Package ‘xcms’

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Author Colin A. Smith <csmith@scripps.edu>,
    Ralf Tautenhahn <rtautenh@gmail.com>,
    Steffen Neumann <sneumann@ibp-halle.de>,
    Paul Benton <hpbenton@scripps.edu>,
    Christopher Conley <cjconley@ucdavis.edu>,
    Johannes Rainer <Johannes.Rainer@eurac.edu>
Maintainer Steffen Neumann <sneumann@ibp-halle.de>
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Description Framework for processing and visualization of chromatographically
    separated and single-spectra mass spectral data. Imports from AIA/ANDI NetCDF,
    mzXML, mzData and mzML files. Preprocesses data for high-throughput, untargeted
    analyte profiling.
License GPL (>= 2) + file LICENSE
URL http://metlin.scripps.edu/download/ and
    https://github.com/sneumann/xcms
VignetteBuilder knitr
BugReports https://github.com/sneumann/xcms/issues/new
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    ‘functions-utils.R’ ‘functions-xcmsEIC.R’
    ‘functions-xcmsFragments.R’ ‘functions-xcmsRaw.R’
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absent-methods

Determine which peaks are absent / present in a sample class

Description

Determine which peaks are absent / present in a sample class

Arguments

object : xcmsSet-class object
class : Name of a sample class from sampclass
minfrac : minimum fraction of samples necessary in the class to be absent/present

Details

Determine which peaks are absent / present in a sample class. The functions treat peaks that are only present because of fillPeaks correctly, i.e., does not count them as present.

Value

An logical vector with the same length as nrow(groups(object)).

Methods

object = "xcmsSet" absent(object, ...) present(object, ...)

See Also

group diffreport

AutoLockMass-methods

Automatic parameter for Lock mass fixing AutoLockMass ~

Description

AutoLockMass - This function decides where the lock mass scans are in the xcmsRaw object. This is done by using the scan time differences.

Arguments

object : An xcmsRaw-class object

Value

AutoLockMass A numeric vector of scan locations corresponding to lock Mass scans

Methods

object = "xcmsRaw" signature(object = "xcmsRaw")
c-methods

Author(s)

Paul Benton, <hpaul.benton08@imperial.ac.uk>

Examples

```r
## Not run: library(xcms)
library(faahKO) ## These files do not have this problem to correct for but just for an example
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xr<-xcmsRaw(cdffiles[1])
xr
##Lets assume that the lockmass starts at 1 and is every 100 scans
lockMass<-xcms:::makeacqNum(xr, freq=100, start=1)
##these are equalvent
lockmass2<-AutoLockMass(xr)
all((lockmass == lockmass2) == TRUE)
ob<-stitch(xr, lockMass)
## End(Not run)
```

c-methods

Combine xcmsSet objects

Description

Combines the samples and peaks from multiple xcmsSet objects into a single object. Group and retention time correction data are discarded. The profinfo list is set to be equal to the first object.

Arguments

- `xs1` xcmsSet object
- `...` xcmsSet objects

Value

A xcmsSet object.

Methods

- `xs1 = "xcmsRaw"` `c(xs1, ...)`

Author(s)

Colin A. Smith, <csmith@scripps.edu>

See Also

- `xcmsSet-class`
**calibrate-methods**

* Calibrate peaks for correcting unprecise m/z values

**Description**

Calibrate peaks of a xcmsSet via a set of known masses

**Arguments**

- **object**
  - a xcmsSet object with uncalibrated m/z

- **calibrants**
  - a vector or a list of vectors with reference m/z-values

- **method**
  - the used calibrating-method, see below

- **mzppm**
  - the relative error used for matching peaks in ppm (parts per million)

- **mzabs**
  - the absolute error used for matching peaks in Da

- **neighbours**
  - the number of neighbours from which the one with the highest intensity is used (instead of the nearest)

- **plotres**
  - can be set to TRUE if wanted a result-plot showing the found m/z with the distances and the regression

**Value**

- **object**
  - a xcmsSet with one or more samples

- **calibrants**
  - for each sample different calibrants can be used, if a list of m/z-vectors is given. The length of the list must be the same as the number of samples, alternatively a single vector of masses can be given which is used for all samples.

- **method**
  - "shift" for shifting each m/z, "linear" does a linear regression and adds a linear term to each m/z. "edgeshift" does a linear regression within the range of the m/z-calibrants and a shift outside.

**Methods**

```r
object = "xcmsSet"    calibrate(object, calibrants, method="linear", mzabs=0.0001, mzppm=5, neighbours=3, plotres=FALSE)
```

**See Also**

* xcmsSet-class
Description

Collecting Peaks into xcmsFragments from several MS-runs using xcmsSet and xcmsRaw.

Arguments

object (empty) xcmsFragments-class object
xs A xcmsSet-class object which contains picked ms1-peaks from several experiments
compMethod ("floor", "round", "none"): compare-method which is used to find the parent peak of a MSnpeak through comparing the MZ-values of the MS1peaks with the MSnParentPeaks.
sthresh, mzgap, uniq
these are the parameters for the getspec-peakpicker included in xcmsRaw.

Details

After running collect(xFragments,xSet) The peak table of the xcmsFragments includes the ms1Peaks from all experiments stored in a xcmsSet-object. Further it contains the relevant msN-peaks from the xcmsRaw-objects, which were created temporarily with the paths in xcmsSet.

Value

A matrix with columns:

peakID unique identifier of every peak
MSnParentPeakID PeakID of the parent peak of a msLevel>1 - peak, it is 0 if the peak is msLevel 1.
msLevel The msLevel of the peak.
rt retention time of the peak midpoint
mz the mz-Value of the peak
intensity the intensity of the peak
sample the number of the sample from the xcmsSet
GroupPeakMSn Used for grouped xcmsSet groups
CollisionEnergy The collision energy of the fragment

Methods

object = "xcmsFragments" collect(object, ...)
diffreport-methods

Create report of analyte differences

Description

Create a report showing the most significant differences between two sets of samples. Optionally create extracted ion chromatograms for the most significant differences.

Arguments

- **object**: the xcmsSet object
- **class1**: character vector with the first set of sample classes to be compared
- **class2**: character vector with the second set of sample classes to be compared
- **filebase**: base file name to save report. .tsv file and _eic will be appended to this name for the tabular report and EIC directory, respectively. if blank nothing will be saved
- **eicmax**: number of the most significantly different analytes to create EICs for
- **eicwidth**: width (in seconds) of EICs produced
- **sortpval**: logical indicating whether the reports should be sorted by p-value
- **classeic**: character vector with the sample classes to include in the EICs
- **value**: intensity values to be used for the diffreport. If value="into", integrated peak intensities are used. If value="maxo", maximum peak intensities are used. If value="intb", baseline corrected integrated peak intensities are used (only available if peak detection was done by findPeaks.centWave).
- **metlin**: mass uncertainty to use for generating link to Metlin metabolite database. the sign of the uncertainty indicates negative or positive mode data for M+H or M-H calculation. a value of FALSE or 0 removes the column
- **h**: Numeric variable for the height of the eic and boxplots that are printed out.
- **w**: Numeric variable for the width of the eic and boxplots print out made.
- **mzdec**: Number of decimal places of title m/z values in the eic plot.
- **...**: optional arguments to be passed to mt.teststat

Details

This method handles creation of summary reports with statistics about which analytes were most significantly different between two sets of samples. It computes Welch’s two-sample t-statistic for each analyte and ranks them by p-value. It returns a summary report that can optionally be written out to a tab-separated file.

Additionally, it does all the heavy lifting involved in creating superimposed extracted ion chromatograms for a given number of analytes. It does so by reading the raw data files associated with the samples of interest one at a time. As it does so, it prints the name of the sample it is currently reading. Depending on the number and size of the samples, this process can take a long time.

If a base file name is provided, the report (see Value section) will be saved to a tab separated file. If EICs are generated, they will be saved as 640x480 PNG files in a newly created subdirectory.
However this parameter can be changed with the commands arguments. The numbered file names correspond to the rows in the report.

Chromatographic traces in the EICs are colored and labeled by their sample class. Sample classes take their color from the current palette. The color a sample class is assigned is dependent its order in the xcmsSet object, not the order given in the class arguments. Thus levels(sampclass(object))[1] would use color palette()[1] and so on. In that way, sample classes maintain the same color across any number of different generated reports.

When there are multiple sample classes, xcms will produce boxplots of the different classes and will generate a single anova p-value statistic. Like the eic’s the plot number corresponds to the row number in the report.

Value

A data frame with the following columns:

- **fold**: mean fold change (always greater than 1, see tstat for which set of sample classes was higher)
- **tstat**: Welch’s two sample t-statistic, positive for analytes having greater intensity in class2, negative for analytes having greater intensity in class1
- **pvalue**: p-value of t-statistic
- **anova**: p-value of the anova statistic if there are multiple classes
- **mzmed**: median m/z of peaks in the group
- **mzmin**: minimum m/z of peaks in the group
- **mzmax**: maximum m/z of peaks in the group
- **rtmed**: median retention time of peaks in the group
- **rtmin**: minimum retention time of peaks in the group
- **rtmax**: maximum retention time of peaks in the group
- **npeaks**: number of peaks assigned to the group
- **Sample Classes**: number samples from each sample class represented in the group
- **metlin**: A URL to metlin for that mass
- **Sample Names**: integrated intensity value for every sample

Methods

```r
object = "xcmsSet" diffreport(object, class1 = levels(sampclass(object))[1], class2 = levels(sampclass(object))[2], filebase = ..., sortpval = TRUE, classeic = c(class1, class2), value = c("into", "maxo", "intb"), metlin = FALSE, h = 480, w = 640, mzdec = 2, ...)
```

See Also

`xcmsSet-class, mt.teststat, palette`
etg  

Empirically Transformed Gaussian function

Description

A general function for asymmetric chromatographic peaks.

Usage

etg(x, H, t1, tt, k1, kt, lambda1, lambdat, alpha, beta)

Arguments

- **x**: times to evaluate function at
- **H**: peak height
- **t1**: time of leading edge inflection point
- **tt**: time of trailing edge inflection point
- **k1**: leading edge parameter
- **kt**: trailing edge parameter
- **lambda1**: leading edge parameter
- **lambdat**: trailing edge parameter
- **alpha**: leading edge parameter
- **beta**: trailing edge parameter

Value

The function evaluated at times x.

Author(s)

Colin A. Smith, <csmith@scripps.edu>

References

Description

For each sample, identify peak groups where that sample is not represented. For each of those peak groups, integrate the signal in the region of that peak group and create a new peak.

Arguments

object the \texttt{xcmsSet} object
method the filling method

Details

After peak grouping, there will always be peak groups that do not include peaks from every sample. This method produces intensity values for those missing samples by integrating raw data in peak group region. According to the type of raw-data there are 2 different methods available. for filling gcms/lcms data the method "chrom" integrates raw-data in the chromatographic domain, whereas "MSW" is used for peaklists without retention-time information like those from direct-infusion spectra.

Value

A \texttt{xcmsSet} objects with filled in peak groups.

Methods

\texttt{object = "xcmsSet" fillPeaks(object, method="")}

See Also

\texttt{xcmsSet-class, getPeaks}
Arguments

object the xcmsSet object
nSlaves number of slaves/cores to be used for parallel peak filling. MPI is used if installed, otherwise the snow package is employed for multicore support. If none of the two packages is available it uses the parallel package for parallel processing on multiple CPUs of the current machine.
expand.mz Expansion factor for the m/z range used for integration.
expand.rt Expansion factor for the retention time range used for integration.

Details

After peak grouping, there will always be peak groups that do not include peaks from every sample. This method produces intensity values for those missing samples by integrating raw data in peak group region. In a given group, the start and ending retention time points for integration are defined by the median start and end points of the other detected peaks. The start and end m/z values are similarly determined. Intensities can be still be zero, which is a rather unusual intensity for a peak. This is the case if e.g. the raw data was thresholded, and the integration area contains no actual raw intensities, or if one sample is miscalibrated, such that the raw data points are (just) outside the integration area.

Importantly, if retention time correction data is available, the alignment information is used to more precisely integrate the proper region of the raw data. If the corrected retention time is beyond the end of the raw data, the value will be not-a-number (NaN).

Value

A xcmsSet objects with filled in peak groups (into and maxo).

Methods

object = "xcmsSet" fillPeaks.chrom(object, nSlaves=0,expand.mz=1,expand.rt=1)

See Also

xcmsSet-class, getPeaks fillPeaks

---

fillPeaks.MSW-methods Integrate areas of missing peaks in FTICR-MS data

Description

For each sample, identify peak groups where that sample is not represented. For each of those peak groups, integrate the signal in the region of that peak group and create a new peak.

Arguments

object the xcmsSet object
Details

After peak grouping, there will always be peak groups that do not include peaks from every sample. This method produces intensity values for those missing samples by integrating raw data in peak group region. In a given group, the start and ending m/z values for integration are defined by the median start and end points of the other detected peaks.

Value

A xcmsSet objects with filled in peak groups.

Methods

object = "xcmsSet" fillPeaks.MSW(object)

See Also

xcmsSet-class, getPeaks fillPeaks

findMZ

Find fragment ions in xcmsFragment objects

Description

This is a method to find a fragment mass with a ppm window in a xcmsFragment object

Usage

findMZ(object, find, ppmE=25, print=TRUE)

Arguments

object xcmsFragment object type
find The fragment ion to be found
ppmE the ppm error window for searching
print If we should print a nice little report

Details

The method simply searches for a given fragment ion in an xcmsFragment object type given a certain ppm error window

Value

A data frame with the following columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PrecursorMz</td>
<td>The precursor m/z of the fragment</td>
</tr>
<tr>
<td>MSnParentPeakID</td>
<td>An index ID of the location of the precursor peak in the xcmsFragment object</td>
</tr>
<tr>
<td>msLevel</td>
<td>The level of the found fragment ion</td>
</tr>
<tr>
<td>rt</td>
<td>the Retention time of the found ion</td>
</tr>
</tbody>
</table>
findneutral

mz the actual m/z of the found fragment ion

intensity The intensity of the fragment ion

sample Which sample the fragment ion came from

GroupPeakMSn an ID if the peaks were grouped by an xcmsSet grouping

CollisionEnergy The collision energy of the precursor scan

Author(s)

H. Paul Benton, <hpaul.beonton08@imperial.ac.uk>

References


See Also

findneutral,

Examples

## Not run:
library(msdata)
mzdatapath <- system.file("iontrap", package = "msdata")
mzdatafiles<list.files(mzdatapath, pattern = "extracted.mzData", recursive = TRUE, full.names = TRUE)
x <- xcmsSet(mzdatafiles, method = "MS1")
## takes only one file from the file set
xfrag <- xcmsFragments(x)
found<-findMZ(xfrag, 657.3433, 50)

## End(Not run)

findneutral Find neutral losses in xcmsFragment objects

Description

This is a method to find a neutral loss with a ppm window in a xcmsFragment object

Usage

findneutral(object, find, ppmE=25, print=TRUE)

Arguments

object xcmsFragment object type
find The neutral loss to be found
ppmE the ppm error window for searching
print If we should print a nice little report
findneutral

Details

The method searches for a given neutral loss in an xcmsFragment object type given a certain ppm error window. The neutral losses are generated between neighbouring ions. The resulting data frame shows the whole scan in which the neutral loss was found.

Value

A data frame with the following columns:

- **PrecursorMz**: The precursor m/z of the neutral losses
- **MSnParentPeakID**: An index ID of the location of the precursor peak in the xcmsFragment object
- **msLevel**: The level of the found fragment ion
- **rt**: The Retention time of the found ion
- **mz**: the actual m/z of the found fragment ion
- **intensity**: The intensity of the fragment ion
- **sample**: Which sample the fragment ion came from
- **GroupPeakMSn**: an ID if the peaks were grouped by an xcmsSet grouping
- **CollisionEnergy**: The collision energy of the precursor scan

Author(s)

H. Paul Benton, <hpbenton@scripps.edu>

References


See Also

findMZ.

Examples

```
## Not run:
library(msdata)
mzdatapath <- system.file("iontrap", package = "msdata")
mzdatafiles<-list.files(mzdatapath, pattern = "extracted.mzData", recursive = TRUE, full.names = TRUE)
x <- xcmsSet(mzdatafiles, method = "MS1")
## takes only one file from the file set
xfrag <- xcmsFragments(x)
found<-findneutral(xfrag, 58.1455, 50)
## End(Not run)
```
**Description**

A number of peak pickers exist in XCMS. `findPeaks` is the generic method.

**Arguments**

- `object` `xcmsRaw-class` object
- `method` Method to use for peak detection. See details.
- `...` Optional arguments to be passed along

**Details**

Different algorithms can be used by specifying them with the `method` argument. For example to use the matched filter approach described by Smith et al (2006) one would use: `findPeaks(object, method="matchedFilter")`. This is also the default.

Further arguments given by `...` are passed through to the function implementing the method.

A character vector of `nicknames` for the algorithms available is returned by `getOption("BioC")$xcms$findPeaks.methods`. If the nickname of a method is called "centWave", the help page for that specific method can be accessed with `?findPeaks.centWave`.

**Value**

A matrix with columns:

- `mz` weighted (by intensity) mean of peak m/z across scans
- `mzmin` m/z of minimum step
- `mzmax` m/z of maximum step
- `rt` retention time of peak midpoint
- `rtmin` leading edge of peak retention time
- `rtmax` trailing edge of peak retention time
- `into` integrated area of original (raw) peak
- `maxo` maximum intensity of original (raw) peak

and additional columns depending on the chosen method.

**Methods**

`object = "xcmsRaw"` `findPeaks(object, ...)`

**See Also**

`findPeaks.matchedFilter findPeaks.centWave findPeaks.addPredictedIsotopeFeatures findPeaks.centWaveWithPredictedIsotopeROIs xcmsRaw-class`
findPeaks.addPredictedIsotopeFeatures-methods

Feature detection based on predicted isotope features for high resolution LC/MS data

Description

Peak density and wavelet based feature detection aiming at isotope peaks for high resolution LC/MS data in centroid mode

Arguments

- **object**: xcmsSet object
- **ppm**: maximal tolerated m/z deviation in consecutive scans, in ppm (parts per million)
- **peakwidth**: Chromatographic peak width, given as range (min,max) in seconds
- **prefilter**: prefilter=c(k,I). Prefilter step for the first phase. Mass traces are only retained if they contain at least k peaks with intensity >= I.
- **mzCenterFun**: Function to calculate the m/z center of the feature: \( \text{wMean}\): intensity weighted mean of the feature m/z values, \( \text{mean}\): mean of the feature m/z values, \( \text{apex}\): use m/z value at peak apex, \( \text{wMeanApex}\): intensity weighted mean of the m/z value at peak apex and the m/z value left and right of it, \( \text{meanApex}\): mean of the m/z value at peak apex and the m/z value left and right of it.
- **integrate**: Integration method. If =1 peak limits are found through descent on the mexican hat filtered data, if =2 the descent is done on the real data. Method 2 is very accurate but prone to noise, while method 1 is more robust to noise but less exact.
- **mzdiff**: minimum difference in m/z for peaks with overlapping retention times, can be negative to allow overlap
- **fitgauss**: logical, if TRUE a Gaussian is fitted to each peak
- **scanrange**: scan range to process
- **noise**: optional argument which is useful for data that was centroided without any intensity threshold, centroids with intensity < noise are omitted from ROI detection
- **sleep**: number of seconds to pause between plotting peak finding cycles
- **verbose.columns**: logical, if TRUE additional peak meta data columns are returned
- **xcmsPeaks**: peak list picked using the centWave algorithm with parameter verbose.columns set to TRUE (columns scmin and scmax needed)
- **snthresh**: signal to noise ratio cutoff, definition see below.
- **maxcharge**: max. number of the isotope charge.
- **maxiso**: max. number of the isotope peaks to predict for each detected feature.
- **mzIntervalExtension**: logical, if TRUE predicted isotope ROIs (regions of interest) are extended in the m/z dimension to increase the detection of low intensity and hence noisy peaks.
Details

This algorithm is most suitable for high resolution LC/[TOF,OrbiTrap,FTICR]-MS data in centroid mode. In the first phase of the method isotope ROIs (regions of interest) in the LC/MS map are predicted. In the second phase these mass traces are further analysed. Continuous wavelet transform (CWT) is used to locate chromatographic peaks on different scales. The resulting peak list and the given peak list (xcmsPeaks) are merged and redundant peaks are removed.

Value

A matrix with columns:

- \(mz\) weighted (by intensity) mean of peak m/z across scans
- \(mz\text{min}\) m/z peak minimum
- \(mz\text{max}\) m/z peak maximum
- \(rt\) retention time of peak midpoint
- \(rt\text{min}\) leading edge of peak retention time
- \(rt\text{max}\) trailing edge of peak retention time
- \(\text{into}\) integrated peak intensity
- \(\text{intb}\) baseline corrected integrated peak intensity
- \(\text{maxo}\) maximum peak intensity
- \(\text{sn}\) Signal/Noise ratio, defined as \((\text{maxo} - \text{baseline})/\text{sd}\), where \(\text{maxo}\) is the maximum peak intensity, \(\text{baseline}\) the estimated baseline value and \(\text{sd}\) the standard deviation of local chromatographic noise.
- \(\text{egauss}\) RMSE of Gaussian fit
  
  if \(\text{verbose.columns}\) is TRUE additionally:

- \(\mu\) Gaussian parameter \(\mu\)
- \(\sigma\) Gaussian parameter \(\sigma\)
- \(h\) Gaussian parameter \(h\)
- \(f\) Region number of m/z ROI where the peak was localised
- \(\text{dppm}\) m/z deviation of mass trace across scans in ppm
- \(\text{scale}\) Scale on which the peak was localised
- \(\text{scpos}\) Peak position found by wavelet analysis
- \(\text{scmin}\) Left peak limit found by wavelet analysis (scan number)
- \(\text{scmax}\) Right peak limit found by wavelet analysis (scan number)

Methods

\(\text{object} = \text{"xcmsRaw"}\)  
\text{findPeaks.centWave}(\text{object}, \text{ppm}=25, \text{peakwidth}=c(20,50), \text{prefilter}=c(3,100))

Author(s)

Ralf Tautenhahn
findPeaks.centWave-methods

References

Ralf Tautenhahn, Christoph Böttcher, and Steffen Neumann "Highly sensitive feature detection for high resolution LC/MS" BMC Bioinformatics 2008, 9:504
Hendrik Treutler and Steffen Neumann. "Prediction, detection, and validation of isotope clusters in mass spectrometry data" Submitted to Metabolites 2016, Special Issue “Bioinformatics and Data Analysis”

See Also

findPeaks.centWave findPeaks-methods xcmsRaw-class

findPeaks.centWave-methods

Feature detection for high resolution LC/MS data

Description

Peak density and wavelet based feature detection for high resolution LC/MS data in centroid mode

Arguments

object xcmsSet object
ppm maximal tolerated m/z deviation in consecutive scans, in ppm (parts per million)
peakwidth Chromatographic peak width, given as range (min,max) in seconds
snthresh signal to noise ratio cutoff, definition see below.
prefilter prefilter=c(k,I). Prefilter step for the first phase. Mass traces are only retained if they contain at least k peaks with intensity >= I.
mzCenterFun Function to calculate the m/z center of the feature: wMean intensity weighted mean of the feature m/z values, mean mean of the feature m/z values, apex use m/z value at peak apex, wMeanApex3 intensity weighted mean of the m/z value at peak apex and the m/z value left and right of it, meanApex3 mean of the m/z value at peak apex and the m/z value left and right of it.
integrate Integration method. If =1 peak limits are found through descent on the mexican hat filtered data, if =2 the descent is done on the real data. Method 2 is very accurate but prone to noise, while method 1 is more robust to noise but less exact.
mzdiff minimum difference in m/z for peaks with overlapping retention times, can be negative to allow overlap
fitgauss logical, if TRUE a Gaussian is fitted to each peak
scanrange scan range to process
noise optional argument which is useful for data that was centroided without any intensity threshold, centroids with intensity < noise are omitted from ROI detection
sleep number of seconds to pause between plotting peak finding cycles
verbose.columns logical, if TRUE additional peak meta data columns are returned
findPeaks.centWave-methods

ROI.list

A optional list of ROIs that represents detected mass traces (ROIs). If this list is empty (default) then centWave detects the mass trace ROIs, otherwise this step is skipped and the supplied ROIs are used in the peak detection phase. Each ROI object in the list has the following slots: scmin start scan index, scmax end scan index, mzmin minimum m/z, mzmax maximum m/z, length number of scans, intensity summed intensity.

firstBaselineCheck

logical, if TRUE continuous data within ROI is checked to be above 1st baseline

roiScales

numeric, optional vector of scales for each ROI in ROI.list to be used for the centWave-wavelets

Details

This algorithm is most suitable for high resolution LC/[TOF,OrbiTrap,FTICR]-MS data in centroid mode. In the first phase of the method mass traces (characterised as regions with less than ppm m/z deviation in consecutive scans) in the LC/MS map are located. In the second phase these mass traces are further analysed. Continuous wavelet transform (CWT) is used to locate chromatographic peaks on different scales.

Value

A matrix with columns:

mz  weighted (by intensity) mean of peak m/z across scans
mzmin  m/z peak minimum
mzmax  m/z peak maximum
rt  retention time of peak midpoint
rtmin  leading edge of peak retention time
rtmax  trailing edge of peak retention time
into  integrated peak intensity
intb  baseline corrected integrated peak intensity
maxo  maximum peak intensity
sn  Signal/Noise ratio, defined as (maxo - baseline)/sd, where maxo is the maximum peak intensity, baseline the estimated baseline value and sd the standard deviation of local chromatographic noise.
e gauss  RMSE of Gaussian fit
mu  Gaussian parameter mu
sigma  Gaussian parameter sigma
h  Gaussian parameter h
f  Region number of m/z ROI where the peak was localised
dppm  m/z deviation of mass trace across scans in ppm
scale  Scale on which the peak was localised
scpos  Peak position found by wavelet analysis
scmin  Left peak limit found by wavelet analysis (scan number)
scmax  Right peak limit found by wavelet analysis (scan number)
Methods

\[
\text{object} = "\text{xcmsRaw}\"
\]

\[\text{findPeaks.centWave(object, ppm=25, peakwidth=c(20,50), snthresh=10, prefilter=c(3,100), mzCenterFun="wMean", integrate=1, scanrange=numeric(), noise=0, sleep=0, verbose.columns=FALSE, ROI.list=list()), firstBaselineCheck=TRUE, roiScales=NULL}\]

Author(s)

Ralf Tautenhahn

References

Ralf Tautenhahn, Christoph Böttcher, and Steffen Neumann "Highly sensitive feature detection for high resolution LC/MS" BMC Bioinformatics 2008, 9:504

See Also

\[\text{findPeaks-methods xcmsRaw-class}\]

Description

Peak density and wavelet based feature detection for high resolution LC/MS data in centroid mode with additional peak picking of isotope features on basis of isotope peak predictions

Arguments

- **object**: xcmsSet object
- **ppm**: maximal tolerated m/z deviation in consecutive scans, in ppm (parts per million)
- **peakwidth**: Chromatographic peak width, given as range (min,max) in seconds
- **snthresh**: signal to noise ratio cutoff, definition see below.
- **prefilter**: prefilter=c(k,I). Prefilter step for the first phase. Mass traces are only retained if they contain at least k peaks with intensity >= I.
- **mzCenterFun**: Function to calculate the m/z center of the feature: \(w\text{mean}\) intensity weighted mean of the feature m/z values, \(\text{mean}\) mean of the feature m/z values, apex use m/z value at peak apex, \(w\text{mean}3\) intensity weighted mean of the m/z value at peak apex and the m/z value left and right of it, \(\text{mean}3\) mean of the m/z value at peak apex and the m/z value left and right of it.
- **integrate**: Integration method. If =1 peak limits are found through descent on the mexican hat filtered data, if =2 the descent is done on the real data. Method 2 is very accurate but prone to noise, while method 1 is more robust to noise but less exact.
- **mzdif**: minimum difference in m/z for peaks with overlapping retention times, can be negative to allow overlap
- **fitgauss**: logical, if TRUE a Gaussian is fitted to each peak
- **scanrange**: scan range to process
noise  optional argument which is useful for data that was centroided without any intensity threshold, centroids with intensity < noise are omitted from ROI detection

sleep  number of seconds to pause between plotting peak finding cycles

verbose.columns  logical, if TRUE additional peak meta data columns are returned

ROI.list  A optional list of ROIs that represents detected mass traces (ROIs). If this list is empty (default) then centWave detects the mass trace ROIs, otherwise this step is skipped and the supplied ROIs are used in the peak detection phase. Each ROI object in the list has the following slots: start scan index, end scan index, m/z minimum m/z, m/z maximum m/z, length number of scans, intensity summed intensity.

firstBaselineCheck  logical, if TRUE continuous data within ROI is checked to be above 1st baseline

roiScales  numeric, optional vector of scales for each ROI in ROI.list to be used for the centWave-wavelets

snthreshIsoROIs  signal to noise ratio cutoff for predicted isotope ROIs, definition see below.

maxcharge  max. number of the isotope charge.

maxiso  max. number of the isotope peaks to predict for each detected feature.

mzIntervalExtension  logical, if TRUE predicted isotope ROIs (regions of interest) are extended in the m/z dimension to increase the detection of low intensity and hence noisy peaks.

Details

This algorithm is most suitable for high resolution LC/{TOF,OrbiTrap,FTICR}-MS data in centroid mode. The centWave algorithm is applied in two peak picking steps as follows. In the first peak picking step ROIs (regions of interest, characterised as regions with less than ppm m/z deviation in consecutive scans) in the LC/MS map are located and further analysed using continuous wavelet transform (CWT) for the localization of chromatographic peaks on different scales. In the second peak picking step isotope ROIs in the LC/MS map are predicted further analysed using continuous wavelet transform (CWT) for the localization of chromatographic peaks on different scales. The peak lists resulting from both peak picking steps are merged and redundant peaks are removed.

Value

A matrix with columns:

mz  weighted (by intensity) mean of peak m/z across scans
mzmin  m/z peak minimum
mzmax  m/z peak maximum
rt  retention time of peak midpoint
rtmin  leading edge of peak retention time
rtmax  trailing edge of peak retention time
into  integrated peak intensity
intb  baseline corrected integrated peak intensity
maxo  maximum peak intensity
### Description

Massifquant is a Kalman filter (KF) based feature detection for XC-MS data in centroid mode (currently in experimental stage). Optionally allows for calling the method "centWave" on features discovered by Massifquant to further refine the feature detection; to do so, supply any additional parameters specific to centWave (even more experimental). The method may be conveniently called through the `xcmsSet(...)` method.
Arguments

The following arguments are specific to Massifquant. Any additional arguments supplied must correspond as specified by the method findPeaks.centWave.

An xcmsRaw object.

**object**

Numeric: Suggested values: (0.1-3.0). This setting helps determine the Kalman Filter prediction margin of error. A real centroid belonging to a bona fide feature must fall within the KF prediction margin of error. Much like in the construction of a confidence interval, criticalVal loosely translates to be a multiplier of the standard error of the prediction reported by the Kalman Filter. If the features in the XC-MS sample have a small mass deviance in ppm error, a smaller critical value might be better and vice versa.

**consecMissedLimit**

Integer: Suggested values: (1,2,3). While a feature is in the process of being detected by a Kalman Filter, the Kalman Filter may not find a predicted centroid in every scan. After 1 or more consecutive failed predictions, this setting informs Massifquant when to stop a Kalman Filter from following a candidate feature.

**prefilter**

Numeric Vector: (Positive Integer, Positive Numeric): The first argument is only used if (withWave = 1); see centWave for details. The second argument specifies the minimum threshold for the maximum intensity of a feature that must be met.

**peakwidth**

Integer Vector: (Positive Integer, Positive Integer): Only the first argument is used for Massifquant, which specifies the minimum feature length in time scans. If centWave is used, then the second argument is the maximum feature length subject to being greater than the minimum feature length.

**ppm**

The minimum estimated parts per million mass resolution a feature must possess.

**unions**

Integer: set to 1 if apply t-test union on segmentation; set to 0 if no t-test to be applied on chromatographically continuous features sharing same m/z range. Explanation: With very few data points, sometimes a Kalman Filter stops tracking a feature prematurely. Another Kalman Filter is instantiated and begins following the rest of the signal. Because tracking is done backwards to forwards, this algorithmic defect leaves a real feature divided into two segments or more. With this option turned on, the program identifies segmented features and combines them (merges them) into one with a two sample t-test. The potential danger of this option is that some truly distinct features may be merged.

**withWave**

Integer: set to 1 if turned on; set to 0 if turned off. Allows the user to find features first with Massifquant and then filter those features with the second phase of centWave, which includes wavelet estimation.

**checkBack**

Integer: set to 1 if turned on; set to 0 if turned off. The convergence of a Kalman Filter to a feature’s precise m/z mapping is very fast, but sometimes it incorporates erroneous centroids as part of a feature (especially early on). The "scan-Back" option is an attempt to remove the occasional outlier that lies beyond the converged bounds of the Kalman Filter. The option does not directly affect identification of a feature because it is a postprocessing measure; it has not shown to be a extremely useful thus far and the default is set to being turned off.

Details

This algorithm’s performance has been tested rigorously on high resolution LC/OrbiTrap, TOF-MS data in centroid mode. Simultaneous kalman filters identify features and calculate their area.
under the curve. The default parameters are set to operate on a complex LC-MS Orbitrap sample. Users will find it useful to do some simple exploratory data analysis to find out where to set a minimum intensity, and identify how many scans an average feature spans. The "consecMissedLimit" parameter has yielded good performance on Orbitrap data when set to (2) and on TOF data it was found best to be at (1). This may change as the algorithm has yet to be tested on many samples. The "criticalValue" parameter is perhaps most difficult to dial in appropriately and visual inspection of peak identification is the best suggested tool for quick optimization. The "ppm" and "checkBack" parameters have shown less influence than the other parameters and exist to give users flexibility and better accuracy.

Value

If the method findPeaks.massifquant(...) is used, then a matrix is returned with rows corresponding to features, and properties of the features listed with the following column names. Otherwise, if centWave feature is used also (withWave = 1), or Massifquant is called through the xcmsSet(...) method, then their corresponding return values are used.

- **mz**: weighted m/z mean (weighted by intensity) of the feature
- **mzmin**: m/z lower boundary of the feature
- **mzmax**: m/z upper boundary of the feature
- **rtmin**: starting scan time of the feature
- **rtmax**: starting scan time of the feature
- **into**: the raw quantitation (area under the curve) of the feature.
- **area**: feature area that is not normalized by the scan rate.

Methods

```r
object = "xcmsRaw" findPeaks.massifquant(object, ppm=10, peakwidth=c(20,50), snthresh=10, prefilter=c(3,100), mzCenterFun="wMean", ... sleep=0, verbose.columns=FALSE, criticalValue = 1.125, consecMissedLimit = 2, unions = 1, checkBack = 0, withWave = 0)
```

Author(s)

Christopher Conley

References


See Also

`findPeaks-methods xcmsSet xcmsRaw xcmsRaw-class`

Examples

```r
library(faahKO)
library(xcms)
#load all the wild type and Knock out samples
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
# run the massifquant analysis
xset <- xcmsSet(cdffiles, method = "massifquant",
```
Find peaks in the chromatographic time domain of the profile matrix.

**Arguments**

- **object** (`xcmsRaw` object)
- **fwhm** full width at half maximum of matched filtration gaussian model peak. Only used to calculate the actual sigma, see below.
- **sigma** standard deviation (width) of matched filtration model peak
- **max** maximum number of peaks per extracted ion chromatogram
- **snthresh** signal to noise ratio cutoff
- **step** step size to use for profile generation
- **steps** number of steps to merge prior to filtration
- **mzdiff** minimum difference in m/z for peaks with overlapping retention times
- **index** return indicies instead of values for m/z and retention times
- **sleep** number of seconds to pause between plotting peak finding cycles
- **scanrange** scan range to process

**Details**

The method calculates the profile matrix (i.e. intensities in bins along the M/Z dimension) on the fly using one of the methods described on the `profBin` help page.

**Value**

A matrix with columns:

- **mz** weighted (by intensity) mean of peak m/z across scans
- **mzmin** m/z of minimum step
- **mzmax** m/z of maximum step
- **rt** retention time of peak midpoint
- **rtmin** leading edge of peak retention time
- **rtmax** trailing edge of peak retention time
- **into** integrated area of original (raw) peak
**findPeaks.MS1-methods**

intf  
integrated area of filtered peak  
maxo  
maximum intensity of original (raw) peak  
maxf  
maximum intensity of filtered peak  
i  
rank of peak identified in merged EIC (<= max)  

**Methods**

```r
findPeaks.matchedFilter(object, fwhm = 30, sigma = fwhm/2.3548, max = 5, snthresh = 10, step = 0.1, steps = 2, mzdiff = 0.8 - step*steps, index = FALSE, sleep = 0, scanrange = numeric())
```

**Author(s)**

Colin A. Smith, <csmith@scripps.edu>

**See Also**

- findPeaks-methods
- xcmsRaw-class

**Description**

Collecting Tandem MS or MS$^n$ Mass Spectrometry precursor peaks as annotated in XML raw file

**Arguments**

- object: xcmsRaw object

**Details**

Some mass spectrometers can acquire MS1 and MS2 (or MS$^n$ scans) quasi simultaneously, e.g. in data dependent tandem MS or DDIT mode.

Since xcmsFragments attaches all MS$^n$ peaks to MS1 peaks in xcmsSet, it is important that findPeaks and xcmsSet do not miss any MS1 precursor peak.

To be sure that all MS1 precursor peaks are in an xcmsSet, findPeaks.MS1 does not do an actual peak picking, but simply uses the annotation stored in mzXML, mzData or mzML raw files.

This relies on the following XML tags:

- **mzData**:
  ```xml
  <spectrum id="463"> <spectrumInstrument msLevel="2">
  <cvParam cvLabel="psi" accession="PSI:1000039" name="TimeInSeconds" value="92.7743"/>
  </spectrumInstrument> <precursor msLevel="1" spectrumRef="461">
  <cvParam cvLabel="psi" accession="PSI:1000040" name="MassToChargeRatio" value="462.091"/>
  <cvParam cvLabel="psi" accession="PSI:1000042" name="Intensity" value="366.674"/>
  </precursor> </spectrum>
  </spectrum>
  ```

- **mzXML**:  
  ```xml
  <scan num="17" msLevel="2" retentionTime="PT1.5224S"> <precursorMz precursorIntensity="125245">220.1828003</precursorMz>
  </scan>
  ```

Several mzXML and mzData converters are known to create incomplete files, either without intensities (they will be set to 0) or without the precursor retention time (then a reasonably close rt will be chosen. NYI).
Value
A matrix with columns:

- \( m_z, m_{z \text{min}}, m_{z \text{max}} \)
  annotated MS1 precursor selection mass
- \( r_t, r_{t \text{min}}, r_{t \text{max}} \)
  annotated MS1 precursor retention time
- \( \text{into, maxo, sn} \)
  annotated MS1 precursor intensity

Methods
```
object = \"xcmsRaw\" findPeaks.MS1(object)
```

Author(s)
Steffen Neumann, <sneumann@ipb-halle.de>

See Also
- `findPeaks-methods`
- `xcmsRaw-class`

---

Feature detection for single-spectrum non-chromatography MS data

Description
Processing Mass Spectrometry direct-injection spectrum by using wavelet based algorithm.

Arguments
- `object` xcmsSet object
- `snthresh` signal to noise ratio cutoff
- `scales` scales of CWT
- `nearbyPeak` Determine whether to include the nearby small peaks of major peaks. TRUE by default
- `sleep` number of seconds to pause between plotting peak finding cycles
- `verbose.columns` additional peak meta data columns are returned

Details
This is a wrapper around the peak picker in the bioconductor package MassSpecWavelet calling 'cwt', 'get.localMaximum.cwt', 'get.ridge', 'identify.majorPeaks' and tuneIn.peakInfo.
Value

A matrix with columns:

- **mz**: m/z value of the peak at the centroid position
- **mzmin**: m/z value at the start-point of the peak
- **mzmax**: m/z value at the end-point of the peak
- **rt**: always -1
- **rtmin**: always -1
- **rtmax**: always -1
- **into**: integrated area of original (raw) peak
- **maxo**: intensity of original (raw) peak at the centroid position
- **intf**: always NA
- **maxf**: maximum MSW-filter response of the peak
- **sn**: Signal/Noise ratio

Methods

```r
object = "xcmsRaw" findPeaks.MSW(object, snthresh=3, scales=seq(1,22,3), nearbyPeak=TRUE,
```

Author(s)

Steffen Neumann, Joachim kutzera, <sneumann|jkutzer@ipb-halle.de>

See Also

- `findPeaks-methods`  
- `xcmsRaw-class`  
- `peakDetectionCWT`

Description

Generate multiple extracted ion chromatograms for m/z values of interest. For `xcmsSet` objects, reread original raw data and apply precomputed retention time correction, if applicable.

Note that this method will always return profile, not raw data (with profile data being the binned data along M/Z). See details for further information.

Arguments

- **object**: the `xcmsRaw` or `xcmsSet` object
- **mzrange**: Either a two column matrix with minimum or maximum m/z or a matrix of any dimensions containing columns `mzmin` and `mzmax`. If not specified, the method for `xcmsRaw` returns the base peak chromatogram (BPC, i.e. the most intense signal for each RT across all m/z).

For `xcmsSet` objects the group data will be used if `mzrange` is not provided.
getPeaks-methods

rtrange A two column matrix the same size as mzrange with minimum and maximum retention times between which to return EIC data points. If not specified, the method returns the chromatogram for the full RT range. For xcmsSet objects, it may also be a single number specifying the time window around the peak to return EIC data points.

step step (bin) size to use for profile generation. Note that a value of step = 0 is not supported.

groupidx either character vector with names or integer vector with indices of peak groups for which to get EICs

sampleidx either character vector with names or integer vector with indices of samples for which to get EICs

rt "corrected" for using corrected retention times, or "raw" for using raw retention times

Details

In contrast to the rawEIC method, that extracts the actual raw values, this method extracts them from the object’s profile matrix (or if the provided step argument does not match the profStep of the object the profile matrix is calculated on the fly and the values returned).

Value

For xcmsSet and xcmsRaw objects, an xcmsEIC object.

Methods

object = "xcmsRaw" getEIC(object, mzrange, rtrange = NULL, step = 0.1)

object = "xcmsSet" getEIC(object, mzrange, rtrange = 200, groupidx, sampleidx = sampnames(object), rt = c("corrected", "raw"))

See Also

xcmsRaw-class, xcmsSet-class, xcmsEIC-class, rawEIC

getPeaks-methods Get peak intensities for specified regions

Description

Integrate extracted ion chromatograms in pre-defined defined regions. Return output similar to findPeaks.

Arguments

object the xcmsSet object

peakrange matrix or data frame with 4 columns: mzmin, mzmax, rtmin, rtmax (they must be in that order or named)

step step size to use for profile generation
Value

A matrix with columns:

- **i**: rank of peak identified in merged EIC (\(<= \max\)), always NA
- **mz**: weighted (by intensity) mean of peak m/z across scans
- **mzmin**: m/z of minimum step
- **mzmax**: m/z of maximum step
- **ret**: retention time of peak midpoint
- **retmin**: leading edge of peak retention time
- **retmax**: trailing edge of peak retention time
- **into**: integrated area of original (raw) peak
- **intf**: integrated area of filtered peak, always NA
- **maxo**: maximum intensity of original (raw) peak
- **maxf**: maximum intensity of filtered peak, always NA

Methods

- object = "xcmsRaw" getPeaks(object, peakrange, step = 0.1)

See Also

- xcmsRaw-class

---

Description

Return the data from a single mass scan using the numeric index of the scan as a reference.

Arguments

- **object**: the xcmsRaw object
- **scan**: integer index of scan. if negative, the index numbered from the end
- **mzrange**: limit data points returned to those between in the range, range(mzrange)

Value

A matrix with two columns:

- **mz**: m/z values
- **intensity**: intensity values

Methods

- object = "xcmsRaw" getScan(object, scan, mzrange = numeric()) getMsnScan(object, scan, mzrange = numeric())

See Also

- xcmsRaw-class, getSpec
getSpec-methods

Get average m/z and intensity values for multiple mass scans

Description

Return full-resolution averaged data from multiple mass scans.

Arguments

object the xcmsRaw object
...
arguments passed to profRange used to specify the spectral segments of interest for averaging

Details

Based on the mass points from the spectra selected, a master unique list of masses is generated. Every spectra is interpolated at those masses and then averaged.

Value

A matrix with two columns:

mz m/z values
intensity intensity values

Methods

object = "xcmsRaw" getSpec(object, ...)

See Also

xcmsRaw-class, profRange, getScan

getXcmsRaw-methods

Load the raw data for one or more files in the xcmsSet

Description

Reads the raw data applies eventual retention time corrections and waters Lock mass correction and returns it as an xcmsRaw object (or list of xcmsRaw objects) for one or more files of the xcmsSet object.

Arguments

object the xcmsSet object
sampleidx The index of the sample for which the raw data should be returned. Can be a single number or a numeric vector with the indices. Alternatively, the file name can be specified.
profmethod The profile method.
profstep The profile step.
rt Whether corrected or raw retention times should be returned.
...
Additional arguments submitted to the xcmsRaw function.
group-methods

Value
A single xcmsRaw object or a list of xcmsRaw objects.

Methods

object = "xcmsSet" getXcmsRaw(object, sampleidx=1, profmethod=profinfo(object)$method, profstep=...)

Author(s)
Johannes Rainer, <johannes.rainer@eurac.edu>

See Also
xcmsRaw-class.

description
A number of grouping (or alignment) methods exist in XCMS, group is the generic method.

Arguments

object xcmsSet-class object
method Method to use for grouping. See details.
... Optional arguments to be passed along

details
Different algorithms can be used by specifying them with the method argument. For example to use
the density-based approach described by Smith et al (2006) one would use: group(object, method="density").
This is also the default.
Further arguments given by ... are passed through to the function implementing the method.
A character vector of nicknames for the algorithms available is returned by getOption("BioC")$xcms$group.methods.
If the nickname of a method is called "mzClust", the help page for that specific method can be ac-
cessed with ?group.mzClust.

Value
An xcmsSet object with peak group assignments and statistics.

Methods

object = "xcmsSet" group(object, ...)

See Also
group.density group.mzClust group.nearest xcmsSet-class.
**group.density**  
*Group peaks from different samples together*

**Description**

Group peaks together across samples using overlapping m/z bins and calculation of smoothed peak distributions in chromatographic time.

**Arguments**

- **object**: the xcmsSet object
- **minfrac**: minimum fraction of samples necessary in at least one of the sample groups for it to be a valid group
- **minsamp**: minimum number of samples necessary in at least one of the sample groups for it to be a valid group
- **bw**: bandwidth (standard deviation or half width at half maximum) of gaussian smoothing kernel to apply to the peak density chromatogram
- **mzwid**: width of overlapping m/z slices to use for creating peak density chromatograms and grouping peaks across samples
- **max**: maximum number of groups to identify in a single m/z slice
- **sleep**: seconds to pause between plotting successive steps of the peak grouping algorithm. peaks are plotted as points showing relative intensity. identified groups are flanked by dotted vertical lines.

**Value**

An xcmsSet object with peak group assignments and statistics.

**Methods**

```r
object = "xcmsSet"  group(object, bw = 30, minfrac = 0.5, minsamp = 1, mzwid = 0.25, max = 50,

```

**See Also**

- `xcmsSet-class`
- `density`

---

**group.mzClust**  
*Group Peaks via High Resolution Alignment*

**Description**

Runs high resolution alignment on single spectra samples stored in a given xcmsSet.
group.nearest

**Arguments**

object: a `xcmsSet` with peaks
mzppm: the relative error used for clustering/grouping in ppm (parts per million)
mzabs: the absolute error used for clustering/grouping
minsamp: set the minimum number of samples in one bin
minfrac: set the minimum fraction of each class in one bin

**Value**

Returns a `xcmsSet` with slots `groups` and `groupindex` set.

**Methods**

```r
object = "xcmsSet"  # group(object, method="mzClust", mzppm = 20, mzabs = 0, minsamp = 1, minfrac=0)
```

**References**

Saira A. Kazmi, Samiran Ghosh, Dong-Guk Shin, Dennis W. Hill and David F. Grant

*Alignment of high resolution mass spectra: development of a heuristic approach for metabolomics.*


**See Also**

`xcmsSet-class`

**Examples**

```r
## Not run:
library(msdata)
mzdatapath <- system.file("fticr", package = "msdata")
mzdatafiles <- list.files(mzdatapath, recursive = TRUE, full.names = TRUE)
xs <- xcmsSet(method="MSW", files=mzdatafiles, scales=c(1,7), SNR.method='data.mean', winSize.noise=500, peakThr=80000, amp.Th=0.005)
xsg <- group(xs, method="mzClust")
## End(Not run)
```

---

**group.nearest**

*Group peaks from different samples together*

**Description**

Group peaks together across samples by creating a master peak list and assigning corresponding peaks from all samples. It is inspired by the alignment algorithm of mzMine. For further details check [http://mzmine.sourceforge.net/](http://mzmine.sourceforge.net/) and


Currently, there is no equivalent to `minfrac` or `minsamp`. 
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>the xcmsSet object</td>
</tr>
<tr>
<td>mzVsRTbalance</td>
<td>Multiplicator for mz value before calculating the (euclidean) distance between two peaks.</td>
</tr>
<tr>
<td>mzCheck</td>
<td>Maximum tolerated distance for mz.</td>
</tr>
<tr>
<td>rtCheck</td>
<td>Maximum tolerated distance for RT.</td>
</tr>
<tr>
<td>kNN</td>
<td>Number of nearest Neighbours to check</td>
</tr>
</tbody>
</table>

Value

An xcmsSet object with peak group assignments and statistics.

Methods

```r
object = "xcmsSet"
group(object, mzVsRTbalance=10, mzCheck=0.2, rtCheck=15, kNN=10)
```

See Also

xcmsSet-class, group.density and group.mzClust

Examples

```r
## Not run: library(xcms)
library(faahKO) ## These files do not have this problem to correct for but just for an example
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xset <- xcmsSet(cdffiles)
gxset <- group(xset, method="nearest")
# this is the same as
# gxset <- group.nearest(xset)
nrow(gxset@groups) == 1096 # the number of features before minFrac

post.minFrac <- function(object, minFrac=0.5){
  ix.minFrac <- sapply(1:length(unique(sampclass(object))), function(x, object, mf){
    meta <- groups(object)
    minFrac.idx <- numeric(length=nrow(meta))
    idx <- which(meta[,levels(sampclass(object))[x]] >= mf*length(which(levels(sampclass(object))[x] == sampclass(object))))
    minFrac.idx[idx]<-1
    return(minFrac.idx)
  }, object, minFrac)
  ix.minFrac <- as.logical(apply(ix.minFrac, 1, sum))
  ix <- which(ix.minFrac == TRUE)
  return(ix)
}

## using the above function we can get a post processing minFrac
ix <- post.minFrac(gxset)

gxset.post <- gxset # copy the xcmsSet object
gxset.post@groupidx <- gxset@groupidx[ix]
gxset.post@groups <- gxset@groups[ix,]
```
groupnames-methods

Generate unique names for peak groups

Description
Allow linking of peak group data between classes using unique group names that remain the same as long as no re-grouping occurs.

Arguments
- **object**: the `xcmsSet` or `xcmsEIC` object
- **mzdec**: number of decimal places to use for m/z
- **rtdec**: number of decimal places to use for retention time
- **template**: a character vector with existing group names whose format should be emulated

Value
A character vector with unique names for each peak group in the object. The format is `M[m/z]T[time in seconds]`.

Methods
- `object = "xcmsSet"` (object, mzdec = 0, rtdec = 0, template = NULL)
- `object = "xcmsEIC"` (object)

See Also
`xcmsSet-class, xcmsEIC-class`

groupval-methods

Extract a matrix of peak values for each group

Description
Generate a matrix of peak values with rows for every group and columns for every sample. The value included in the matrix can be any of the columns from the `xcmsSet` peaks slot matrix. Collisions where more than one peak from a single sample are in the same group get resolved with one of several user-selectable methods.

Arguments
- **object**: the `xcmsSet` object
- **method**: conflict resolution method, "medret" to use the peak closest to the median retention time or "maxint" to use the peak with the highest intensity
- **value**: name of peak column to enter into returned matrix, or "index" for index to the corresponding row in the peaks slot matrix
- **intensity**: if method == "maxint", name of peak column to use for intensity
Value

A matrix with rows for every group and columns for every sample. Missing peaks have NA values.

Methods

```r
object = "xcmsSet" groupval(object, method = c("medret", "maxint"), value = "index", intensity = "into")
```

See Also

- `xcmsSet-class`

---

### Descriptions

Plot log intensity image of a xcmsRaw object

Create log intensity false-color image of a xcmsRaw object plotted with m/z and retention time axes

**Arguments**

- `x` xcmsRaw object
- `col` vector of colors to use for the image
- `...` arguments for `profRange`

**Methods**

```r
x = "xcmsRaw" image(x, col = rainbow(256), ...)
```

**Author(s)**

Colin A. Smith, `<csmith@scripps.edu>`

**See Also**

- `xcmsRaw-class`
**levelplot-methods**

Plot log intensity image of a xcmsRaw object

**Description**

Create an image of the raw (profile) data m/z against retention time, with the intensity color coded.

**Arguments**

- `x`: xcmsRaw object.
- `log`: Whether the intensity should be log transformed.
- `col.regions`: The color ramp that should be used for encoding of the intensity.
- `rt`: Whether the original (rt="raw") or the corrected (rt="corrected") retention times should be used.
- `...`: Arguments for profRange.

**Methods**

- `x = "xcmsRaw"`  
  
  levelplot(x, log=TRUE, col.regions=colorRampPalette(brewer.pal(9, "YlOrRd"))(256), ...)  

- `x = "xcmsSet"`  
  
  levelplot(x, log=TRUE, col.regions=colorRampPalette(brewer.pal(9, "YlOrRd"))(256), rt="raw", ...)  

**Author(s)**

Johannes Rainer, <johannes.rainer@eurac.edu>

**See Also**

xcmsRaw-class, xcmsSet-class

**loadRaw-methods**

Read binary data from a source

**Description**

This function extracts the raw data which will be used an xcmsRaw object. Further processing of data is done in the xcmsRaw constructor.

**Arguments**

- `object`: Specification of a data source (such as a file name or database query)

**Details**

The implementing methods decide how to gather the data.
Value

A list containing elements describing the data source. The `rt`, `scanindex`, `tic`, and `acquisitionNum` components each have one entry per scan. They are "parallel" in the sense that `rt[1]`, `scanindex[1]`, and `acquisitionNum[1]` all refer to the same scan. The list contain the following components:

- **rt**: Numeric vector with acquisition time (in seconds) for each scan
- **tic**: Numeric vector with Total Ion Count for each scan
- **scanindex**: Integer vector with starting positions of each scan in the `mz` and `intensity` components. It is an exclusive offset, so `scanindex[i]` is the offset in `mz` and `intensity` before the beginning of scan `i`. This means that the `mz` (respectively `intensity`) values for scan `i` would be from `scanindex[i] + 1` to `scanindex[i + 1]`
- **mz**: Concatenated vector of m/z values for all scans
- **intensity**: Concatenated vector of intensity values for all scans

Methods

signature(object = "xcmsSource")

Uses `loadRaw, xcmsSource-method` to extract raw data. Subclasses of `xcmsSource` can provide different ways of fetching data.

Author(s)

Daniel Hackney, <dan@haxney.org>

See Also

`xcmsRaw-class, xcmsSource`

**medianFilter**

Apply a median filter to a matrix

Description

For each element in a matrix, replace it with the median of the values around it.

Usage

`medianFilter(x, mrad, nrad)`

Arguments

- **x**: numeric matrix to median filter
- **mrad**: number of rows on either side of the value to use for median calculation
- **nrad**: number of rows on either side of the value to use for median calculation

Value

A matrix whose values have been median filtered
Copy MSn data in an xcmsRaw to the MS slots

Description

The MS2 and MSn data is stored in separate slots, and cannot directly be used by e.g. findPeaks(). msn2xcmsRaw() will copy the MSn spectra into the "normal" xcmsRaw slots.

Usage

msn2xcmsRaw(xmsn)

Arguments

xmsn

an object of class xcmsRaw that contains spectra read with includeMSn=TRUE

Details

The default gap value is determined from the 90th percentile of the pair-wise differences between adjacent mass values.

Value

An xcmsRaw object

Author(s)

Steffen Neumann <sneumann@ipb-halle.de>

See Also

xcmsRaw.

Examples

msnfile <- system.file("MSMSpos20_6.mzML", package = "msdata")
xrmsn <- xcmsRaw(msnfile, includeMSn=TRUE)
xr <- msn2xcmsRaw(xrmsn)
p <- findPeaks(xr, method="centWave")
**peakPlots-methods**  
Plot a grid of a large number of peaks

**Description**
Plot extracted ion chromatograms for many peaks simultaneously, indicating peak integration start and end points with vertical grey lines.

**Arguments**
- **object**: the `xcmsRaw` object
- **peaks**: matrix with peak information as produced by `findPeaks`
- **figs**: two-element vector describing the number of rows and the number of columns of peaks to plot, if missing then an approximately square grid that will fit the number of peaks supplied
- **width**: width of chromatogram retention time to plot for each peak

**Details**
This function is intended to help graphically analyze the results of peak picking. It can help estimate the number of false positives and improper integration start and end points. Its output is very compact and tries to waste as little space as possible. Each plot is labeled with rounded m/z and retention time separated by a space.

**Methods**
```
signature(object = "xcmsSet") plotPeaks(object, peaks, figs, width = 200)
```

**See Also**
`xcmsRaw-class, findPeaks, split.screen`

---

**peakTable-methods**  
Create report of aligned peak intensities

**Description**
Create a report showing all aligned peaks.

**Arguments**
- **object**: the `xcmsSet` object
- **filebase**: base file name to save report. `.tsv` file and `_eic` will be appended to this name for the tabular report and EIC directory, respectively. If blank nothing will be saved
- **...**: arguments passed down to `groupval`, which provides the actual intensities.
This method handles creation of summary reports similar to `diffreport`. It returns a summary report that can optionally be written out to a tab-separated file.

If a base file name is provided, the report (see Value section) will be saved to a tab-separated file.

**Value**

A data frame with the following columns:

- **mz**: median m/z of peaks in the group
- **mzmin**: minimum m/z of peaks in the group
- **mzmax**: maximum m/z of peaks in the group
- **rt**: median retention time of peaks in the group
- **rtmin**: minimum retention time of peaks in the group
- **rtmax**: maximum retention time of peaks in the group
- **npeaks**: number of peaks assigned to the group

**Sample Classes**: number of samples from each sample class represented in the group

**Sample Names**: integrated intensity value for every sample

**Methods**

```r
object = "xcmsSet"  peakTable(object, filebase = character(), ...)
```

**Examples**

```r
## Not run:
library(faahKO)
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xs<-xcmsSet(cdf files)
xs<-group(xs)
peakTable(xs, filebase="peakList")
## End(Not run)
```
**plot.xcmsEIC**

Plot extracted ion chromatograms from multiple files

**Description**

Batch plot a list of extracted ion chromatograms to the current graphics device.

**Arguments**

- **x**
  the xcmsEIC object

- **y**
  optional xcmsSet object with peak integration data

- **groupid**
  either character vector with names or integer vector with indicies of peak groups for which to plot EICs

- **sampleidx**
  either character vector with names or integer vector with indicies of samples for which to plot EICs

- **rtrange**
  a two column matrix with minimum and maximum retention times between which to return EIC data points
  if it has the same number of rows as the number groups in the xcmsEIC object, then sampleidx is used to subset it. otherwise, it is repeated over the length of sampleidx
  it may also be a single number specifying the time window around the peak for which to plot EIC data

- **col**
  color to use for plotting extracted ion chromatograms. if missing and y is specified, colors are taken from unclass(sampclass(y)) and the default palette
  if it is the same length as the number groups in the xcmsEIC object, then sampleidx is used to subset it. otherwise, it is repeated over the length of sampleidx

- **legtext**
  text to use for legend. if NULL and y is specified, legend text is taken from the sample class information found in the xcmsSet

- **peakint**
  logical, plot integrated peak area with darkened lines (requires that y also be specified)

- **sleep**
  seconds to pause between plotting EICs

- **...**
  other graphical parameters

**Value**

A xcmsSet object.

**Methods**

```r
x = "xcmsEIC" plot.xcmsEIC(x, y, groupidx = groupnames(x), sampleidx = sampnames(x), rtrange = x@rtrange, col = rep(1, length(sampleidx)), legtext = NULL, peakint = TRUE, sleep = 0, ...)```

**Author(s)**

Colin A. Smith, <csmith@scripps.edu>

**See Also**

`xcmsEIC-class`, `png`, `pdf`, `postscript`,
plotChrom-methods

Plot extracted ion chromatograms from the profile matrix

Description

Uses the pre-generated profile mode matrix to plot averaged or base peak extracted ion chromatograms over a specified mass range.

Arguments

- **object**: the xcmsRaw object
- **base**: logical, plot a base-peak chromatogram
- **ident**: logical, use mouse to identify and label peaks
- **fitgauss**: logical, fit a gaussian to the largest peak
- **vline**: numeric vector with locations of vertical lines
- **...**: arguments passed to profRange

Value

If **ident** == TRUE, an integer vector with the indecies of the points that were identified. If **fitgauss** == TRUE, a nls model with the fitted gaussian. Otherwise a two-column matrix with the plotted points.

Methods

**object** = "xcmsRaw" plotChrom(object, base = FALSE, ident = FALSE, fitgauss = FALSE, 

See Also

xcmsRaw-class

plotEIC-methods

Plot extracted ion chromatograms for specified m/z range

Description

Plot extracted ion chromatogram for m/z values of interest. The raw data is used in contrast to plotChrom which uses data from the profile matrix.

Arguments

- **object**: xcmsRaw object
- **mzrange**: m/z range for EIC. Uses the full m/z range by default.
- **rtrange**: retention time range for EIC. Uses the full retention time range by default.
- **scanrange**: scan range for EIC
- **mzdec**: Number of decimal places of title m/z values in the eic plot.
- **type**: Specifics how the data should be plotted (by default as a line).
- **add**: If the EIC should be added to an existing plot.
- **...**: Additional parameters passed to the plotting function (e.g. col etc).
Value

A two-column matrix with the plotted points.

Methods

object = "xcmsRaw" plotEIC(object, mrange = numeric(), rrange = numeric(), scanrange = numeric())

Author(s)

Ralf Tautenhahn

See Also

rawEIC, xcmsRaw-class

plotPeaks-methods

Plot a grid of a large number of peaks

Description

Plot extracted ion chromatograms for many peaks simultaneously, indicating peak integration start and end points with vertical grey lines.

Arguments

object the xcmsRaw object
peaks matrix with peak information as produced by findPeaks
figs two-element vector describing the number of rows and the number of columns of peaks to plot, if missing then an approximately square grid that will fit the number of peaks supplied
width width of chromatogram retention time to plot for each peak

Details

This function is intended to help graphically analyze the results of peak picking. It can help estimate the number of false positives and improper integration start and end points. Its output is very compact and tries to waste as little space as possible. Each plot is labeled with rounded m/z and retention time separated by a space.

Methods

object = "xcmsRaw" plotPeaks(object, peaks, figs, width = 200)

See Also

xcmsRaw-class, findPeaks, split.screen
plotQC

Plot m/z and RT deviations for QC purposes without external reference data

Description

Use "democracy" to determine the average m/z and RT deviations for a grouped xcmsSet, and dependency on sample or absolute m/z

Usage

plotQC(object, sampNames, sampColors, sampOrder, what)

Arguments

object A grouped xcmsSet
sampNames Override sample names (e.g. with simplified names)
sampColors Provide a set of colors (default: monochrome ?)
sampOrder Override the order of samples, e.g. to bring them in order of measurement to detect time drift
what A vector of which QC plots to generate. "mzdevhist": histogram of m/z deviations. Should be gaussian shaped. If it is multimodal, then some peaks seem to have a systematically higher m/z deviation "rtdevhist": histogram of RT deviations. Should be gaussian shaped. If it is multimodal, then some peaks seem to have a systematically higher RT deviation "mzdevmass": Shows whether m/z deviations are absolute m/z dependent, could indicate miscalibration "mzdevtime": Shows whether m/z deviations are RT dependent, could indicate instrument drift "mzdevsample": median m/z deviation for each sample, indicates outliers "rtdevsample": median RT deviation for each sample, indicates outliers

Details

plotQC() is a wrapper to create a set of diagnostic plots. For the m/z deviations, the median of all m/z within one group are assumed.

Value

No return value

Author(s)

Michael Wenk, Michael Wenk <michael.wenk@student.uni-halle.de>

Examples

library(faahKO)
xsg <- group(faahko)

plotQC(xsg, what="mzdevhist")
plotQC(xsg, what="rtdevhist")
plotQC(xsg, what="mzdevmass")
plotQC(xsg, what="mzdevtime")
plotQC(xsg, what="mzdevsample")
plotQC(xsg, what="rtdevsample")

---

plotRaw-methods  Scatterplot of raw data points

Description

Produce a scatterplot showing raw data point location in retention time and m/z. This plot is more useful for centroided data than continuum data.

Arguments

- **object**: the xcmsRaw object
- **mzrange**: numeric vector of length >= 2 whose range will be used to select the masses to plot
- **rtrange**: numeric vector of length >= 2 whose range will be used to select the retention times to plot
- **scanrange**: numeric vector of length >= 2 whose range will be used to select scans to plot
- **log**: logical, log transform intensity
- **title**: main title of the plot

Value

A matrix with the points plotted.

Methods

**object** = "xcmsRaw" plotRaw(object, mzrange = numeric(), rtrange = numeric(), scanrange = numeric(), log=FALSE, title=)

See Also

xcmsRaw-class

---

plotrt-methods  Plot retention time deviation profiles

Description

Use corrected retention times for each sample to calculate retention time deviation profiles and plot each on the same graph.
**plotScan-methods**

**Arguments**
- **object** the xcmsSet object
- **col** vector of colors for plotting each sample
- **ty** vector of line and point types for plotting each sample
- **leg** logical plot legend with sample labels
- **densplit** logical, also plot peak overall peak density

**Methods**

```r
object = "xcmsSet" plotrt(object, col = NULL, ty = NULL, leg = TRUE, densplit = FALSE)
```

**See Also**
- `xcmsSet-class`, `retcor`

---

**plotScan-methods**

*Plot a single mass scan*

**Description**

Plot a single mass scan using the impulse representation. Most useful for centroided data.

**Arguments**
- **object** the xcmsRaw object
- **scan** integer with number of scan to plot
- **mzrange** numeric vector of length >= 2 whose range will be used to select masses to plot
- **ident** logical, use mouse to interactively identify and label individual masses

**Methods**

```r
object = "xcmsRaw" plotScan(object, scan, mzrange = numeric(), ident = FALSE)
```

**See Also**
- `xcmsRaw-class`
**plotSpec-methods**  
*Plot mass spectra from the profile matrix*

**Description**
Uses the pre-generated profile mode matrix to plot mass spectra over a specified retention time range.

**Arguments**
- `object`: the `xcmsRaw` object
- `ident`: logical, use mouse to identify and label peaks
- `vline`: numeric vector with locations of vertical lines
- `...`: arguments passed to `profRange`

**Value**
- If `ident == TRUE`, an integer vector with the indecies of the points that were identified. Otherwise a two-column matrix with the plotted points.

**Methods**
- `object = "xcmsRaw"` plotSpec(object, ident = FALSE, vline = numeric(0), ...)

**See Also**
- `xcmsRaw-class`

**plotSurf-methods**  
*Plot profile matrix 3D surface using OpenGL*

**Description**
This method uses the rgl package to create interactive three dimensional representations of the profile matrix. It uses the terrain color scheme.

**Arguments**
- `object`: the `xcmsRaw` object
- `log`: logical, log transform intensity
- `aspect`: numeric vector with aspect ratio of the m/z, retention time and intensity components of the plot
- `...`: arguments passed to `profRange`
Details

The rgl package is still in development and imposes some limitations on the output format. A bug in the axis label code means that the axis labels only go from 0 to the aspect ratio constant of that axis. Additionally the axes are not labeled with what they are.

It is important to only plot a small portion of the profile matrix. Large portions can quickly overwhelm your CPU and memory.

Methods

object = "xcmsRaw" plotSurf(object, log = FALSE, aspect = c(1, 1, .5), ...)

See Also

xcmsRaw-class

---

plotTIC-methods  Plot total ion count

Description

Plot chromatogram of total ion count. Optionally allow identification of target peaks and viewing/identification of individual spectra.

Arguments

object the xcmsRaw object
ident logical, use mouse to identify and label chromatographic peaks
msident logical, use mouse to identify and label spectral peaks

Value

If ident == TRUE, an integer vector with the indecies of the points that were identified. Otherwise a two-column matrix with the plotted points.

Methods

object = "xcmsRaw" plotTIC(object, ident = FALSE, msident = FALSE)

See Also

xcmsRaw-class
profMedFilt-methods  Median filtering of the profile matrix

Description

Apply a median filter of given size to a profile matrix.

Arguments

- **object**: the `xcmsRaw` object
- **massrad**: number of m/z grid points on either side to use for median calculation
- **scanrad**: number of scan grid points on either side to use for median calculation

Methods

```r
object = "xcmsRaw" profMedFilt(object, massrad = 0, scanrad = 0)
```

See Also

- `xcmsRaw-class, medianFilter`

profMethod-methods  Get and set method for generating profile data

Description

These methods get and set the method for generating profile (matrix) data from raw mass spectral data. It can currently be **bin**, **binlin**, **binlinbase**, or **intlin**.

Methods

```r
object = "xcmsRaw" profMethod(object)
```

See Also

- `xcmsRaw-class, profMethod, profBin, plotSpec, plotChrom, findPeaks`
profRange-methods

Specify a subset of profile mode data

Description
Specify a subset of the profile mode matrix given a mass, time, or scan range. Allow flexible user entry for other functions.

Arguments
object
the xcmsRaw object
mzrange
single numeric mass or vector of masses
rtrange
single numeric time (in seconds) or vector of times
scanrange
single integer scan index or vector of indices
...
arguments to other functions

Details
This function handles selection of mass/time subsets of the profile matrix for other functions. It allows the user to specify such subsets in a variety of flexible ways with minimal typing.

Because R does partial argument matching, mzrange, scanrange, and rtrange can be specified in short form using m=, s=, and t=, respectively. If both a scanrange and rtrange are specified, then the rtrange specification takes precedence.

When specifying ranges, you may either enter a single number or a numeric vector. If a single number is entered, then the closest single scan or mass value is selected. If a vector is entered, then the range is set to the range() of the values entered. That allows specification of ranges using shortened, slightly non-standard syntax. For example, one could specify 400 to 500 seconds using any of the following: \texttt{t=c(400,500)}, \texttt{t=c(500,400)}, or \texttt{t=400:500}. Use of the sequence operator (:) can save several keystrokes when specifying ranges. However, while the sequence operator works well for specifying integer ranges, fractional ranges do not always work as well.

Value
A list with the following items:
mzrange
numeric vector with start and end mass
masslab
textual label of mass range
massidx
integer vector of mass indices
scanrange
integer vector with start and end scans
scanlab
textual label of scan range
scanidx
integer vector of scan range
rtrange
numeric vector of start and end times
timelab
textual label of time range

Methods
\texttt{object = "xcmsRaw"} profRange(object, mzrange = numeric(), rtrange = numeric(), scanrange = numeric(), ...)
See Also

xcmsRaw-class

profStep-methods  Get and set m/z step for generating profile data

Description

These methods get and set the m/z step for generating profile (matrix) data from raw mass spectral data. Smaller steps yield more precision at the cost of greater memory usage.

Methods

object = "xcmsRaw" profStep(object)

See Also

xcmsRaw-class, profMethod

Examples

## Not run:
library(faahKO)
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xset <- xcmsRaw(cdffiles[1])

xset
plotSurf(xset, mass=c(200,500))

profStep(xset)<-0.1 ## decrease the bin size to get better resolution
plotSurf(xset, mass=c(200, 500))
##works nicer on high resolution data.
## End(Not run)

rawEIC-methods  Get extracted ion chromatograms for specified m/z range

Description

Generate extracted ion chromatogram for m/z values of interest. The raw data is used in contrast to getEIC which uses data from the profile matrix (i.e. values binned along the M/Z dimension).

Arguments

object  xcmsRaw object
mzrange  m/z range for EIC
rtrange  retention time range for EIC
scanrange  scan range for EIC
Value
A list of:

- `scan`          scan number
- `intensity`     added intensity values

Methods

```r
object = "xcmsRaw"  rawEIC(object, mzrange = numeric(), rtrange = numeric(), scanrange = numeric(), log = FALSE)
```

Author(s)
Ralf Tautenhahn

See Also

- `xcmsRaw-class`
- `plotRaw` for plotting the raw intensities

Description

Returns a matrix with columns for time, m/z, and intensity that represents the raw data from a chromatography mass spectrometry experiment.

Arguments

- `object`          The container of the raw data
- `mzrange`         Subset by m/z range
- `rtrange`         Subset by retention time range
- `scanrange`       Subset by scan index range
- `log`             Whether to log transform the intensities

Value

A numeric matrix with three columns: time, m/z and intensity.

Methods

```r
object = "xcmsRaw"  rawMat(object, mzrange = numeric(), rtrange = numeric(), scanrange = numeric(), log = FALSE)
```

Author(s)
Michael Lawrence

See Also

- `plotRaw` for plotting the raw intensities
retcor-methods

Correct retention time from different samples

Description

To correct differences between retention times between different samples, a number of methods exist in XCMS. retcor is the generic method.

Arguments

- **object**: `xcmsSet-class` object
- **method**: Method to use for retention time correction. See details.
- **...**: Optional arguments to be passed along

Details

Different algorithms can be used by specifying them with the `method` argument. For example, to use the approach described by Smith et al (2006) one would use: `retcor(object, method="loess")`. This is also the default.

Further arguments given by `...` are passed through to the function implementing the method.

A character vector of nicknames for the algorithms available is returned by `getOption("BioC")$xcms$retcor.methods`. If the nickname of a method is called "loess", the help page for that specific method can be accessed with `?retcor.loess`.

Value

An `xcmsSet` object with corrected retention times.

Methods

- `object = "xcmsSet"` retcor(object, ...)

See Also

`retcor.loess retcor.obiwarp xcmsSet-class`. 

retcor.obiwarp

Align retention times across samples with Obiwap

Description

Calculate retention time deviations for each sample. It is based on the code at [http://obi-warp.sourceforge.net/](http://obi-warp.sourceforge.net/). However, this function is able to align multiple samples, by a center-star strategy.

For the original publication see

Chromatographic Alignment of ESI-LC-MS Proteomics Data Sets by Ordered Bijective Interpolated Warping John T. Prince and, Edward M. Marcotte Analytical Chemistry 2006 78 (17), 6140-6152
Arguments

- **object**: the `xcmsSet` object
- **plottype**: if deviation plot retention time deviation
- **profStep**: step size (in m/z) to use for profile generation from the raw data files
- **center**: the index of the sample all others will be aligned to. If center==NULL, the sample with the most peaks is chosen as default.
- **col**: vector of colors for plotting each sample
- **ty**: vector of line and point types for plotting each sample
- **response**: Responsiveness of warping. 0 will give a linear warp based on start and end points. 100 will use all bijective anchors
- **distFunc**: DistFunc function: cor (Pearson’s R) or cor_opt (default, calculate only 10% diagonal band of distance matrix, better runtime), cov (covariance), prd (product), euc (Euclidean distance)
- **gapInit**: Penalty for Gap opening, see below
- **gapExtend**: Penalty for Gap enlargement, see below
- **factorDiag**: Local weighting applied to diagonal moves in alignment.
- **factorGap**: Local weighting applied to gap moves in alignment.
- **localAlignment**: Local rather than global alignment
- **initPenalty**: Penalty for initiating alignment (for local alignment only) Default: 0

Default gap penalties: (gapInit, gapExtend) [by distFunc type]: 'cor' = '0.3,2.4' 'cov' = '0.11.7' 'prd' = '0.7.8' 'euc' = '0.9,1.8'

Value

An `xcmsSet` object

Methods

```r
retcor(object, method="obiwarp", plottype=c("none", "deviation"), profStep=1, center=NULL, col=NULL, ty=NULL, response=1, distFunc="cor_opt", gapInit=NULL, gapExtend=NULL, factorDiag=2, factorGap=1, localAlignment=0, initPenalty=0)
```

See Also

`xcmsSet-class`.

Description

These two methods use “well behaved” peak groups to calculate retention time deviations for every time point of each sample. Use smoothed deviations to align retention times.
Arguments

- **object**: the xcmsSet object
- **missing**: number of missing samples to allow in retention time correction groups
- **extra**: number of extra peaks to allow in retention time correction correction groups
- **smooth**: either "loess" for non-linear alignment or "linear" for linear alignment
- **span**: degree of smoothing for local polynomial regression fitting
- **family**: if gaussian fitting is by least-squares with no outlier removal, and if symmetric
  a re-descending M estimator is used with Tukey's biweight function, allowing
  outlier removal
- **plottype**: if deviation plot retention time deviation points and regression fit, and if mdevden
  also plot peak overall peak density and retention time correction peak density
- **col**: vector of colors for plotting each sample
- **ty**: vector of line and point types for plotting each sample

Value

An xcmsSet object

Methods

```r
object = "xcmsSet" retcor(object, missing = 1, extra = 1, smooth = c("loess", "linear"),
                           span = .2, family = c("gaussian", "symmetric"),
                           plottype = c("none", "deviation", "mdevden"),
                           col = NULL, ty = NULL)
```

See Also

- xcmsSet-class, loess retcor.obiwarp
- retexp

Description

Expands (or contracts) the retention time window in each row of a matrix as defined by the retmin
and retmax columns.

Usage

```r
retexp(peakrange, width = 200)
```

Arguments

- **peakrange**: matrix with columns retmin and retmax
- **width**: new width for the window

Value

The altered matrix.

Author(s)

Colin A. Smith, <csmith@scripps.edu>
sampnames-methods

See Also
   getEIC

Description

Return sample names for an object

Value

A character vector with sample names.

Methods

object = "xcmsEIC"  sampnames(object)
object = "xcmsSet"   sampnames(object)

See Also

xcmsSet-class, xcmsEIC-class

specDist-methods  Distance methods for xcmsSet, xcmsRaw and xsAnnotate

Description

There are several methods for calculating a distance between two sets of peaks in xcms. specDist is the generic method.

Arguments

object  a xcmsSet or xcmsRaw.
method  Method to use for distance calculation. See details.
...     mzabs, mzppm and parameters for the distance function.

Details

Different algorithms can be used by specifying them with the method argument. For example to use the "meanMZmatch" approach with xcmsSet one would use: specDist(object, peakIDs1, peakIDs2, method="meanMZmatch"). This is also the default.

Further arguments given by ... are passed through to the function implementing the method.

A character vector of nicknames for the algorithms available is returned by getOption("BioC")$xcms$specDist.methods. If the nickname of a method is called "meanMZmatch", the help page for that specific method can be accessed with ?specDist.meanMZmatch.
specDist.cosine

Value

mzabs maximum absolute deviation for two matching peaks
mzppm relative deviations in ppm for two matching peaks
symmetric use symmetric pairwise m/z-matches only, or each match

Methods

object = "xcmsSet" specDist(object, peakIDs1, peakIDs2,...)
object = "xsAnnotate" specDist(object, PSpec1, PSpec2,...)

Author(s)

Joachim Kutzer, <jkutzer@ipb-halle.de>

---

specDist.cosine a Distance function based on matching peaks

Description

This method calculates the distance of two sets of peaks using the cosine-distance.

Usage

specDist.cosine(peakTable1, peakTable2, mzabs=0.001, mzppm=10, mzExp=0.6, intExp=3, nPdiff=2, nPmin=8, symmetric=FALSE)

Arguments

peakTable1 a Matrix containing at least m/z-values, row must be called "mz"
peakTable2 the matrix for the other m/z-values
mzabs maximum absolute deviation for two matching peaks
mzppm relative deviations in ppm for two matching peaks
symmetric use symmetric pairwise m/z-matches only, or each match
mzExp the exponent used for mz
intExp the exponent used for intensity
nPdiff the maximum nrow-difference of the two peaktables
nPmin the minimum absolute sum of peaks from both peaktables

Details

The result is the cosine-distance of the product from weighted factors of mz and intensity from matching peaks in the two peaktables. The factors are calculated as wFact = mz^mzExp * int^intExp. If no distance is calculated (for example because no matching peaks were found) the return-value is NA.

Methods

peakTable1 = "matrix", peakTable2 = "matrix" specDist.cosine(peakTable1, peakTable2, mzabs = 0.001, mzppm = 10, mzExp = 0.6, intExp = 3, nPdiff = 2, nPmin = 8, symmetric = FALSE)
**specDist.meanMZmatch**

**Author(s)**

Joachim Kutzera, <jkutzer@ipb-halle.de>

---

**Description**

This method calculates the distance of two sets of peaks.

**Usage**

```r
specDist.meanMZmatch(peakTable1, peakTable2, matchdist=1, matchrate=1, mzabs=0.001, mzppm=10, symmetric=TRUE)
```

**Arguments**

- `peakTable1`: a Matrix containing at least m/z-values, row must be called "mz"
- `peakTable2`: the matrix for the other m/z-values
- `mzabs`: maximum absolute deviation for two matching peaks
- `mzppm`: relative deviations in ppm for two matching peaks
- `symmetric`: use symmetric pairwise m/z-matches only, or each match
- `matchdist`: the weight for value one (see details)
- `matchrate`: the weight for value two

**Details**

The result of the calculation is a weighted sum of two values. Value one is the mean absolute difference of the matching peaks, value two is the relation of matching peaks and non matching peaks. If no distance is calculated (for example because no matching peaks were found) the return-value is NA.

**Methods**

```r
peakTable1 = "matrix", peakTable2 = "matrix"     specDist.meanMZmatch(peakTable1, peakTable2, matchdist=1, matchrate=1, mzabs=0.001, mzppm=10, symmetric=TRUE)
```

**Author(s)**

Joachim Kutzera, <jkutzer@ipb-halle.de>
specDist.peakCount-methods

*a Distance function based on matching peaks*

**Description**

This method calculates the distance of two sets of peaks by just returning the number of matching peaks (m/z-values).

**Usage**

```
specDist.peakCount(peakTable1, peakTable2, mzabs=0.001, mzppm=10, symmetric=FALSE)
```

**Arguments**

- `peakTable1`: a Matrix containing at least m/z-values, row must be called "mz"
- `peakTable2`: the matrix for the other m/z-values
- `mzabs`: maximum absolute deviation for two matching peaks
- `mzppm`: relative deviations in ppm for two matching peaks
- `symmetric`: use symmetric pairwise m/z-matches only, or each match

**Methods**

- `peakTable1 = "matrix", peakTable2 = "matrix"`  
- `specDist.peakCount(peakTable1, peakTable2, mzppm=10, symmetric=FALSE)`

**Author(s)**

Joachim Kutzera, <jkutzer@ipb-halle.de>

---

specNoise  

*Calculate noise for a sparse continuum mass spectrum*

**Description**

Given a sparse continuum mass spectrum, determine regions where no signal is present, substituting half of the minimum intensity for those regions. Calculate the noise level as the weighted mean of the regions with signal and the regions without signal. If there is only one raw peak, return zero.

**Usage**

```
specNoise(spec, gap = quantile(diff(spec[, "mz"]), 0.9))
```

**Arguments**

- `spec`: matrix with named columns mz and intensity
- `gap`: threshold above which to data points are considered to be separated by a blank region and not bridged by an interpolating line
specPeaks

Details

The default gap value is determined from the 90th percentile of the pair-wise differences between adjacent mass values.

Value

A numeric noise level

Author(s)

Colin A. Smith, <csmith@scripps.edu>

See Also

getSpec, specPeaks

Description

Given a spectrum, identify and list significant peaks as determined by several criteria.

Usage

specPeaks(spec, sn = 20, mzgap = 0.2)

Arguments

spec          matrix with named columns mz and intensity
sn            minimum signal to noise ratio
mzgap         minimal distance between adjacent peaks, with smaller peaks being excluded

Details

Peaks must meet two criteria to be considered peaks: 1) Their s/n ratio must exceed a certain threshold. 2) They must not be within a given distance of any greater intensity peaks.

Value

A matrix with columns:

mz            m/z at maximum peak intensity
intensity     maximum intensity of the peak
fwhm          full width at half max of the peak

Author(s)

Colin A. Smith, <csmith@scripps.edu>

See Also

gSpec, specNoise
split.xcmsRaw  

*Divide an xcmsRaw object*

**Description**

Divides the scans from a xcmsRaw object into a list of multiple objects. MS$^n$ data is discarded.

**Arguments**

- `x`: xcmsRaw object
- `f`: factor such that `factor(f)` defines the scans which go into the new xcmsRaw objects
- `drop`: logical indicating if levels that do not occur should be dropped (if `f` is a `factor` or a list).
- `...`: further potential arguments passed to methods.

**Value**

A list of xcmsRaw objects.

**Methods**

```r
xr = "xcmsRaw"
split(x, f, drop = TRUE, ...)
```

**Author(s)**

Steffen Neumann, <sneumann(at)ipb-halle.de>

**See Also**

- `xcmsRaw-class`

---

split.xcmsSet  

*Divide an xcmsSet object*

**Description**

Divides the samples and peaks from a xcmsSet object into a list of multiple objects. Group data is discarded.

**Arguments**

- `xs`: xcmsSet object
- `f`: factor such that `factor(f)` defines the grouping
- `drop`: logical indicating if levels that do not occur should be dropped (if `f` is a `factor` or a list).
- `...`: further potential arguments passed to methods.
SSgauss

Description

This selfStart model evaluates the Gaussian model and its gradient. It has an initial attribute that will evaluate the initial estimates of the parameters mu, sigma, and h.

Value

A numeric vector of the same length as x. It is the value of the expression \( h \times \exp\left(-\frac{(x-mu)^2}{2*sigma^2}\right) \), which is a modified gaussian function where the maximum height is treated as a separate parameter not dependent on sigma. If arguments mu, sigma, and h are names of objects, the gradient matrix with respect to these names is attached as an attribute named gradient.

Author(s)

Colin A. Smith, <csmith@scripps.edu>

See Also

nls, selfStart
**stitch-methods**

**Correct gaps in data**

**Description**

Fixes gaps in data due to calibration scans or lock mass. Automatically detects file type and calls the relevant method. The mzXML file keeps the data the same length in time but overwrites the lock mass scans. The netCDF version adds the scans back into the data thereby increasing the length of the data and correcting for the unseen gap.

**Arguments**

- **object**: An `xcmsRaw-class` object
- **lockMass**: A dataframe of locations of the gaps
- **freq**: The intervals of the lock mass scans
- **start**: The starting lock mass scan location, default is 1

**Details**

`makeacqNum` takes locates the gap using the starting lock mass scan and it’s intervals. This data frame is then used in `stitch` to correct for the gap caused by the lock mass. Correction works by using scans from either side of the gap to fill it in.

**Value**

`stitch` A corrected `xcmsRaw-class` object

`makeacqNum` A numeric vector of scan locations corresponding to lock Mass scans

**Methods**

- **object = "xcmsRaw"** `stitch(object, lockMass=numeric())`
- **object = "xcmsRaw"** `makeacqNum(object, freq=numeric(), start=1)`

**Author(s)**

Paul Benton, <hpaul.benton08@imperial.ac.uk>

**Examples**

```r
## Not run: library(xcms)
library(faahKO) # These files do not have this problem to correct for but just for an example
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xr<-xcmsRaw(cdffiles[1])
xr
## Lets assume that the lockmass starts at 1 and is every 100 scans
lockMass<-xcms:::makeacqNum(xr, freq=100, start=1)
## these are equal
lockmass<-AutoLockMass(xr)
ob<-stitch(xr, lockMass)
ob```
#plot the old data before correction
foo <- rawEIC(xr, m = c(200, 210), scan = c(80, 140))
plot(foo$scan, foo$intensity, type = "h")

#plot the new corrected data to see what changed
foo <- rawEIC(ob, m = c(200, 210), scan = c(80, 140))
plot(foo$scan, foo$intensity, type = "h")

## End(Not run)

updateObject, xcmsSet-method

Update an xcmsSet object

Description

This method updates an old xcmsSet object to the latest definition.

Usage

## S4 method for signature 'xCMS'
updateObject(object, ..., verbose = FALSE)

Arguments

object     The xcmsSet object to update.
...        Optional additional arguments. Currently ignored.
verbose    Currently ignored.

Value

An updated xcmsSet containing all data from the input object.

Author(s)

Johannes Rainer

valueCount2ScanIndex

Create index vector for internal C calls

Description

Simple helper function that converts the number of values per scan/spectrum to an integer vector that can be passed to the base xcms functions/downstream C functions.

Usage

valueCount2ScanIndex(valCount)
verify.mzQuantM

Arguments

valCount   Numeric vector representing the number of values per spectrum.

Value

An integer vector with the index (0-based) in the mz or intensity vectors indicating the start of a spectrum.

Author(s)

Johannes Rainer

----------------------------------

verify.mzQuantM       Verify an mzQuantML file

Description

Export in XML data formats: verify the written data

Usage

verify.mzQuantML(filename, xsdfilename)

Arguments

filename   filename (may include full path) for the output file. Pipes or URLs are not allowed.

xsdfilename   Filename of the XSD to verify against (may include full path)

Details

The verify.mzQuantML() function will verify an PSI standard format mzQuantML document against the XSD schema, see http://www.psidev.info/mzquantml

Value

None.

See Also

write.mzQuantML
write.cdf-methods

Save an xcmsRaw object to file

Description
Write the raw data to a (simple) CDF file.

Arguments

object  the xcmsRaw object
filename  filename (may include full path) for the CDF file. Pipes or URLs are not allowed.

Details
Currently the only application known to read the resulting file is XCMS. Others, especially those which build on the AndiMS library, will refuse to load the output.

Value
None.

Methods

object = "xcmsRaw" write.cdf(object, filename)

See Also

xcmsRaw-class, xcmsRaw.

write.mzdata-methods

Save an xcmsRaw object to a file

Description
Write the raw data to a (simple) mzData file.

Arguments

object  the xcmsRaw object
filename  filename (may include full path) for the mzData file. Pipes or URLs are not allowed.

Details
This function will export a given xcmsRaw object to an mzData file. The mzData file will contain a <spectrumList> containing the <spectrum> with mass and intensity values in 32 bit precision. Other formats are currently not supported. Any header information (e.g. additional <software> information or <cvParams>) will be lost. Currently, also any MSn information will not be stored.
Value
None.

Methods

\texttt{object = "xcmsRaw" write.mzdata(object, filename)}

See Also
\texttt{xcmsRaw-class, xcmsRaw,}

\texttt{write.mzQuantML-methods}

\textit{Save an xcmsSet object to an PSI mzQuantML file}

Description
Export in XML data formats: Write the processed data in an xcmsSet to mzQuantML.

Arguments

\begin{itemize}
  \item \texttt{object} the xcmsRaw or xcmsSet object
  \item \texttt{filename} filename (may include full path) for the output file. Pipes or URLs are not allowed.
\end{itemize}

Details
The \texttt{write.mzQuantML()} function will write a (grouped) xcmsSet into the PSI standard format mzQuantML, see \url{http://www.psidev.info/mzquantml}

Value
None.

Methods

\texttt{object = "xcmsSet" write.mzQuantML(object, filename)}

See Also
\texttt{xcmsSet-class, xcmsSet, verify.mzQuantML,}
writeMzTab

Save a grouped xcmsSet object in mzTab-1.1 format file

Description

Write the grouped xcmsSet to an mzTab file.

Arguments

- **object**
  the xcmsSet object

- **filename**
  filename (may include full path) for the mzTab file. Pipes or URLs are not allowed.

Details

The mzTab file format for MS-based metabolomics (and proteomics) is a lightweight supplement to the existing standard XML-based file formats (mzML, mzIdentML, mzQuantML), providing a comprehensive summary, similar in concept to the supplemental material of a scientific publication. mzTab files from xcms contain small molecule sections together with experimental metadata and basic quantitative information. The format is intended to store a simple summary of the final results.

Value

None.

Usage

```
object = "xcmsSet" writeMzTab(object, filename)
```

See Also

`xcmsSet-class, xcmsSet`

Examples

```
library(faahKO)
xs <- group(faahko)

mzt <- data.frame(character(0))
mzt <- xcms:::mzTabHeader(mzt,
    version="1.1.0", mode="Complete", type="Quantification",
    description="faahKO",
    xset=xs)
mzt <- xcms:::mzTabAddSME(mzt, xs)
xcms:::writeMzTab(mzt, "faahKO.mzTab")
```
xcms-deprecated

Deprecated functions in package ‘xcms’

Description

These functions are provided for compatibility with older versions of ‘xcms’ only, and will be defunct at the next release.

Details

The following functions/methods are deprecated.

- xcmsPapply: this function is no longer available and the use of bplapply is suggested.

xcmsEIC-class

Class xcmsEIC, a class for multi-sample extracted ion chromatograms

Description

This class is used to store and plot parallel extracted ion chromatograms from multiple sample files. It integrates with the xcmsSet class to display peak area integrated during peak identification or fill-in.

Objects from the Class

Objects can be created with the getEIC method of the xcmsSet class. Objects can also be created by calls of the form new("xcmsEIC", ...).

Slots

- eic: list containing named entries for every sample. for each entry, a list of two column EIC matrices with retention time and intensity
- mzrange: two column matrix containing starting and ending m/z for each EIC
- rtrange: two column matrix containing starting and ending time for each EIC
- rt: either "raw" or "corrected" to specify retention times contained in the object
- groupnames: group names from xcmsSet object used to generate EICs

Methods

- groupnames signature(object = "xcmsEIC"): get groupnames slot
- mzrange signature(object = "xcmsEIC"): get mzrange slot
- plot signature(x = "xcmsEIC"): plot the extracted ion chromatograms
- rtrange signature(object = "xcmsEIC"): get rtrange slot
- sampnames signature(object = "xcmsEIC"): get sample names

Note

No notes yet.
Author(s)
Colin A. Smith, <csmith@scripps.edu>

See Also
getEIC

---

**xcmsFileSource-class**  
*Base class for loading raw data from a file*

**Description**

Data sources which read data from a file should inherit from this class. The xcms package provides classes to read from netCDF, mzData, mzXML, and mzML files using xcmsFileSource.

This class should be considered virtual and will not work if passed to `loadRaw-methods`. The reason it is not explicitly virtual is that there does not appear to be a way for a class to be both virtual and have a data part (which lets functions treat objects as if they were character strings).

This class validates that a file exists at the path given.

**Objects from the Class**

xcmsFileSource objects should not be instantiated directly. Instead, create subclasses and instantiate those.

**Slots**

`.Data`: Object of class "character". File path of a file from which to read raw data as the object’s data part

**Extends**

Class "character", from data part. Class "xcmsSource", directly.

**Methods**

xcmsSource signature(object = "character"): Create an xcmsFileSource object referencing the given file name.

**Author(s)**

Daniel Hackney <dan@haxney.org>

**See Also**

xcmsSource
**xcmsFragments**

*Constructor for xcmsFragments objects which holds Tandem MS peaks*

**Description**

EXPERIMENTAL FEATURE

xcmsFragments is an object similar to xcmsSet, which holds peaks picked (or collected) from one or several xcmsRaw objects.

There are still discussions going on about the exact API for MS^n$ data, so this is likely to change in the future. The code is not yet pipeline-ified.

**Usage**

```
xcmsFragments(xs, ...)  
```

**Arguments**

- **xs**
  
  A `xcmsSet-class` object which contains picked ms1-peaks from one or several experiments

- **...**
  
  further arguments to the `collect` method

**Details**

After running `collect(xFragments,xSet)` the peaktable of the xcmsFragments includes the ms1Peaks from all experiments stored in a xcmsSet-object. Further it contains the relevant MSn-peaks from the xcmsRaw-objects, which were created temporarily with the paths in xcmsSet.

**Value**

An xcmsFragments object.

**Author(s)**

Joachim Kutzera, Steffen Neumann, <sneumann@ipb-halle.de>

**See Also**

`xcmsFragments-class`, `collect`
Class xcmsFragments, a class for handling Tandem MS and MS^n data

Description

This class is similar to xcmsSet because it stores peaks from a number of individual files. However, xcmsFragments keeps Tandem MS and e.g. Ion Trap or Orbitrap MS^n peaks, including the parent ion relationships.

Objects from the Class

Objects can be created with the xcmsFragments constructor and filled with peaks using the collect method.

Slots

- peaks: matrix with columns peakID (MS1 parent in corresponding xcmsSet), MSnParentPeakID (parent peak within this xcmsFragments), msLevel (e.g. 2 for Tandem MS), rt (retention time in case of LC data), mz (fragment mass-to-charge), intensity (peak intensity extracted from the original xcmsSet), sample (the index of the rawData-file).
- MS2spec: This is a list of matrices. Each matrix in the list is a single collected spectra from collect. The column ID’s are mz, intensity, and full width half maximum(fwhm). The fwhm column is only relevant if the spectra came from profile data.
- specinfo: This is a matrix with reference data for the spectra in MS2spec. The column id’s are preMZ, AccMZ, rtmin, rtmax, ref, CollisionEnergy. The preMZ is precursor mass from the MS1 scan. This mass is given by the XML file. With some instruments this mass is only given as nominal mass, therefore a AccMZ is given which is a weighted average mass from the MS1 scan of the collected spectra. The retention time is given by rtmin and rtmax. The ref column is a pointer to the MS2spec matrix spectra. The collisionEnergy column is the collision Energy for the spectra.

Methods

- collect signature(object = "xcmsFragments"): gets a xcmsSet-object, collects ms1-peaks from it and the msn-peaks from the corresponding xcmsRaw-files.
- plotTree signature(object = "xcmsFragments"): prints a (text based) pseudo-tree of the peak-table to display the dependencies of the peaks among each other.
- show signature(object = "xcmsFragments"): print a human-readable description of this object to the console.

Note

No notes yet.

Author(s)

S. Neumann, J. Kutzera
xcmsPapply

References

A parallel effort in metabolite profiling data sharing: http://metlin.scripps.edu/

See Also

xcmsRaw

deprecated: xcmsPapply

Description

This function is deprecated, use bplapply instead.

An apply-like function which uses Rmpi to distribute the processing evenly across a cluster. Will use a non-MPI version if distributed processing is not available.

Usage

```
xcmsPapply(arg_sets, papply_action, papply_commondata = list(),
            show_errors = TRUE, do_trace = FALSE, also_trace = c())
```

Arguments

- `arg_sets`: a list, where each item will be given as an argument to `papply\_action`
- `papply_action`: A function which takes one argument. It will be called on each element of `arg\_sets`
- `papply_commondata`: A list containing the names and values of variables to be accessible to the `papply\_action`. 'attach' is used locally to import this list.
- `show_errors`: If set to TRUE, overrides Rmpi’s default, and messages for errors which occur in R slaves are produced.
- `do_trace`: If set to TRUE, causes the `papply\_action` function to be traced. i.e. Each statement is output before it is executed by the slaves.
- `also_trace`: If supplied an array of function names, as strings, tracing will also occur for the specified functions.

Details

Similar to apply and lapply, applies a function to all items of a list, and returns a list with the corresponding results.

Uses Rmpi to implement a pull idiom in order to distribute the processing evenly across a cluster. If Rmpi is not available, or there are no slaves, implements this as a non-parallel algorithm.

xcmsPapply is a modified version of the papply function from package papply 0.2 (Duane Currie). Parts of the slave function were wrapped in try() to make it failsafe and progress output was added.

Make sure Rmpi was installed properly by executing the example below. Rmpi was tested with

- OpenMPI: Unix, http://www.open-mpi.org/, don’t forget to export MPI_ROOT before installing Rmpi e.g. export MPI_ROOT=/usr/lib/openmpi
Value
A list of return values from papply\_action. Each value corresponds to the element of arg\_sets used as a parameter to papply\_action

Note
Does not support distributing recursive calls in parallel. If papply is used inside papply\_action, it will call a non-parallel version

Author(s)
Duane Currie <duane.currie@acadiau.ca>, modified by Ralf Tautenhahn <rtautenh@ipb-halle.de>.

References
http://ace.acadiau.ca/math/ACMMaC/software/papply/

Examples
```r
## Not run:
library(Rmpi)
library(xcms)
	number_lists <- list(1:10,4:40,2:27)

mpi.spawn.Rslaves(nslaves=2)

results <- xcmsPapply(number_lists,sum)

results

mpi.close.Rslaves()

## End(Not run)
```

---

### xcmsPeaks-class

A matrix of peaks

Description
A matrix of peak information. The actual columns depend on how it is generated (i.e. the findPeaks method).

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

Slots
`.Data`: The matrix holding the peak information
Extends


Methods

None yet. Some utilities for working with peak data would be nice.

Author(s)

Michael Lawrence

See Also

findPeaks for detecting peaks in an xcmsRaw.

---

**xcmsRaw**

*Constructor for xcmsRaw objects which reads NetCDF/mzXML files*

**Description**

This function handles the task of reading a NetCDF/mzXML file containing LC/MS or GC/MS data into a new xcmsRaw object. It also transforms the data into profile (maxrix) mode for efficient plotting and data exploration.

**Usage**

```r
xcmsRaw(filename, profstep = 1, profmethod = "bin", profparam = list(), includeMSn=FALSE, mslevel=NULL, scanrange=NULL)

deepCopy(object)
```

**Arguments**

- `filename` path name of the NetCDF or mzXML file to read
- `profstep` step size (in m/z) to use for profile generation
- `profmethod` method to use for profile generation
- `profparam` extra parameters to use for profile generation
- `includeMSn` only for XML file formats: also read MS^n$ (Tandem-MS of Ion-/Orbi- Trap spectra)
- `mslevel` move data from mslevel into normal MS1 slots, e.g. for peak picking and visualisation
- `scanrange` scan range to read
- `object` An xcmsRaw object
xlmsRaw

Details

The scanrange to import can be restricted, otherwise all MS1 data is read. If profstep is set to 0, no profile matrix is generated. Unless includeMSn=TRUE only first level MS data is read, not MS/MS, etc.

deepCopy(xraw) will create a copy of the xcmsRaw object with its own copy of mz and intensity data in xraw@env.

Value

A xcmsRaw object.

Author(s)

Colin A. Smith, <csmith@scripps.edu>

References

NetCDF file format: http://my.unidata.ucar.edu/content/software/netcdf/
http://www.astm.org/Standards/E2077.htm
http://www.astm.org/Standards/E2078.htm

mzXML file format: http://sashimi.sourceforge.net/software_glossolalia.html

PSI-MS working group who developed mzData and mzML file formats: http://www.psidev.info/index.php?q=node/80


See Also

xcmsRaw-class, profStep, profMethod xcmsFragments

Examples

```r
## Not run:
library(xcms)
library(faahKO)
cdfpath <- system.file("cdf", package = "faahKO")
cdffiles <- list.files(cdfpath, recursive = TRUE, full.names = TRUE)
xr<-xcmsRaw(cdffiles[1])
xr
##This gives some information about the file
names(attributes(xr))
## Lets have a look at the structure of the object
str(xr)

# same but with a preview of each slot in the object
#50... lets have a look at how this works
head(xr@scanindex)
#1] 0 429 860 1291 1718 2140
xr@env$mz[425:430]
#1] 596.3 597.0 597.3 598.1 599.3 200.1
##We can see that the 429 index is the last mz of scan 1 therefore...

mz.scan1<-xr@env$mz[[1+xr@scanindex[1]]]:xr@scanindex[2]]
intensity.scan1<-xr@env$intensity[[1+xr@scanindex[1]]]:xr@scanindex[2]]
plot(mz.scan1, intensity.scan1, type="h", main=paste("Scan 1 of file", basename(cdffiles[1]), sep=""))
```

## the easier way :p
scan1<-getScan(xr, 1)
head(scan1)
plotScan(xr, 1)

## End(Not run)

### xcmsRaw-class

**Class xcmsRaw, a class for handling raw data**

#### Description

This class handles processing and visualization of the raw data from a single LC/MS or GS/MS run. It includes methods for producing a standard suite of plots including individual spectra, multi-scan average spectra, TIC, and EIC. It will also produce a feature list of significant peaks using matched filtration.

#### Objects from the Class

Objects can be created with the `xcmsRaw` constructor which reads data from a NetCDF file into a new object.

#### Slots

- **acquisitionNum**: acquisitionNum
- **env**: environment with three variables: `mz` - concatenated m/z values for all scans, `intensity` - corresponding signal intensity for each m/z value, and `profile` - matrix representation of the intensity values with columns representing scans and rows representing equally spaced m/z values
- **filepath**: Path to the raw data file
- **gradient**: matrix with first row, `time`, containing the time point for interpolation and successive columns representing solvent fractions at each point
- **msnAcquisitionNum**: for each scan a unique acquisition number as reported via "spectrum id" (mzData) or "<scan num=...>" and "<scanOrigin num=...>" (mzXML)
- **msnCollisionEnergy**: "CollisionEnergy" (mzData) or "collisionEnergy" (mzXML)
- **msnLevel**: for each scan the "msLevel" (both mzData and mzXML)
- **msnPrecursorCharge**: "ChargeState" (mzData) and "precursorCharge" (mzXML)
- **msnPrecursorIntensity**: "Intensity" (mzData) or "precursorIntensity" (mzXML)
- **msnPrecursorMz**: "MassToChargeRatio" (mzData) or "precursorMz" (mzXML)
- **msnPrecursorScan**: "spectrumRef" (both mzData and mzXML)
- **msnRt**: Retention time of the scan
- **msnScanindex**: msnScanindex
- **mzrange**: numeric vector of length 2 with minimum and maximum m/z values represented in the profile matrix
- **polarity**: polarity
- **profmethod**: character value with name of method used for generating the profile matrix
profparam: profparam

scanindex: integer vector with starting positions of each scan in the mz and intensity variables (note that index values are based off a 0 initial position instead of 1)

scantime: numeric vector with acquisition time (in seconds) for each scan
tic: numeric vector with total ion count (intensity) for each scan

mslevel: Numeric representing the MS level that is present in MS1 slot. This slot should be accessed through its getter method mslevel.

scanrange: Numeric of length 2 specifying the scan range (or NULL for the full range). This slot should be accessed through its getter method scanrange.

Methods

findPeaks signature(object = "xcmsRaw"): feature detection using matched filtration in the chromatographic time domain

getEIC signature(object = "xcmsRaw"): get extracted ion chromatograms in specified m/z ranges. This will return the total ion chromatogram (TIC) if the m/z range corresponds to the full m/z range (i.e. sum of all signals per retention time across all m/z).

getPeaks signature(object = "xcmsRaw"): get data for peaks in specified m/z and time ranges

getScan signature(object = "xcmsRaw"): get m/z and intensity values for a single mass scan

getSpec signature(object = "xcmsRaw"): get average m/z and intensity values for multiple mass scans

image signature(x = "xcmsRaw"): get data for peaks in specified m/z and time ranges

levelplot Create an image of the raw (profile) data m/z against retention time, with the intensity color coded.

mslevel Getter method for the mslevel slot.

plotChrom signature(object = "xcmsRaw"): plot a chromatogram from profile data

plotRaw signature(object = "xcmsRaw"): plot locations of raw intensity data points

plotScan signature(object = "xcmsRaw"): plot a mass spectrum of an individual scan from the raw data

plotSpec signature(object = "xcmsRaw"): plot a mass spectrum from profile data

plotSurf signature(object = "xcmsRaw"): experimental method for plotting 3D surface of profile data with rgl.

plotTIC signature(object = "xcmsRaw"): plot total ion count chromatogram

profinfo signature(object = "xcmsRaw"): returns a list containing the profile generation method and step (profile m/z step size) and eventual additional parameters to the profile function.

profMedFilt signature(object = "xcmsRaw"): median filter profile data in time and m/z dimensions

profMethod<- signature(object = "xcmsRaw"): change the method of generating the profile matrix

profMethod signature(object = "xcmsRaw"): get the method of generating the profile matrix

profMz signature(object = "xcmsRaw"): get vector of m/z values for each row of the profile matrix

profRange signature(object = "xcmsRaw"): interpret flexible ways of specifying subsets of the profile matrix
profStep <- signature(object = "xcmsRaw"): change the m/z step used for generating the profile matrix
profStep signature(object = "xcmsRaw"): get the m/z step used for generating the profile matrix
revMz signature(object = "xcmsRaw"): reverse the order of the data points for each scan
scanrange Getter method for the scanrange slot.
sortMz signature(object = "xcmsRaw"): sort the data points by increasing m/z for each scan
stitch signature(object = "xcmsRaw"): Raw data correction for lock mass calibration gaps.

Note
No notes yet.

Author(s)
Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

References
A parallel effort in metabolite profiling data sharing: http://metlin.scripps.edu/

See Also
xcmsRaw

xcmsSet

Constructor for xcmsSet objects which finds peaks in NetCDF/mzXML files

Description
This function handles the construction of xcmsSet objects. It finds peaks in batch mode and pre-sorts files from subdirectories into different classes suitable for grouping.

Usage

xcmsSet(files = NULL, snames = NULL, sclass = NULL, phenoData = NULL,
        profmethod = "bin", profparam = list(),
        polarity = NULL, lockMassFreq=FALSE,
        mslevel=NULL, nSlaves=0, progressCallback=NULL,
        scanrange = NULL, BPPARAM = bpparam(), ...)

Arguments

files path names of the NetCDF/mzXML files to read
snames sample names. By default the file name without extension is used.
sclass sample classes.
phenoData: data.frame or AnnotatedDataFrame defining the sample names and classes and other sample related properties. If not provided, the argument sclass or the subdirectories in which the samples are stored will be used to specify sample grouping.

profmethod: Method to use for profile generation. Supported values are "bin", "binlin", "binlinbase" and "intlin" (for methods profBin, profBinLin, profBinLinBase and profIntLin, respectively). See help on profBin for a complete list of available methods and their supported parameters.

profparam: parameters to use for profile generation.

polarity: filter raw data for positive/negative scans

lockMassFreq: Performs correction for Waters LockMass function

mslevel: perform peak picking on data of given mslevel

nSlaves: DEPRECATED, use BPPARAM argument instead.

progressCallback: function to be called, when progress changes (useful for GUIs)

scanrange: scan range to read

BPPARAM: a BiocParallel parameter object to control how and if parallel processing should be performed. Such objects can be created by the SerialParam, MulticoreParam or SnowParam functions.

... further arguments to the findPeaks method of the xcmsRaw class

Details

The default values of the files, snames, sclass, and phenoData arguments cause the function to recursively search for readable files. The filename without extension is used for the sample name. The subdirectory path is used for the sample class. If the files contain both positive and negative spectra, the polarity can be selected explicitly. The default (NULL) is to read all scans.

If phenoData is provided, it is stored to the phenoData slot of the returned xcmsSet class. If that data.frame contains a column named "class", its content will be returned by the sampclass method and thus be used for the group/class assignment of the individual files (e.g. for peak grouping etc.). For more details see the help of the xcmsSet-class.

The step size (in m/z) to use for profile generation can be submitted either using the profparam argument (e.g. profparam=list(step=0.1)) or by submitting step=0.1. By specifying a value of 0 the profile matrix generation can be skipped.

The feature/peak detection algorithm can be specified with the method argument which defaults to the "matchFilter" method (findPeaks.matchedFilter). Possible values are returned by getOption("BioC")$xcms$findPeaks.methods.

The lock mass correction allows for the lock mass scan to be added back in with the last working scan. This correction gives better reproducibility between sample sets.

Value

A xcmsSet object.

Note

The arguments profmethod and profparam have no influence on the feature/peak detection. The step size parameter step for the profile generation in the findPeaks.matchedFilter peak detection algorithm can be passed using the ...
**Author(s)**
Colin A. Smith, <csmith@scripps.edu>

**See Also**
xcmsSet-class, findPeaks, profStep, profMethod, profBin, xcmsPapply

---

**Description**
This class transforms a set of peaks from multiple LC/MS or GC/MS samples into a matrix of preprocessed data. It groups the peaks and does nonlinear retention time correction without internal standards. It fills in missing peak values from raw data. Lastly, it generates extracted ion chromatograms for ions of interest.

**Details**
The `phenoData` slot (and `phenoData` parameter in the `xcmsSet` function) is intended to contain a data.frame describing all experimental factors, i.e. the samples along with their properties. If this data.frame contains a column named "class", this will be returned by the `sampclass` method and will thus be used by all methods to determine the sample grouping/class assignment (e.g. to define the colors in various plots or for the `group` method).

The `sampclass<-` method adds or replaces the “class” column in the `phenoData` slot. If a data.frame is submitted to this method, the interaction of its columns will be stored into the “class” column.

Also, similar to other classes in Bioconductor, the `$` method can be used to directly access all columns in the `phenoData` slot (e.g. use `xset$name` on a `xcmsSet` object called “xset” to extract the values from a column named “name” in the `phenoData` slot).

**Objects from the Class**
Objects can be created with the `xcmsSet` constructor which gathers peaks from a set NetCDF files. Objects can also be created by calls of the form `new("xcmsSet", ...).

**Slots**
- **peaks**: matrix containing peak data
- **filled**: a vector with peak indices of peaks which have been added by a `fillPeaks` method,
- **groups**: matrix containing statistics about peak groups
- **groupidx**: list containing indices of peaks in each group
- **phenoData**: a data frame containing the experimental design factors
- **rt**: list containing two lists, `raw` and `corrected`, each containing retention times for every scan of every sample
- **filepaths**: character vector with absolute path name of each NetCDF file
- **profinfo**: list containing the values method - profile generation method, and step - profile m/z step size and eventual additional parameters to the profile function.
- **dataCorrection** logical vector filled if the waters Lock mass correction parameter is used.
xcmsSet-class

polarity: a string ("positive" or "negative" or NULL) describing whether only positive or negative scans have been used reading the raw data.

progressInfo: progress informations for some xcms functions (for GUI)

progressCallback: function to be called, when progressInfo changes (for GUI)

mslevel: Numeric representing the MS level on which the peak picking was performed (by default on MS1). This slot should be accessed through its getter method mslevel.

scanrange: Numeric of length 2 specifying the scan range (or NULL for the full range). This slot should be accessed through its getter method scanrange.

Methods

  c  signature("xcmsSet"): combine objects together

  filepaths<- signature(object = "xcmsSet"): set filepaths slot

  filepaths signature(object = "xcmsSet"): get filepaths slot

  diffreport signature(object = "xcmsSet"): create report of differentially regulated ions including EICs

  fillPeaks signature(object = "xcmsSet"): fill in peak data for groups with missing peaks

  getEIC signature(object = "xcmsSet"): get list of EICs for each sample in the set

  getXcmsRaw signature(object = "xcmsSet", sampleidx = 1, profmethod = profMethod(object), profstep = profStep(object), profparam = profinfo(object), mslevel = NULL, scanrange = NULL, rt = c("corrected", "raw"), BPPARAM = bpparam()):
read the raw data for one or more files in the xcmsSet and return it. The default parameters will apply all settings used in the original xcmsSet call to generate the xcmsSet object to be applied also to the raw data. Parameter sampleidx allows to specify which raw file(s) should be loaded. Argument BPPARAM allows to setup parallel processing.

  groupidx<- signature(object = "xcmsSet"): set groupidx slot

  groupidx signature(object = "xcmsSet"): get groupidx slot

  groupnames signature(object = "xcmsSet"): get textual names for peak groups

  groups<- signature(object = "xcmsSet"): set groups slot

  groups signature(object = "xcmsSet"): get groups slot

  groupval signature(object = "xcmsSet"): get matrix of values from peak data with a row for each peak group

  group signature(object = "xcmsSet"): find groups of peaks across samples that share similar m/z and retention times

  mslevel Getter method for the mslevel slot.

  peaks<- signature(object = "xcmsSet"): set peaks slot

  peaks signature(object = "xcmsSet"): get peaks slot

  plotrt signature(object = "xcmsSet"): plot retention time deviation profiles

  profinfo<- signature(object = "xcmsSet"): set profinfo slot

  profinfo signature(object = "xcmsSet"): get profinfo slot

  profMethod signature(object = "xcmsSet"): extract the method used to generate the profile matrix.

  profStep signature(object = "xcmsSet"): extract the profile step used for the generation of the profile matrix.

  retcor signature(object = "xcmsSet"): use initial grouping of peaks to do nonlinear loess retention time correction
Description

This virtual class provides an implementation-independent way to load mass spectrometer data from various sources for use in an `xcmsRaw` object. Subclasses can be defined to enable data to be loaded from user-specified sources. The virtual class `xcmsFileSource` is included out of the box which contains a file name as a character string.

When implementing child classes of `xcmsSource`, a corresponding `loadRaw-methods` method must be provided which accepts the `xcmsSource` child class and returns a list in the format described in `loadRaw-methods`.

References

A parallel effort in metabolite profiling data sharing: [http://metlin.scripps.edu/](http://metlin.scripps.edu/)

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>

Author(s)

Colin A. Smith, <csmith@scripps.edu>, Johannes Rainer <johannes.rainer@eurac.edu>
Objects from the Class

A virtual Class: No objects may be created from it.

Author(s)

Daniel Hackney, <dan@haxney.org>

See Also

`xcmsSource-methods` for creating `xcmsSource` objects in various ways.

---

```
xcmsSource-methods  Create an xcmsSource object in a flexible way
```

Description

Users can define alternate means of reading data for `xcmsRaw` objects by creating new implementations of this method.

Methods

```
signature(object = "xcmsSource")  Pass the object through unmodified.
```

Author(s)

Daniel Hackney, <dan@haxney.org>

See Also

`xcmsSource`
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