Package ‘CorrectOverloadedPeaks’

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Type Package

Title Correct Overloaded Peaks from GC-APCI-MS Data

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Description Analyzes and modifies metabolomics raw data (generated using GC-APCI-MS, Gas Chromatography-Atmospheric Pressure Chemical Ionization-Mass Spectrometry) to correct overloaded signals, i.e. ion intensities exceeding detector saturation leading to a cut-off peak. Data in xcmsRaw format are accepted as input and mzXML files can be processed alternatively. Overloaded signals are detected automatically and modified using a Gaussian or Isotopic-Ratio approach. QC plots are generated and corrected data are stored within the original xcmsRaw or mzXML respectively to allow further processing.

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VignetteBuilder knitr

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Imports xcms, XML, digest, bitops

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CorrectOverloadedPeaks

Correct Overloaded Peaks from GC-MS data.

Description

CorrectOverloadedPeaks will take an xcmsRaw data structure and search for overloaded peaks within the mass traces, based on further parameters. It will correct overloaded peaks automatically using a Gaussian or IsotopicRatio approach, generate QC plots and write the corrected data back into the original xcmsRaw.

Usage

CorrectOverloadedPeaks(data = NULL, method = c("Isoratio", "Gauss", "EMG")[,], detection_limit = 1, ds = NULL, silent = TRUE, testing = FALSE, attotwm = FALSE, region = NULL, peak = NULL)

Arguments

data An xcmsRaw-object or an mzXML-object as imported by read.mzXML.

method Either Gauss or EMG (usually better results) or Isoratio (more robust for non gaussian peak shapes).

detection_limit If=1 only peaks hitting detector saturation (ds) will be corrected, can be lowered to 0.95 to catch also peaks going into saturation.

ds Detector saturation. Will be determined based on data if not specified explicitly.

silent QC-plots will be generated if silent=FALSE and additional Warnings() will be generated.

testing Will automatically set silent=FALSE and store all extracted regions with overloaded peaks in the working directory as cor_df_all.RData.

attotwm All-the-Time-of-the-World-Mode. If calculation time doesn’t matter try this out. :)

region From an initial QC-Plot file you may reprocess a specific overloaded region. Dont forget to specify the ds parameter explicitly.

peak You may further restrict the reprocessing to a specific peak within the region.
**FitGaussPeak**

**Details**

This is a high level function to batch pre-process Metabolomics data which are partially overloaded before continuing with the standard workflow of peak identification etc. It relies internally on `FitGaussPeak` and `FitPeakByIsotopicRatio` to modify data of individual intensity signal. Basically the function aims to identify automatically overloaded regions and extracts base peak chromatograms for all overloaded m/z traces within these regions, which are corrected and put back into the original data structure. For simplicity some potentially interesting parameters are hidden at the top of the function definition. They have been set to values determined empirically to be working for a Bruker impact II MS (high-res QTOF) coupled to GC and LC via APCI and ESI respectively. For more details please see [http://dx.doi.org/10.1021/acs.analchem.6b02515](http://dx.doi.org/10.1021/acs.analchem.6b02515).

**Value**

An corrected xcmsRaw- or mzXML-object which can be exported to file. Additionally a QC-plot pdf-file if silent=FALSE.

**References**

[http://dx.doi.org/10.1021/acs.analchem.6b02515](http://dx.doi.org/10.1021/acs.analchem.6b02515)

**See Also**

- ModelGaussPeak
- FitGaussPeak
- FitPeakByIsotopicRatio
- read.mzXML
- write.mzXML

**Examples**

```r
#load xcmsRaw test data, then correct, plot and return reconstructed data
data("xcmsRaw_data")
CorrectOverloadedPeaks(data=xcmsRaw_data, method="Gauss", silent=FALSE)

#load mzXML test data
data(mzXML_data)
CorrectOverloadedPeaks(data=mzXML_data, method="EMG", silent=FALSE)
```

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**FitGaussPeak**  
*Extrapolate a flat top peak using a Gauss approach.*

**Description**

FitGaussPeak will take retention time (’x’) and intensity (’y’) data and extrapolate all points above a certain threshold based on further parameters using a Gaussian approach.
FitGaussPeak

Usage

FitGaussPeak(x, y, scale_range = c(1, 100), steps = 10, cutoff = 0.95,
  idx = NULL, weight_front = 0.5, strip_data = "none",
  account_for_baseline_offset = TRUE, method = c("Gauss", "EMG")[1],
  silent = TRUE, fix_sd = NULL, ...)

Arguments

x  A numeric vector, retention times.
y  A numeric vector, ion intensities.
scale_range  Specifies the expected range for the true peak to exceed the observed, where
  scale_range=c(1,100) would assume anything between not overloaded and 100-fold
  overloaded.
steps  Specifies a step parameter used to create a sequence within 'scale_range' to test
  for good fits, higher=more precision, fewer=faster.
cutoff  Overloaded peaks will be screwed from gaussian shape already when approach-
  ing detector saturation (DS), cutoff=0.95 ensures that points just before DS will
  not be used to model fit.
idx  If not NULL, 'idx' is expected to specify points to correct explicitly (as a numeric-
  vector within 1:length(x)).
weight_front  A weighting parameter to punish deviations in peak front and tail differently;
  0.5=use front/tail equally, 1=use only front, 0=use only tail.
strip_data  Use all provided data if 'none' (default). Strip 'front' or 'tail' data in case you
  observe peak fronting or tailing respectively.
account_for_baseline_offset  If TRUE will substract min(y) from y before fitting parameters.
method  The method for peak shape calculation. Can be ‘Gauss’ or ‘EMG’ (exponen-
  tially modified gauss).
silent  For testing purposes some QC-plot will be generated if silent=FALSE.
fix_sd  Supply a fix standard deviation (sd) for the peak or leave NULL to estimate sd
  within function.
...  passed to the QC plot function, e.g. ‘main’ or ‘xlab’.

Details

This function is mainly used internally (CorrectOverloadedPeaks) but can be of value on it’s
own to test brute force peak reconstruction given that appropriate base peak chromatograms are
available.

Value

An annotated plot of the mass spectrum and detailed information within the console (if silent=FALSE)
and the optimal fitted data points (vector of length(y), returned invisible).
FitPeakByIsotopicRatio

Examples

```r
#load test data
data("xcmsRaw_data")
str(xcmsRaw_data)

# extract base peak chromatogram and plot
int <- slot(xcmsRaw_data, "env")$intensity
scans <- slot(xcmsRaw_data, "scanindex")
time <- slot(xcmsRaw_data, "scantime")
bpc_raw <- apply(cbind(scans, c(scans[-1], length(int))), 1, function(x)(max(int[x[1]:x[2]])))
plot(y=bpc_raw, x=time, type="l", main="BasePeak Chromatogram",
     ylab="Intensity", xlab="Retention Time")

#correct one overloaded peak, plot and return reconstructed data
peak595s_idx <- c(133:163)
FitGaussPeak(y=bpc_raw[peak595s_idx], x=time[peak595s_idx], silent=FALSE)

# assume tailing in the peak and leave out tail data in fit calculation
FitGaussPeak(y=bpc_raw[peak595s_idx], x=time[peak595s_idx], strip_data="tail", silent=FALSE)
```

FitPeakByIsotopicRatio

*Extrapolate a flat top peak using isotopic ratios.*

Description

FitPeakByIsotopicRatio will take a data frame containing peak data for retention time ('RT'), as well as mass and intensity information of M0, M+1 and M+2 and extrapolate all points above a certain threshold for Int_M0 based on further parameters using an IsotopicRatio approach.

Usage

```r
FitPeakByIsotopicRatio(cor_df = NULL, idx = NULL, silent = TRUE)
```

Arguments

- `cor_df` A data frame containing information about the overloaded area; columns=(Scan, RT, mz0, int0, mz1, int1, mz2, int2, modified).
- `idx` If not NULL, 'idx' is expected to specify points to correct explicitly (as a numeric-vector within 1:length(x)).
- `silent` For testing purposes some QC-plot will be generated if silent=FALSE.
Details

Isotopic ratios within ion traces of molecules can be considered stable. If this ratio is changed because one molecule, let's say the M+0, is exceeding the detector range while another (say M+1) is still quantifiable, we therefore may attempt to modify M+0 by multiplying the values of M+1 with a constant (the stable ratio). This constant is determined ideally from the values within the peak front. As this function is mainly used internally (CorrectOverloadedPeaks), it is not very flexible with respect to the input format. Please prepare a dataframe according to the parameter specifications or process a file using CorrectOverloadedPeaks with testing=TRUE, which will generate a list structure of such dataframes.

Value

An annotated plot of the mass spectrum and detailed information within the console. Main result will be returned invisible.

Examples

```r
# load test data
data("xcmsRaw_data")

# plot EIC for 350.165
par(mfrow=c(1,3))
xcms::plotEIC(xcmsRaw_data, mzrange=matrix(c(350.16,350.17), nrow=1))
# process example data with testing=TRUE for one individual peak to get the extracted data.frame
# necessary for FitPeakByIsotopicRatio
CorrectOverloadedPeaks(data=xcmsRaw_data, method="Isoratio", testing=TRUE, region=4, peak=2)
load("cor_df_all.RData")

# correct, plot and return reconstructed data
FitPeakByIsotopicRatio(cor_df=cor_df_all[[4]][[2]], silent=FALSE)

# plot (corrected) EIC for 350.165
xcms::plotEIC(xcmsRaw_data, mzrange=matrix(c(350.16,350.17), nrow=1))
```

---

**ModelGaussPeak**

Create and modify parameters of an artificial chromatographic peak.

**Description**

ModelGaussPeak will create a potentially overloaded gaussian peak of requested width and height.

**Usage**

ModelGaussPeak(\(height = 10^7\), \(width = 4\), \(scan\_rate = 10\), \(e = 0\),
\(ds = 10^7\), \(base\_line = 10^2\))
Arguments

- **height**  
  True peak height (=intensity counts).

- **width**  
  Peak width in time units (preferably seconds).

- **scan_rate**  
  Is determining the resolution of data points per time unit (preferably seconds).

- **e**  
  Error term giving the percent amount of deviation from the ideal gaussian curve for individual data points.

- **ds**  
  Detector saturation. Intensity values will be cut off at this point if requested.

- **base_line**  
  Defines if peak is supposed to have a higher base level.

Details

The main task of **ModelGaussPeak** is to create peak data in gaussian shape for testing. Width is meant in the chromatographic sense, i.e. the time between peak front and tail hitting the baseline.

Value

Dataframe with columns 'rt' and 'int'.

Examples

```r
ylim <- c(0,10^7)
par(mfrow=c(1,5))
pk <- ModelGaussPeak(height=10^7, width=4, scan_rate=10, e=0, ds=10^7, base_line=10^2)
plot(pk,ylim=ylim,main="standard")
pk <- ModelGaussPeak(height=10^7, width=4, scan_rate=10, e=0, ds=8*10^6, base_line=10^2)
plot(pk,ylim=ylim,main="flat top")
pk <- ModelGaussPeak(height=10^7, width=4, scan_rate=10, e=0, ds=8*10^6, base_line=10^5)
plot(pk,ylim=ylim,main="high baseline")
pk <- ModelGaussPeak(height=10^7, width=4, scan_rate=10, e=0.05, ds=8*10^6, base_line=10^5)
plot(pk,ylim=ylim,main="e=5%")
pk <- ModelGaussPeak(height=10^7, width=4, scan_rate=5, e=0.05, ds=8*10^6, base_line=10^5)
plot(pk,ylim=ylim,main="sr=5")
```

---

**mzXML_data**  
_A test dataset of class mzXML._

Description

A test dataset imported by read.mzXML() from a GC-APCI measurement on a Bruker impact II, exported by Compass to an mzXML file.

Usage

data("mzXML_data")
Format
The full format depends on the source mzXML (different vendors export different fields). However, raw data should be stored within list element 'scan' containing sublist elements for 'mass' and 'peaks'. The class-attribute needs to be 'mzXML' such that CorrectOverloadedPeaks can recognize it.

read.mzXML
Read a standard mzXML

Description
read.mzXML is a copy from the caMassClass package which is no longer actively on CRAN.

Usage
read.mzXML(filename)

Arguments
filename A mzXML file as exported by vendor software.

Details
The main task of read.mzXML and write.mzXML functions is to extract and save scan data of mzXML files. In addition attempt is made to keep all other sections of mzXML file as unparsed XML code, so the data can be extracted latter or saved into new mzXML files. Those unparsed sections are stored as XML text.

Value
A generic R object of class mzXML.

write.mzXML
Write a standard mzXML

Description
write.mzXML is a copy from the caMassClass package which is no longer actively on CRAN

Usage
write.mzXML(mzXML, filename, precision = c("32", "64"))
Arguments

- **mzXML**: The generic mzXML object
- **filename**: A mzXML filename to export to.
- **precision**: Either '32' or '64' byte.

Details

The main task of `read.mzXML` and `write.mzXML` functions is to extract and save scan data of mzXML files. In addition attempt is made to keep all other sections of mzXML file as unparsed XML code, so the data can be extracted latter or saved into new mzXML files. Those unparsed sections are stored as XML text.

Value

Nothing. mzXML object is exported to filename. If it was imported using `read.mzXML` it should contain all previous fields.

---

**xcmsRaw_data**

A test dataset of class xcmsRaw.

Description

A few seconds extracted from a GC-APCI-MS run using a Bruker impact II.

Usage

```r
data("xcmsRaw_data")
```

Format

The format is based on class 'xcmsRaw' [package "xcms"] with several slots. The slots which will be used by the functions are 'env', 'scantime' and 'scanindex'. Only individual intensity values within 'env$intensity' will be modified.
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