSets.

names: Returns the names of MSnSets, if available.

show: Display the object by printing a short summary.

lapply(x, FUN, ...) Apply function FUN to each element of the input x. If the application of FUN returns and MSnSet, then the return value is an MSnSetList, otherwise a list.

Author(s)

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See Also

The commonFeatureNames function to select common features among MSnSet instances.

Examples

library("prolocdata")
data(tan2009r1)
data(tan2009r2)

## The MSnSetList class
## an unnamed example
msnl <- MSnSetList(list(tan2009r1, tan2009r2))
## a named example
msnl <- MSnSetList(list(A = tan2009r1, B = tan2009r2))

names(msnl)
msnsets(msnl)
length(msnl)
objlog(msnl)

msnl[[1]] ## an MSnSet

msnl[[1]] ## an MSnSetList of length 1
## MzTab-class

### Parse MzTab files

### Description

The MzTab class stores the output of a basic parsing of a mzTab file. It contains metadata (a list), comments (a character vector), and at least one of the following data types: proteins, peptides, PSMs and small molecules (as data.frames). At this stage, the metadata and data are only minimally parsed. More specific data extraction and preparation are delegated to more specialised functions, such as the as(object, "MSnSetList") method and readMzTabData for proteomics data.

Note that no attempts are made to verify the validity of the mzTab file.

### Objects from the Class

Objects can be created by calls to the constructor MzTab that takes a single mzTab file as input.

The objects can subsequently be coerced to MSnSetList instances with as(object, "MSnSetList"). The resulting MSnSetList contains possibly empty MSnSet instances for proteins, peptide and PSMs, respectively named "Proteins", "Peptides" and "PSMs".

The assaydata slots of the two former are populated with the protein_abundance_assay[1-n] and peptide_abundance_assay[1-n] columns in the mzTab file. No abundance values are defined for the latter. The respective feature names correspond to protein accessions, peptide sequences and PSM identifiers, possibly made unique as by appending sequence numbers to duplicates.
MzTab-class

Slots

Metadata: Object of class "list" storing the metadata section.
Filename: Object of class "character" storing the original file name.
Proteins: Object of class "data.frame" storing the protein data.
Peptides: Object of class "data.frame" storing the peptide data.
PSMs: Object of class "data.frame" storing the PSM data.
SmallMolecules: Object of class "data.frame" storing the small molecules data.
Comments: Object of class "character" storing the comments that were present in the file.

Accessors

metadata signature(x = "MzTab"): returns the meta data list.
mzTabMode signature(x = "MzTab"): returns the mode (complete or summary) of the mzTab data. A shortcut for metadata(x)\$`mzTab-mode`.
mzTabType signature(x = "MzTab"): returns the type (quantification or identification) of the mzTab data. A shortcut for metadata(x)\$`mzTab-type`.
fileName signature(object = "MzTab"): returns the file name of the original mzTab file.
peptides signature(object = "MzTab"): returns the peptide data.frame.
proteins signature(object = "MzTab"): returns the proteins data.frame.
psms signature(object = "MzTab"): returns the PSMS data.frame.
smallMolecules signature(object = "MzTab"): returns the small molecules data.frame.
comments signature(object = "MzTab"): returns the comments.

Author(s)

Laurent Gatto, with contributions from Richard Cotton (see https://github.com/lgatto/MSnbase/issues/41).

References

The mzTab format is a light-weight, tab-delimited file format for proteomics data. See https://code.google.com/p/mztab/ for details and specifications.

Examples

```r
## Test files from the mzTab development repository
fls <- c("Cytidine.mzTab", "MTBLS2.mztab",
         "PRIDE_Exp_Complete_Ac_1643.xml-mztab.txt",
         "PRIDE_Exp_Complete_Ac_16649.xml-mztab.txt",
         "SILAC_CQI.mzTab", "SILAC_SQ.mzTab",
         "iTRAQ_CQI.mzTab", "iTRAQ_SQI.mzTab",
         "labelfree_CQI.mzTab", "labelfree_SQI.mzTab",
         "lipidomics-HFD-LD-study-PL-DG-SM.mzTab",
         "lipidomics-HFD-LD-study-TG.mzTab")
baseurl <- "https://mztab.googlecode.com/svn/examples/"

## a list of mzTab objects
mzt <- sapply(file.path(baseurl, fls), MzTab)
stopifnot(length(mzt) == length(fls))

mzt[[4]]

dim(proteins(mzt[[4]]))
dim(psms(mzt[[4]]))

prots4 <- proteins(mzt[[4]])
class(prots4)
prots4[1:5, 1:4]
```

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 parameters.

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".
NAnnotatedDataFrame-class

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=1f,
     varMetadata=metaData,
     multiplex=length(mplx),
     multiLabels=mplx)
Normalise methods

Description

The `normalise` method (also available as `normalize`) performs basic normalisation on spectra intensities of single spectra ("Spectrum" or "Spectrum2" objects), whole experiments ("MSnExp" objects) or quantified expression data ("MSnSet" objects).

Raw spectra and experiments are normalised using max or sum only. For MSMS spectra could be normalised to their precursor additionally. Each peak intensity is divided by the highest intensity in the spectrum, the sum of intensities or the intensity of the precursor. These methods aim at facilitating relative peaks heights between different spectra.

The method parameter for "MSnSet" can be one of sum, max, quantiles, center.mean, center.median, quantiles.robust or vsn. For sum and max, each feature's reporter intensity is divided by the maximum or the sum respectively. These two methods are applied along the features (rows). center.mean and center.median translate the respective sample (column) intensities according to the column mean or median. Using quantiles or quantiles.robust applies (robust) quantile normalisation, as implemented in `normalize.quantiles` and `normalize.quantiles.robust` of the preprocessCore package. vsn uses the `vsn2` function from the vsn package. Note that the latter also glog-transforms the intensities. See respective manuals for more details and function arguments.

A scale method, mimicking the base scale method exists for "MSnSet" instances. See `?base::scale` for details.

Arguments

- `object` An object of class "Spectrum", "Spectrum2", "MSnExp" or "MSnSet".
- `method` A character vector of length one that describes how to normalise the object. See description for details.
- `...` Additional arguments passed to the normalisation function.

Methods

The `normalise` methods:

```r
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.
signature(object = "Spectrum2", method = "character", precursorIntensity) Normalises the object peak intensities using method. If method == "precursor", precursorIntensity allows to specify the intensity of the precursor manually.
```
The scale method:
signature(x = "MsnSet", center = "logical", scale = "logical") See ?base::scale.

Examples

```r
## quantifying full experiment
data(msnset)
msnset.nrm <- normalise(msnset, "quantiles")
msnset.nrm
```

npcv

Non-parametric coefficient of variation

Description

Calculates a non-parametric version of the coefficient of variation where the standard deviation is replaced by the median absolute deviations (see mad for details) and divided by the absolute value of the mean.

Usage

```r
npcv(x, na.rm = TRUE)
```

Arguments

- `x` A numeric.
- `na.rm` A logical (default is TRUE indicating whether NA values should be stripped before the computation of the median absolute deviation and mean.

Details

Note that the mad of a single value is 0 (as opposed to NA for the standard deviation, see example below).

Value

A numeric.

Author(s)

Laurent Gatto

Examples

```r
set.seed(1)
npcv(rnorm(10))
replicate(10, npcv(rnorm(10)))
npcv(1)
mad(1)
sd(1)
```
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 features 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(msnset)
n <- 2
msnset <- topN(msnset, groupBy = fData(msnset)$ProteinAccession, n)
m <- nQuants(msnset, fcol = "ProteinAccession")
msnset2 <- combineFeatures(msnset,
                        groupBy = fData(msnset)$ProteinAccession,
                        fun = sum)
stopifnot(dim(n) == dim(msnset2))
head(exprs(msnset2))
head(exprs(msnset2) * (n/m))
**pickPeaks-methods**  
Peak Detection for 'MSnExp' or 'Spectrum' instances

**Description**

This method performs a peak picking on individual spectra (Spectrum instances) or whole experiments (MSnExp instances) to create centroided spectra. For noisy spectra there are currently two different noise estimators, the Median Absolute Deviation (method = "MAD") and Friedman’s Super Smoother (method = "SuperSmoother"), as implemented in the MALDIquant::detectPeaks and MALDIquant::estimateNoise functions respectively.

**Methods**

signature(x = "MSnExp", halfWindowSize = "integer", method = "character", SNR = "numeric", verbose = FALSE)

Performs the peak picking for all spectra in an MSnExp instance. method could be "MAD" or "SuperSmoother", halfWindowSize controls the window size of the peak picking algorithm. The resulting window size is \( 2 \times \text{halfWindowSize} + 1 \). The size should be nearly (or slightly larger) the FWHM (full width at half maximum). A local maximum is considered as peak if its intensity is SNR times larger than the estimated noise. The arguments ... are passed to the noise estimator functions. Currently only the method = "SuperSmoother" accepts additional arguments, e.g. span. Please see supsmu for details. This method displays a progress bar if verbose = TRUE. Returns an MSnExp instance with centroided spectra.

signature(x = "Spectrum", method = "character", halfWindowSize = "integer", ...)

Performs the peak picking for the spectrum (Spectrum instance). This method is the same as above but returns a centroided Spectrum instead of an MSnExp object. It has no verbose argument. Please read the details for the above MSnExp method.

**Author(s)**

Sebastian Gibb <mail@sebastiangibb.de>

**References**


**See Also**

`clean`, `removePeaks`, `smooth` and `trimMz` for other spectra processing methods.

**Examples**

```r
sp1 <- new("Spectrum1",
    intensity = c(1:6, 5:1),
    mz = 1:11)
sp2 <- pickPeaks(sp1)
intensity(sp2)
```
data(itraqdata)
itraqdata2 <- pickPeaks(itraqdata)
processingData(itraqdata2)

### plot-methods

#### Plotting 'Spectrum' object(s)

**Description**

These methods plot mass spectra MZ values against the intensities. 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 `ggplotR` system. An object of class 'ggplot' is returned invisibly.

If a single "Spectrum2" and a "character" representing a valid peptide sequence are passed as argument, the expected fragment ions are calculated and matched/annotated on the spectrum plot.

**Arguments**

- **x**: Objects of class "Spectrum", "Spectrum2" or "MSnExp" to be plotted.
- **y**: Missing, "Spectrum" or "character".
- **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 histograms, 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 histogram bars for centroided reporter ions plots. Default is 0.01. See below for more details.

**Methods**

```r
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 = TRUE) 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.

signature(x = "Spectrum2", y = "character", orientation = "numeric", add = "logical", col = "character") Plots a single MS2 spectrum and annotates the fragment ions based on the matching between the peaks in x and the fragment peaks calculated from the peptide sequence y. The default values are orientation=1, add=FALSE, col="#74ADD1", pch=NA, xlab="m/z", ylab="intensity", ylim=c(0, 1), tolerance=0.1, relative=FALSE, type=c("b", "y"), modifications=c(C=160.030649), z=1, fragments=MSnbase:::calculateFragments_Spectrum2 and fragments.cex=0.75. Additional arguments ... are passed to plot.default.

Author(s)
Laurent Gatto <lg390@cam.ac.uk> and Sebastian Gibb

See Also
calculateFragments to calculate ions produced by fragmentation and plot.Spectrum.Spectrum to plot and compare 2 spectra and their shared peaks.

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

itraqdata2 <- pickPeaks(itraqdata)
i <- 14
s <- as.character(FData(itraqdata2)[i, "PeptideSequence"])
plot(itraqdata2[[1]], s, main = s)
Arguments

- **x**: Object of class "Spectrum".
- **y**: Object of class "Spectrum".
- **...**: Further arguments passed to internal functions.

Methods

```r
signature(x = "Spectrum", y = "Spectrum", ...) Plots two spectra against each other. Common peaks are drawn in a slightly darker colour. The ... arguments are passed to the internal functions. Currently tolerance, relative, sequences and most of the plot.default arguments (like xlim, ylim, main, xlab, ylab, ...) are supported. You could change the tolerance (default 25e-6) and decide whether this tolerance should be applied relative (default relative = TRUE) or absolute (relative = FALSE) to find and colour common peaks. Use a character vector of length 2 to provide sequences which would be used to calculate and draw the corresponding fragments. If sequences are given the type argument (default: type=c("b", "y") specify the fragment types which should calculated. Also it is possible to allow some modifications. Therefore you have to apply a named character vector for modifications where the name corresponds to the one-letter-code of the modified amino acid (default: Carbamidomethyl modifications=c(C=160.030649)). See calculateFragments for details.
```

Author(s)

Sebastian Gibb <mail@sebastiangibb.de>

See Also

More spectrum plotting available in `plot.Spectrum`.

Examples

```r
## find path to a mzXML file
file <- dir(system.file(package = "MSnbase", dir = "extdata"),
                   full.name = TRUE, pattern = "mzXML$")

## create basic MSnExp
msexp <- readMSData(file)

## centroid them
msexp <- pickPeaks(msexp)

## plot the first against the second spectrum
plot(msexp[[1]], msexp[[2]])

## add sequence information
plot(msexp[[1]], msexp[[2]], sequences=c("VESITARHGEVLQLRPK",
                                         "IDGQWTHQWLKK"))

itraqdata2 <- pickPeaks(itraqdata)
```
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 ggplotR system. An object of class 'ggplot' is returned invisibly.

Arguments

- **object**: An object of class "MSnExp" 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 "MSnExp" 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

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

```r
itraqdata
plotDensity(itraqdata, z="ionCount")
plotDensity(itraqdata, z="peaks.count")
plotDensity(itraqdata, z="precursor.mz")
```
The delta m/z 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 suggest that it might work.

The methods make use 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object of class MSnExp or mzRamp (from the mzR package) containing MS2 spectra.</td>
</tr>
<tr>
<td>reporters</td>
<td>An object of class &quot;ReporterIons&quot; that defines which reporter ion peaks to set to 0. The default value NULL leaves the spectra as they are.</td>
</tr>
<tr>
<td>subset</td>
<td>A numeric between 0 and 1 to use a subset of object’s MS2 spectra.</td>
</tr>
<tr>
<td>percentage</td>
<td>The percentage of most intense peaks to be used for the plot. Default is 0.1.</td>
</tr>
<tr>
<td>precMz</td>
<td>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 precursorMz method.</td>
</tr>
<tr>
<td>precMzWidth</td>
<td>A numeric of length 1 that specifies the width around the precursor m/z where peaks are set to 0. Default is 2.</td>
</tr>
<tr>
<td>bw</td>
<td>A numeric specifying the bandwidth to be used to bin the delta m/z value to plot the histogram. Default if 1. See geom_histogram for more details.</td>
</tr>
<tr>
<td>xlim</td>
<td>A numeric of length 2 specifying the range of delta m/z to plot on the histogram. Default is c(40, 200).</td>
</tr>
<tr>
<td>withLabels</td>
<td>A logical defining if amino acid residue labels are plotted on the figure. Default is TRUE.</td>
</tr>
</tbody>
</table>
size

A numeric of length 1 specifying the font size of amino acids 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 illustration 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


See Also

The plotDensity and plot2d methods for other QC plots.

Examples

mzdplot <- plotMzDelta(itraqdata,
  subset = 0.5,
  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)
**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 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**

```r
data(msnset)
exprs(msnset)[sample(prod(dim(msnset)), 120)] <- NA

head(is.na(msnset))
table(is.na(msnset))
ageimage(msnset)

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

---

**precSelection**  
*Number of precursor selection events*
Description

precSelection computes the number of selection events each precursor ions has undergone in an 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 "MSnExp".
n The number of decimal places to round the precursor MZ to. Is passed to the round 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.
**pSet-class**

### 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. identification 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.

```r
[ 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 'code-processingData' slot) from which the individual object’s spectra where read from.
```
PSet-class

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 PMID 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. Additional arguments are currently ignored.
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.
scanIndex signature(object = "pSet"): Accessor for spectra scan indices.
collisionEnergy signature(object = "pSet"): Accessor for MS2 spectra collision energies.
intensity signature(object = "pSet", ...): Accessor for spectra intensities, returned as named list. Additional arguments are currently ignored.
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. Additional arguments are currently ignored.
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.
precAcquisitionNum signature(object = "pSet"): Accessor for MS2 precursor scan numbers.
precScanNum see precAcquisitionNum.
rtime signature(object = "pSet", ...): Accessor for spectra retention times. Additional arguments are currently ignored.
purityCorrect-methods

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, filename, edit = TRUE)` helps the user to create such a matrix. The function can be used in two ways. If given an integer `x`, it is used as the dimension of the square matrix (i.e. the number of reporter ions). For TMT6-plex and iTRAQ4-plex, default values taken from manufacturer's certification sheets are used as templates, but batch specific values should be used whenever possible. Alternatively, the filename of a csv spreadsheet can be provided. The sheet should define the correction factors as illustrated below (including
reporter names in the first column and header row) and the corresponding correction matrix is calculated. Examples of such csv files are available in the package’s extdata directory. Use 
\[\text{dir(system.file("extdata", package = "MSnbase"), pattern = "PurityCorrection", full.names = TRUE)}\]
to locate them. If \text{edit = TRUE}, the the matrix can be edited before it is returned.

Arguments

- \text{object} 
  An object of class "\text{MSnSet}".

- \text{impurities} 
  A square 'matrix' of dim equal to \text{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:

<table>
<thead>
<tr>
<th>reporter</th>
<th>% of -2</th>
<th>% of -1</th>
<th>% of +1</th>
<th>% of +2</th>
</tr>
</thead>
<tbody>
<tr>
<td>114</td>
<td>0.0</td>
<td>1.0</td>
<td>5.9</td>
<td>0.2</td>
</tr>
<tr>
<td>115</td>
<td>0.0</td>
<td>2.0</td>
<td>5.6</td>
<td>0.1</td>
</tr>
<tr>
<td>116</td>
<td>0.0</td>
<td>3.0</td>
<td>4.5</td>
<td>0.1</td>
</tr>
<tr>
<td>117</td>
<td>0.1</td>
<td>4.0</td>
<td>3.5</td>
<td>0.1</td>
</tr>
</tbody>
</table>

The impurity table will be

\[\begin{bmatrix}
0.929 & 0.059 & 0.002 & 0.000 \\
0.020 & 0.923 & 0.056 & 0.001 \\
0.000 & 0.030 & 0.924 & 0.045 \\
0.000 & 0.001 & 0.040 & 0.923
\end{bmatrix}\]

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

Similarly, for TMT 6-plex tags, we observe

<table>
<thead>
<tr>
<th>reporter</th>
<th>% of -3</th>
<th>% of -2</th>
<th>% of -1</th>
<th>% of +1</th>
<th>% of +2</th>
<th>% of +3</th>
</tr>
</thead>
<tbody>
<tr>
<td>126</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>6.1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>127</td>
<td>0</td>
<td>0</td>
<td>0.5</td>
<td>6.7</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>128</td>
<td>0</td>
<td>0</td>
<td>1.1</td>
<td>4.2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>129</td>
<td>0</td>
<td>0</td>
<td>1.7</td>
<td>4.1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>130</td>
<td>0</td>
<td>0</td>
<td>1.6</td>
<td>2.1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>131</td>
<td>0</td>
<td>0.2</td>
<td>3.2</td>
<td>2.8</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

and obtain the following impurity correction matrix

\[\begin{bmatrix}
0.939 & 0.061 & 0.000 & 0.000 & 0.000 & 0.000 \\
0.005 & 0.928 & 0.067 & 0.000 & 0.000 & 0.000 \\
0.000 & 0.011 & 0.947 & 0.042 & 0.000 & 0.000 \\
0.000 & 0.000 & 0.017 & 0.942 & 0.041 & 0.000
\end{bmatrix}\]
For iTRAQ 8-plex, given the following correction factors (to make such a matrix square, if suffices to add -4, -3, +3 and +4 columns filled with zeros):

<table>
<thead>
<tr>
<th>TAG</th>
<th>-2</th>
<th>-1</th>
<th>+1</th>
<th>+2</th>
</tr>
</thead>
<tbody>
<tr>
<td>113</td>
<td>0</td>
<td>2.5</td>
<td>3</td>
<td>0.1</td>
</tr>
<tr>
<td>114</td>
<td>0</td>
<td>1</td>
<td>5.9</td>
<td>0.2</td>
</tr>
<tr>
<td>115</td>
<td>0</td>
<td>2</td>
<td>5.6</td>
<td>0.1</td>
</tr>
<tr>
<td>116</td>
<td>0</td>
<td>3</td>
<td>4.5</td>
<td>0.1</td>
</tr>
<tr>
<td>117</td>
<td>0.1</td>
<td>4</td>
<td>3.5</td>
<td>0.1</td>
</tr>
<tr>
<td>118</td>
<td>0.1</td>
<td>2</td>
<td>3</td>
<td>0.1</td>
</tr>
<tr>
<td>119</td>
<td>0.1</td>
<td>2</td>
<td>4</td>
<td>0.1</td>
</tr>
<tr>
<td>121</td>
<td>0.1</td>
<td>2</td>
<td>3</td>
<td>0.1</td>
</tr>
</tbody>
</table>

we calculate the impurity correction matrix shown below

<table>
<thead>
<tr>
<th></th>
<th>113</th>
<th>114</th>
<th>115</th>
<th>116</th>
<th>117</th>
<th>118</th>
<th>119</th>
<th>121</th>
</tr>
</thead>
<tbody>
<tr>
<td>% report 113</td>
<td>0.944</td>
<td>0.030</td>
<td>0.001</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>% report 114</td>
<td>0.010</td>
<td>0.929</td>
<td>0.059</td>
<td>0.002</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>% report 115</td>
<td>0.000</td>
<td>0.020</td>
<td>0.923</td>
<td>0.056</td>
<td>0.001</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>% report 116</td>
<td>0.000</td>
<td>0.000</td>
<td>0.030</td>
<td>0.924</td>
<td>0.045</td>
<td>0.001</td>
<td>0.000</td>
<td>0.000</td>
</tr>
<tr>
<td>% report 117</td>
<td>0.000</td>
<td>0.000</td>
<td>0.001</td>
<td>0.040</td>
<td>0.923</td>
<td>0.035</td>
<td>0.001</td>
<td>0.000</td>
</tr>
<tr>
<td>% report 118</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.001</td>
<td>0.020</td>
<td>0.948</td>
<td>0.030</td>
<td>0.001</td>
</tr>
<tr>
<td>% report 119</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.001</td>
<td>0.020</td>
<td>0.938</td>
<td>0.040</td>
</tr>
<tr>
<td>% report 121</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0.001</td>
<td>0.020</td>
<td>0.948</td>
</tr>
</tbody>
</table>

Finally, for a TMT 10-plex impurity matrix

<table>
<thead>
<tr>
<th></th>
<th>-2</th>
<th>-1</th>
<th>1</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>126</td>
<td>0.0</td>
<td>0.00</td>
<td>4.69 (127C)</td>
<td>0.0 (128N)</td>
</tr>
<tr>
<td>127N</td>
<td>0.0</td>
<td>0.40</td>
<td>6.50 (128N)</td>
<td>0.0 (128C)</td>
</tr>
<tr>
<td>127C</td>
<td>0.0</td>
<td>0.20 (126)</td>
<td>4.60 (128C)</td>
<td>0.3 (129N)</td>
</tr>
<tr>
<td>128N</td>
<td>0.0</td>
<td>0.90 (127N)</td>
<td>4.70 (129N)</td>
<td>0.2 (129C)</td>
</tr>
<tr>
<td>128C</td>
<td>0.1 (126)</td>
<td>0.53 (127C)</td>
<td>2.59 (129C)</td>
<td>0.0 (130N)</td>
</tr>
<tr>
<td>129N</td>
<td>0.0 (127N)</td>
<td>0.73 (128N)</td>
<td>2.49 (130N)</td>
<td>0.0 (130C)</td>
</tr>
<tr>
<td>129C</td>
<td>0.0 (127C)</td>
<td>1.30 (128C)</td>
<td>2.50 (130C)</td>
<td>0.0 (131)</td>
</tr>
<tr>
<td>130N</td>
<td>0.0 (128N)</td>
<td>1.20 (129N)</td>
<td>2.80 (131)</td>
<td>2.7</td>
</tr>
<tr>
<td>130C</td>
<td>0.1 (128C)</td>
<td>2.90 (129C)</td>
<td>2.90</td>
<td>0.0</td>
</tr>
<tr>
<td>131</td>
<td>0.0 (129N)</td>
<td>2.36 (130N)</td>
<td>1.43</td>
<td>0.0</td>
</tr>
</tbody>
</table>

the impurity correction matrix is
These examples are provided as defaults impurity correction matrices in `makeImpuritiesMatrix`.

**Methods**

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

**Examples**

```r
## quantifying full experiment
data(msnset)
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.crrct <- purityCorrect(msnset, impurities)
head(exprs(msnset))
head(exprs(msnset.crrct))
processingData(msnset.crrct)

## default impurity matrix for iTRAQ 8-plex
makeImpuritiesMatrix(8, edit = FALSE)

## default impurity matrix for TMT 10-plex
makeImpuritiesMatrix(10, edit = FALSE)
```

**quantify-methods**

Quantifies 'MSnExp' and 'Spectrum' objects

**Description**

This method quantifies individual "Spectrum" objects or full "MSnExp" experiments. Current, MS2-level isobar tagging using iTRAQ and TMT (or any arbitrary peaks of interest, see "ReporterIons")
and MS2-level label-free quantitation (spectral counting, spectral index or spectral abundance factor) are available.

Isobaric tag peaks of single spectra or complete experiments can be quantified using appropriate methods. Label-free quantitation is available only for MSnExp experiments.

Since version 1.13.5, parallel quantitation is supported by the BiocParallel package and controlled by the BPPARAM argument.

Arguments

- **object**: An instance of class "Spectrum" (isobaric tagging only) or "MSnExp".
- **method**: Peak quantitation method. For isobaric tags, 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).
  - For label-free quantitation, one of "SI" (spectral index), "S\_gi" (global intensity spectral index), "S\_in" (normalised spectral index), "SAF" (spectral abundance factor) or "NSAF" (normalised spectral abundance factor).
  - Finally, the simple "count" method counts the occurrence of the respective spectra (at this stage all 1s) that can then be used as input to combineFeatures to implement spectra counting.

- **reporters**: An instance of class "ReporterIons" that defines the peak(s) to be quantified. For isobaric tagging only.

- **strict**: For isobaric tagging only. If strict is FALSE (default), the quantitation is performed using data points along the entire width of a peak. If strict is set to TRUE, once the apex(es) is/are identified, only data points within apex +/- width of reporter (see "ReporterIons") are used for quantitation.

- **BPPARAM**: Support for parallel processing using the BiocParallel infrastructure. When missing (default), the default registered BiocParallelParam parameters are applied using bpparam(). Alternatively, one can pass a valid BiocParallelParam parameter instance: SnowParam, MulticoreParam, DoparParam,... see the BiocParallel package for details.

- **parallel**: Deprecated. Please see BPPARAM.

- **qual**: Should the qual slot be populated. Default is TRUE.

- **verbose**: Verbose of the output (only for MSnExp objects).

- **...**: Further arguments passed to the quantitation functions.

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).

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.
Note that for label-free, spectra that have not been identified (the corresponding fields in the feature data are populated with NA values) or that have been uniquely assigned to a protein (the nprot feature data is greater that 1) are removed prior to quantitation. The latter does not apply for method = "count" but can be applied manually with removeMultipleAssignment.

Methods

signature(object = "MSnExp", method = "character", reporters = "ReporterIons", verbose = "logical", ...)  
For isobaric tagging, 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.

For label-free quantitation, the respective quantitation methods and normalisations are applied to the spectra. These methods require two additional arguments (...), namely the protein accession of identifiers (fcol, with default value "accession") and the protein lengths (plength, with default value "length"). These values are available of the identification data had been collated using addIdentificationData.  
An object of class "MSnSet" is returned containing the quantified feature expression and all meta data inherited from the MSnExp object argument.

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

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, names 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> and Sebastian Gibb <mail@sebastiangibb.de>

References


Examples

```r
## Quantifying a full experiment using iTRAQ4-plex tagging
data(itraqdata)
```
readIspyData

Reads an ispy2 result spreadsheet 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 <pdc35@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

Description

Reads a 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.
readMSData

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

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".

Examples

data(itraqdata)
writeMgfData(itraqdata, con="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=1e-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
file <- dir(system.file(package="MSnbase",dir="extdata"),
            full.name=TRUE,
            pattern= "test.mgf")
(x <- readMgfData(file))
x[[2]]
precursorMz(x[[2]])
precursorIntensity(x[[2]])
precursorMz(x[[1]])
precursorIntensity(x[[1]]) # was not in test.mgf
scanIndex(x)
**readMSnSet**

`msLevel` MS level spectra to be read. Use '1' for MS1 spectra or 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 `removePeaks` 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 `clean` 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**

```r
file <- dir(system.file(package="MSnbase",dir="extdata"),
    full.name=TRUE,
    pattern="mzXML$")
aa <- readMSnData(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. `readMSnSet2` is a simple version that takes a single text spreadsheet as input and extracts the expression data and feature meta-data to create and `MSnSet`. 
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, ...)

readMSnSet2(file, ecol, fnames, ...)

Arguments

Arguments directly passed to readExpressionSet. The description is from the readExpressionSet documentation page.

(exprsFile) 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) File or connection from which to read phenotypic data. read.AnnotatedDataFrame is called with this as its file argument and further arguments given by phenoDataArgs.

(experimentDataFile) File or connection from which to read experiment data. read.MIAME is called with this as its file argument and further arguments given by experimentDataArgs.

(notesFile) File or connection from which to read notes; readLines is used to input the file.

(path) (optional) directory in which to find all the above files.

(annotation) A single character string indicating the annotation associated with this ExpressionSet.

(exprsArgs) A list of arguments to be used with read.table when reading in the expression matrix.

(phenoDataArgs) A list of arguments to be used (with read.AnnotatedDataFrame) when reading the phenotypic data.

(experimentDataArgs) A list of arguments to be used (with read.MIAME) when reading the experiment data.

(sep, header, quote, stringsAsFactors, row.names) arguments used by the read.table-like functions.
readMsnSet

widget A boolean value indicating whether widgets can be used. Widgets are NOT yet implemented for `read.AnnotatedDataFrame`.

Further arguments that can be passed on to the `read.table`-like functions. Additional argument, specific to `readMsnSet`:

featureDataFile (character) File or connection from which to read feature data. `read.AnnotatedDataFrame` is called with this as its file argument and further arguments given by `phenoDataArgs`.

featureDataArgs A list of arguments to be used (with `read.AnnotatedDataFrame`) when reading the phenotypic data.

Arguments for `readMsnSet2`:

file A character indicating the spreadsheet file. Default is to read the file as a comma-separated values (csv). If different, use the additional arguments, passed to `read.csv`, to parametrise file import.

ecol A numeric indicating the indices of the columns to be used as expression values. Can also be a character indicating the names of the columns. Caution must be taken of the column names are composed of special characters like '(' or '-' that will be converted to a '.'. If `ecol` does not match, the error message will display the column names are see by R.

fnames An optional character indicating the column to be used as feature names.

Value

An instance of the `MSnSet` class.

Author(s)

Laurent Gatto <lg390@cam.ac.uk>

See Also

The `grepEcols` and `getEcols` helper functions to identify the `ecol` values. The `MSnbase-io` vignette illustrates these functions in detail. It can accessed with `vignette("MSnbase-io")`.

Examples

```r
## 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

**Read an 'mzTab' file**

**Description**

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

**Usage**

\[
\text{readMzTabData}(\text{file}, \text{what} = \text{c("PRT", "PEP", "PSM")}, \text{version} = \text{c("1.0", "0.9")}, \text{verbose} = \text{TRUE})
\]

**Arguments**

- **file**: A character with the mzTab file to be read in.
- **what**: One of "PRT", "PEP" or "PSM", defining which of protein, peptide PSMs section should be returned as an MSnSet.
- **version**: A character defining the format specification version of the mzTab file. Default is "1.0". Version "0.9" is available of backwards compatibility. See `readMzTabData_v0.9` for details.
- **verbose**: Produce verbose output.

**Value**

An instance of class MSnSet.

**Author(s)**

Laurent Gatto

**See Also**

See MzTab and MSNSetList for details about the inners of readMzTabData.

**Examples**

```r
testfile <- "https://mztab.googlecode.com/svn/examples/PRIDE_Exp_Complete_Ac_16649.xml-mztab.txt"
prot <- readMzTabData(testfile, "PRT")
prot
head(fData(prot))
head(exprs(prot))
psms <- readMzTabData(testfile, "PSM")
psms
head(fData(psms))
```
readMzTabData_v0.9  

Read an 'mzTab' file

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_v0.9(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

testfile <- "http://mztab.googlecode.com/svn/legacy/jmztab-1.0/examples/mztab_itraq_example.txt"
prot <- readMzTabData_v0.9(testfile, "PRT")
prot
pep <- readMzTabData_v0.9(testfile, "PEP")
pep
removeNoId-methods

Removes non-identified features

Description

The method removes non-identified features in MSnExp and MSnSet instances using relevant information from the featureData slot of a user-provide filtering vector of logicals.

Methods

signature(object = "MSnExp", fcol = "pepseq", keep = NULL) Removes the feature from object that have a feature fcol (default is "pepseq") equal to NA. Alternatively, one can also manually define keep, a vector of logical, defining the feature to be retained.

signature(object = "MSnSet", fcol = "pepseq", keep = NULL) As above of MSnSet instances.

Author(s)

Laurent Gatto <lg390@cam.ac.uk>

See Also

MSnExp and MSnSet.

Examples

quantfile <- dir(system.file(package = "MSnbase", dir = "extdata"),
                 full.name = TRUE, pattern = "mzXML$")
identfile <- dir(system.file(package = "MSnbase", dir = "extdata"),
                 full.name = TRUE, pattern = "dummyITRAQ.mzid")
msexp <- readMSData(quantfile)
msexp <- addIdentificationData(msexp, identfile)
fData(msexp)$pepseq
length(msexp)

## using default fcol
msexp2 <- removeNoId(msexp)
length(msexp2)
fData(msexp2)$pepseq

## using keep
print(fvarLabels(msexp))
(k <- fData(msexp)$'ms-gf:evalue' > 75)
k[is.na(k)] <- FALSE
k
msexp3 <- removeNoId(msexp, keep = k)
length(msexp3)
fData(msexp3)$pepseq
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.

If the spectrum is in profile mode, ranges of successive non-0 peaks <= t are set to 0. If the spectrum is centroided, then individual peaks <= t are set to 0. See the example below for an illustration.

Note that the number of peaks is not changed; the peaks below the threshold are set to 0 and the object is not cleared 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(itraqdata2)) == 0)
table(unlist(intensity(itraqdata2)) == 0)
processingData(itraqdata2)

## difference between centroided and profile peaks

int <- c(104, 57, 32, 33, 118, 76, 38, 39, 52, 140, 52, 88, 394, 71, 408, 94, 2032)
sp <- new("Spectrum2",
    intensity = int,
    centroided = FALSE,
    mz = seq_len(length(int)))

## unchanged, as ranges of peaks <= 500 considered
intensity(removePeaks(sp, 500))

centroided(sp) <- TRUE
## different!
intensity(removePeaks(sp, 500))

---

**removeReporters-methods**

Removes reporter ion tag peaks

---

**Description**

This method 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

```r
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 an 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. Additional arguments are currently ignored.

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


See Also

TMT6 or iTRAQ4 for readily available examples.

Examples

```r
## 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]
```

smooth-methods

Smooths 'MSnExp' or 'Spectrum' instances

Description

This method smooths individual spectra (Spectrum instances) or whole experiments (MSnExp instances). Currently, the Savitzky-Golay-Smoothing (method = "SavitzkyGolay") and the Moving-Average-Smoothing (method = "MovingAverage") are available, as implemented in the MALDIquant::smoothIntensity function. Additional methods might be added at a later stage.

Methods

```r
signature(x = "MSnExp", method = "character", halfWindowSize = "integer", verbose = "logical", ...)
Smooths all spectra in MSnExp. method could be "SavitzkyGolay" or "MovingAverage". \code{halfWindowSize} controls the window size of the filter. The resulting window size is \code{2 * halfWindowSize + 1}. The best size differs depending on the selected \code{method}.
```
should be lower than \textit{fwhm} of the peaks at half maximum; please find details in Bromba and Ziegler.

The arguments \code{...} are passed to the internal functions. Currently the only supported argument is \code{polynomialorder}
(default: 3) for \code{method="SavitzkyGolay} to control the polynomial order of the Savitzky-Golay Filter. This method displays a progress bar if \code{verbose = TRUE}. Returns an \texttt{MSnExp} instance with smoothed spectra.

\begin{verbatim}
signature(x = "Spectrum", method = "character", halfWindowSize = "integer", ...)  
Smoothes the spectrum (\texttt{Spectrum} instance). This method is the same as above but returns a smoothed \texttt{Spectrum} instead of an \texttt{MSnExp} object. It has no \code{verbose} argument. Please read the details for the above \texttt{MSnExp} method.
\end{verbatim}

Author(s)

Sebastian Gibb <mail@sebastiangibb.de>

References


See Also

clean, pickPeaks, removePeaks and trimMz for other spectra processing methods.

Examples

\begin{verbatim}
sp1 <- new("Spectrum1",  
        intensity = c(1:6, 5:1),  
        mz = 1:11)
sp2 <- smooth(sp1, method = "MovingAverage", halfWindowSize = 2)
intensity(sp2)

data(itraqdata)
itraqdata2 <- smooth(itraqdata,  
        method = "MovingAverage",  
        halfWindowSize = 2)
processingData(itraqdata2)
\end{verbatim}

Spectrum-class

\begin{verbatim}
The "Spectrum" Class
\end{verbatim}

Description

Virtual container for spectrum data common to all different types of spectra. A Spectrum object can not be directly instanciated. Use "Spectrum1" and "Spectrum2" instead.
Spectrum-class

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') of 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.

scanIndex(object) Returns the scan index 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.

mzLevel(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. Additional arguments are currently ignored.

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. Additional arguments are currently ignored.
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. Additional arguments are currently ignored.

bin signature(object = "Spectrum"): Bins Spectrum. See bin documentation for more details and examples.

clean signature(object = "Spectrum"): Removes unused 0 intensity data points. See clean documentation for more details and examples.

compareSpectra signature(object1 = "Spectrum", object2 = "Spectrum"): Compares spectra. See compareSpectra documentation for more details and examples.

pickPeaks signature(object = "Spectrum"): Performs the peak picking to generate a centroided spectrum. See pickPeaks documentation for more details and examples.

plot signature(x = "Spectrum", y = "missing"): Plots intensity against mz. See plot.Spectrum documentation for more details.

plot signature(x = "Spectrum", y = "Spectrum"): Plots two spectra above/below each other. See plot.Spectrum.Spectrum documentation for more details.

plot signature(x = "Spectrum", y = "character"): Plots an MS2 level spectrum and its highlight the fragmentation peaks. See plot.Spectrum.character 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 that a threshold t. See removePeaks documentation for more details and examples.

smooth signature(x = "Spectrum"): Smooths spectrum. See smooth 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.

isEmpty signature(x = "Spectrum"): Checks if the x is an empty Spectrum.

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 instanciated directly.

Author(s)
Laurent Gatto <lg390@cam.ac.uk>

See Also
Instaciable sub-classes "Spectrum1" and "Spectrum2" for MS1 and MS2 spectra.
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 if 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 ion (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


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. Accessed with the precScanNum or precAcquisitionNum methods.

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

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 an 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.
precAcquisitionNum: Returns the precursor's acquisition number.
precScanNum: See precAcquisitionNum.
calculateFragments signature(sequence = "character", object = "Spectrum2"): Calculates and matches the theoretical fragments of a peptide sequence with the ones observed in a spectrum. See calculateFragments 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.

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. The TMT10 instance corresponds to the 10-plex version.

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
TMT10
References


See Also

iTRAQ4.

Examples

TMT6
TMT6[1:2]

TMT10

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>
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` 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

```r
## 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=1e-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 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

```r
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


### See Also

Functions to generate metadata (`makeMTD`), peptide data (`makePEP`) and proteins (`makePRT`), `readMzTabData` to create "MsnSet" instances from an mzTab file.

### Examples

```r
mzTabFile <- tempfile()
data(msnset)
pep <- msnset
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,
```
xic-methods  

**Extracted ion chromatograms**

### Description

These methods produce an extracted ion chromatogram given mass-spectrometry data and an ion to be extracted. In addition to the object (see 'Methods' section below), additional arguments are

- **mz** A numeric specifying the ion mass to be extracted.
- **width** The M/Z extraction width. Default is 0.5.
- **rtlim** The retention time limit to be displayed. When missing (default), the complete range of the matching extracted ions is plotted.
- **npeaks** The number of peaks to be annotated. Default is 3.
- **charge** The charge of the ion to be extracted. This value is optional; when provided, the mass of the ion (mz above) will first be divided by its charge before extraction.
- **clean** A logical, defining if the XIC data should be cleaned before plotting. Default is TRUE. See `clean` for details.
- **legend** A logical defining if the figure should be annotated.
- **plot** A logical defining if the plot should be rendered.
- **points** A logical specifying if points should be added to for each individual MS spectrum. Annotated peaks are coloured in orange and MS2 spectra with precursor M/Z matching the extracted ion are highlighted in red.

- **hd** The header data.frame corresponding to the object input. `hd` is generated automatically and can generally be omitted.

... Additional arguments passed to the `plot` function.

Note: the methods are currently not vectorised.

xcms::plotEIC provides a similar functionality.

### Value

The methods invisibly return the data.frame with the XIC intensities (column `int`), retention times (column `rt`) and extracted M/Z values (column `mz`) used to generate the figure.

### Methods

- `signature(object = "character")` Plots the XIC for the mass-spectrometry data stored in the object file. The file format must be support by mzR. See `mzR::openMSfile` for details.

- `signature(object = "mzRramp")` Plots the XIC for the mzRramp instance. See the mzR package for details.
Examples

```r
## Not run:
library("RforProteomics")
(f <- getPX0000001mzXML())
ms <- openMSfile(f)
x <- xic(ms, mz = 636.925, width = 0.01)
head(x)
xic(ms, mz = 636.925, width = 0.01,
    npeaks = 1,
    rtlim = c(2000, 2300))

## End(Not run)
```
Index

*Topic chron
  formatRt, 25
*Topic classes
  FeatComp-class, 19
  FeaturesOfInterest-class, 21
  MIAPe-class, 43
  MSMap-class, 47
  MSExp-class, 49
  MSProcess-class, 52
  MSNSet-class, 53
  MSNSetList-class, 58
  MZTab-class, 60
  NAnnotatedDataFrame-class, 62
  pSet-class, 76
  Reporterions-class, 97
  Spectrum-class, 100
  Spectrum1-class, 103
  Spectrum2-class, 104
*Topic datasets
  itRAQ4, 34
  itraqdata, 35
  TMT6, 105
*Topic documentation, internal
  missing-data, 46
*Topic file
  readIspyData, 85
  readMgfData, 87
  readMSData, 88
  readMSnSet, 89
  writeMgfData-methods, 107
*Topic manip
  readIspyData, 85
  readMSData, 88
  readMSnSet, 89
*Topic methods
  addIdentificationData-methods, 4
  bin-methods, 7
  calculateFragments-methods, 8
  chromatogram-methods, 10
  clean-methods, 11
  compareSpectra-methods, 16
  exprsToRatios-methods, 18
  extractPrecSpectra-methods, 18
  impute-methods, 29
  normalise-methods, 64
  pickPeaks-methods, 67
  plot-methods, 68
  plot.Spectrum.Spectrum-methods, 69
  plot2d-methods, 71
  plotDensity-methods, 72
  plotMzDelta-methods, 73
  plotNA-methods, 74
  purityCorrect-methods, 79
  quantify-methods, 82
  removeNoId-methods, 94
  removePeaks-methods, 95
  removeReporters-methods, 96
  smooth-methods, 99
  trimMz-methods, 106
  writeMgfData-methods, 107
  xic-methods, 110
*Topic package
  MSnbase-package, 3
*Topic utilities
  formatRt, 25
  [,MSnSet,ANY,ANY,ANY-method
   (MSnSet-class), 53
  [,MSnSet,ANY,ANY-method (MSnSet-class),
   53
  [,MSnSet-method (MSnSet-class), 53
  [,MSnSetList,ANY,ANY,ANY-method
   (MSnSetList-class), 58
  [,MSnSetList,ANY,missing,missing-method
   (MSnSetList-class), 58
  [,Reporterions,ANY,ANY,ANY-method
   (Reporterions-class), 97
  [,Reporterions,ANY,ANY-method
   (Reporterions-class), 97

112
INDEX
113

addIdentificationData, MSnSet, mzIDCollection-method (MSnSet-class), 53
addIdentificationData-methods, 4
analyser, MIAPE-method (MIAPE-class), 43
analyser, MSnSet-method (MSnSet-class), 53
analyser, pSet-method (pSet-class), 76
analyserDetails, MIAPE-method (MIAPE-class), 43
analyserDetails, pSet-method (pSet-class), 76
analyserDetails, pSet-method (pSet-class), 76
analyserDetails, pSet-method (pSet-class), 76
as.data.frame, as.matrix, MIAPE-method (MIAPE-class), 43
as.data.frame, ExpressionSet (ExpressionSet-class), 53
as.matrix, FoICollection (FeaturesOfInterest-class), 21
as.matrix, FoICollection (FeaturesOfInterest-class), 21
AssayData, 53
assayData, pSet-method (pSet-class), 76
averageMSnSet, 6, 20
averageMSnSet, bin, 16, 17, 50, 102
averageMSnSet, bin (bin-methods), 7
averageMSnSet, bin (bin-methods), 7
calculateFragments, 69, 70, 105
filterNA, 75
filterNA (MSnSet-class), 53
filterNA, matrix-method (MSnSet-class), 53
filterNA, MSnSet-method (MSnSet-class), 53
filterZero (MSnSet-class), 53
filterZero, matrix-method (MSnSet-class), 53
filterZero, MSnSet-method (MSnSet-class), 53
fnamesIn (FeaturesOfInterest-class), 21
fnamesIn, FeaturesOfInterest, data.frame-method (FeaturesOfInterest-class), 21
fnamesIn, FeaturesOfInterest, matrix-method (FeaturesOfInterest-class), 21
fnamesIn, FeaturesOfInterest, MSnSet-method (FeaturesOfInterest-class), 21
fnamesIn-methods (FeaturesOfInterest-class), 21
foi (FeaturesOfInterest-class), 21
foi, FeaturesOfInterest-method (FeaturesOfInterest-class), 21
foi, FoICollection-method (FeaturesOfInterest-class), 21
foi-methods (FeaturesOfInterest-class), 21
FoICollection (FeaturesOfInterest-class), 21
FoICollection, list-method (FeaturesOfInterest-class), 21
FoICollection, missing-method (FeaturesOfInterest-class), 21
FoICollection-class (FeaturesOfInterest-class), 21
FoICollection-methods (FeaturesOfInterest-class), 21
formatR, 25
fromFile (Spectrum-class), 100
fromFile, pSet-method (pSet-class), 76
fromFile, Spectrum-method (Spectrum-class), 100
fvarLabels, pSet-method (pSet-class), 76
fvarMetadata, pSet-method (pSet-class), 76
geom_histogram, 73
get.amino.acids, 25
get.atomic.mass, 26
getCode, 91
getCode (grepEcols), 27
getCode, exprsToRatios-methods, 18
getCode, variableName, 27
getCode, grep, 28
getCode, grepEcols, 27, 91
header (pSet-class), 76
header, pSet, missing-method (pSet-class), 76
header, pSet, numeric-method (pSet-class), 76
hist, 7
idSummary (MSnSet-class), 53
idSummary, MSnExp-method (MSnExp-class), 49
idSummary, MSnSet-method (MSnSet-class), 53
image, 29
image, MSnSet-method (MSnSet-class), 53
image2 (MSnSet-class), 53
imageNA2, 28, 46
imp.norm, 30
impute, 55
impute (impute-methods), 29
impute, MSnSet-method (impute-methods), 29
impute-methods, 29
impute, knn, 30
impute, MinDet, 30
impute, MinProb, 31
impute, QRILC, 30
imputeMethods (impute-methods), 29
instrumentCustomisations (MIAPE-class), 43
instrumentCustomisations, MIAPE-method (MIAPE-class), 43
instrumentCustomisations, pSet-method (pSet-class), 76
instrumentManufacturer (MIAPE-class), 43
instrumentManufacturer, MIAPE-method (MIAPE-class), 43
instrumentManufacturer, pSet-method (pSet-class), 76
instrumentModel (MIAPE-class), 43
instrumentModel, MIAPE-method (MIAPER-class), 43
INDEX

instrumentModel, pSet-method (pSet-class), 76
intensity(Spectrum-class), 100
intensity, pSet-method (pSet-class), 76
intensity, Spectrum-method (Spectrum-class), 100
ionCount(Spectrum-class), 100
ionCount, pSet-method (pSet-class), 76
ionCount, Spectrum-method (Spectrum-class), 100
ionSource (MIAPE-class), 43
ionSource, MIAPE-method (MIAPE-class), 43
ionSource, MSnSet-method (MSnSet-class), 53
ionSource, pSet-method (pSet-class), 76
ionSourceDetails (MIAPE-class), 43
ionSourceDetails, MIAPE-method (MIAPE-class), 43
ionSourceDetails, pSet-method (pSet-class), 76
iPQF, 13, 32, 33
is.na, MSnSet, 55
is.na, MSnSet (plotNA-methods), 74
isEmpty, Spectrum-method (Spectrum-class), 100
iTraq4, 34, 99, 106
iTraq5 (iTraq4), 34
iTraq8 (iTraq4), 34
iTraq9 (iTraq4), 34
itraqdata, 35

lapply, MSnSetList-method (MSnSetList-class), 58
length (pSet-class), 76
length, FeaturesOfInterest-method (FeaturesOfInterest-class), 21
length, FoICollection-method (FeaturesOfInterest-class), 21
length, MSnSetList-method (MSnSetList-class), 58
length, pSet-method (pSet-class), 76
length, ReporterIons-method (ReporterIons-class), 97
length-method (ReporterIons-class), 97
lengths, FoICollection-method (FeaturesOfInterest-class), 21
listOf, 35
log, MSnSet-method (MSnSet-class), 53

ma_plot, 56
mad, 65
makeImpuritiesMatrix (purityCorrect-methods), 79
makeMTD, 36, 41, 43, 109
makePEP, 38, 39, 43, 109
makePRT, 38, 41, 41, 109
MAplot, MSnSet-method (MSnSet-class), 53
meanSdPlot, 55
meanSdPlot, MSnSet-method (MSnSet-class), 53
metadata, MzTab-method (MzTab-class), 60
MIAME, 45
MIAME, 3, 50, 54, 55, 77, 79
MIAPE (MIAPE-class), 43
MIAPE-class, 43
MIAxE, 45
missing-data, 46
missingdata (missing-data), 46
ms2df (MSnSet-class), 53
msInfo (MIAPE-class), 43
msInfo, MIAPE-method (MIAPE-class), 43
msInfo, MSnSet-method (MSnSet-class), 53
msInfo, pSet-method (pSet-class), 76
msLevel (Spectrum-class), 100
msLevel, MSmap-method (MSmap-class), 47
msLevel, pSet-method (pSet-class), 76
msLevel, Spectrum-method (Spectrum-class), 100
MSmap (MSmap-class), 47
msMap (MSmap-class), 47
msMap, MSmap-method (MSmap-class), 47
MSmap-class, 47
MSnbase (MSnbase-package), 3
MSnbase-package, 3
MSnExp. 3–5, 18, 53, 64, 68, 71, 72, 76, 79, 82, 83, 87–89, 94, 96, 97, 101, 103–105, 107
MSnExp (MSnExp-class), 49
MSnExp-class, 49
MSnProcess (MSnProcess-class), 52
MSnProcess-class, 52
MSnSet. 3–5, 12, 13, 15, 16, 18, 20, 21, 31, 36, 37, 39, 41, 53, 58, 64, 66, 80, 83–86, 89, 91–94, 101, 109
MSnSet (MSnSet-class), 53
msnset (itraqdata), 35
INDEX

MSnSet-class, 53
msnset2(itraqdata), 35
MSnSetList, 60, 92
MSnSetList(MSnSetList-class), 58
MSnSet-class, 58
msnsets(MSnSetList-class), 58
multiLabels
  (NAnnotatedDataFrame-class), 62
multiLabels, NAnnotatedDataFrame-method
  (NAnnotatedDataFrame-class), 62
multiplex (NAnnotatedDataFrame-class), 62
multiplex, NAnnotatedDataFrame-method
  (NAnnotatedDataFrame-class), 62
mva.pairs, 56
mz (Spectrum-class), 100
mz, MSmap-method (MSmap-class), 47
mz, pSet-method (pSet-class), 76
mz, ReporterIons-method
  (ReporterIons-class), 97
mz, Spectrum-method (Spectrum-class), 100
mzRes (MSmap-class), 47
mzRes, MSmap-method (MSmap-class), 47
MzTab, 59, 92
MzTab (MzTab-class), 60
MzTab-class, 60
mzTabMode (MzTab-class), 60
mzTabType (MzTab-class), 60

names, FeatComp-method (FeatComp-class), 19
names, MSnSetList-method
  (MSnSetList-class), 58
names, ReporterIons-method
  (ReporterIons-class), 97
NAnnotatedDataFrame, 87, 88
NAnnotatedDataFrame
  (NAnnotatedDataFrame-class), 62
NAnnotatedDataFrame-class, 62
nasset (impute-methods), 29
ncol, MSmap-method (MSmap-class), 47
normalise, 21, 54
normalise (normalise-methods), 64
normalise, MSnExp-method
  (normalise-methods), 64
normalise, MSnSet-method
  (normalise-methods), 64
normalise, Spectrum-method
  (normalise-methods), 64
normalise, Spectrum2-method
  (normalise-methods), 64
normalise-methods, 64
normalize(normalise-methods), 64
normalize, MSnExp-method
  (normalise-methods), 64
normalize, MSnSet-method
  (normalise-methods), 64
normalize, Spectrum-method
  (normalise-methods), 64
normalize, Spectrum2-method
  (normalise-methods), 64
normalize-methods (normalise-methods), 64
normalize-methods, 64
normalize, quantiles, 64
normalize, quantiles.robust, 64
notes, MIAPE-method (MIAPE-class), 43
notes, pSet-method (pSet-class), 76
notes<, MIAPE-method (MIAPE-class), 43
npcv, 6, 65
nQuants, 55, 66
nrow, MSmap-method (MSmap-class), 47
objlog (MSnSetList-class), 58
otherInfo, MIAPE-method (MIAPE-class), 43
pca, 30
pData, pSet-method (pSet-class), 76
peaksCount (Spectrum-class), 100
peaksCount, pSet, missing-method
  (pSet-class), 76
peaksCount, pSet, numeric-method
  (pSet-class), 76
peaksCount, Spectrum, missing-method
  (Spectrum-class), 100
peptides, MzTab-method (MzTab-class), 60
phenoData, 50, 53, 77
phenoData, pSet-method (pSet-class), 76
pickPeaks, 8, 17, 50, 100, 102
pickPeaks (pickPeaks-methods), 67
pickPeaks, MSnExp-method (MSnExp-class), 49
pickPeaks, Spectrum-method
  (Spectrum-class), 100
pickPeaks-methods, 67
plot (plot-methods), 68
plot, MSmap, missing-method
  (MSmap-class), 47
plot, MSnExp (MSnExp-class), 49
plot.MSnExp.missing-method (MSnExp-class), 49
plot,Spectrum.missing-method (plot-methods), 68
plot,Spectrum,Spectrum-method (plot.Spectrum-Spectrum-methods), 69
plot,Spectrum-method (plot-methods), 68
plot,Spectrum2.character-method (plot-methods), 68
plot-methods, 68
plot.default, 70
plot.MSnExp, 50
plot.MSnExp (plot-methods), 68
plot.Spectrum, 70, 102
plot.Spectrum (plot-methods), 68
plot.Spectrum.character, 102
plot.Spectrum.Spectrum, 69, 102
plot.Spectrum.Spectrum-methods, 69
plot2d, 50, 72, 74
plot2d (plot2d-methods), 71
plot2d, data.frame-method (plot2d-methods), 71
plot2d, MSnExp-method (plot2d-methods), 71
plot2d-methods, 71
plot3D (MSmap-class), 47
plot3D, MSmap-method (MSmap-class), 47
plotDensity, 51, 71, 72, 74
plotDensity (plotDensity-methods), 72
plotDensity, data.frame-method (plotDensity-methods), 72
plotDensity, MSnExp-method (plotDensity-methods), 72
plotDensity-methods, 72
plotMzDelta, 51, 71
plotMzDelta (plotMzDelta-methods), 73
plotMzDelta, MSnExp-method (plotMzDelta-methods), 73
plotMzDelta, mZRamp-method (plotMzDelta-methods), 73
plotMzDelta-methods, 73
plotNA, 46, 55, 56
plotNA (plotNA-methods), 74
plotNA, matrix-method (plotNA-methods), 74
plotNA, MSnSet-method (plotNA-methods), 74
plotNA-methods, 74
polarity (Spectrum1-class), 103
polarity, pSet-method (pSet-class), 76
polarity, Spectrum-method (Spectrum1-class), 103
precAcquisitionNum (Spectrum2-class), 104
precAcquisitionNum, pSet-method (pSet-class), 76
precAcquisitionNum, Spectrum-method (Spectrum2-class), 104
precScanNum (Spectrum2-class), 104
precScanNum, pSet-method (pSet-class), 76
precScanNum, Spectrum-method (Spectrum2-class), 104
precSelection, 75
precSelectionTable (precSelection), 75
precursorCharge (Spectrum2-class), 104
precursorCharge, pSet-method (pSet-class), 76
precursorCharge, Spectrum-method (Spectrum2-class), 104
precursorIntensity (Spectrum2-class), 104
precursorIntensity, pSet-method (pSet-class), 76
precursorIntensity, Spectrum-method (Spectrum2-class), 104
precursorMz, 73
precursorMz (Spectrum2-class), 104
precursorMz, pSet-method (pSet-class), 76
precursorMz, Spectrum-method (Spectrum2-class), 104
processingData (pSet-class), 76
processingData, MSnSet-method (MSnSet-class), 53
processingData, pSet-method (pSet-class), 76
proteins, MzTab-method (MzTab-class), 60
protocolData, 50, 54, 77
protocolData, pSet-method (pSet-class), 76
pSet, 49–51, 54, 77
pSet (pSet-class), 76
pSet-class, 76
psms, MzTab-method (MzTab-class), 60
pubMedIds, MIAPE-method (MIAPE-class), 43
pubMedIds, pSet-method (pSet-class), 76
pubMedIds<-, MIAPE-method (MIAPE-class), 43
purityCorrect, 54
purityCorrect (purityCorrect-methods), 79
purityCorrect, MSnSet, matrix-method (MSnSet-class), 53
purityCorrect, MSnSet-method (MSnSet-class), 53
purityCorrect-methods, 79
qual (MSnSet-class), 53
qual, MSnSet-method (MSnSet-class), 53
quantify, 34, 35, 51, 53, 57, 98, 102, 105
quantify (quantify-methods), 82
quantify, MSnExp, character-method (MSnExp-class), 49
quantify, MSnExp-method (MSnExp-class), 49
quantify, Spectrum, character-method (Spectrum-class), 100
quantify, Spectrum-method (Spectrum-class), 100
quantify-methods, 82
read.AnnotatedDataFrame, 90, 91
read.csv, 91
read.MIAME, 90
read.table, 90, 91
readExpressionSet, 89
readIspyData, 85
readLines, 28, 90
readMgfData, 87, 89, 108
readMSData, 49, 51, 86, 87, 88
readMSnSet, 89
readMSnSet2, 28
readMSnSet2 (readMSnSet), 89
readMzTabData, 92, 109
readMzTabData_v0.9, 92, 93
removeMultipleAssignment, 84
removeMultipleAssignment-method (MSnSet-class), 53
removeMultipleAssignment, MSnExp-method (MSnExp-class), 49
removeMultipleAssignment, MSnSet-method (MSnSet-class), 53
removeMultipleAssignment-method (MSnSet-class), 53
removeNoId, 51, 56
removeNoId (removeNoId-methods), 94
removeNoId, MSnExp-method (MSnExp-class), 49
removeNoId, MSnSet-method (MSnSet-class), 53
removeNoId-methods, 94
removePeaks, 8, 12, 17, 51, 52, 67, 89, 97, 100, 102, 107
removePeaks (removePeaks-methods), 95
removePeaks, MSnExp-method (MSnExp-class), 49
removePeaks, Spectrum-method (Spectrum-class), 100
removePeaks-methods, 95
removeReporters, 51, 105
removeReporters (removeReporters-methods), 96
removeReporters, MSnExp-method (MSnExp-class), 49
removeReporters, Spectrum-method (Spectrum-class), 104
removeReporters-methods, 96
reporterColors (ReporterIons-class), 97
reporterColors, ReporterIons-method (ReporterIons-class), 97
reporterColors-method (ReporterIons-class), 97
reporterColours (ReporterIons-class), 97
reporterColours, ReporterIons-method (ReporterIons-class), 97
reporterColours-method (ReporterIons-class), 97
reporterIons (ReporterIons-class), 97
reporterIons-class, 97
reporterNames (ReporterIons-class), 97
reporterNames, ReporterIons-method (ReporterIons-class), 97
reporterNames-method (ReporterIons-class), 97
reporterNames<-, ReporterIons, ANY-method (ReporterIons-class), 97
reporterNames<-, ReporterIons, character-method
trimMz-methods, 106
unique1 (FeatComp-class), 19
unique1,FeatComp-method
  (FeatComp-class), 19
unique1,methods (FeatComp-class), 19
unique2 (FeatComp-class), 19
unique2,FeatComp-method
  (FeatComp-class), 19
unique2,methods (FeatComp-class), 19
unsplit,MSnSetList,factor-method
  (MSnSetList-class), 58
updateFeatureNames (MSnSet-class), 53
updateFvarLabels (MSnSet-class), 53
updateSampleNames (MSnSet-class), 53
varLabels,pSet-method (pSet-class), 76
varMetadata,pSet-method (pSet-class), 76
Versioned, 22, 45, 50, 52, 54, 63, 77, 98, 101, 103
  104
VersionedBiobase, 50, 54, 77
Versions, 50, 54, 77
vsn2, 64
width (ReporterIons-class), 97
width,ReporterIons-method
  (ReporterIons-class), 97
width-method (ReporterIons-class), 97
write.exprs, 57
write.exprs (MSnSet-class), 53
write.exprs,MSnSet-method
  (MSnSet-class), 53
writeMgfData, 87
writeMgfData (writeMgfData-methods), 107
writeMgfData,MSnExp-method
  (writeMgfData-methods), 107
writeMgfData,Spectrum-method
  (writeMgfData-methods), 107
writeMgfData-methods, 107
writeMzTabData, 93, 108
xic (xic-methods), 110
xic,character-method (xic-methods), 110
xic,mzRramp-method (xic-methods), 110
xic-methods, 110