Package 'CAMERA'

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Title Collection of annotation related methods for mass spectrometry data

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Imports methods, xcms, RBGL, graph, graphics, grDevices, stats, utils, Hmisc, igraph

Suggests faahKO, RUnit, BiocGenerics, multtest

Enhances Rmpi, snow

Description Annotation of peaklists generated by xcms, rule based annotation of isotopes and adducts, isotope validation, EIC correlation based tagging of unknown adducts and fragments

License GPL (>= 2)

ByteCompile TRUE

URL http://msbi.ipb-halle.de/msbi/CAMERA/

BugReports https://github.com/sneumann/CAMERA/issues/new

biocViews ImmunoOncology, MassSpectrometry, Metabolomics

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Contents

annotate-methods *Automatic deconvolution/annotation of LC/ESI-MS data*

Description

Wrapper skript for automatic annotation of isotope peaks, adducts and fragments for a (grouped) xcmsSet `xs`. The function returns an xsAnnotate object.

Usage

```
annotate(object, sample=NA, nSlaves=1, sigma=6, perfwhm=0.6,
  cor_eic_th=0.75, graphMethod="hcs", pval=0.05, calcCiS=TRUE,
  calcIso=FALSE, calcCaS=FALSE, maxcharge=3, maxiso=4, minfrac=0.5,
  ppm=5, mzabs=0.015, quick=FALSE, psg_list=NULL, rules=NULL,
  polarity="positive", multiplier=3, max_peaks=100 ,intval="into")
```

Arguments

`object`	xcmsSet with peak group assignments
`sample`	xsAnnotate: Sample selection for grouped xcmsSet, see xsAnnotate-class
`nSlaves`	xsAnnotate: Use parallel CAMERA mode, require Rmpi
`sigma`	groupFWHM: multiplier of the standard deviation
`perfwhm`	groupFWHM: percentage of FWHM width
`cor_eic_th`	groupCorr: correlation threshold (0..1)
`graphMethod`	groupCorr: Method selection for grouping peaks after correlation analysis into pseudospectra
`pval`	groupCorr: significant correlation threshold
`calcCiS`	groupCorr: Use correlation inside samples for peak grouping
`calcIso`	groupCorr: Use isotopic relationship for peak grouping
`calcCaS`	groupCorr: Use correlation across samples for peak grouping
`maxcharge`	findIsotopes: max. ion charge
`maxiso`	findIsotopes: max. number of expected isotopes
`minfrac`	findIsotopes: The percentage number of samples, which must satisfy the C12/C13 rule for isotope annotation
`ppm`	General ppm error
`mzabs`	General absolut error in m/z
`quick`	Use only groupFWHM and findIsotopes
`psg_list`	Calculation will only be done for the selected groups
`rules`	findAdducts: User defined ruleset
`polarity`	findAdducts: Which polarity mode was used for measuring of the ms sample
`multiplier`	findAdducts: If no ruleset is provided, calculate ruleset with max. number n of [nM+x] clusterions
`max_peaks`	How much peaks will be calculated in every thread using the parallel mode
`intval`	General used intensity value (into, maxo, intb)

Details

Batch script for annotation of an (grouped) xcmsSet `xs`. Generates an xsAnnotate object by calling all involved functions for the annotation step. Function list: 1: groupFWHM() , 2: findIsotopes() , 3: groupCorr(), 4: findAdducts() Return the xsAnnotate object, which inherits all annotations. For more information about the parameters see the specific function manpages.

Value

`annotate` returns an xsAnnotate object. For more information about the xsAnnotate object see xsAnnotate-class.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

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

`annotateDiffreport` *Automatic deconvolution/annotation of LC/ESI-MS data*

Description

Wrapper function for the xcms diffreport and the annotate function. Returns a diffreport within the annotation results.

Usage

```
annotateDiffreport(object, sample=NA, nSlaves=1, sigma=6, perfwhm=0.6,
  cor_eic_th=0.75, cor_exp_th = 0.75, graphMethod="hcs", pval=0.05, calcCiS=TRUE,
   calcIso=FALSE, calcCaS=FALSE, maxcharge=3, maxiso=4, minfrac=0.5,
   ppm=5, mzabs=0.015, quick=FALSE, psg_list=NULL, rules=NULL,
   polarity="positive", multiplier=3, max_peaks=100, intval="into",
   pval_th = NULL, fc_th = NULL, sortpval=TRUE, ...)
```

Arguments

`object`	xcmsSet with peak group assignments
`sample`	xsAnnotate: Sample selection for grouped xcmsSet, see xsAnnotate-class
`nSlaves`	xsAnnotate: Use parallel CAMERA mode, require Rmpi
`sigma`	groupFWHM: multiplier of the standard deviation
`perfwhm`	groupFWHM: percentage of FWHM width

cor_eic_th	groupCorr: Correlation threshold for EIC correlation (0..1)
cor_exp_th	groupCorr: Threshold for intensity correlations across samples (0..1)
graphMethod	groupCorr: Method selection for grouping peaks after correlation analysis into pseudospectra
pval	groupCorr: significant correlation threshold
calcCiS	groupCorr: Use correlation inside samples for peak grouping
calcIso	groupCorr: Use isotopic relationship for peak grouping
calcCaS	groupCorr: Use correlation across samples for peak grouping
maxcharge	findIsotopes: max. ion charge
maxiso	findIsotopes: max. number of expected isotopes
minfrac	findIsotopes: The percentage number of samples, which must satisfy the C12/C13 rule for isotope annotation
ppm	General ppm error
mzabs	General absolut error in m/z
quick	Use only groupFWHM and findIsotopes
psg_list	Calculation will only be done for the selected groups
rules	findAdducts: User defined ruleset
polarity	findAdducts: Which polarity mode was used for measuring of the ms sample
multiplier	findAdducts: If no ruleset is provided, calculate ruleset with max. number n of [nM+x] clusterions
max_peaks	How much peaks will be calculated in every thread using the parallel mode
intval	General used intensity value (into, maxo, intb)
pval_th	pval threshold. Creates a new psg_list. A pseudospectra is selected if it contains peaks, with pval < pval_th
fc_th	Same as pval. Select those groups with contains peaks with fold-change > fc_th. Pval_th and fc_th can be combined
sortpval	Sort diffreport after pvalues
...	Diffreport parameters see diffreport

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

annotateDiffreport returns an diffreport, see diffreport, within additional columns containing the annotation results.

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,metlin = TRUE)

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

---

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

Description

Calculate the correlation across samples. Filtering correlation with specific parameters and returns a correlation matrix.

Usage

```
calcCaS(object,corval=0.75, pval=0.05, intval="into")
```

Arguments

object	The xsAnnotate object
corval	Correlation threshold for positive hits
pval	P-Value threshold for significance level of correlation
intval	Selection of the intensity values that should be used in the correlation analysis. Can be into, maxo or intb.

Details

Calculate pearson correlation between the peak intensites over all samples. Afterwards use cor.test for returning only significant correlation. Returns only those correlation, which are above both threshold. Set corval and pval to 0 to get the unfiltered correlation matrix. If the object is pregrouped with groupFWHM, then the correlation is only calculated between peaks within a pseudospectrum. Otherwise between all peaks.

Value

A matrix with 4 columns:

x	peak index according to peaktable
y	peak index according to peaktable
cor	correlation value between peak x and peak y
ps	pseudospektrum index for both peaks

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

See Also

calcCiS groupCorr xsAnnotate-class

Examples

```
library(CAMERA)
#Multiple sample
library(faahKO)
xs.grp       <- group(faahko)
#create xsAnnotate object
xsa          <- xsAnnotate(xs.grp)
#generate pseudospectra
xsa.group    <- groupFWHM(xsa)
#calculate correlation
correlationMatrix <- calcCaS(xsa.group)
```

---

calcCiS-methods *Calculate peak distance matrix after EIC correlation*

Description

Processing an xsAnnotate object and correlates peak EIC curves from one pseudospectrum, using a precalculated EIC matrix (getAllPeakEICs). It return a weighted edge list as distance matrix between peaks according to the correlation analysis. The edge value is the pearson correlation coefficent. The list can be used as input for calcPC.

Usage

```
calcCiS(object, EIC=EIC, corval=0.75, pval=0.05, psg_list=NULL)
```

Arguments

object	The xsAnnotate object
EIC	EIC Matrix
corval	Correlation threshold for the EIC correlation
pval	pvalue for testing correlation of significance
psg_list	Vector of pseudospectra indices. The correlation analysis will be only done for those 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. Only correlation with a higher value than the correlation threshold and significant p-values will be returned.

Value

A matrix with 4 columns:

x	peak index
y	peak index
cor	correlation value
ps	pseudospectrum index, which contains x and y

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

See Also

calcCaS groupCorr getAllPeakEICs xsAnnotate-class

---

calcIsotopes-methods *Calculate isotope distance matrix from xsAnnotate object*

Description

Processing an xsAnnotate object with annotated isotopes (findIsotopes). It return a weighted edge list as distance matrix between peaks according to the isotope annotation. The edge value for recognized isotopes is 1 for all cases. The list can be used as input for calcPC.

Arguments

object	xsAnnotate object

Value

A matrix with 4 columns:

x	peak index
y	peak index
cor	edge value, always 1
ps	pseudospectrum index, which contains x and y

Methods

object = "xsAnnotate" `calcIsotopes(object)`

Author(s)

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

See Also

calcPC xsAnnotate-class

---

calcPC-methods *Peakclustering into pseudospectra according to a distance matrix*

Description

A number of clustering methods exist in CAMERA. `calcPC` is the generic method.

Usage

```
calcPC(object, method, ...)
```

Arguments

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

Details

This algorithms cluster peaks from a xsAnnotate object into pseudospectra according to a provided distance matrix. Therefore all peaks are transformend into a graph, with peaks as nodes and the value from the distance matrix as edges. Afterwards a graph separation algorithm is applied, which searches in the graph for clusters. See the manpages of the specific clustering algorithms for more information.

If the xsAnnotate is pregrouped, for example groupFWHM, only the already existing groups will be further processed.

The different algorithms that can be used by specifying them with the method argument. For example to use the highly connected subgraphs approach by E. Hartuv, R. Shamir, (1999), one would use: calcPC(object, method="hcs"). This is also the default, see calcPC.hcs.

Further arguments given by ... are passed through to the function implementing the method, which are most likely ajc. The parameter ajc is the peak distance matrix.

getOption("BioC")$CAMERA$findPeaks.methods returns a character vector of *nicknames* for the algorithms available.

The function returns a xsAnnotate object with grouping information, as list of peak indices. They are stored as object@pspectra.

See Also

calcPC.lpc calcPC.hcs xsAnnotate-class

---

calcPC.hcs *Peakclustering into pseudospectra with the highly connected subgraphs approach*

Description

Cluster peaks from an xsAnnotate object into pseudospectra

Arguments

object	xsAnnotate object
ajc	Weighted symbolic edge list as four column matrix ("x","y","cor","ps"). Columns x,y are peak indices, cor the edge value and ps the pseudospectrum index, where both peaks occur.
psg_list	additional vector ps pseudospectra indices, which are used in the clustering. If set to NULL all pseudospectra will be processed.

Details

In some cases, is the peak grouping after retentiontime with groupFWHM not enough to separate co-elution compounds. Therefore groupCorr use additional correlation analysis to achieve a separation. calcPC is part of this approach, which takes the calculated weighted edge list and performs the graph clustering. It returns an xsAnnotate object with further separated pseudospectra.

Methods

object = "xsAnnotate" calcPC.hcs(object, ajc=NULL, psg_list=NULL)

Author(s)

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

See Also

calcPC groupCorr highlyConnSG xsAnnotate-class

---

calcPC.lpc *Peakclustering into pseudospectra with the label-propagation-community algorithm*

Description

Cluster peaks from an xsAnnotate object into pseudospectra

Arguments

object	xsAnnotate object
ajc	Weighted symbolic edge list as four column matrix ("x","y","cor","ps"). Columns x,y are peak indices, cor the edge value and ps the pseudospectrum index, where both peaks occur.
psg_list	additional vector ps pseudospectra indices, which are used in the clustering. If set to NULL all pseudospectra will be processed.

Details

In some cases, is the peak grouping after retentiontime with groupFWHM not enough to separate co-elution compounds. Therefore groupCorr use additional correlation analysis to achieve a separation. calcPC is part of this approach, which takes the calculated weighted edge list and performs the graph clustering. It returns an xsAnnotate object with further separated pseudospectra.

Methods

object = "xsAnnotate" `calcPC.lpc(object, ajc=NULL, psg_list=NULL)`

Author(s)

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

See Also

calcPC groupCorr xsAnnotate-class label.propagation.community

cleanParallel *Cleans up with spawned slave processes after use*

Description

The spawned slaves processes, which are created within the parallel mode, are closed explicit.

Usage

```
cleanParallel(object)
```

Arguments

object	xsAnnotate object

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

```
## Not run:   library(CAMERA)
  file <- system.file('mzML/MM14.mzML', package = "CAMERA")
  xs   <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
  an   <- xsAnnotate(xs, polarity="positive", nSlaves=2)
  an   <- groupFWHM(an)
  an   <- findAdducts(an)
  cleanParallel(an)

## End(Not run)
```

combinexsAnnos *Check CAMERA ion species annotation due to matching with opposite ion mode*

Description

This function check annoations of ion species with the help of a sample from opposite ion mode. As first step it searches for pseudospectra from the positive and the negative sample within a retention time window. For every result the m/z differences between both samples are matched against specific rules, which are combinations from pos. and neg. ion species. As example M+H and M-H with a m/z difference of 2.014552. If two ions matches such a difference, the ion annotations are changed (previous annotation is wrong), confirmed or added. Returns the peaklist from one ion mode with recalculated annotations.

Usage

```
combinexsAnnos(xsa.pos, xsa.neg, pos=TRUE, tol=2, ruleset=NULL)
```

Arguments

xsa.pos	xsAnnotate object with positive ion mode
xsa.neg	xsAnnotate object with neagtive ion mode
pos	If TRUE the peaklist from the positive mode is returned, if FALSE the negative
tol	Retention time window in seconds
ruleset	Matrix of matching rules, see example

Details

Both xsAnnotate object should be full processed (grouping and annotation). Without previous annotation the resulting peaklist only includes annotation with matches peaks from both mode according to the rule(s). With ruleset=NULL the function only looks for M+H/M-H pairs. The ruleset is a two column matrix with includes rule indices from the rule table of both xsAnnotate objects. ruleset <- cbind(1,1) would create the M+H/M-H rule, since the first rule of xsa.pos@ruleset and xsa.neg@ruleset is M+H respectively M-H. Only rules with identical charge can be combined!

Value

Returns a (normal) CAMERA peaklist with a additional column neg. Mode or pos. Mode, where matching peaks from the opposite mode are noted.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
 ## Not run:
 #Searches for M+H/M-H combinations within a retention time window of 2 seconds
 peaklist.pos <- combinexsAnnos(xsa.pos, xsa.neg, tol=2)

## End(Not run)
```

---

compoundLibraries *The supported compound databases*

Description

Returns a set of supported compound databases

Usage

```
compoundLibraries()
```

Value

Vector of supported compound databases

Author(s)

Hendrik Treutler

Examples

```
compoundLibraries()
```

`compoundQuantiles` *compoundQuantiles constructor*

Description

constructor of class compoundQuantiles

Usage

```
compoundQuantiles(compoundLibrary = "kegg", massWindowSize = 50)
```

Arguments

`compoundLibrary`	the database; see compoundLibraries() for a list of supported databases
`massWindowSize`	the mass window size for grouping compounds; see massWindowSizes(compoundLibrary = "kegg") for a list of supported databases for e.g. the database kegg

Value

the compoundQuantiles object

Author(s)

Hendrik Treutler

Examples

```
cpObj <- compoundQuantiles()
```

compoundQuantiles-class

Class compoundQuantiles encapsulates compound statistics from different databases.

Description

The user is able to get the expected number of atoms of element e (C, N, ...) for a compound of mass m for a q-quantile. I.e. getAtomCount(object = compoundQuantiles(), element = e, mass = m, quantile = q) returns the number of atoms of element e in a compound of mass m in the lowest-(q*100) (sorted ascending by the possible number of atoms of element e for compounds of such mass).

The user is able to get the expected proportion between the intensities of two isotope peaks for a compound of mass m for a q-quantile. I.e. getIsotopeProportion(object = compoundQuantiles(), isotope1 = i1, isotope2 = i2, mass = m, quantile = q) returns the isotope proportion i1 / i2 for a compound of mass m in the lowest-(q*100) (sorted ascending by the possible isotope proportions for compounds of such mass).

Objects from the Class

Objects can be created with the `compoundQuantiles` constructor.

Slots

`compoundLibrary`: The compound library to rely on (kegg, chebi, ...)

`massWindowSize`: The mass window size of the compound statistics (25, 100, ...)

`minCompoundMass`: Minimum compound mass for which there are statistics

`maxCompoundMass`: Maximum compound mass for which there are statistics

`numberOfMassWindows`: Number of mass windows

`numberOfIsotopes`: Number of isotopes for which there are isotope ratio quantiles

`isotopeSet`: The set of isotopes for which there are isotope ratio quantiles

`elementSet`: The set of elements for which there are element count statistics

`quantileSet`: The set of quantiles for which there are isotope ratio statistics

`eleCounters_e_q_mw`: Three dimensional array containing the element count statistics (element, quantile, mass window index)

`proportions_i_q_mw`: Three dimensional array containing the isotope ratio quantiles relative to the monoisotopic peak (isotope index, quantile, mass window index)

Methods

getAtomCount `signature(object = "xsAnnotate")`: returns the number of atoms of the specified element for the given quantile and mass window index

getIsotopeProportion,compoundQuantiles-method `signature(object = "xsAnnotate")`: returns the isotope ratio of the specified isotope for the given quantile and mass window index relative to the monoisotopic peak

Note

No notes yet.

Author(s)

Hendrik Treutler, <hendrik.treutler@ipb-halle.de>

See Also

compoundQuantiles getAtomCount getIsotopeProportion

---

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, max_peaks=100, psg_list=NULL, intval="maxo")
```

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
intval	choose intensity values. Allowed values are into, maxo, intb

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('mzML/MM14.mzML', 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 *Deconvolute/Annotate LC/ESI-MS data*

Description

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

Usage

```
findIsotopes(object, maxcharge=3, maxiso=4, ppm=5, mzabs=0.01, intval=c("maxo","into","intb"), minfr
```

Arguments

object	the xsAnnotate object
maxcharge	max. number of the isotope charge
maxiso	max. number of the isotope peaks
ppm	ppm error for the search
mzabs	allowed variance for the search
intval	choose intensity values for C12/C13 check. Allowed values are into, maxo, intb
minfrac	in case of multiple samples, percentaged value of samples, which have to contain the correct C12/C13 ratio and are not NA
isotopeMatrix	four column m/z-diff and ratio Matrix, for matching isotopic peaks.
filter	Should C12/C13 filter be applied

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 funtion. The itensity of the C13 isotope peak is checked against the C12 of proper ratio. In the case of mulitiple sample, all samples will be tested. Minfrac describe the minimal percentaged of samples, which must passed the test. If peaks are NA, then this sample is skipped and the ratio is (found correct C12/C13 ratio) / (samples containing C12 and C13 peak).

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

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

`findIsotopesWithValidation`

Deconvolute/Annotate LC/ESI-MS data

Description

Annotate validated isotope clusters for a xsAnnotate object. Returns a xsAnnotate object with annotated isotopes. Validation of isotope clusters is based on statistics of the KEGG database implemented in S4 class object `compoundQuantiles`.

Usage

```
findIsotopesWithValidation(object, maxcharge=3, ppm=5, mzabs=0.01, intval=c("maxo","into","intb"), v
```

Arguments

`object`	the `xsAnnotate` object
`maxcharge`	max. number of the isotope charge
`ppm`	ppm error for the search
`mzabs`	allowed variance for the search
`intval`	choose intensity values for C12/C13 check. Allowed values are into, maxo, intb
`validateIsotopePatterns`	logical, if TRUE putative isotope clusters are validated based on KEGG database statistics.
`database`	the database which is the basis for isotope cluster validation. One of `compoundLibraries()`.

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 funtion. The ratios between isotope peaks are checked against the mass–specific $99%$ confidence interval based on statistics of the KEGG database.

Author(s)

Hendrik Treutler <hendrik.treutler@ipb-halle.de>

References

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

findIsotopes

Examples

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

---

findKendrickMasses *Find specfic mass defects using Kendrick mass scales*

Description

Todo

Usage

```
findKendrickMasses(object, masses=c(14, 14.01565),
maxHomologue=4, error=0.002, time=60, intval="maxo",
plot=FALSE)
```

Arguments

object	xsAnnotate object
masses	nominal mass and exact mass
error	allowed mass difference in Da for matching Kendrick mass defect
maxHomologue	max number of homologue
time	allowed retention time difference between homologues
intval	intensity value (allowed values: maxo,into or intb)
plot	plot hits

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

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

#With specific selected sample
xsa     <- xsAnnotate(xs)
#Screen for substance with CH2 differences
findKendrickMasses(xsa, masses=c(14, 14.01565), plot=TRUE)
```

---

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('mzML/MM14.mzML', package = "CAMERA")
xs   <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
an   <- xsAnnotate(xs)
an   <- groupFWHM(an)
#Searches for Peaks with water loss
xs.pseudo <- findNeutralLoss(an,mzdiff=18.01,mzabs=0.01)
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

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.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

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

`getAllPeakEICs` *Generate EIC information from raw data*

Description

Generate EIC data out of the raw data, according to the peak peaker information.

Usage

```
getAllPeakEICs(object, index)
```

Arguments

`object`	The `xsAnnotate` object
`index`	Sample index vector, with the same length as the number of peaks. Encoding from with sample the peak should be extracted. If all peaks should be generated from the same sample set index = rep(sample index, peak count)

Details

The function extract from the raw data the EIC curves. Therefore all .netcdf, .mzML etc. files must be acessable. It returns a list with two item.

Value

A list with items:

`EIC`	EIC Matrix with rows = number of peaks and columns = maxscans. It contains mostly NA values and only in that part, where a peak had been found, the intensity information.
`scantimes`	Scantimes of each sample

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

See Also

`xsAnnotate-class`

Examples

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

#create xsAnnotate object
xsa          <- xsAnnotate(xs.grp)
#generate pseudospectra
xsa.group    <- groupFWHM(xsa)

#calculate correlation
tmp <- getAllPeakEICs(xsa.group,index=rep(1,nrow(xsa.group@groupInfo)))
#extract EIC matrix
EIC.matrix <- tmp$EIC;
```

`getAtomCount,compoundQuantiles-method`

The number of atoms of the given element

Description

Returns the number of atoms the specified element in a compound of the specified mass for the specified quantile level

Usage

```
## S4 method for signature 'compoundQuantiles'
getAtomCount(object, element, mass, quantile)
```

Arguments

`object`	A compoundQuantiles object
`element`	The element of interest specified by element symbol
`mass`	The mass of the compound specified in atomic units (=dalton)
`quantile`	The quantile level for the number of atoms

Value

The number of atoms

Author(s)

Hendrik Treutler

Examples

```
cpObj <- compoundQuantiles()

compoundMass <- 503
quantileLow   <- 0.05
quantileHigh  <- 0.95
element <- "C"
countLow  <- getAtomCount(object = cpObj, element = element, mass = compoundMass, quantile = quantileLow)
countHigh <- getAtomCount(object = cpObj, element = element, mass = compoundMass, quantile = quantileHigh)

print(paste("The ", (quantileHigh - quantileLow) * 100, "% confidence interval for the number of atoms of element ",
```

---

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", sampleIndex=NULL)
```

Arguments

object	xsAnnotate object
number	Set to NULL extract all isotope cluster or to specific chosen ones
value	Which intensity values should be extracted. Allowed values are: maxo, into, intb
sampleIndex	Selection vector with indexes to select from which sample(s) the intensity values should be retrieved. If set to NULL the sample is selected, which has been chosen for the pseudospectra in the grouping step

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, see getPeaklist.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
#single sample
library(CAMERA)
file <- system.file('mzML/MM14.mzML', 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)

#Select from multiple samples

isolist <- getIsotopeCluster(an, sampleIndex=c(1,2,5))

##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)
```

---

getIsotopeProportion,compoundQuantiles-method

The proportion of the intensities of two isotope peaks

Description

Returns the proportion of the intensities of isotope1 versus isotope2 for a compound of the given mass for the given quantile level

Usage

```
## S4 method for signature 'compoundQuantiles'
getIsotopeProportion(object, isotope1, isotope2,
  mass, quantile)
```

Arguments

object	A compoundQuantiles object
isotope1	The divident isotope ranging from 0 (the monoisotopic peak) to 5
isotope2	The divisor isotope ranging from 0 (the monoisotopic peak) to 5
mass	The mass of the compound specified in atomic units (=dalton)
quantile	The quantile level for the isotope proportion

Value

The isotope proportion

Author(s)

Hendrik Treutler

Examples

```
cpObj <- compoundQuantiles(compoundLibrary = "kegg")

compoundMass <- 503
isotope1 <- 0
isotope2 <- 1
quantileLow   <- 0.05
quantileHigh  <- 0.95

propLow  <- getIsotopeProportion(object = cpObj, isotope1 = isotope1, isotope2 = isotope2, mass = compoundMass, qua
propHigh <- getIsotopeProportion(object = cpObj, isotope1 = isotope1, isotope2 = isotope2, mass = compoundMass, qua
print(paste("The ", (quantileHigh - quantileLow) * 100, "% confidence interval for the proportion of isotopes ", iso
```

---

getPeaklist *Generate the annotatad peaklist*

Description

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

Usage

```
getPeaklist(object, intval="into")
```

Arguments

object	xsAnnotate object
intval	Choose intensity values. Allowed values are into, maxo, intb, intf, maxf, area, depending on the feature detection algorithm used.

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('mzML/MM14.mzML', 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 peaklist of one or more pseudospectra*

Description

Extract group(s) from a xsAnnotate object. Returns a peaklist as matrix 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 or more of these so called "pseudo spectra groups" with include the peaklist with there annotations. The annotation depends on a before called findAdducts() (and findIsotopes()). Important: 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('mzML/MM14.mzML', package = "CAMERA")
xs   <- xcmsSet(c(file), method="centWave", ppm=30, peakwidth=c(5,10))
an   <- xsAnnotate(xs)
an   <- groupFWHM(an)
#For one group
peaklist <- getpspectra(an, 1)
#For two groups
peaklist <- getpspectra(an, c(1,2))
```

`getReducedPeaklist` *Generate reduced peaklist from the annotatad peaklist*

Description

Extract information from an xsAnnotate object. Returns a reduced peaklist with annotated peaks. For any putative compound in the pcgroup, all found adducts are pooled into one putative compound per group. Thus, the reduced peaklist only contains one annotated adduct per pcgroup.

Usage

```
getReducedPeaklist(object, method = "median", intval = "into", default.adduct.info = "first", mzrt.ra
```

Arguments

`object`	xsAnnotate object.
`method`	Choose reduction method. Allowed values are "sum", "median", "maxint", "pca".
`intval`	Choose intensity values. Allowed values are "into", "maxo", "intb".
`default.adduct.info`	Choose method to select adduct information. Allowed values are "first", "maxint", "maxpeaks"
`mzrt.range`	If TRUE, max and min values of mz and rt values of all adducts winthin a pcgroup are saved (not recommended).
`npeaks.sum`	If TRUE, the sum of all peaks of all adducts within a pcgroup is saved (not recommended).
`cleanup`	If TRUE, NA values and negative abundances are being set to zero and constant features (rows) are being removed.

Details

This function extracts a reduced peaktable from an xsAnnotate object. Normally, all adducts are grouped for any putative compounds and saved within the peaklist (see method getPeaklist). However, for statistical computation it is sometimes better to only work with putative compounds rather than with all of their adducts. Thus, this function pools all adducts for any putative compound into one putative compound per pcgroup. There are several methods to choose from how this is being done. Selection methods: "sum": The intensities of adducts are summed for each sample. "median" (default): The median intensities of adducts is calculated for each sample. "maxint": Only the adduct with the highest intensities throughout the samples is returned. "pca": A Principal Component Analysis is being performed for the adducts for the samples. and the PC1 values are taken as intensity information. Select mz / rt methods: "first" (default): The mz & rt information of the first adduct are taken. "maxint": The mz & rt information of the adduct that has highest intensities are taken. "maxpeaks": The mz & rt information of the adduct that has the most peaks are taken. In addition, when mzrt.range is TRUE, the min and max values of all mz and rt found in a group are stored within mzmin, mzmax and rtmin and rtmax (not recommended). In addition, when npeaks.sum is TRUE, all peaks within a pcgroup are summed (not recommended).

Author(s)

Kristian Peters <kpeters@ipb-halle.de>

Examples

```
library(CAMERA)
file <- system.file('mzML/MM14.mzML', 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.reduced <- getReducedPeaklist(an)
```

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

Description

Peak grouping after correlation information into pseudospectrum groups for an xsAnnotate object. Return an xsAnnotate object with grouping information.

Usage

```
groupCorr(object,cor_eic_th=0.75, pval=0.05, graphMethod="hcs",
calcIso = FALSE, calcCiS = TRUE, calcCaS = FALSE, psg_list=NULL, xraw=NULL,
cor_exp_th=0.75, intval="into", ...)
```

Arguments

object	The xsAnnotate object
cor_eic_th	Correlation threshold for EIC correlation
pval	p-value threshold for testing correlation of significance
graphMethod	Clustering method for resulting correlation graph. See calcPC for more details.
calcIso	Include isotope detection informationen for graph clustering
calcCiS	Calculate correlation inside samples
calcCaS	Calculate correlation accross samples
psg_list	Vector of pseudospectra indices. The correlation analysis will be only done for those groups
xraw	Optional xcmsRaw object, which should be used for raw data extraction
cor_exp_th	Threshold for intensity correlations across samples
intval	Selection of the intensity values (such as "into") that should be used in the correlation analysis. See getPeaklist for all allowed values.
...	Additional parameter

Details

The algorithm calculates different informations for group peaks into so called pseudospectra. This pseudospectra contains peaks, with have a high correlation between each other. So far three different kind of information are available. Correlation of intensities across samples (need more than 3 samples), EIC correlation between peaks inside a sample and additional the informationen about recognized isotope cluster can be included. After calculation of all these informations, they are combined as edge value into a graph object. A following graph clustering algorithm separate the peaks (nodes in the graph) into the pseudospectra.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

See Also

calcCiS calcCaS calcPC xsAnnotate-class

Examples

```
library(CAMERA)
file        <- system.file('mzML/MM14.mzML', 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 for using isotope information
an.grp.corr <- groupCorr(an.iso, calcIso=TRUE);

#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
xsa.grp.corr <- groupCorr(xsa.iso, calcIso=TRUE)

#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
#We use also correlation across sample
xsa.grp.corr <- groupCorr(xsa.iso, psg_list=index, calcIso=TRUE, calcCaS=TRUE)
#Note: Group 1 and 4 have no subgroups
```

---

groupDen *Density-Grouping of LC/ESI-MS data*

Description

Group peaks of a xsAnnotate object according to peak distributions in chromatographic time into pseudospectra-groups. Works analogous as the group.density method of xcms. Returns xsAnnotate object with pseudospectra informations.

Usage

```
groupDen(object, bw = 5 , ...)
```

Arguments

object	the xsAnnotate object
bw	bandwidth (standard deviation or half width at half maximum) of gaussian smoothing kernel to apply to the peak density chromatogram
...	Further Arguments, NYI

Details

The grouping strongly depends on the bw parameter. For an UPLC a good starting point is smaller or around 1.

Value

Returns a grouped xsAnnotate object.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
#Single sample
file <- system.file('mzML/MM14.mzML', package = "CAMERA")
xs   <- xcmsSet(file, method="centWave", ppm=30, peakwidth=c(5,10))
xsa   <- xsAnnotate(xs)
xsa.grp   <- groupDen(xsa, bw=0.5)

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

#With specific selected sample
xsa     <- xsAnnotate(xs, sample=1)
xsa.grp <- groupDen(xsa)

#With automatic selection
xsa.auto     <- xsAnnotate(xs)
xsa.grp.auto <- groupDen(xsa.auto)
```

---

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

Description

Group peaks of a xsAnnotate object according to their retention time into pseudospectra-groups. Uses the peak FWHMs as grouping borders. Returns xsAnnotate object with pseudospectra informations.

Usage

```
groupFWHM(object, sigma = 6 , perfwhm = 0.6, intval = "maxo")
```

Arguments

object	the xsAnnotate object
sigma	the multiplier of the standard deviation
perfwhm	percentage of the width of the FWHM
intval	intensity values for ordering. Allowed values are into, maxo, intb

Details

Every peak that shares a retention time with a selected peak will be part of the group. Same timepoint is defined about the Rt_med +/- FWHM * perfwhm. For a single sample `xcmsSet`, the selection of peaks starts at the most abundant and goes down to the least abundant. With a multiple sample set, the automatic selection uses the most abundant peak as an representative for every feature group, according to the xcms grouping. With the xsAnnotate sample parameter, a sample selection can be defined to use only specific samples. See `xsAnnotate-class` for further information. The FWHM (full width at half maximum) of a peak is estimated as FWHM = SD * 2.35. For the calculation of the SD, the peak is assumed as normal distributed.

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

```
library(CAMERA)
#Single sample
file <- system.file('mzML/MM14.mzML', 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 specific 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)
```

---

massWindowSizes *The supported mass window sizes*

Description

Returns the set of supported mass window sizes for the given compound database

Usage

```
massWindowSizes(libraryName = "kegg")
```

Arguments

`libraryName`	The compound database

Value

Vector of supported mass window sizes

Author(s)

Hendrik Treutler

Examples

```
massWindowSizes()
```

`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 mzML 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 "mzML": 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 "mzML/MM14.mzML"
  ..@ profinfo :List of 2
  .. ..$ method: chr "bin"
  .. ..$ step  : num 0.1
  ..@ polarity : chr(0)
```

Details

The corresponding raw mzData files are located in the mzML 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.

Usage

```
plotPsSpectrum(object, pspec=1:length(object@pspectra), log=FALSE, value="into", maxlabel=0, title=N
```

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.
cexMulti	Cex multiplier for peak labels
...	Additional parameter for function plot

Value

None.

Methods

signature(object = "xsAnnotate") object deriviving from class "xsAnnotate"

Author(s)

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

See Also

xsAnnotate-class, png, pdf, postscript,

psDist-methods *Distance methods for xsAnnotate*

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

object1	a xsAnnotate object with pseudospectra
object2	a xsAnnotate object with pseudospectra
PSpec1	index of pseudospectrum in object1
PSpec2	index of pseudospectrum in object2
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 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 all the algorithms which are available is returned by getOption("BioC")$xcms$specDis
If the nickname of a method is called "meanMZmatch", the help page for that specific method can be accessed with ?specDist.meanMZmatch.

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

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

Author(s)

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

pspec2metfrag *Export the putative fragments as MetFrag query files*

Description

MetFrag is an in-silico metabolite identification system, which aims to putatively identify compounds from fragmentation MS data, expecially from tandem-MS, but also in-source fragments might give additional hints on top of the accurate mass of the precursor alone.

Usage

```
pspec2metfrag(object, pspecidx=NULL, filedir=NULL)
pspec2metfusion(object, pspecidx=NULL, filedir=NULL)
```

Arguments

object	an xsAnnotate object
pspecidx	Index of pspectra to export, if NULL then all are exported.
filedir	Directory for placement of batch query files

Details

For each spectrum in pspecidx (or all in the xsAnnotate object), for each [M] mass hypothesis, remove all non-fragment peaks (isotopes, clusters, adducts) and pass them to MetFrag and MetFusion batch query files.

Value

Returns a list

Author(s)

Carsten Kuhl <ckuhl@ipb-halle.de>

Examples

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

pspec2metfrag(an, pspecidx=c(1))
```

ruleSet *Class* ruleSet

Description

The class ruleSet is used to read lists of ions, adducts and neutral losses, and compile the dynamic ruleSet from those. This makes it possible to modify the default rules for certain analytical settings.

Slots

ionlistfile: File of known charged ions, an example is found in CAMERA/lists/ions.csv .

neutrallossfile: File of known neutral losses, an example is found in CAMERA/lists/neutralloss.csv.

neutraladditionfile: File of known adducts, an example is found in CAMERA/lists/lists/neutraladdition.csv .

ionlist: Known charged ions.

neutralloss: Known neutral losses.

neutraladdition: Known adducts.

maxcharge: .

mol : .

nion : .

nnloss : .

nnadd : .

nh : .

polarity : Polarity of the ruleSet.

rules: data.frame of resulting mass differences, this is the dynamic ruleSet.

lib.loc Path to local R library

Extends

Class "Versioned", directly.

Methods

Methods implemented for ruleSet

setDefaultLists signature(object = "ruleSet"): Set filenames for the lists shipped with CAMERA.

readLists signature(object = "ruleSet"): Read and parse the lists from the files.

setDefaultParams signature(object = "ruleSet"): Set the default parameters for rule generation.

setParams signature(object = "ruleSet"): Set the parameters for rule generation.

generateRules signature(object = "ruleSet"): Create the rules in ruleSet@rules .

Author(s)

Steffen Neumann and Carsten Kuhl

Examples

```
r <- new("ruleSet");
r2 <- setDefaultLists(r) ;
r3 <- readLists(r2) ;
r4 <- setDefaultParams(r3) ;
r5 <- generateRules(r4)
dim(r5@rules)
```

---

xsAnnotate *xsAnnotate constructor for an provided xcmsSet object*

Description

This function deals with the construction of an xsAnnotate object. It extracts the peaktable from a provided xcmsSet, which is used for all further analysis. The xcmsSet can be a single sample or multiple sample experiment. Since some functions needs the raw data a selection algorithm must be choosen in the case of a multiple sample. CAMERA includes two different strategies: A defined selection of samples (sample = indices of samples) or the default automatic solution (sample = NA). The automatic solution chooses the best sample for a specifc groups called pseudospectrum, see groupFWHM and groupCorr. It returns a xsAnnotate object, see xsAnnotate-class.

Usage

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

Arguments

xs	a xcmsSet object
sample	Indices of the group xcmsSet sample, that are used for the EIC correlation step. For automatic selection don't set a value. For use all samples simply define sample = c(1:n), with n = number of samples.
nSlaves	For parallel mode set nSlaves higher than 1, but not higher than the number of cpu cores.
polarity	Set polarity mode: "positive" or "negative"

Value

A xsAnnotate object.

Author(s)

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

See Also

xsAnnotate-class

Examples

```
library(faahKO)
xs <- group(faahko)
xsa <- xsAnnotate(xs, sample=c(1:12))

#With automatic selection
xsa.autoselect <- xsAnnotate(xs)
```

---

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

Description

This class transforms a xcmsSet object with peaks from multiple LC/MS or GC/MS samples into a set of annotation results. It contains searching algorihms for isotopes and adducts, peak grouping algorithms to find connected peak, which originate from the same molecule.

Objects from the Class

Objects can be created with the xsAnnotate constructor which include the peaktable from a provided xcmsSet. Objects can also be created by calls of the form new("xsAnnotate", ...).

Slots

annoGrp: Assignment of mass hypotheses to correlation groups

annoID: The assignemnt 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 there peak IDs

psSamples: List containing information with sample was sample was selecteted as representative (automatic selection)

ruleset: A dataframe describing the mass difference rules used for the annotion

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)

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

See Also

`xsAnnotate`

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