

CAMERA

April 20, 2011

annotatedDiffreport *Deconvolute/Annotate LC/ESI-MS data*

Description

Wrapper function for the `xcms` `diffreport` and the `annotate` function. Returns a `diffreport` with the result from the annotation progress.

Usage

```
annotatedDiffreport(object, sample=NA, sigma = 6, perfwth = 0.6, cor_eic_th = 0.7,
  multiplier = 3, polarity = "positive", nSlaves = 1, psg_list =
  rules = NULL, class1 = levels(sampclass(object))[1], class2 = le
  eicmax = 0, eicwidth = 200, sortpval = TRUE, classeic = c(class
  metlin = FALSE, h = 480, w = 640, ...)
```

Arguments

<code>object</code>	<code>xcmsSet</code> with peak group assignments
<code>sample</code>	Index of which sample is used for the correlation, NA for auto-selection
<code>sigma</code>	Isotopic peak relationship table
<code>perfwth</code>	Adduct/Fragment peak relationship table
<code>cor_eic_th</code>	correlation threshold (0..1)
<code>maxcharge</code>	max charge of the ions
<code>maxiso</code>	max number of isotopes
<code>ppm</code>	ppm error
<code>mzabs</code>	absolut error
<code>multiplier</code>	max. number n of [nM+x] clusterions
<code>polarity</code>	Which polarity mode was used for measuring of the ms sample
<code>nSlaves</code>	Number of slaves for parallel calculation (Warning: Beta)
<code>psg_list</code>	Index-list of pseudospectra. Only for those ones will the annotation be calculated. Useful as a speed-up
<code>pval_th</code>	pval threshold. Creates a new <code>psg_list</code> . A pseudospectra is selected if it contains peaks, with <code>pval < pval_th</code>

<code>fc_th</code>	Same as <code>pval</code> . Select those groups with contains peaks with fold-change > <code>fc_th</code> . <code>Pval_th</code> and <code>fc_th</code> can be combined
<code>quick</code>	If <code>quick</code> is TRUE, only <code>groupFWHM</code> and <code>findIsotopes</code> will be calculated. Useful for preselecting groups with <code>psg_list</code>
<code>rules</code>	User defined ruleset
<code>class1</code>	character vector with the first set of sample classes to be compared
<code>class2</code>	character vector with the second set of sample classes to be compared
<code>filebase</code>	base file name to save report, <code>.tsv</code> file and <code>_eic</code> will be appended to this name for the tabular report and EIC directory, respectively. if blank nothing will be saved
<code>eicmax</code>	number of the most significantly different analytes to create EICs for
<code>eicwidth</code>	width (in seconds) of EICs produced
<code>sortpval</code>	logical indicating whether the reports should be sorted by p-value
<code>classeic</code>	character vector with the sample classes to include in the EICs
<code>value</code>	intensity values to be used for the diffreport. If <code>value="into"</code> , integrated peak intensities are used. If <code>value="maxo"</code> , maximum peak intensities are used. If <code>value="intb"</code> , baseline corrected integrated peak intensities are used (only available if peak detection was done by <code>findPeaks.centWave</code>).
<code>metlin</code>	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
<code>h</code>	Numeric variable for the height of the eic and boxplots that are printed out.
<code>w</code>	Numeric variable for the width of the eic and boxplots print out made.
<code>...</code>	optional arguments to be passed to <code>mt.teststat</code>

Details

Batch script wrapper for combining the annotation and the diffreport for a (grouped) `xcmsSet` `xs`. Function list: 1: `diffreport()`, 2: `groupFWHM()`, 3: `findIsotopes()`, 4: `groupCorr()`, 5: `findAdducts()` For a speedup calculation users can create a quick run, with `quick = TRUE` to preselect pseudospectra of interest. The indices of those pseudospectra are set with `psg_list` in a second run. On the other hand, a automatic selection with `pval_th` and/or `fc_th` can be performed. Returns the normal `xcms` diffreport table, with the additional CAMERA slots

Value

`annotate` returns an `xsAnnotate` object. For more information about see [xsAnnotate-class](#)

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
#Multiple sample
library(CAMERA)
library(faahKO)
xs.grp      <- group(faahko)
```

```

xs.fill    <- fillPeaks(xs.grp)

#fast preselection
diffreport <- annotateDiffreport(xs.fill,quick=TRUE)
index <- c(1,18,35,45,56) #Make only for those grps a adduct annotation
diffreport2 <- annotateDiffreport(xs.fill,psg_list=index)

#automatic selection, all groups with peaks p-val < 0.05 and fold-change > 3
diffreport <- annotateDiffreport(xs.fill,pval_th=0.05,fc=3)

```

 annotate

Deconvolute/Annotate LC/ESI-MS data

Description

Annotate isotope peaks, adducts and fragments for a (grouped) `xcmsSet` `xs`. Returns a `xsAnnotate` object.

Usage

```
annotate(object, sigma = 6, perfw hm = 0.6, cor_eic_th = 0.75, maxcharge = 3, max
```

Arguments

<code>object</code>	<code>xcmsSet</code> with peak group assignments
<code>sigma</code>	Isotopic peak relationship table
<code>perfw hm</code>	Adduct/Fragment peak relationship table
<code>cor_eic_th</code>	correlation threshold (0..1)
<code>maxcharge</code>	max charge of the ions
<code>maxiso</code>	max number of isotopes
<code>ppm</code>	ppm error
<code>mzabs</code>	absolut error
<code>multiplier</code>	max. number <code>n</code> of <code>[nM+x]</code> clusterions
<code>sample</code>	Index of which sample is used for the correlation, NA for auto-selection
<code>quick</code>	Use only <code>groupFWHM</code> and <code>findIsotopes</code>
<code>psg_list</code>	Calculation will only be done for the selected groups
<code>polarity</code>	Which polarity mode was used for measuring of the ms sample
<code>nSlaves</code>	Number of slaves for parallel calculation (Warning: Beta)
<code>max_peaks</code>	If run in parallel mode, value defines how much peaks will be calculated in every thread

Details

Batch script for a annotation for a (grouped) `xcmsSet` `xs`. Generate intern a `xsAnnotate` object and calls the member function for the annotation step. Function list: 1: `groupFWHM()`, 2: `findIsotopes()`, 3: `groupCorr()`, 4: `findAdducts()` Return the `xsAnnotate` object which all the annotations. For more information see the funtion manpages.

Value

annotate returns an xsAnnotate object. For more information about see [xsAnnotate-class](#)

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
xsa <- annotate(xs)
```

findAdducts-methods

Calculate Adducts and Annotate LC/ESI-MS Spectra

Description

Annotate adducts (and fragments) for a xsAnnotate object. Returns a xsAnnotate object with annotated pseudospectra.

Usage

```
findAdducts(object, ppm=5, mzabs=0.015, multiplier=3, polarity=NULL, rules=NULL)
```

Arguments

object	the xsAnnotate object
ppm	ppm error for the search
mzabs	allowed variance for the search
multiplier	highest number(n) of allowed clusterion [nM+ion]
polarity	Which polarity mode was used for measuring of the ms sample
rules	personal ruleset or with NULL standard ruleset will be calculated
max_peaks	If run in parralel mode, this number defines how much peaks will be calculated in every thread
psg_list	Vector of pseudospectra indices. The correlation analysis will be only done for those groups

Details

Adducts (and fragments) are annotated for a xsAnnotate object. For every pseudospectra group, generated bei groupFWHM and groupCorr, all possible Adducts are calculated and mapped to the peaks. If at least two adducts match, a possible molecule-mass for the group can be calculated. After the annotation every masshypothese is checked against the charge of the calculated isotopes. It is recommend to call findIsotopes() before the annotation step.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
an <- findIsotopes(an) # optional but recommended.
# an <- groupCorr(an) # optional but very recommended step
an <- findAdducts(an,polarity="positive")
peaklist <- getPeaklist(an) # get the annotated peak list
```

findIsotopes-methods

Deconvolute/Annotate LC/ESI-MS data

Description

Annotate isotope peaks for a `xsAnnotate` object. Returns a `xsAnnotate` object with annotated isotopes.

Arguments

<code>object</code>	the <code>xsAnnotate</code> object
<code>maxcharge</code>	max. number of the isotope charge
<code>maxiso</code>	max. number of the isotope peaks
<code>ppm</code>	ppm error for the search
<code>mzabs</code>	allowed variance for the search

Details

Isotope peaks are annotated for a `xsAnnotate` object according to given rules (`maxcharge`, `maxiso`). The algorithm benefits from a earlier grouping of the data, with `groupFWHM`. Generates a list of all possible isotopes, which is stored in `object@isotopes`. Those isotope information will be used in the `groupCorr` function.

Methods

```
object = "xsAnnotate" findIsotopes(object, maxcharge=3, maxiso=3, ppm=5,
mzabs=0.01)
```

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
an <- findIsotopes(an)
```

findNeutralLoss *Find pseudospectra that contains a specific neutral loss*

Description

The method searches in every pseudospectra for a distance between two ions matching a provided mass difference. It returns a xcmsSet object containing the matching peaks.

Usage

```
findNeutralLoss(object, mzdiff=NULL, mzabs=0, mzppm=10)
```

Arguments

object	xsAnnotate object
mzdiff	neutral loss in Dalton
mzabs	absolut allowed mass difference
mzppm	relative allowed mass difference

Details

The function needs a xsAnnotate object after groupCorr or groupFWHM. The resulting object is a artificial xcmsSet, where the peaks with the specific neutral loss are stored in xcmsSet@peaks.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
xs.pseudo <- findNeutralLoss(an,mzdiff=18.01,mzabs=0.01) #Searches for Peaks with water
xs.pseudo@peaks #show Hits
```

`findNeutralLossSpecs`*Find pseudospectra that contains a specific neutral loss*

Description

The method searches in every pseudospectra for a distance between two ions matching a provided mass difference. It returns a boolean vector with the length equals to the number of pseudospectra, where a hit is marked with TRUE.

Usage

```
findNeutralLossSpecs(object, mzdiff=NULL, mzabs=0, mzppm=10)
```

Arguments

<code>object</code>	xsAnnotate object
<code>mzdiff</code>	neutral loss in Dalton
<code>mzabs</code>	absolut allowed mass difference
<code>mzppm</code>	relative allowed mass difference

Details

The function needs a xsAnnotate object after groupCorr or groupFWHM.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
hits <- findNeutralLossSpecs(an,mzdiff=18.01,mzabs=0.01) #Searches for Pseudospectra with
```

`getIsotopeCluster` *Retrieve the annotatad isotopes*

Description

Extract all annotated isotope cluster. Returns a list with one element per cluster. A element contains the charge of the molecule and a peakmatrix with mz and intensity value.

Usage

```
getIsotopeCluster(object, number=NULL, value="maxo")
```

Arguments

object	xsAnnotate object
number	Set to NULL extract all isotope cluster or to specific choosen ones
value	Which intensity values should be extracted. Allowed values are: maxo, into, intb

Details

This method extract the isotope annotation from a xsAnnotate object. The order of the resulting list is the same as the one in the peaklist. In the case of a multiple sample the intensity value for a peak is retrieved from the sample, which has been choosen for the pseudospectra in the grouping step.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
#single sample
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
an <- findIsotopes(an)
isolist <- getIsotopeCluster(an)
isolist[[10]] #get IsotopeCluster 10

#multiple sample
library(faahKO)
xs <- group(faahko)
xs <- fillPeaks(xs)
an <- xsAnnotate(xs)
an <- groupFWHM(an)
an <- findIsotopes(an)
isolist <- getIsotopeCluster(an)

##Interaction with Rdisop
## Not run:
library(Rdisop)
isotopes.decomposed <- lapply(isolist, function(x) {
  decomposeIsotopes(x$peaks[,1], x$peaks[,2], z=x$charge);
}) #decomposed isotope cluster, filter steps are recommended

## End(Not run)
```

getPeaklist

Retrieve the annotatad peaklist

Description

Extract all information from an xsAnnotate object. Returns a peaklist with annotated peaks.

Usage

```
getPeaklist(object)
```

Arguments

object xsAnnotate object

Details

This function extract the peaktable from an xsAnnotate object, containing three additional columns (isotopes, adducts, pseudospectrum) with represents the annotation results. For a grouped xcmsSet it returns the grouped peaktable.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
an <- findIsotopes(an)
an <- findAdducts(an,polarity="positive")
peaklist <- getPeaklist(an)
```

getpspectra

Retrieve a spectra-group peaklist

Description

Extract one group from a xsAnnotate object. Returns a peaklist with annotated peaks.

Usage

```
getpspectra(object, grp)
```

Arguments

object xsAnnotate object
grp index of pseudo-spectra-group

Details

xsAnnotate groups LC/MS Peaklist after there EIC correlation and FWHM. These function extract one of these so called "pseudo spectra groups" with include the peaklist with there annotations. The annotation depends on a before called findAdducts() (and findIsotopes()). Attention: The indices for the isotopes, are those from the whole peaklist. See getPeaklist().

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(c(file), method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)
peaklist <- getpspectra(an, 1)
```

groupCorr-methods *EIC correlation grouping of LC/ESI-MS data*

Description

Grouping the peaks after the correlation of the EICs into pseudospectragroups for a xsAnnotate object. Return a xsAnnotate object with group information.

Usage

```
groupCorr(object, cor_eic_th=0.75, psg_list = NULL, polarity = NA)
```

Arguments

object	The xsAnnotate object
cor_eic_th	Correlation threshold for the EIC correlation
psg_list	Vector of pseudospectra indices. The correlation analysis will be only done for those groups
polarity	Optional feature, that ensure that [M+H] ⁺ , [M+Na] ⁺ , [M+K] ⁺ in pos. mode and [M-H] ⁻ [M+Cl] ⁻ ions in neg. mode will not be seperated in different groups

Details

The algorithm correlates the EIC of a every peak with all others, to find the peaks that belong to one substance. LC/MS data should grouped with groupFWHM first. This step reduce the runtime a lot and increased the number of correct classifications. If you perform the findIsotope step first, annotated isotopes will always be in the same group.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
file      <- system.file('mzdata/MM14.mzdata', package = "CAMERA");
xs        <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5, 10));
an        <- xsAnnotate(xs);
an.group  <- groupFWHM(an);
an.iso    <- findIsotopes(an.group); #optional step
index     <- c(1,4); #Only group one and four will be calculate
an.grp.corr <- groupCorr(an.iso, psg_list=index, polarity="positive");

#For csv output
# write.csv(file="peaklist_with_isotopes.csv", getPeaklist(an))

#Multiple sample
library(faahKO)
xs.grp    <- group(faahko)

#With selected sample
xsa       <- xsAnnotate(xs.grp, sample=1)
xsa.group <- groupFWHM(xsa)
xsa.iso   <- findIsotopes(xsa.group) #optional step
index     <- c(1,4) #Only group one and four will be calculate
xsa.grp.corr <- groupCorr(xsa.iso, psg_list=index, polarity="positive")

#With automatic selection
xsa.auto  <- xsAnnotate(xs.grp)
xsa.grp   <- groupFWHM(xsa.auto)
xsa.iso   <- findIsotopes(xsa.grp) #optional step
index     <- c(1,4) #Only group one and four will be calculate
xsa.grp.corr <- groupCorr(xsa.iso, psg_list=index, polarity="positive")
#Note: Group 1 and 4 have no subgroups
```

groupFWHM-methods *FWHM-Grouping of LC/ESI-MS data*

Description

Group peaks of one `xsAnnotate` object after the FWHM of there retentiontimes into pseudospectra-groups. Returns a `xsAnnotate` object with group information.

Usage

```
groupFWHM(object, sigma = 6 , perfwhm = 0.6)
```

Arguments

<code>object</code>	the <code>xsAnnotate</code> object
<code>sigma</code>	the multiplier of the standard deviation
<code>perfwhm</code>	percentage of the width of the FWHM

Details

Every peak who eluated at the same time as a selected peak, will be part of the group. Same time is defined about the $Rt_med \pm FWHM * perfwhm$. For single sample the selection of peaks starts at the most abundant and goes down the smaller ones. In a multiple sample set you can define a sample, that will be used for the process or use the automatic selection. This select the most abundant peak as an representative for every peak group. Peak group means here those ones from the xcms grouping. The FWHM (full width at half maximum) of a peak is estimated as $FWHM = SD * 2.35$. The calculation of the SD, the peak is assumed as a normal distribution.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
#Single sample
file <- system.file('mzdata/MM14.mzdata', package = "CAMERA")
xs <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an <- xsAnnotate(xs)
an <- groupFWHM(an)

#Multiple sample
library(faahKO)
xs <- group(faahko)
#With selected sample
xs.anno <- xsAnnotate(xs, sample=1)
xs.group <- groupFWHM(xs.anno)

#With automatic selection
xs.anno.auto <- xsAnnotate(xs)
xs.group.auto <- groupFWHM(xs.anno.auto)
```

mm14

Extract of marker mixture 14 LC/MS data

Description

xcmsSet object containing quantitated LC/MS peaks from a marker mixture. The data is a centroided subset from 117-650 m/z and 271-302 seconds with 134 peaks. Positive ionization mode data in mzData file format.

Usage

```
data(mm14)
```

Format

The format is:

```

Formal class 'xcmsSet' [package "xcms"] with 8 slots
  @ peaks      : num [1:83, 1:11] 117 117 118 119 136
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : NULL
  .. .. ..$ : chr [1:11] "mz" "mzmin" "mzmax" "rt"
  ..@ groups   : logi[0 , 0 ]
  ..@ groupidx : list()
  ..@ phenoData:'data.frame': 1 obs. of  1 variable:
  .. ..$ class: Factor w/ 1 level "mzdata": 1
  ..@ rt       :List of 2
  .. ..$ raw    :List of 1
  .. .. ..$ : num [1:112] 270 271 271 271 272 ...
  .. ..$ corrected:List of 1
  .. .. ..$ : num [1:112] 270 271 271 271 272 ...
  ..@ filepaths: chr "mzdata/MM14.mzdata"
  ..@ profinfo  :List of 2
  .. ..$ method: chr "bin"
  .. ..$ step   : num 0.1
  ..@ polarity  : chr(0)

```

Details

The corresponding raw mzData files are located in the mzData subdirectory of this package.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Source

<http://doi:10.1186/1471-2105-9-504>

References

Data originally reported in "Highly sensitive feature detection for high resolution LC/MS" BMC Bioinformatics; 2008; 9:504.

plotEICs-methods *Plot extracted ion chromatograms from (multiple) Pseudospectra*

Description

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

Arguments

object	the xsAnnotate object
xraw	xcmsRaw object underlying the the xsAnnotate
maxlabel	How many m/z labels to print
sleep	seconds to pause between plotting EICs
...	other graphical parameters

Value

None.

Methods

```
object = "xsAnnotate" plotEICs(object, xraw, pspec=1:length(object@pspectra),
                               maxlabel=0, sleep=0)
```

Author(s)

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

See Also

[xsAnnotate-class](#), [png](#), [pdf](#), [postscript](#),

plotPsSpectrum-methods

Plot a Pseudospectrum

Description

Plot a pseudospectrum, with the most intense peaks labelled, to the current graphics device.

Arguments

object	the xsAnnotate object
pspec	ID of the pseudospectrum to print
log	Boolean, whether the log(intensity) should be shown
value	Which of a peak's intensities should be used
maxlabel	How many m/z labels to print
title	Main title of the Plot
mzrange	Which m/z range should plotted
sleep	Time (in seconds) to wait between successive Spectra, if multiple pspec are requested.

Value

None.

Methods

```
object = "xsAnnotate" plotPsSpectrum(object, pspec=NULL, log=FALSE, value="maxo",
                                     maxlabel=0, title=NULL, mzrange=numeric() sleep=0)
```

Author(s)

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

See Also

[xsAnnotate-class](#), [png](#), [pdf](#), [postscript](#),

Description

The package `xcms` contains several methods for calculating a distance between two sets of peaks. The CAMERA method `psDist` is the generic wrapper to use these methods for processing two pseudospectra from two different `xsAnnotate` objects.

Arguments

<code>object1</code>	a <code>xsAnnotate</code> object with pseudospectra
<code>object2</code>	a <code>xsAnnotate</code> object with pseudospectra
<code>PSpec1</code>	index of pseudospectrum in <code>object1</code>
<code>PSpec2</code>	index of pseudospectrum in <code>object2</code>
<code>method</code>	method to use for distance calculation. See details.
<code>...</code>	<code>mzabs</code> , <code>mzppm</code> 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 one would use: `specDist(object1, object2, pspectrum1, pspectrum2, 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`. If the nickname of a method is called "meanMZmatch", the help page for that specific method can be accessed with `?specDist.meanMZmatch`.

Value

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

Methods

object1 = "xsAnnotate" `specDist(object1, object2, pspectrum1, pspectrum2, method, ...)`

Author(s)

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

xsAnnotate-class *Class xsAnnotate, a class for annotate peak data*

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.

Objects from the Class

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

Slots

`annoGrp`: Assignment of mass hypotheses to correlation groups
`annoID`: The assignment of peaks to the mass difference rule used
`derivativeIons`: List with annotation result for every peak
`formula`: Matrix containing putative sum formula (intended for future use)
`isoID`: Matrix containing IDs and additional of all annotated isotope peaks
`groupInfo`: (grouped) Peaktable with "into" values
`isotopes`: List with annotated isotopid results for every peak
`polarity`: A single string with the polarity mode of the peaks
`pspectra`: List contains all pseudospectra with their peak IDs
`psSamples`: List containing information with sample was selected as representative (automatic selection)
`ruleset`: A dataframe describing the mass difference rules used for the annotation
`runParallel`: Flag if CAMERA runs in serial or parallel mode
`sample`: Number of the used xcmsSet sample (beforehand sample selection)
`xcmsSet`: The embedded xcmsSet

Methods

groupFWHM signature(object = "xsAnnotate"): group the peak data after the FWHM of the retention time
groupCorr signature(object = "xsAnnotate"): group the peak data after the correlation of the EICs
findIsotopes signature(object = "xsAnnotate"): search for possible isotopes in the spectra
findAdducts signature(object = "xsAnnotate"): search for possible adducts in the spectra
plotEICs signature(object = "xsAnnotate"): plot EICs of pseudospectra

Note

No notes yet.

Author(s)

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See Also

[xsAnnotate](#)

xsAnnotate	<i>Constructor for a xsAnnotate object which one assigned xcmsSet object</i>
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Description

This function handles the construction of xsAnnotate object. It extract the peaktable from a given xcmsSet, which is used for all further analysis. The xcmsSet can be a single sample or multiple sample experiment. Since some functions needs to go back into the raw data, the selection algorithm must be chosen for a multiple sample. CAMERA includes two different strategies: A fixed selection, which sample = index of sample, or the default automatic solution (sample = NA). The automatic solution chooses the best sample for a specific groups called pseudospectrum, see groupFWHM and groupCorr.

Usage

```
xsAnnotate(xs = NULL, sample=NA, nSlaves = 1)
```

Arguments

xs	a xcmsSet object
sample	Index of the group xcmsSet sample, that is used for the EIC correlations step. For automatic selection don't set a value.
nSlaves	For parallel mode set nSlaves higher than 1, but not higher than the number of cpu cores.

Value

A xsAnnotate object.

Author(s)

Carsten Kuhl, <ckuhl@ipb-halle.de>

See Also

[xsAnnotate-class](#)

Examples

```
library(faahKO)
xs <- group(faahko)
xs.anno <- xsAnnotate(xs, sample=1)
#With automatic selection
xs.anno.autoselect <- xsAnnotate(xs)
```

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