Package ‘PROcess’

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**align**

*Align peaks for a specified precision.*

**Description**

A vector of peaks are expanded to a collection of intervals, ‘eps’ * m/z of the peak to the left and right of the peak position. They are then aligned using the method of intersection graphs by Gentleman and Vandal.

**Usage**

`align(pVec, eps = 0.003)`

**Arguments**

- `pVec`: A vector of peaks.
- `eps`: A user specified precision of peak position.

**Value**

A vector of aligned peaks.

**References**


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**avesd**

*Compute the Average Standard Deviation for a Set of Spectra and a Given Cutoff Point*

**Description**

Compute the Average Standard Deviation for a Set of Spectra and a Given Cutoff Point

**Usage**

`avesd(Ma, cutoff)`

**Arguments**

- `Ma`: A matrix with rows the m/z values and columns samples/spectra
- `cutoff`: A number of m/z

**Details**

For a given cutoff point, the standard deviation of all spectra will be calculated at each m/z above this cutoff point. The resulting sd’s are then averaged and returned.

**Value**

A real number.
aveSpec

Compute mean spectrum of a set of spectra

Description

Compute mean spectrum of a set of spectra.

Usage

aveSpec(nVec)

Arguments

nVec A character vector of file names.

Details

'aveSpec' computes the point-wise mean of intensities of a set of spectra over the whole range of the m/z values.

Value

A matrix with 2 columns, the first being the m/z values and the 2nd being the average of intensities corresponding to the m/z value in the first column of the same row.

Author(s)

Xiaochun Li

Examples

testfs <- dir(system.file("Test", package = "PROcess"), full.names=TRUE)
testAve <- aveSpec(testfs)

binning

Binning the Mass Spectrometry Data

Description

The function 'binning' takes a matrix of spectra and constructs a matrix of intensities of reduced dimensions based on a equally spaced mesh of 'breaks' intervals over the entire m/z range.

Usage

binning(Ma, breaks = 400)

Arguments

Ma a matrix of spectra by column.
breaks number of bins, or equally-spaced intervals for the image of reduced resolution
Baseline Subtraction

Description

This function estimates the baseline and then removes baseline from the raw spectrum.

Usage

bslnoff(f, breaks = 200, qntl = 0, method = c("loess", "approx"), bw = 0.005, plot = FALSE, ...)

Arguments

f

a matrix with M/Z values in the first column and intensities in the second column

breaks

number of breaks set to M/Z values for finding the local minima or points below a certain quantile of intensities; breaks -1 equally spaced intervals on the log M/Z scale.

qntl

if 0, find local minima; if >0 find intensities < qntl*100th quantile locally.

method

"loess" or "approx" (linear interpolation).

bw

the bandwidth to be passed to loess.

plot

TRUE or FALSE, if true, it will plot the raw spectrum, the estimated baseline and the baseline subtracted spectrum.

...

Further parameters that get passed on to plot.

Value

A matrix of two columns: the first column being the M/Z values same as the input, and the second column being the baseline subtracted spectra.

Author(s)

Xiaochun Li

Examples

fdat <- system.file("Test", package = "PROcess")
fs <- list.files(fdat, pattern="\.*csv\.*", full.names=TRUE)
f1 <- read.files(fs[1])
fcut <- f1[f1[,1]>0,]
bseoff <- bslnoff(fcut, method="loess", plot=TRUE, bw=0.1)
title(basename(fs[1]))
gelmap

Plot the image of a set of spectra

Description

This function takes its argument as a intensity matrix of a set of spectra and plots the image as a heatmap.

Usage

gelmap(Ma, cols = gray(seq(1, 0, by = -0.01)), at.mz = NULL, at.col = NULL, cexCol = 0.2 + 1/log10(nc))

Arguments

Ma
a matrix of intensities; spectra are arranged column-wise.
cols
a vector of color to represent continuum of intensities.
at.mz
a vector of m/z values where labels are desired.
at.col
a vector of sample indices, useful to label particular samples. If NULL, samples will be labelled from down up by 1:ncol(Ma).
cexCol
text size of the sample labels.

See Also

See Also binning.

getMzs

Extract M/Z values from the biomarker dataframe.

Description

Turn column names of the biomarker dataframe to numeric M/Z values.

Usage

getMzs(df)

Arguments

df
The biomarker dataframe with rows as spectra and columns as biomarkers.

Value

A numeric vector.
getPeaks  

**Peak Detection**

**Description**

For given threshold criteria, find peaks.

**Usage**

```r
getPeaks(bseoffM, peakinfofile, SoN = 2, span = 81, sm.span=11, zerothrsh=2, area.w = 0.003, ratio = 0.2)
```

**Arguments**

- `bseoffM`: a matrix holding the baseline-subtracted spectra, with row-names as the m/z values and column-names as the spectrum names.
- `peakinfofile`: a `.csv` file in the same format as Ciphergen’s peak info file, with 5 columns data. More details later.
- `SoN`: see `isPeak()`.
- `span`: see `isPeak()`.
- `sm.span`: see `isPeak()`.
- `zerothrsh`: ignore peaks whose intensity values are below `zerothrsh`.
- `area.w`: see `isPeak()`.
- `ratio`: see `isPeak()`.

**Details**

For given threshold criteria, detect peaks and write the following columns of information into `peakinfofile`, spectrum name (Spectrum.Tag), spectrum sequential number (Spectrum.), peak sequential number within a spectrum (Peak.), relative intensity (Intensity) and the m/z value where the relative intensity occurs (Substance.Mass).

**Author(s)**

Xiaochun Li

**See Also**

`rmBaseline`

**Examples**

```r
eexample(renorm)
peakfile <- paste(tempdir(),"testpeakinfo.csv", sep="/"
getPeaks(rtM, peakfile)```
getPeaks2  

**Quantify peaks for individual spectra.**

**Description**
For a vector of given peak locations, quantify peaks for individual spectra.

**Usage**
getPeaks2(bseoffM, pVec, eps = 0.003)

**Arguments**
- **bseoffM**: A matrix of intensities, with rows the m/z values and columns samples.
- **pVec**: A vector of given peak locations.
- **eps**: Relative precision of peak location.

**Details**
Each peak is expanded to an interval, eps * m/z to the left and right of the peak. Intensities of individual spectra are quantified by the maxima in this interval.

**Value**
A matrix of intensities with rows the peaks 'pVec' and column the samples. The m/z values of 'pVec' is stored as the 'rownames' of the returned matrix.

---

intg  

**Integration**

**Description**
This function calculates the integration of y with respect to x.

**Usage**
intg(y, x)

**Arguments**
- **x**: A vector of real values, not necessarily sorted.
- **y**: A vector of function values at x.

**Details**
(x,y)s are sorted according to ascending x values and then the integration is calculated as sum of the products of average of adjacent y values and the difference of adjacent x values.
is.multiple

Author(s)

Xiaochun Li

Examples

x <- seq(0, 1, length=100)
y <- x^2
intg(y, x)

Find multiple-charged polypeptides.

is.multiple

Description

For each of the polypeptides in a vector, find its multiple-charged species in the vector.

Usage

is.multiple(v, k = 2, eps = 0.003)

Arguments

v a vector of polypeptides.
k a vector of integers, that is, multiples of interest.
eps a user specified precision of peak position.

Details

If abs(v-k*u)/v <= eps, then v is considered to be u with k charges.

Value

A list named with the m/z values of polypeptides who have multiple-charged species; each component is a named vector of polypeptides with number of charges as names.

Examples

bmks <- c(2360.25, 2666.34, 3055.72, 3058.04, 3776.94, 3778.24, 3779.53, 4712.37, 7559.76, 4587.03, 4589.88, 9155.59, 13298.7)
is.multiple(bmks, k=2:5)
isPeak

Locate Peaks in a Spectrum

Description

Find local maxima of a spectrum.

Usage

```r
isPeak(f, SoN = 2, span = 81, sm.span=11, plot=FALSE, add = FALSE, zerothrsh=2, area.w = 0.003, ratio = 0.2, ...)
```

Arguments

- `f`: a matrix of two columns representing a spectrum, with the first column the m/z value and second the intensity.
- `SoN`: signal to noise ratio criterion for peak detection.
- `span`: parameter for estimating local variance before peak detection; default is 81 points, that is, 40 points to the left and right of a point of which the variance is being estimated.
- `sm.span`: parameter for smoothing the spectrum before peak detection; default is 11 points, that is, 5 points to the left and right of a point being smoothed.
- `plot`: logical, plot the smoothed spectrum and peaks?
- `add`: add to the existing raw and baseline-subtracted plot?
- `zerothrsh`: ignore peaks whose intensity values are below zerothrsh.
- `area.w`: the neighbourhood of a peak m/z, m/z*(1-area.w, 1+area.w) to calculate area of the peak.
- `ratio`: if area/max(area) > ratio, the peak is retained.
- `...`: further arguments that get passed on to `plot`.

Details

A spectrum is smoothed first using the nearest 'span' neighbours. A larger span 'sm.span' is needed to estimate the local variation so that it is not overestimated due to the peaks nearby. Then potential peaks are identified using Ripley’s ‘peaks’ function with ‘span’ points. Peaks that satisfy the conditions that the (smoothed) signal to noise ratio is greater than ‘SoN’ and that the smoothed signal is greater than 1.64 * mad(sm) are returned.

Value

A data frame with five components, 'peak', 'smooth', 'mz' and 'sigmas', each of length the number of rows in ‘f’. ‘peak’ is logical indicating whether there is a peak or not (Y/N), ‘smooth’ the smooth of the spectrum, ‘mz’ the same as ‘f[,1]’, ‘sigmas’ the estimates of local variation and ‘area’ the area associated with each peak after the first pass.

Author(s)

Xiaochun Li
Examples

```r
example(bslnoff)
pkobj <- isPeak(bseoff, span=81, sm.span=11, plot=TRUE)
```

---

### lnn

Estimate Signal and Variation of a Spectrum

**Description**

Estimate the signal and the variation of a spectrum.

**Usage**

```r
lnn(x, span = 21, sm.span = 11)
```

**Arguments**

- `x`: a vector of real values.
- `span`: the window width for estimation of local variation.
- `sm.span`: the window width for estimation of the signal of `x`.

**Details**

The signal of a spectrum is estimated by moving average and its local variation is estimated by moving 'mad', possibly in a large window.

**Value**

A list with two components:

- `fitted`: estimated signal,
- `sigma`: estimated local variation.

---

### peaks

Peak Detection

**Description**

Finds the local maxima, local noise and its associated standard deviations in a vector.

**Usage**

```r
peaks(x, span = 3)
noise(x, span = 5)
sigma(x, span = 5)
```
Arguments

- **x**: a vector.
- **span**: a local maximum is defined as an element in a sequence which is greater than all other elements within a window of width ‘span’ centered at that element. The default value is 3, meaning that a peak is bigger than both of its neighbors. Local noise is defined as an element minus the mean of all elements within a window of width ‘span’ centered at that element. Local standard deviation of an element is defined as the standard deviation of all elements within a window of width ‘span’ centered at that element.

Value

- a logical vector of the same length as `series` indicating where the peaks are.

Author(s)

Xiaochun Li

Examples

```r
x <- seq(0, 10*pi, by=0.1)
y <- sin(x)*x
plot(x,y, type="l")
is.max <- peaks(y)
points(x[is.max],y[is.max], pch=21, bg="red")
legend(2, 25, legend = "Peaks",pch = 19, col="red", bty = "n")

# can be used for local minima too:
# is.min <- peaks(-y)
# points(x[is.min],y[is.min], pch=21, bg="blue")
```

Description

Align peaks of spectra in ‘peakinfofile’ and find biomarkers by a procedure described in Gentleman and Geyer (1994).

Usage

```r
pk2bmkr(peakinfofile, bseoffM, bmkfile, eps = 0.003, binary = F,p.fltr = 0.1)
```

Arguments

- **bseoffM**: a matrix holding the baseline-subtracted spectra, with row-names as the m/z values and column-names as the spectrum names.
- **bmkfile**: a `.csv` file in the same format as Ciphergen’s biomarker file, with spectra (samples) as columns, and biomarkers as rows.
quality

expected experimental variation in the m/z values.
output intensity or binary peak presence/absence signals.
a number between 0 and 1. If a proto-biomarker is identified as peak in > p.fltr x 100 percent of spectra, it’s kept in ‘bmkfile’.

Value

A dataframe with spectra as rows and biomarkers as columns. Spectrum labels and biomarker positions may be in the names of the dataframe.

Author(s)

Xiaochun Li

References


See Also

rmBaseline, getPeaks

Examples

e.example(getPeaks)

bmkfile <- paste(tempdir(),"testbiomarker.csv",sep="/"

testBio <- pk2bmkr(peakfile, rtM, bmkfile)

## plot biomarker intensities of the 2 spectra

mzs <- as.numeric(rownames(rtM))

matplot(mzs, rtM, type="l", xlim=c(1000, 10000))

bks <- getMzs(testBio)

abline(v=bks, col="green")

quality

Quality Check on a Set of Spectra

Compute three quality parameters for a set of spectra.

Usage

quality(Ma, peakinfofile, cutoff)

Arguments

Ma a Matrix where the baseline-subtracted spectra are stored column wise.
peakinfofile a ‘.csv’ file in the same format as Ciphergen’s peak info file, with 5 columns data. See Details of getPeaks.
cutoff The point in m/z below which spectra are cutoff.
Details

The quality parameters are computed a la fashion de Mani. 1. Estimate noise by moving average with a 5 point window. 2. Estimate the noise envelop by 3 times the standard deviation of noise in a 251 point moving window. 3. Compute the area under the baseline-subtracted curve, area0. 4. Compute the area after subtracting the noise envelop from the baseline-subtracted curve, area1. 5. Parameter 'Quality' is defined as area1/area0. 6. Parameter 'Retain' is defined as the number of points with height above 5 times the noise envelop over total number of points in the spectrum. 7. Detect peaks in each spectrum by getPeaks or Ciphergen software. 8. Parameter 'peak' is defined as the number of peaks in a spectrum divided by the mean number of peaks across spectra.

A spectrum is considered to be of poor quality if Quality<0.4, Retain<0.1 and peak<0.5 simultaneously.

Value

A matrix with three named columns, 'Quality', 'Retain' and 'peak', with spectrum file names as row names.

Author(s)

Xiaochun Li

Examples

eexample(getPeaks)
qualRes <- quality(testM, peakfile, cutoff=1500)

Description

Read a Spectrum from a Comma Delimited File, maybe compressed.

Usage

read.files(fn)

Arguments

fn  path to a `.csv` file, possibly compressed.
renorm  Renormalize Spectra

Description

Renormalize spectra for m/z values greater than ‘cutoff’.

Usage

renorm(Ma, cutoff)

Arguments

Ma  a matrix, with rows the m/z values and the columns the samples.
cutoff  a real value, before which the portion of a spectrum will be ignored.

Details

A sample of spectra will be normalized to have the same AUC, the median of the AUCs of spectra. Each AUC is calculated as the sum of the intensities whose m/z values are greater than ‘cutoff’.

Value

A matrix, with rows the m/z values and the columns the samples. Only rows with m/z values greater than ‘cutoff’ are kept.

Examples

example(rmBaseline)
rtM <- renorm(testM, cutoff=1500)

rmBaseline  Batch Baseline Subtraction.

Description

Baseline subtraction from each raw spectrum in ‘fldr’.

Usage

rmBaseline(fldr, bseoffrda = NULL, breaks = 200, qntl = 0,
method = "loess", bw = 0.1,
SpecNames = list.files(fldr, pattern = "\.*csv\.*")
specZoom

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fldr</td>
<td>a path to where the raw spectra are stored</td>
</tr>
<tr>
<td>bseoffrda</td>
<td>optional; name of the file (with extension .rda) where the baseline-subtracted spectra, a matrix with row-names as the m/z values and column-names as the spectrum tags, will be saved to.</td>
</tr>
<tr>
<td>breaks</td>
<td>see bslnoff().</td>
</tr>
<tr>
<td>qntl</td>
<td>see bslnoff().</td>
</tr>
<tr>
<td>method</td>
<td>see bslnoff().</td>
</tr>
<tr>
<td>bw</td>
<td>see bslnoff().</td>
</tr>
<tr>
<td>SpecNames</td>
<td>a vector of character strings as spectrum names.</td>
</tr>
</tbody>
</table>

Value

A matrix whose columns correspond to baseline-subtracted spectra with row-names as the m/z values and column-names as the spectrum names.

Author(s)

Xiaochun Li

See Also

'bslnoff'.

Examples

testdir <- system.file("Test", package = "PROcess")
testM <- rmBaseline(testdir)

```
specZoom(pks, xlim = NULL, cols = c("cyan", "red", "black"), ...)
```

Description

Function for plotting an object returned by isPeak.

Usage

```
specZoom(pks, xlim = NULL, cols = c("cyan", "red", "black"), ...)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pks</td>
<td>an object (a list) returned by isPeak.</td>
</tr>
<tr>
<td>xlim</td>
<td>a range of m/z values over which a zoomed-in view of the spectrum is desired.</td>
</tr>
<tr>
<td>cols</td>
<td>a vector of color specification for the smooth (signal), peaks and local noise.</td>
</tr>
<tr>
<td>...</td>
<td>further arguments that get passed on to plot.</td>
</tr>
</tbody>
</table>

Examples

```
example(isPeak)
specZoom(pkobj, xlim=c(5000, 10000))
```
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