Package ‘flagme’

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Title Analysis of Metabolomics GC/MS Data

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Description Fragment-level analysis of gas chromatography - mass spectrometry metabolomics data

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R topics documented:

`addAMDISPeaks` *Add AMDIS peak detection results*

Description

Reads ASCII ELU-format files (output from AMDIS) and attaches them to an already created `peaksDataset` object

Usage

```
addAMDISPeaks(object,fns=dir(,"[Eu][Ll][Uu]"),verbose=TRUE,...)
```

Arguments

`object`	a `peaksDataset` object.
`fns`	character vector of same length as `object@rawdata` (user ensures the order matches)
`verbose`	whether to give verbose output, default `TRUE`
`...`	arguments passed on to `parseELU`

Details

Repeated calls to `parseELU` to add peak detection results to the original `peaksDataset` object.

Value

`peaksDataset` object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`parseELU`, `peaksDataset`

Examples

```
# need access to CDF (raw data) and ELU files
require(gcspikelite)
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")

# full paths to file names
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# create a 'peaksDataset' object and add AMDIS peaks to it
pd<-peaksDataset(cdfFiles[1],mz=seq(50,550),rtrange=c(7.5,8.5))
pd<-addAMDISPeaks(pd,eluFiles[1])
```

`addChromaTOFPeaks` *Add ChromaTOF peak detection results*

Description

Reads ASCII tab-delimited format files (output from ChromaTOF) and attaches them to an already created `peaksDataset` object

Usage

```
addChromaTOFPeaks(object,fns=dir(,"[Tt][Xx][Tx]"),rtDivide=60,verbose=TRUE,...)
```

Arguments

object	a peaksDataset object.
fns	character vector of same length as object@rawdata (user ensures the order matches)
rtDivide	number giving the amount to divide the retention times by.
verbose	whether to give verbose output, default TRUE
...	arguments passed on to parseChromaTOF

Details

Repeated calls to parseChromaTOF to add peak detection results to the original peaksDataset object.

Value

peaksDataset object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

parseChromaTOF, peaksDataset

Examples

```
# need access to CDF (raw data) and ChromaTOF files
require(gcspikelite)
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")

# full paths to file names
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
# [not run] cTofFiles<-dir(gcmsPath,"txt",full=TRUE)

# create a 'peaksDataset' object and add ChromaTOF peaks to it
pd<-peaksDataset(cdfFiles[1],mz=seq(50,550),rtrange=c(7.5,8.5))
# [not run] pd<-addChromTOFPeaks(pd,...)
```

addXCMSPeaks *Add xcms/CAMERA peak detection results*

Description

Reads the raw data using xcms, group each extracted ion according to their retention time using CAMERA and attaches them to an already created `peaksDataset` object

Usage

```
addXCMSPeaks(files, object, peakPicking=c('cwt','mF'), ...)
```

Arguments

`files`	character vector of same length as `object@rawdata` (user ensures the order matches)
`object`	a `peaksDataset` object.
`peakPicking`	Methods to use for peak detection. See details.
`...`	arguments passed on to `xcmsSet` and `annotate`

Details

Repeated calls to xcmsSet and annotate to perform peak-picking and deconvolution. The peak detection results are added to the original `peaksDataset` object. Two peak detection alorithms are available: continuous wavelet transform (peakPicking=c('cwt')) and the matched filter approach (peakPicking=c('mF')) described by Smith et al (2006). For further information consult the xcms package manual.

Value

`peaksDataset` object

Author(s)

Riccardo Romoli <riccardo.romoli@unifi.it>

See Also

`peaksDataset` `findPeaks.matchedFilter` `findPeaks.centWave` `xcmsRaw-class`

Examples

```
# need access to CDF (raw data)
require(gcspikelite)
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")

# full paths to file names
cdfFiles <- dir(gcmsPath, "CDF", full=TRUE)
```

```
# create a 'peaksDataset' object and add XCMS peaks to it
pd <- peaksDataset(cdfFiles[1], mz=seq(50,550), rtrange=c(7.5,8.5))
pd <- addXCMSPeaks(cdfFiles[1], pd, peakPicking=c('mF'),
                   snthresh=3, fwhm=4, step=1, steps=2, mzdiff=0.5)
```

---

betweenAlignment *Data Structure for "between" alignment of many GCMS samples*

Description

This function creates a "between" alignment (i.e. comparing merged peaks)

Usage

```
betweenAlignment(pD, cAList, pAList, impList, filterMin = 1, gap = 0.7,
                     D = 10, usePeaks = TRUE, df = 30, verbose = TRUE,
                         metric = 2,  type = 2, penality = 0.2)
```

Arguments

`pD`	a `peaksDataset` object
`cAList`	`list` of `clusterAlignment` objects, one for each experimental group
`pAList`	`list` of `progressiveAlignment` objects, one for each experimental group
`impList`	`list` of imputation lists
`filterMin`	minimum number of peaks within a merged peak to be kept in the analysis
`gap`	gap parameter
`D`	retention time penalty parameter
`usePeaks`	logical, whether to use peaks (if `TRUE`) or the full 2D profile alignment (if `FALSE`)
`df`	distance from diagonal to calculate similarity
`verbose`	logical, whether to print information
`metric`	numeric, different algorithm to calculate the similarity matrix between two mass spectrum. `metric=1` call `normDotProduct()`; `metric=2` call `ndpRT()`; `metric=3` call `corPrt()`
`type`	numeric, two different type of alignment function
`penality`	penalization applied to the matching between two mass spectra if `(t1-t2)>D`

Details

`betweenAlignment` objects gives the data structure which stores the result of an alignment across several "pseudo" datasets. These pseudo datasets are constructed by merging the "within" alignments.

Value

`betweenAlignment` object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`multipleAlignment`

Examples

```
require(gcspikelite)
## see 'multipleAlignment'
```

`calcTimeDiffs` *Calculate retention time shifts from profile alignments*

Description

This function takes the set of all pairwise profile alignments and use these to estimate retention time shifts between each pair of samples. These will then be used to normalize the retention time penalty of the signal peak alignment.

Usage

```
calcTimeDiffs(pd,ca.full,verbose=TRUE)
```

Arguments

`pd`	a `peaksDataset` object
`ca.full`	a `clusterAlignment` object, fit with
`verbose`	logical, whether to print out information

Details

Using the set of profile alignments,

Value

`list` of same length as `ca.full@alignments` with the matrices giving the retention time penalties.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

peaksAlignment, clusterAlignment

Examples

```
require(gcspikelite)

# paths and files
gcmsPath <- paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles <- dir(gcmsPath,"CDF",full=TRUE)
eluFiles <- dir(gcmsPath,"ELU",full=TRUE)

# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
pd <- addAMDISPeaks(pd,eluFiles[1:2])

# pairwise alignment using all scans
fullca <- clusterAlignment(pd, usePeaks=FALSE, df=100)

# calculate retention time shifts
timedf <- calcTimeDiffs(pd, fullca)
```

---

clusterAlignment — *Data Structure for a collection of all pairwise alignments of GCMS runs*

Description

Store the raw data and optionally, information regarding signal peaks for a number of GCMS runs

Usage

```
clusterAlignment(pD, runs=1:length(pD@rawdata), timedf=NULL,
                 usePeaks=TRUE, verbose=TRUE, ...)
```

Arguments

`pD`	a `peaksDataset` object.
`runs`	vector of integers giving the samples to calculate set of pairwise alignments over.
`timedf`	list (length = the number of pairwise alignments) of matrices giving the expected time differences expected at each pair of peaks used with `usePeaks=TRUE`, passed to `peaksAlignment`
`usePeaks`	logical, `TRUE` uses `peakdata` list, `FALSE` uses `rawdata` list for computing similarity.
`verbose`	logical, whether to print out info.
`...`	other arguments passed to `peaksAlignment`

Details

clusterAlignment computes the set of pairwise alignments.

Value

`clusterAlignment` object

Author(s)

Mark Robinson, Riccardo Romoli

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksDataset`, `peaksAlignment`

Examples

```
require(gcspikelite)

# paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath, "CDF", full=TRUE)
eluFiles <- dir(gcmsPath, "ELU", full=TRUE)

# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2], mz=seq(50,550), rtrange=c(7.5,8.5))
pd <- addAMDISPeaks(pd, eluFiles[1:2])

ca <- clusterAlignment(pd, gap=0.5, D=0.05, df=30, metric=1, type=1)
```

compress *Compress an alignment object*

Description

Many of the peaks are not similar. So, the set of pairwise similarity matrices can be compressed.

Usage

```
compress(object,verbose=TRUE,...)
decompress(object,verbose=TRUE,...)
```

Arguments

object	a `peaksAlignment`, `peaksAlignment` or `peaksAlignment` object to be compressed
verbose	logical, whether to print out information
...	further arguments

Details

Using sparse matrix representations, a significant compression can be achieved. Here, we use the `matrix.csc` class of the `SpareM` package.

Value

an object of the same type as the input object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksAlignment`, `clusterAlignment`, `progressiveAlignment`

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data, peak detection results
pd<-peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
pd<-addAMDISPeaks(pd,eluFiles[1:2])

# pairwise alignment (it is compressed by default)
ca<-clusterAlignment(pd, usePeaks = TRUE, df = 20, metric=1, type=1)
object.size(ca)

# decompress
ca<-decompress(ca)
object.size(ca)
```

---

corPrt   *Retention Time Penalized Correlation*

Description

This function calculates the similarity of all pairs of peaks from 2 samples, using the spectra similarity and the rretention time differencies

Usage

```
corPrt(d1, d2, t1, t2, D, penality=0.2)
```

Arguments

d1	data matrix for sample 1
d2	data matrix for sample 2
t1	vector of retention times for sample 1
t2	vector of retention times for sample 2
D	retention time window for the matching
penality	penalization applied to the matching between two mass spectra if `(t1-t2)>D`

Details

Computes the Pearson carrelation between every pair of peak vectors in the retention time window (`D`)and returns the similarity matrix.

Value

matrix of similarities

Author(s)

Riccardo Romoli

See Also

peaksAlignment

Examples

```
## Not Run
require(gcspikelite)
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath,"CDF", full=TRUE)
## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550), rtrange=c(7.5,10.5))
pd <- addXCMSPeaks(files=cdfFiles[1:3], object=pd, peakPicking=c('mF'),
                   snthresh=3, fwhm=10,  step=0.1, steps=2, mzdiff=0.5,
                   sleep=0)
## review peak picking
plot(pd, rtrange=c(7.5, 10.5), runs=c(1:3))

r <- corPrt(pd@peaksdata[[1]], pd@peaksdata[[2]],
           pd@peaksrt[[1]], pd@peaksrt[[2]], D=50, penality=0.2)
## End (Not Run)
```

---

dp *Dynamic programming algorithm, given a similarity matrix*

Description

This function calls C code for a bare-bones dynamic programming algorithm, finding the best cost path through a similarity matrix.

Usage

```
dp(M,gap=.5,big=10000000000,verbose=FALSE)
```

Arguments

M	similarity matrix
gap	penalty for gaps
big	large value used for matrix margins
verbose	logical, whether to print out information

Details

This is a pretty standard implementation of a bare-bones dynamic programming algorithm, with a single gap parameter and allowing only simple jumps through the matrix (up, right or diagonal).

Value

`list` with element `match` with the set of pairwise matches.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`normDotProduct`

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data, peak detection results
pd<-peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
pd<-addAMDISPeaks(pd,eluFiles[1:2])

# similarity matrix
r<-normDotProduct(pd@peaksdata[[1]],pd@peaksdata[[2]])

# dynamic-programming-based matching of peaks
v<-dp(r,gap=.5)
```

`dynRT` *dynRT*

Description

Dynamic Retention Time Based Alignment algorithm, given a similarity matrix

Usage

```
dynRT(S)
```

Arguments

`S`	similarity matrix

Details

This function align two chromatograms finding the maximum similarity among the mass spectra

Value

list containing the matched peaks between the two chromatograms. The number represent position of the spectra in the S matrix

Author(s)

riccardo.romoli@unifi.it

Examples

```
require(gcspikelite)
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath,"CDF", full=TRUE)
## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550),
    rtrange=c(7.5,10.5))
pd <- addXCMSPeaks(files=cdfFiles[1:3], object=pd,
    peakPicking=c('mF'),snthresh=3, fwhm=10,  step=0.1, steps=2,
    mzdiff=0.5, sleep=0)
## review peak picking
plot(pd, rtrange=c(7.5, 10.5), runs=c(1:3))
## similarity
r <- ndpRT(pd@peaksdata[[1]], pd@peaksdata[[2]], pd@peaksrt[[1]],
    pd@peaksrt[[2]], D=50)
## dynamic retention time based alignment algorithm
v <- dynRT(S=r)
```

`eitherMatrix-class` *The* `eitherMatrix` *class*

Description

A container to store either matrix or matrix.csc objects

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksAlignment`

`exportSpectra` *exportSpectra*

Description

Write the deconvoluted mass spectra to an external file

Usage

```
exportSpectra(object, sample, spectraID, normalize = TRUE)
```

Arguments

`object`	an object of class "peaksDataset" where to keep the mass spectra; both abundance (y) than m/z (x)
`sample`	character, the sample from were to plot the mass spectra
`spectraID`	numerical, a vector containing the index of the spectra to be plotted.
`normalize`	logical, if TRUE normalize the intensity of the mass peak to 100, the most abundant is 100 are scaled consequetially

Details

Write a .msp file of the deconvoluted mass spectra. Usfull to try to identify the unknown spectra using NIST Search.

Value

a .msp file ready to be read using NIST search

Author(s)

riccardo.romoli@unifi.it

gatherInfo *Gathers abundance informations from an alignment*

Description

Given an alignment table (indices of matched peaks across several samples) such as that within a progressiveAlignment or multipleAlignment object, this routines goes through the raw data and collects the abundance of each fragment peak, as well as the retention times across the samples.

Usage

```
gatherInfo(pD, obj, newind = NULL, method = c("apex"), findmzind = TRUE,
           useTIC = FALSE, top = NULL, intensity.cut = 0.05)
```

Arguments

pD	a peaksDataset object, to get the abundance data from
obj	either a multipleAlignment or progressiveAlignment object
newind	list giving the
method	method used to gather abundance information, only apex implemented currently.
findmzind	logical, whether to take a subset of all m/z indices
useTIC	logical, whether to use total ion current for abundance summaries
top	only use the top top peaks
intensity.cut	percentage of the maximum intensity

Details

This procedure loops through the the table of matched peaks and gathers the

Value

Returns a list (of lists) for each row in the alignment table. Each list has 3 elements:

mz	a numerical vector of the m/z fragments used
rt	a numerical vector for the exact retention time of each peak across all samples
data	matrix of fragment intensities. If useTIC = TRUE, this matrix will have a single row

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

imputePeaks

Examples

```
require(gcspikelite)

## paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep = "/")
cdfFiles <- dir(gcmsPath, "CDF", full = TRUE)
eluFiles <- dir(gcmsPath, "ELU", full = TRUE)

## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2], mz = seq(50, 550), rtrange = c(7.5, 8.5))
pd <- addAMDISPeaks(pd, eluFiles[1:2])

## multiple alignment
ma <- multipleAlignment(pd, c(1,1), wn.gap = 0.5, wn.D = 0.05, bw.gap = 0.6,
                        bw.D = 0.2, usePeaks = TRUE, filterMin = 1, df = 50,
                        verbose = TRUE, metric = 1, type = 1)

## gather apex intensities
d <- gatherInfo(pd, ma)

## table of retention times
nm <- list(paste("MP", 1:length(d), sep = ""), c("S1", "S2"))
rts <- matrix(unlist(sapply(d, .subset, "rt")), byrow = TRUE, nc = 2,
              dimnames = nm)
```

---

imputePeaks *Imputatin of locations of peaks that were undetected*

Description

Using the information within the peaks that are matched across several runs, we can impute the location of the peaks that are undetected in a subset of runs

Usage

```
imputePeaks(pD, obj, typ = 1, obj2 = NULL, filterMin = 1, verbose = TRUE)
```

Arguments

pD	a peaksDataset object
obj	the alignment object, either multipleAlignment or progressiveAlignment, that is used to infer the unmatched peak locations
typ	type of imputation to do, 1 for simple linear interpolation (default), 2 only works if obj2 is a clusterAlignment object
obj2	a clusterAlignment object
filterMin	minimum number of peaks within a merged peak to impute
verbose	logical, whether to print out information

Details

If you are aligning several samples and for a (small) subset of the samples in question, a peak is undetected, there is information within the alignment that can be useful in determining where the undetected peak is, based on the surrounding matched peaks. Instead of moving forward with missing values into the data matrices, this procedures goes back to the raw data and imputes the location of the apex (as well as the start and end), so that we do not need to bother with post-hoc imputation or removing data because of missing components.

We realize that imputation is prone to error and prone to attributing intensity from neighbouring peaks to the unmatched peak. We argue that this is still better than having to deal with these in statistical models after that fact. This may be an area of future improvement.

Value

list with 3 elements apex, start and end, each masked matrices giving the scan numbers of the imputed peaks.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

multipleAlignment, progressiveAlignment, peaksDataset

Examples

```
require(gcspikelite)

## paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep = "/")
cdfFiles <- dir(gcmsPath,"CDF", full = TRUE)
eluFiles <- dir(gcmsPath,"ELU", full = TRUE)
```

```
## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz = seq(50,550), rtrange = c(7.5,8.5))
pd <- addAMDISPeaks(pd, eluFiles[1:3])

## alignments
ca <- clusterAlignment(pd, gap = 0.5, D = 0.05, df = 30, metric = 1, type = 1)
pa <-progressiveAlignment(pd, ca, gap = 0.6, D = 0.1, df = 30)

v <- imputePeaks(pd, pa, filterMin = 1)
```

---

multipleAlignment-class

Data Structure for multiple alignment of many GCMS samples

Description

Store the raw data and optionally, information regarding signal peaks for a number of GCMS runs

Usage

```
multipleAlignment(pd, group, bw.gap = 0.8, wn.gap = 0.6, bw.D = 0.20,
                         wn.D = 0.05, filterMin = 1, lite = FALSE, usePeaks = TRUE,
                            df = 50, verbose = TRUE, timeAdjust = FALSE,
                           doImpute = FALSE, metric = 2, type = 2, penality = 0.2)
```

Arguments

pd	a peaksDataset object
group	factor variable of experiment groups, used to guide the alignment algorithm
bw.gap	gap parameter for "between" alignments
wn.gap	gap parameter for "within" alignments
bw.D	distance penalty for "between" alignments
wn.D	distance penalty for "within" alignments
filterMin	minimum number of peaks within a merged peak to be kept in the analysis
lite	logical, whether to keep "between" alignment details (default, FALSE)
usePeaks	logical, whether to use peaks (if TRUE) or the full 2D profile alignment (if FALSE)
df	distance from diagonal to calculate similarity
verbose	logical, whether to print information
timeAdjust	logical, whether to use the full 2D profile data to estimate retention time drifts (Note: time required)
doImpute	logical, whether to impute the location of unmatched peaks
metric	numeric, different algorithm to calculate the similarity matrix between two mass spectrum. metric=1 call normDotProduct(); metric=2 call ndpRT(); metric=3 call corPrt()
type	numeric, two different type of alignment function
penality	penalization applied to the matching between two mass spectra if (t1-t2)>D

Details

multipleAlignment is the data structure giving the result of an alignment across several GCMS runs.

Multiple alignments are done progressively. First, all samples with the same `tg$Group` label with be aligned (denoted a "within" alignment). Second, each group will be summarized into a pseudo-data set, essentially a spectrum and retention time for each matched peak of the within-alignment. Third, these "merged peaks" are aligned in the same progressive manner, here called a "between" alignment.

Value

`multipleAlignment` object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksDataset`, `betweenAlignment`, `progressiveAlignment`

Examples

```
require(gcspikelite)

## paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep = "/")
cdfFiles <- dir(gcmsPath, "CDF", full = TRUE)
eluFiles <- dir(gcmsPath, "ELU", full = TRUE)

## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2], mz = seq(50, 550), rtrange = c(7.5, 8.5))
pd <- addAMDISPeaks(pd,eluFiles[1:2])

## multiple alignment
ma <- multipleAlignment(pd, c(1, 1), wn.gap = 0.5, wn.D = 0.05, bw.gap = 0.6,
                        bw.D = 0.2, usePeaks = TRUE, filterMin = 1, df = 50,
                        verbose = TRUE, metric = 1, type = 1)
```

ndpRT *Retention Time Penalized Normalized Dot Product*

Description

This function calculates the similarity of all pairs of peaks from 2 samples, using the spectra similarity and the rretention time differencies

Usage

```
ndpRT(s1, s2, t1, t2, D)
```

Arguments

s1	data matrix for sample 1
s2	data matrix for sample 2
t1	vector of retention times for sample 1
t2	vector of retention times for sample 2
D	retention time window for the matching

Details

Computes the normalized dot product between every pair of peak vectors in the retention time window (D)and returns a similarity matrix.

Value

matrix of similarities

Author(s)

Riccardo Romoli

See Also

peaksAlignment

Examples

```
## Not Run
require(gcspikelite)
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath,"CDF", full=TRUE)

                                        # read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550), rtrange=c(7.5,10.5))
pd <- addXCMSPeaks(files=cdfFiles[1:3], object=pd, peakPicking=c('mF'),
```

```
                    snthresh=3, fwhm=10,  step=0.1, steps=2, mzdiff=0.5,
                    sleep=0)
## review peak picking
plot(pd, rtrange=c(7.5, 10.5), runs=c(1:3))

r <- ndpRT(pd@peaksdata[[1]], pd@peaksdata[[2]],
           pd@peaksrt[[1]], pd@peaksrt[[2]], D=50)
## End (Not Run)
```

---

normDotProduct *Normalized Dot Product*

Description

This function calculates the similarity of all pairs of peaks from 2 samples, using the spectra similarity

Usage

```
normDotProduct(x1,x2,t1=NULL,t2=NULL,df=max(ncol(x1),ncol(x2)),D=100000,timedf=NULL,verbose=FALSE)
```

Arguments

x1	data matrix for sample 1
x2	data matrix for sample 2
t1	vector of retention times for sample 1
t2	vector of retention times for sample 2
df	distance from diagonal to calculate similarity
D	retention time penalty
timedf	matrix of time differences to normalize to. if NULL, 0 is used.
verbose	logical, whether to print out information

Details

Efficiently computes the normalized dot product between every pair of peak vectors and returns a similarity matrix. C code is called.

Value

matrix of similarities

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

dp, peaksAlignment

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data, peak detection results
pd<-peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
pd<-addAMDISPeaks(pd,eluFiles[1:2])

r<-normDotProduct(pd@peaksdata[[1]],pd@peaksdata[[2]])
```

---

parseChromaTOF *Parser for ChromaTOF files*

Description

Reads ASCII ChromaTOF-format files from AMDIS (Automated Mass Spectral Deconvolution and Identification System)

Usage

```
parseChromaTOF(fn,min.pc=.01,mz=seq(85,500),rt.cut=.008,rtrange=NULL,skip=1,rtDivide=60)
```

Arguments

`fn`	ChromaTOF filename to read.
`min.pc`	minimum percent of maximum intensity.
`mz`	vector of mass-to-charge bins of raw data table.
`rt.cut`	the difference in retention time, below which peaks are merged together.
`rtrange`	retention time range to parse peaks from, can speed up parsing if only interested in a small region (must be `numeric` vector of length 2)
`skip`	number of rows to skip at beginning of the ChromaTOF
`rtDivide`	multiplier to divide the retention times by (default: 60)

Details

parseChromaTOF will typically be called by addChromaTOFPeaks, not called directly.

Peaks that are detected within rt.cut are merged together. This avoids peaks which are essentially overlapping.

Fragments that are less than min.pc of the maximum intensity fragment are discarded.

Value

list with components peaks (table of spectra – rows are mass-to-charge and columns are the different detected peaks) and tab (table of features for each detection), according to what is stored in the ChromaTOF file.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

addAMDISPeaks

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
tofFiles<-dir(gcmsPath,"tof",full=TRUE)

# parse ChromaTOF file
cTofList<-parseChromaTOF(tofFiles[1])
```

---

parseELU *Parser for ELU files*

Description

Reads ASCII ELU-format files from AMDIS (Automated Mass Spectral Deconvolution and Identification System)

Usage

```
parseELU(f,min.pc=.01,mz=seq(50,550),rt.cut=.008,rtrange=NULL)
```

Arguments

f	ELU filename to read.
min.pc	minimum percent of maximum intensity.
mz	vector of mass-to-charge bins of raw data table.
rt.cut	the difference in retention time, below which peaks are merged together.
rtrange	retention time range to parse peaks from, can speed up parsing if only interested in a small region (must be numeric vector of length 2)

Details

parseELU will typically be called by addAMDISPeaks, not called directly.

Peaks that are detected within rt.cut are merged together. This avoids peaks which are essentially overlapping.

Fragments that are less than min.pc of the maximum intensity fragment are discarded.

Value

list with components peaks (table of spectra – rows are mass-to-charge and columns are the different detected peaks) and tab (table of features for each detection), according to what is stored in the ELU file.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

addAMDISPeaks

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# parse ELU file
eluList<-parseELU(eluFiles[1])
```

---

peaksAlignment-class *Data Structure for pairwise alignment of 2 GCMS samples*

Description

Store the raw data and optionally, information regarding signal peaks for a number of GCMS runs

Usage

```
peaksAlignment(d1, d2, t1, t2, gap=0.5, D=50, timedf=NULL, df=30,
               verbose=TRUE, usePeaks=TRUE, compress=TRUE, metric=2,
               type=2, penality=0.2)
```

Arguments

`d1`	matrix of MS intensities for 1st sample (if doing a peak alignment, this contains peak apexes/areas; if doing a profile alignment, this contains scan intensities. Rows are m/z bins, columns are peaks/scans.
`d2`	matrix of MS intensities for 2nd sample
`t1`	vector of retention times for 1st sample
`t2`	vector of retention times for 2nd sample
`gap`	gap penalty for dynamic programming algorithm. Not used if `type=2`
`D`	time window (on same scale as retention time differences, `t1` and `t2`. Default scale is seconds.)
`timedf`	list (length = the number of pairwise alignments) of matrices giving the expected time differences expected at each pair of peaks used with `usePeaks=TRUE`.
`df`	integer, how far from the diagonal to go to calculate the similarity of peaks. Smaller value should run faster, but be careful not to choose too low.
`verbose`	logical, whether to print out info.
`usePeaks`	logical, `TRUE` uses `peakdata` list, `FALSE` uses `rawdata` list for computing similarity.
`compress`	logical, whether to compress the similarity matrix into a sparse format.
`metric`	numeric, different algorithm to calculate the similarity matrix between two mass spectrum. `metric=1` call `normDotProduct()`; `metric=2` call `ndpRT()`; `metric=3` call `corPrt()`
`type`	numeric, two different type of alignment function
`penality`	penalization applied to the matching between two mass spectra if `(t1-t2)>D`

Details

peaksAlignment is a hold-all data structure of the raw and peak detection data.

Value

`peaksAlignment` object

Author(s)

Mark Robinson, Riccardo Romoli

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksDataset`, `clusterAlignment`

Examples

```
## see clusterAlignment, it calls peaksAlignment

## Not Run:
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath,"CDF", full=TRUE)

# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550), rtrange=c(7.5,10.5))
pd <- addXCMSPeaks(files=cdfFiles[1:3], object=pd, peakPicking=c('mF'),
                   snthresh=3, fwhm=10,  step=0.1, steps=2, mzdiff=0.5,
                   sleep=0)
## review peak picking
plot(pd, rtrange=c(7.5, 10.5), runs=c(1:3))

## align two chromatogram
pA <- peaksAlignment(pd@peaksdata[[1]], pd@peaksdata[[2]],
                     pd@peaksrt[[1]], pd@peaksrt[[2]], D=50,
                     metric=3, compress=FALSE, type=2, penality=0.2)

plot(pA)
pA@v$match

par(mfrow=c(2,1))
plot(pd@peaksdata[[1]][,15], type='h', main=paste(pd@peaksrt[[1]][[15]]))
plot(pd@peaksdata[[2]][,17], type='h',
     main=paste(pd@peaksrt[[2]][[17]]))
## End (Not Run)
```

peaksDataset *Data Structure for raw GCMS data and peak detection results*

Description

Store the raw data and optionally, information regarding signal peaks for a number of GCMS runs

Usage

```
peaksDataset(fns=dir(,"[Cc][Dd][Ff]"),verbose=TRUE,mz=seq(50,550),rtDivide=60,rtrange=NULL)
```

Arguments

`fns`	character vector, filenames of raw data in CDF format.
`verbose`	logical, if `TRUE` then iteration progress information is output.
`mz`	vector giving bins of raw data table.
`rtDivide`	number giving the amount to divide the retention times by.
`rtrange`	retention time range to limit data to (must be `numeric` vector of length 2)

Details

peaksDataset is a hold-all data structure of the raw and peak detection data.

Value

`peaksDataset` object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data
pd<-peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
show(pd)
```

`plot.peaksDataset` *Plotting functions for GCMS data objects*

Description

Store the raw data and optionally, information regarding signal peaks for a number of GCMS runs

Usage

```
.plotpD(object, runs=1:length(object@rawdata),
       mzind=1:nrow(object@rawdata[[1]]), mind=NULL,
       plotSampleLabels=TRUE, calcGlobalMax=FALSE, peakCex = 0.8,
       plotPeaks=TRUE, plotPeakBoundaries=FALSE, plotPeakLabels=FALSE,
       plotMergedPeakLabels=TRUE, mlwd=3,usePeaks=TRUE,
       plotAcrossRuns=FALSE, overlap=F, rtrange=NULL, cols=NULL, thin=1,
       max.near=median(object@rawrt[[1]]), how.near=50, scale.up=1, ...)

.plotpA(object, xlab="Peaks - run 1", ylab="Peaks - run 2",
       plotMatches=TRUE, matchPch=19, matchLwd=3,
     matchCex=.5, matchCol="black", col=colorpanel(50, "white", "green", "navyblue"),

       breaks=seq(0, 1, length=51), ...)

.plotcA(object, alignment=1, ...)
```

Arguments

`object`	a `peaksDataset`, `peaksAlignment` or `clusterAlignment` object.
`runs`	for `peaksDataset` only: set of run indices to plot
`mzind`	for `peaksDataset` only: set of mass-to-charge indices to sum over (default, all)
`mind`	for `peaksDataset` only: matrix of aligned indices
`plotSampleLabels`	for `peaksDataset` only: logical, whether to display sample labels
`calcGlobalMax`	for `peaksDataset` only: logical, whether to calculate an overall maximum for scaling
`peakCex`	character expansion factor for peak labels
`plotPeaks`	for `peaksDataset` only: logical, whether to plot hashes for each peak
`plotPeakBoundaries`	for `peaksDataset` only: logical, whether to display peak boundaries
`plotPeakLabels`	for `peaksDataset` only: logical, whether to display peak labels
`plotMergedPeakLabels`	for `peaksDataset` only: logical, whether to display 'merged' peak labels
`mlwd`	for `peaksDataset` only: line width of lines indicating the alignment

usePeaks	for peaksDataset only: logical, whether to plot alignment of peaks (otherwise, scans)
plotAcrossRuns	for peaksDataset only: logical, whether to plot across peaks when unmatched peak is given
overlap	for peaksDataset only: logical, whether to plot TIC/XICs overlapping
rtrange	for peaksDataset only: vector of length 2 giving start and end of the X-axis
cols	for peaksDataset only: vector of colours (same length as the length of runs)
thin	for peaksDataset only: when usePeaks=FALSE, plot the alignment lines every thin values
max.near	for peaksDataset only: where to look for maximum
how.near	for peaksDataset only: how far away from max.near to look
scale.up	for peaksDataset only: a constant factor to scale the TICs
plotMatches	for peaksDataset only: logical, whether to plot matches
xlab	for peaksAlignment and clusterAlignment only: x-axis label
ylab	for peaksAlignment and clusterAlignment only: y-axis label
matchPch	for peaksAlignment and clusterAlignment only: match plotting character
matchLwd	for peaksAlignment and clusterAlignment only: match line width
matchCex	for peaksAlignment and clusterAlignment only: match character expansion factor
matchCol	for peaksAlignment and clusterAlignment only: match colour
col	for peaksAlignment and clusterAlignment only: vector of colours for colourscale
breaks	for peaksAlignment and clusterAlignment only: vector of breaks for colourscale
alignment	for peaksAlignment and clusterAlignment only: the set of alignments to plot
...	further arguments passed to the plot or image command

Details

For peakDataset objects, each TIC is scale to the maximum value (as specified by the how.near and max.near values). The many parameters gives considerable flexibility of how the TICs can be visualized.

For peakAlignment objects, the similarity matrix is plotted and optionally, the set of matching peaks. clusterAlignment objects are just a collection of all pairwise peakAlignment objects.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

plotImage, peaksDataset

Examples

```
require(gcspikelite)

## paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath, "CDF", full=TRUE)
eluFiles <- dir(gcmsPath, "ELU", full=TRUE)

## read data
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550), rtrange=c(7.5,8.5))

## image plot
plot(pd, rtrange=c(7.5,8.5), plotPeaks=TRUE, plotPeakLabels=TRUE)
```

---

plotImage *Plot of images of GCMS data*

Description

Image plots (i.e. 2D heatmaps) of raw GCMS profile data

Usage

```
plotImage(object,run=1,rtrange=c(11,13),main=NULL,mzrange=c(50,200),SCALE=log2,...)
```

Arguments

object	a peaksDataset object
run	index of the run to plot an image for
rtrange	vector of length 2 giving start and end of the X-axis (retention time)
main	main title (auto-constructed if not specified)
mzrange	vector of length 2 giving start and end of the Y-axis (mass-to-charge ratio)
SCALE	function called to scale the data (default: log2)
...	further arguments passed to the image command

Details

For peakDataset objects, each TIC is scale to the maximum value (as specified by the how.near and max.near values). The many parameters gives considerable flexibility of how the TICs can be visualized.

For peakAlignment objects, the similarity matrix is plotted and optionally, the set of matching peaks. clusterAlignment objects are just a collection of all pairwise peakAlignment objects.

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

plot, peaksDataset

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data
pd<-peaksDataset(cdfFiles[1],mz=seq(50,550),rtrange=c(7.5,8.5))

# image plot
plotImage(pd,run=1,rtrange=c(7.5,8.5),main="")
```

---

plotMultipleSpectra *plotMultipleSpectra*

Description

Plot the aligned mass spectra

Usage

```
plotMultipleSpectra(object, outList, spectra, fullRange = TRUE,
  normalize = TRUE, ...)
```

Arguments

object	where to keep the mass range of the experiment
outList	where to keep the mass spectra; both abundance than m/z
spectra	a vector containing the index of the spectra to be plotted. Is referred to outList
fullRange	if TRUE uses the mass range of the whole experiment, otherwise uses only the mass range of each plotted spectum
normalize	if TRUE normalize the intensity of the mass peak to 100, the most abundant is 100 consequetially
...	further arguments passed to the 'plot' command

Details

Plot the deconvoluted and aligned mass spectra collected using gatherInfo()

Author(s)

Riccardo Romoli <riccardo.romoli@unifi.it>

Examples

```
## Rd workflow
gcmsPath <- paste(find.package("gcspikelite"), "data", sep = "/")
cdfFiles <- dir(gcmsPath,"CDF", full = TRUE)

# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:4], mz = seq(50,550), rtrange = c(7.5,10.5))
pd <- addXCMSPeaks(files = cdfFiles[1:4], object = pd, peakPicking = c('mF'),
                   snthresh = 2, fwhm = 8,  step = 0.5, steps = 2, mzdiff = 0.5,
                   sleep = 0)
## multiple alignment
ma <- multipleAlignment(pd, c(1,1,2,2), wn.gap = 0.5, wn.D = 0.05, bw.gap = 0.6,
                        bw.D = 0.2, usePeaks = TRUE, filterMin = 1, df = 50,
                        verbose = TRUE, metric = 2, type = 2)

## gather apex intensities
gip <- gatherInfo(pd, ma)
gip[[33]]
plotMultipleSpectra(object = pd, outList = gip, spectra = 33, fullRange = FALSE,
                    normalize = TRUE)
```

`plotSpectra` *plotSpectra*

Description

Plot the mass spectra from the profile matrix

Usage

```
plotSpectra(object, sample, spectraID, normalize = TRUE, ...)
```

Arguments

`object`	an object of class "peaksDataset" where to keep the mass spectra; both abundance (y) than m/z (x)
`sample`	character, the sample from were to plot the mass spectra
`spectraID`	numerical, a vector containing the index of the spectra to be plotted.
`normalize`	logical, if TRUE normalize the intensity of the mass peak to 100, the most abundant is 100 are scaled consequetially
`...`	other parameter passed to the plot() function

Details

Plot the deconvoluted mass spectra from the profile matrix

Author(s)

riccardo.romoli@unifi.it

Examples

```
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath,"CDF", full=TRUE)
# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:3], mz=seq(50,550), rtrange=c(7.5,10.5))
pd <- addXCMSPeaks(files=cdfFiles[1:3], object=pd, peakPicking=c('mF'),
                   snthresh=3, fwhm=10,  step=0.1, steps=2, mzdiff=0.5,
                   sleep=0)
## align two chromatogram
pA <- peaksAlignment(pd@peaksdata[[1]], pd@peaksdata[[2]],
                     pd@peaksrt[[1]], pd@peaksrt[[2]], D=50,
                     metric=3, compress=FALSE, type=2, penality=0.2)
pA@v$match
## plot the mass spectra
par(mfrow=c(2,1))
plotSpectra(object=pd, sample=cdfFiles[1], spectraID=10)
plotSpectra(object=pd, sample=cdfFiles[2], spectraID=12)
```

---

progressiveAlignment-class

Data Structure for progressive alignment of many GCMS samples

---

Description

Performs a progressive peak alignment (clustalw style) of multiple GCMS peak lists

Usage

```
progressiveAlignment(pD, cA, D=50, gap=.5, verbose=TRUE,
                     usePeaks=TRUE, df=30, compress=TRUE, type=2)
```

Arguments

pD	a `peaksDataset` object
cA	a `clusterAlignment` object
D	retention time penalty
gap	gap parameter
verbose	logical, whether to print information
usePeaks	logical, whether to use peaks (if `TRUE`) or the full 2D profile alignment (if `FALSE`)

`df`	distance from diagonal to calculate similarity
`compress`	logical, whether to store the similarity matrices in sparse form
`type`	numeric, two different type of alignment function

Details

The progressive peak alignment we implemented here for multiple GCMS peak lists is analogous to how `clustalw` takes a set of pairwise sequence alignments and progressively builds a multiple alignment. More details can be found in the reference below.

Value

`progressiveAlignment` object

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

`peaksDataset`, `multipleAlignment`

Examples

```
require(gcspikelite)
## paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep="/")
cdfFiles <- dir(gcmsPath, "CDF", full=TRUE)
eluFiles <- dir(gcmsPath, "ELU", full=TRUE)

## read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2], mz=seq(50,550), rtrange=c(7.5,8.5))
pd <- addAMDISPeaks(pd, eluFiles[1:2])

ca <- clusterAlignment(pd, gap=.5, D=.05, df=30, metric=1, type=1)
pa <- progressiveAlignment(pd, ca, gap=.6, D=.1, df=30, type=1)
```

retFatMatrix *retFatMatrix*

Description

Build a fat data matrix

Usage

```
retFatMatrix(object, data, minFilter = 1)
```

Arguments

object	peakDataset object
data	a gatherInfo() object
minFilter	the minimum number for a feature to be returned in the data matrix

Details

This function allows to extract the data from an object created using `gatherInfo` and build a data matrix using the area of the deconvoluted and aligned peaks. The row are the samples while the column represent the different peaks.

Value

A fat data matrix containing the area of the deconvoluted and aligned peaks. The row are the samples while the column represent the different peaks

Author(s)

Riccardo Romoli <riccardo.romoli@unifi.it>

See Also

gatherInfo

Examples

```
require(gcspikelite)
# paths and files
gcmsPath <- paste(find.package("gcspikelite"), "data", sep = "/")
cdfFiles <- dir(gcmsPath,"CDF",full=TRUE)
# read data, peak detection results
pd <- peaksDataset(cdfFiles[1:2], mz=seq(50,550),
                   rtrange=c(7.5,8.5))
pd <- addXCMSPeaks(files=cdfFiles[1:2], object=pd,
                   peakPicking=c('mF'), snthresh=3, fwhm=4,
                   step=1, steps=2, mzdiff=0.5)
```

```
ma <- multipleAlignment(pd = pd, group = c(1,1),
                        filterMin = 1, metric = 2, type = 2)
outList <- gatherInfo(pd, ma)
mtxD <- retFatMatrix(object = pd, data = outList, minFilter = 1)
```

---

rmaFitUnit *Fits a robust linear model (RLM) for one metabolite*

Description

Using `rlm` from MASS, this procedure fits a linear model using all the fragments

Usage

```
rmaFitUnit(u,maxit=5,mzEffect=TRUE,cls=NULL,fitSample=TRUE,fitOrCoef=c("coef","fit"),TRANSFORM=log2
```

Arguments

`u`	a metabolite unit (list object with vectors `mz` and `rt` for m/z and retention times, respectively and a `data` element giving the fragmentxsample intensitity matrix)
`maxit`	maximum number of iterations (default: 5)
`mzEffect`	logical, whether to fit m/z effect (default: `TRUE`)
`cls`	class variable
`fitSample`	whether to fit individual samples (alternative is fit by group)
`fitOrCoef`	whether to return a vector of coefficients (default: "coef"), or an `rlm` object ("fit")
`TRANSFORM`	function to transform the raw data to before fitting (default: `log2`)

Details

Fits a robust linear model.

Value

`list` giving elements of `fragment` and `sample` coefficients (if `fitOrCoef="coef"`) or a `list` of elements from the fitting process (if `fitOrCoef="fit"`)

Author(s)

Mark Robinson

References

Mark D Robinson (2008). Methods for the analysis of gas chromatography - mass spectrometry data *PhD dissertation* University of Melbourne.

See Also

peaksAlignment, clusterAlignment

Examples

```
require(gcspikelite)

# paths and files
gcmsPath<-paste(find.package("gcspikelite"),"data",sep="/")
cdfFiles<-dir(gcmsPath,"CDF",full=TRUE)
eluFiles<-dir(gcmsPath,"ELU",full=TRUE)

# read data, peak detection results
pd<-peaksDataset(cdfFiles[1:2],mz=seq(50,550),rtrange=c(7.5,8.5))
pd<-addAMDISPeaks(pd,eluFiles[1:2])

# pairwise alignment using all scans
fullca<-clusterAlignment(pd, usePeaks = FALSE, df = 100)

# calculate retention time shifts
timedf<-calcTimeDiffs(pd, fullca)
```

Index