

# Package ‘TargetSearch’

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**Type** Package

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**Author** Alvaro Cuadros-Inostroza <acuadros+bioc@gmail.com>,  
Jan Lisec,  
Henning Redestig,  
Matt Hannah

**Maintainer** Alvaro Cuadros-Inostroza <acuadros+bioc@gmail.com>

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TargetSearch-package    *A targeted approach for GC-MS data.*

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### Description

This packages provides a targeted method for GC-MS data analysis. The workflow includes a peak picking algorithm to convert from netcdf files to tab delimited files, retention time correction using retention time markers provided by the user, and a library search using multiple marker masses and retention time index optimisation.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

Maintainer: Alvaro Cuadros-Inostroza <inostroza@mpimp-golm.mpg.de>

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baseline                      *Baseline correction - wrapper function*

---

### Description

This function perform baseline correction by wrapping around the methods implemented on [baselineCorrection](#) and [baselineCorrectionQuant](#).

### Usage

```
baseline(ncdf, bsline_method = c('classic', 'quantiles', 'none'), ...)
```

### Arguments

|               |   |
|---------------|---|
| ncdf          | A list containing the raw chromatogram data. The list can be generated by <a href="#">peakCDFextraction</a> . Expected elements are "Peaks" which is matrix of intensities where the rows are retention times and columns are mass traces, "Time" which is a vector of retention time in seconds. |
| bsline_method | A string to select the baseline retention method. Options are "classic" which implements Chang's method (the old or classic TargetSearch method), "quantiles" the quantiles based method, and "none" which does nothing (returns the same input).   |
| ...           | Extra parameters to be passed to <a href="#">baselineCorrection</a> or <a href="#">baselineCorrectionQuant</a> .  |

### Details

This is a wrapper function around the different baseline correction algorithms. It is not intended to be executed by the average user. Please refer to the respective man pages for details.

**Value**

Returns a list with the same elements as the the input, but the element "Peaks" containing baseline corrected values.

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[Rlcorrect](#), [baselineCorrection](#), [baselineCorrectionQuant](#)

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baselineCorrection     *Baseline correction - Chang's method*

---

**Description**

Function for baseline correction of GC-MS chromatograms using Chang's method described below.

**Usage**

```
baselineCorrection(peaks, threshold = 0.5, alpha = 0.95, bfraction = 0.2,  
                  segments = 100, signalWindow = 10, method = "linear")
```

**Arguments**

|              |  |
|--------------|--|
| peaks        | Either a matrix object of spectra peak intensities to be baseline corrected, where the rows are retention times and columns are mass traces; or, a named list containing an element called "Peaks" which such matrix. The list can be generated by <a href="#">peakCDFextraction</a> |
| threshold    | A numeric value between 0 and 1. A value of one sets the baseline above the noise, 0.5 in the middle of the noise and 0 below the noise.   |
| alpha        | The alpha parameter of the high pass filter.   |
| bfraction    | The percentage of the fragments with the lowest intensities of the filtered signal that are assumed to be baseline signal.   |
| segments     | The number of segments in which the filtered signal is divided.  |
| signalWindow | The window size (number of points) used in the signal windowing step.  |
| method       | The method used to approximate the baseline. "linear" (default) uses linear interpolation. "spline" fits a cubic smoothing spline (warning: really slow).  |

## Details

The baseline correction algorithm is based on the work of Chang et al, and it works as follows. For every mass trace, i.e., columns of matrix peaks, the signal intensity is filtered by a first high pass filter:  $y[i] = \alpha * (y[i-1] + x[i] - x[i-1])$ . The filtered signal is divided into evenly spaced segments (segments) and the standard deviation of each segment is calculated. A percentage (bfraction) of the segments with the lowest values are assumed to be baseline signal and the standard deviation (*stdn*) of the points within those segments is calculated.

Once *stdn* has been determined, the points with absolute filtered values larger than  $2 * \text{stdn}$  are considered signal. After that, the signal windowing step takes every one of the points found to be signal as the center of a signal window (*signalWindow*) and marks the points within that window as signal. The remaining points are now considered to be noise.

The baseline signal is obtained by either using linear interpolation (default) or fitting a cubic smoothing spline taking only the noise. The baseline can be shifted up or down by using the parameter (*threshold*), which is done by the formula:  $B' = B + 2 * (\text{threshold} - 0.5) * 2 * \text{stdn}$ , where *B* is the fitted spline, *stdn* the standard deviation of the noise, and *threshold* a value between 0 and 1. Finally, the corrected signal is calculated by subtracting *B'* to the original signal.

## Value

The output depends on whether the input peaks is a matrix or a list. If it is a matrix, then the function returns a matrix of the same dimensions with the baseline corrected intensities. If instead peaks is a list, then the element called "Peaks" will hold the output.

## Note

This function is intended to be run internally, but it is exported for advanced users.

## Author(s)

Alvaro Cuadros-Inostroza

## References

David Chang, Cory D. Banack and Sirish L. Shah, Robust baseline correction algorithm for signal dense NMR spectra. *Journal of Magnetic Resonance* 187 (2007) 288-292

## See Also

[Rlcorrect](#)

---

`baselineCorrectionQuant`*Baseline correction - quantiles method*

---

### Description

This function perform baseline correction using a quantiles around a moving window algorithm.

### Usage

```
baselineCorrectionQuant(peaks, time, smooth=0, qntl=0.50, width=30,  
                        unit=c("seconds", "points"), steps=10)
```

### Arguments

|                     |   |
|---------------------|---|
| <code>peaks</code>  | Either a matrix object of spectra peak intensities to be baseline corrected, where the rows are retention times and columns are mass traces; or, a named list containing an element called "Peaks" which such matrix and another called "Time" with the retention time in seconds. The list can be generated by <a href="#">peakCDFextraction</a> |
| <code>time</code>   | A vector of retention time in seconds. This parameter is used if <code>peaks</code> is a matrix. Otherwise, the element called "Time" is used instead and this parameter is ignored.  |
| <code>smooth</code> | An integer. Smooth each signal by this number of points using a moving average. Smoothing is disabled if this value is less or equal than 1. Note that the smoothing is applied after the baseline correction.  |
| <code>qntl</code>   | Numeric scalar. The quantile for baseline estimation. The value must be in [0, 1].  |
| <code>width</code>  | numeric scalar. The size of the window centered around a scan for baseline estimation. The size depends on the parameter <code>unit</code> below.   |
| <code>unit</code>   | A string which chooses if the width are points (scans) or seconds.  |
| <code>steps</code>  | Integer scalar greater than zero. To speed up computation, the baseline algorithm does not compute the baseline estimate in each single scan, but in intervals of <code>steps</code> steps. The intermediate points are estimated by simple linear regression.  |

### Details

Applies a quantile based baseline estimation method. The method is applied for each ion mass trace (column of peaks) individually. It simple computes for each data point of the trace the `qntl` quantile, for example the 50% quantile, ie, the median, of all the points which are within a `width` distance or it.

In order for the method to work, select a `width` much larger than the widest peak.

For speed efficiency, and assuming that the baseline is a smooth curve, the quantiles are computed every `steps` points instead. By setting this value to 1, it means compute the baseline for each point. The baseline of the points in between are approximated by linear interpolation.

**Value**

Returns a list with the same elements as the the input, but the element "Peaks" containing baseline corrected values. In case peaks is a matrix, it returns a matrix of the same dimension instead.

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[Rlcorrect](#), [baseline](#), [baselineCorrection](#)

---

checkRimLim

*Visually check retention index marker limits*

---

**Description**

A function to visually check if the retention time search limits of the retention index markers (aka FAMEs) are correct or need some adjustment.

**Usage**

```
checkRimLim(samples, rim, layout, show = TRUE, single = TRUE, extend = 0.5,
  rect.col = "#e7e7e7", mar = c(2, 2, 2, 2), oma = c(3, 3, 2, 0.5),
  cex.main = 1, type = "l", ...)
```

**Arguments**

|          |   |
|----------|---|
| samples  | A <a href="#">tsSample</a> object created by <a href="#">ImportSamples</a> .  |
| rim      | A <a href="#">tsRim</a> object describing the retention index markers. See <a href="#">ImportFameSettings</a> .   |
| layout   | A vector of the form <code>c(nr, nc)</code> to arrange the panel by <code>nr</code> rows and <code>nc</code> columns. If missing then the layout is created automatically.              |
| show     | Logical. If FALSE the plot is not shown, but the data points can be used for further inspection or for custom plots.  |
| single   | Logical. If TRUE a <i>single</i> sample will be selected randomly for plotting. This was the old default behavior. If FALSE all samples will be used for plotting (but see note below). |
| extend   | a numeric coefficient to extend the time window search of the respective time marker. Defaults to 0.5.  |
| rect.col | the color for the background rectangle which indicates the current retention time limits.   |
| mar      | the subplots margins, passed to <a href="#">par()</a> .   |
| oma      | the outer plot margins, passed to <a href="#">par()</a> .   |
| cex.main | The magnification to be used for main titles, passed to <a href="#">par()</a> .   |
| type     | A character vector indicating the type of plots. Default "l" for lines. Passed to <a href="#">matplot()</a> .   |
| ...      | extra plotting arguments passed to <a href="#">matplot()</a> such as <code>col</code> , <code>lty</code> , <code>pch</code> , <code>lwd</code> .  |

## Details

The function takes a `tsSample` object and creates a panel plot of the  $m/z$  traces around the area in which a marker is expected to be, one panel for each marker. By default, a single (random) sample is chosen (see option `single`) for plotting, but it is also possible to visualize many samples at the same time (but see note below).

For multiple sample visualization, it is recommended to use sub-setting for the `samples` and `rim` arguments in order to avoid over crowded plots, specially when there are several samples and several retention index markers. See the examples below.

Plotting options such as `col`, `lty`, `pch`, `lwd` can be passed; these are in turn passed to `matplot()`. Note that these are passed to each panel; it not possible to pass different options to different panels (for example to have different line colors). Moreover, using options such as `xlim` and `ylim` may result in 'empty' plots (because each panel needs its own limits). If different styles are required, then either make your own function from the output or use subsets of the `rim` (`tsRim`) object.

## Value

The output value is either invisible or it depends on the option `single`. If this option is TRUE (the old behavior), then the output will be a list of  $n$  times 2 matrices, each element corresponding to a retention marker. Columns are retention time and intensities of the respective marker's  $m/z$ . The rows can be as many data points are within the search window.

If `single=FALSE`, the output is a list whose length is equal to `length(samples)` and its names are equal to `sampleNames(samples)`. Each element is in turn a list with exactly the same structure described in the paragraph above.

## Note

If `single=TRUE`, all CDF files will be scanned, which can take a significant amount of time to parse, in particular, if there are hundred of them. Also due to this, each panel of the plot could be extremely crowded. It is therefore recommended to use sample sub-setting to reduce this number, as shown in the examples below.

## See Also

`matplot` for plotting parameters, `par` for inner and outer margins parameters, `tsSample`, `sampleNames`, `tsRim`, `ImportFameSettings`

## Examples

```
require(TargetSearchData)

# get the cdf path TargetSearchData
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# import samples (see ImportSamples() for details)
samples <- ImportSamples(file.path(cdfpath, "samples.txt"), CDFpath = cdfpath)

# Import RI markers (see ImportFameSettings())
rim <- ImportFameSettings(file.path(cdfpath, "rimLimits.txt"))
```



```

# choose a sample at random and plot the m/z traces around the retention time window
ret <- checkRimLim(samples, rim)

# to choose a specific sample and marker, use subsetting
ret <- checkRimLim(samples[3], rim[1:2])

# to display many samples at the same time, set the option `single` to `FALSE` and select a subset
# of samples (recommended). In this example the first three samples are chosen.
ret <- checkRimLim(samples[1:3], rim, single=FALSE)

# in general, visualizing all samples (as shown below) at the same time it is not recommended
# for large number of samples.
## Not run:
ret <- checkRimLim(samples, rim, single=FALSE)

## End(Not run)

```

---

FAMEoutliers

*FAME outlier detection*


---

## Description

A function to detect retention time marker (FAME) outliers.

## Usage

```

FAMEoutliers(samples, RImatrix, pdffile = NA, startDay = NA, endDay = NA,
             threshold = 3, group.threshold = 0.05)

```

## Arguments

|                 |   |
|-----------------|---|
| samples         | A tsSample object created by ImportSamples function.  |
| RImatrix        | A retention time matrix of the found retention time markers.                                    |
| pdffile         | A character string naming a PDF file where the FAMEs report will be saved.                      |
| startDay        | A numeric vector with the starting days of your day groups.                                     |
| endDay          | A numeric vector with the ending days of your day groups.                                       |
| threshold       | A standard deviations cutoff to detect outliers.  |
| group.threshold | A numeric cutoff to detect day groups based on hierarchical clustering. Must be between 0. . 1. |

## Details

If no pdffile argument is given, the report will be saved on a file called "TargetSearch-YYYY-MM-DD.FAME-report.pdf", where YYYY-MM-DD is a date.

If both startDay and endDay are not given, the function will try to detect day groups using a hierarchical clustering approach by cutting the tree using group.threshold as cutoff height.

Retention time markers that deviate more than threshold standard deviations from the mean of their day group will be identified as outliers.

**Value**

A logical matrix of the same size of RImatrix. A TRUE value indicates that the retention time marker in that particular sample is an outlier.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[RiCorrect](#), [ImportSamples](#), [TSEExample](#)

**Examples**

```
# load pre-calculated example data and objects
data(TSEExample)

# find the retention marker outliers of the example data and save it in "outlier.pdf"
outliers <- FAMEoutliers(sampleDescription, RImatrix, pdfFile = "outlier.pdf")

# find the outliers (although they are reported in the output PDF file)
apply(outliers, 1, which)
```

---

FindAllPeaks

*Extract peaks from chromatogram files - low level function*

---

**Description**

This function extracts all peaks of a given metabolite in a given RI window. This function is intended for fine-tuning metabolite search parameters.

**Usage**

```
FindAllPeaks(samples, Lib, libID, dev=NULL, mz=NULL, RI=NULL,
             mz_type = c('selMass', 'quantMass', 'topMass'),
             columns = NULL)
```

**Arguments**

|         |   |
|---------|---|
| samples | A tsSample object created by <a href="#">ImportSamples</a> function.  |
| Lib     | A tsLib object created by <a href="#">ImportLibrary</a> function.   |
| libID   | An index (integer or character) value representing the respective metabolite in the reference library Lib. It must be a scalar. |
| dev     | The allowed retention index (RI) deviation or NULL. See details below.  |
| mz      | A list of m/z values to search or NULL.   |

|         |   |
|---------|---|
| RI      | The expected retention index or NULL.   |
| mz_type | whether to search for the selective, quant or top masses of the respective metabolite.  |
| columns | Either NULL, a character vector, or an integer vector. In most cases, leave it as NULL. This parameter is used to configure the column names or positions of RI text files. See the documentation on the <a href="#">text2bin</a> function for further details. |

### Details

The function searches for all peaks of a metabolite in all samples within a RI window. The parameters `dev`, `mz`, and `RI` have preference over the settings of the metabolite indexed by `libID`. In fact, if all of these parameters are not NULL, then `refLib` and `libID` are not used.

The `dev` parameter can either be NULL (as stated above), or a numeric vector. If the length is equal to 1, then the RI search window is the given RI plus or minus `dev`. If the length is 2, then the search window is from `RI + dev[1]` to `RI + dev[2]`. *Note* than in this case `dev[1]` is usually a negative value. An error is raised if the length is greater than 2

The `columns` parameter is only needed for custom text RI files. There is no need to change it.

### Value

It returns a matrix in which each row represent a hit. Note that there can be zero rows if no hits are found. The columns are named and these are:

|     |  |
|-----|--|
| Int | Peak intensity   |
| RI  | Retention Index  |
| RI  | Retention Time   |
| mz  | the searched m/z value                                 |
| fid | the respective file or sample index. An integer value. |

### Note

This is an internal function not intended to be invoked directly, but it is exposed for convenience and advanced users.

In the future it may replace [FindPeaks](#).

See also the function [ri\\_data\\_extract](#) which offers a similar functionality but with different input parameters.

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

[FindPeaks](#), [ri\\_data\\_extract](#),

## Examples

```
# load pre-calculated example data files and objects
require(TargetSearchData)
data(TSExample)

# get and set the RI file path
RIpath(sampleDescription) <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# search all peaks of Valine (GC.3) and selective masses
peaks <- FindAllPeaks(sampleDescription, refLibrary, 'GC.3')
head(peaks)

# a numeric index is also allowed
peaks <- FindAllPeaks(sampleDescription, refLibrary, 3)
head(peaks)

# an asymmetric deviation search
peaks <- FindAllPeaks(sampleDescription, refLibrary, 'GC.3', dev=c(-1000, 2000))
head(peaks)

# search arbitrary masses at arbitrary RI. the reference library and ID
# must be set set to NULL.
peaks <- FindAllPeaks(sampleDescription, NULL, NULL, dev=3000, RI=270000, mz=c(144, 100))
head(peaks)
```

---

FindPeaks

*Extract peaks from chromatogram files*

---

## Description

This function extracts the maximum intensity of a list of masses in a given RI window.

## Usage

```
FindPeaks(my.files, refLib, columns = NULL, showProgressBar = FALSE)
```

## Arguments

|                              |   |
|------------------------------|---|
| <code>my.files</code>        | A character vector naming RI files to be searched.  |
| <code>refLib</code>          | A numeric matrix with three columns or a list of three column matrices. The second column contains the masses and the first and third column contains the RI limits.  |
| <code>showProgressBar</code> | Logical. Should the progress bar be displayed?  |
| <code>columns</code>         | Either NULL, a character vector, or an integer vector. In most cases, leave it as NULL. This parameter is used to configure the column names or positions of RI text files. See the documentation on the <a href="#">text2bin</a> function for further details. |

**Details**

The reference library parameter `refLib` can be either a single three-column matrix or a list of such matrices. If it is a list, the length must match the length of `my.files`. In this case, every component will be used to iteratively search in the corresponding file.

The RI files format can be either "text" or "binary". The type is detected dynamically.

**Value**

A `tsMSdata` object.

**Note**

This is an internal function not intended to be invoked directly.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[medianRILib](#), [sampleRI](#), [peakFind](#), [tsMSdata](#)

**Examples**

```
# load example CDF files
require(TargetSearchData)
# load pre-calculated example data and objects
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
# update RI file path
RIpath(sampleDescription) <- RI.path

my.files <- RIfiles(sampleDescription)
# make a three column matrix: lower RI, mass, upper RI
refLib <- refLib(refLibrary)
head(refLib)

# extract the peaks
peaks <- FindPeaks(my.files, refLib)
```

---

`fixRI`*Fixing Retention Time Index Correction*

---

## Description

This function can be used to correct the detected retention time index (RI) markers or to manually force their location to specific retention times if, for example, the RI markers were not co-injected with the biological samples.

## Usage

```
fixRI(samples, rimLimits, RImatrix=NULL, sampleNames=NULL, quiet=TRUE)
```

## Arguments

|                          |  |
|--------------------------|--|
| <code>samples</code>     | A <code>tsSample</code> object created by <code>ImportSamples</code> function.   |
| <code>rimLimits</code>   | A <code>tsRim</code> object. See <code>ImportFameSettings</code> .   |
| <code>RImatrix</code>    | Optional. A retention time matrix of the found retention time markers that was obtained after running <code>RIcorrect</code> . |
| <code>sampleNames</code> | Optional. A character vector naming the samples that are to be RI corrected.   |
| <code>quiet</code>       | Logical. Do not print a list of converted files.   |

## Details

Sometimes the retention index limits (see `ImportFameSettings`) are not set correctly and you will have to run the peak detection and RI correction function (`RIcorrect`) again, which may take a long time specially if there are many samples.

Instead, a simple approach is to fix the RI limits and use this function to correct the generated RI files. Since these files are much smaller than CDF files (chromatograms), this runs much faster.

Other possibility is that the time positions of one or more RI markers were wrongly detected because there was just simply no peak or the RI markers where not co-injected in some samples. You could manually force the locations of the RI markers. This case is discussed in the “`RICorrection`” vignette.

The behavior of this function depends on whether the parameter `RImatrix` is `NULL` or not. If `NULL`, the RI markers will be searched again (using the settings of `rimLimits` parameters, which you should have already fixed) and the resulting values will be used to correct the RI files. If it is a numeric matrix, then these values will be used to correct the RI files. Note that this matrix dimensions are exactly  $m$  samples (rows) times  $n$  (columns) RI markers.

`sampleNames` controls which samples will be corrected. If `NULL` then all samples will be corrected. It could be character vector (sample names) or a numeric vector representing the sample indexes.

## Value

Invisible `NULL`. It prints the corrected samples if `quiet` is `FALSE`.

**Note**

In case the RI files are in text format and their column names are not standard (for example, when the files were generated with another software), use the global option 'TS\_RI\_columns' or transform the RI files to [TargetSearch](#) binary format. See the documentation in function [text2bin](#).

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[RIcorrect](#), [FAMEoutliers](#), [ImportSamples](#), [ImportFameSettings](#)

**Examples**

```
require(TargetSearchData)
# import refLibrary, rimLimits and sampleDescription.
data(TSExample)
# get the CDF files
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# select a subset of samples
smp <- sampleDescription[1:4]

# update the CDF path
CDFpath(smp) <- cdfpath

# make a copy of the RI markers object
rim <- rimLimits

# mess up the limits of marker 3 (real value is 369 seconds app.)
rimLimits(rim)[3,] <- c(375, 400)

# run RImat (skip CDF-4 conversion)
RImat <- RImat(smp, rim, writeCDF4path=FALSE,
              Window = 15, IntThreshold = 50)

# fix the limits of marker 3
rimLimits(rim)[3,] <- c(360, 400)

# you could run again RImat, but this is faster
fixRI(smp, rim)

# get the RI matrix
RImat <- riMatrix(smp, rim)

# compare the values with the real ones (previously stored in RImat)
stopifnot( all.equal(RImat, RImat[1:4], tolerance=1e-8) )

# manual adjustment or RI markers for sample 3.
# Warning: this is just an example to illustrate how to use this function.
#         don't do this unless you know what you're doing.
```

```
RImat[,3] <- c(252, 311, 369)
fixRI(smp, rim, RImat, 3)
```

---

ImportFameSettings      *Retention time markers settings*

---

## Description

This function imports a list of retention standard markers.

## Usage

```
ImportFameSettings(tmp.file = NA, mass = NA, ...)
```

## Arguments

|                       |  |
|-----------------------|--|
| <code>tmp.file</code> | A character string naming a file with standard markers.      |
| <code>mass</code>     | The m/z standard marker.                                     |
| <code>...</code>      | Other options passed to <a href="#">read.delim</a> function. |

## Details

The standard marker file is a tab-delimited text file with 3 or 4 columns. Column names doesn't matter. They must be in the following order.

- `LowerLimit` - The Retention time lower limit in seconds.
- `UpperLimit` - The Retention time upper limit in seconds.
- `RIstandard` - The RI value of that standard.
- `mass` - The m/z standard marker. This column is optional since it could be set by the `mass` parameter.

If no arguments are given, a default object will be returned.

## Value

A `tsRim` object.

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[RIcorrect](#), [tsRim](#)



## Examples

```
# get the RI marker definition file
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
rim.file <- file.path(cdfpath, "rimLimits.txt")

# set the mass marker to 87
mass <- 87

# load the definition
rimLimits <- ImportFameSettings(rim.file, mass = mass)

# sometimes you need to change the limits of a particular standard
rimLimits(rimLimits)[2,] <- c(410, 450)

# to change the mass value
rimMass(rimLimits) <- 85
```

---

ImportLibrary

*Library import*

---

## Description

These functions import a metabolite library file that will be used to processed the GC-MS data. Two file formats are supported: a tab-delimited format and the more common NIST MSP format.

## Usage

```
ImportLibrary(x, type = "auto", ...)
```

```
ImportLibrary.tab(libfile, fields = NULL, RI_dev = c(2000,1000,200),
  SelMasses = 5, TopMasses = 15, ExcludeMasses = NULL,
  libdata, file.opt=NULL)
```

```
ImportLibrary.msp(libfile, fields = NULL, RI_dev = c(2000,1000,200),
  SelMasses = 5, TopMasses = 15, ExcludeMasses = NULL)
```

## Arguments

- |         |   |
|---------|---|
| x       | A character string or a data.frame. If data.frame, it will be passed to ImportLibrary.tab as parameter libdata. If character, it will be passed as libfile to either ImportLibrary.tab or ImportLibrary.msp according to the file type (option type). |
| libfile | A character string naming a library file. See details.  |
| type    | The library file format. Possible options are "tab" for a tab-delimited file, "msp" for NIST MSP format, or "auto" for autodetection. Default to "auto".  |

|               |   |
|---------------|---|
| fields        | A two component list. Each component contains a regular expression used to parse and extract the fields for retention index and selection masses. Only meaningful for MSP format.   |
| RI_dev        | A three component vector with RI windows.   |
| SelMasses     | The number of selective masses that will be used.   |
| TopMasses     | The number of most intensive masses that will be taken from the spectrum, if no TOP_MASS is provided.   |
| ExcludeMasses | Optional. A vector containing a list of masses that will be excluded.   |
| libdata       | Optional. A data frame with library data. The format is the same as the library file. It is equivalent to importing the library file first with <code>read.table</code> and calling <code>ImportLibrary.tab</code> after. This might be preferable for "fine tuning", for example, if the library file is in CSV format instead of tab-delimited. |
| file.opt      | Optional. A list containing arguments to be passed to <code>read.table</code> .   |
| ...           | Further arguments passed to <code>ImportLibrary.tab</code> or <code>ImportLibrary.msp</code>  |

## Details

`ImportLibrary` is a wrapper for functions `ImportLibrary.tab` and `ImportLibrary.msp` which detects automatically which function should be called.

`ImportLibrary.tab` reads a tab delimited text file by calling the function `read.table` which will be parsed and converted to a `tsLib` object. The following arguments are used by default (which are not exactly the defaults for `read.table`):

```
header=TRUE, sep="\t", quote="", dec=".", fill=TRUE, comment.char="#"
```

The argument `file.opt` can be used to change these options. Other alternative is to import first the file with `read.table` and friends, and call `ImportLibrary` with the resulting `data.frame`. This allows more flexibility with libraries with unusual characters, for example.

These columns are needed:

- libID - A unique identifier for the metabolite.
- Name - The metabolite name.
- RI - The expected RI.
- SEL\_MASS - A list of selective masses separated with semicolon.
- TOP\_MASS - A list of the most abundant masses to be searched, separated with semicolons.
- Win\_k - The RI windows,  $k = 1, 2, 3$ . Mass search is performed in three steps. A RI window required for each one of them.
- SPECTRUM - The metabolite spectrum.  $m/z$  and intensity are separated by spaces and colons.
- QUANT\_MASS - A list of masses that might be used for quantification. One value per metabolite and it must be one of the selective masses. (optional)

The columns Name and RI are mandatory. At least one of columns SEL\_MASS, TOP\_MASS and SPECTRUM must be given as well. By using the parameters SelMasses or TopMasses it is possible to set the selective masses or the top masses from the spectra. The parameter ExcludeMasses is used only when masses are obtained from the spectra. The parameter RI\_dev can be used to set the RI windows. Note that in this case, all metabolites would have the same RI windows.

A unique identifier may be provided as well (libID). This could be an external database identifier. If it is not provided, a random identifier will be created of the form GC.k, k = 1,...,N.

The MSP format is a text file that can be imported/exported from NIST. A typical MSP file looks like this:

```
Name: Pyruvic Acid
Synon: Propanoic acid, 2-(methoxyimino)-, trimethylsilyl ester
Synon: RI: 223090
Synon: SEL MASS: 89|115|158|174|189
Formula: C7H15NO3Si
MW: 189
Num Peaks: 41
  85   8; 86  13; 87   5; 88   4; 89  649;
  90  55; 91  28; 92   1; 98  13; 99  257;
 100 169; 101 30; 102  7; 103 13; 104  1;
 113  3; 114 35; 115 358; 116 44; 117 73;
 118 10; 119  4; 128  2; 129  1; 130 10;
 131  3; 142  1; 143 19; 144  4; 145  1;
 157  1; 158 69; 159 22; 160  4; 173  1;
 174 999; 175 115; 176 40; 177  2; 189 16;
 190  2;
```

```
Name: another metabolite
...
```

Different entries must be separated by empty lines. In order to parse the retention time index (RI) and selective masses (SEL MASS), a two component list containing the field names of RI and SEL\_MASS must be provided by using the parameter fields. In this example, use field = list("RI: ", "SEL MASS: "). Note that ImportLibrary expects to find those fields next to "Synon:". Alternatively, you could provide the RI and SEL\_MASS using the `tsLib` methods.

Libraries for TargetSearch and for different retention index systems, such as VAR5 or MDN35, can be downloaded from <http://gmd.mpimp-golm.mpg.de/>.

### Value

A `tsLib` object.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

### See Also

[ImportSamples](#), [tsLib](#)

### Examples

```
# get the reference library file
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
```

```

lib.file <- file.path(cdfpath, "library.txt")

# Import the reference library
refLibrary <- ImportLibrary(lib.file)

# set new names for the first 3 metabolites
libName(refLibrary)[1:3] <- c("Metab01", "Metab02", "Metab03")

# change the retention time deviations of Metabolite 3
RIdev(refLibrary)[3,] <- c(3000,1500,150)

```

---

ImportSamples

*Sample definitions*


---

### Description

These functions import sample information from either a tab delimited file or a file system path. The sample information contain sample names, CDF files and their measurement day, also known as, measurement run or measurement batch.

### Usage

```
ImportSamples(sampfile, CDFpath, RIpath, ftype=c("binary", "text"), ...)
```

```
ImportSamplesFromDir(CDFpath=".", RIfiles=FALSE, ftype=c("binary", "text"),
verbose=FALSE, ...)
```

### Arguments

|          |   |
|----------|---|
| sampfile | A character string naming a sample file or a data.frame. See details.   |
| CDFpath  | A character string naming a directory where the CDF files are located (by default is the current directory)   |
| RIpath   | A character string naming a directory where the RI corrected text files are/will be located.  |
| RIfiles  | Logical. If TRUE, the function will look for for RI files (RI_*) instead of CDF files (the default).  |
| ftype    | A character string giving the file type for RI files. Options are "binary" and "text".  |
| verbose  | Logical. Show more output if TRUE.  |
| ...      | Extra options whose meaning depend on the function: for ImportSamples, the options will be passed to <a href="#">read.delim</a> , while for ImportSamplesFromDir, these are passed to <a href="#">dir</a> . |

## Details

The sample file is a tab-delimited text file or, alternatively, a data.frame like the one would get by calling [read.delim](#). The following columns are expected, though only the first one below is mandatory.

- CDF\_FILE - The list of baseline corrected CDF files (mandatory).
- MEASUREMENT\_DAY - The day or batch when the sample was measured (optional).
- SAMPLE\_NAME - A unique sample identifier (optional).

The function first looks for columns matching those names. If they are not found, then it looks for columns with the substrings 'cdf', 'day' and 'name' respectively. If the 'cdf' column is not found, the function raises an error, but if 'day' is not found, then it assumes the measurement day is the same for all. Moreover, if the column for sample names/idenfiers is missing, then the function uses the 'cdf' file names as identifiers.

During the column matching, the first match is taken in case of ambiguity. The column order does not matter. Other columns could be included in that file. They won't be used by the script, but will be included in the "sample" R object.

The files given in the 'cdf' column may optionally include a relative path, such as mypath/myfile.cdf, which will be relative to the working directory or relative to the argument CDFpath. Optionally, the file extension can be omitted because 'TargetSearch' adds the .cdf extension automatically if missing. Note: it may fail in case sensitive file systems as a lower case extension is appended.

If the parameter CDFpath is missing, then the current directory is used. If RIpath is missing, the value of CDFpath will be used.

The ftype parameter sets the file format of the RI files, which are created by the function [RIcorrect](#). "text" is the *classic* text format and "binary" is a binary version, designed for speed, of the text format (TargetSearch >= 1.12.0). The file format can be identified by the file extension (".txt" for text, ".dat" for binary), but this is just an indicator: the file format is detected dynamically during file reading. Use the method [fileFormat](#) to set or get this parameter.

The function [ImportSamplesFromDir](#) scans for cdf files in the current or given directory. The search can be made recursive by passing the parameter recursive=TRUE (actually passed to [dir](#)).

The parameter verbose will print a list of detected files is set to TRUE. This can be used for debugging.

## Value

A tsSample object.

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[ImportLibrary](#), [tsSample](#)

## Examples

```
# get the sample definition definition file
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
sample.file <- file.path(cdfpath, "samples.txt")

# set a path where the RI files will be created
RIpath <- "."

# import samples
sampleDescription <- ImportSamples(sample.file, CDFpath = cdfpath, RIpath = RIpath)

# change the sample names. It is required that the names must be unique.
sampleNames(sampleDescription) <- paste("Sample", 1:length(sampleDescription), sep = "_")

# change the file paths (relative to the working path)
CDFpath(sampleDescription) <- "my_cdfs"
RIpath(sampleDescription) <- "my_RIs"
```

---

medianRILib

*Median RI library correction*

---

## Description

Return a tsLib object with the median RI of the selective masses across samples.

## Usage

```
medianRILib(samples, Lib, makeReport = FALSE, pdfFile = "medianLibRep.pdf",
            columns = NULL, showProgressBar = FALSE)
```

## Arguments

|                 |   |
|-----------------|---|
| samples         | A tsSample object created by <a href="#">ImportSamples</a> function.  |
| Lib             | A tsLib object created by <a href="#">ImportLibrary</a> function.   |
| makeReport      | Logical. If TRUE will report the RI deviations for every metabolite in the library.   |
| pdfFile         | The file name where the report will be saved.   |
| columns         | Either NULL, a character vector, or an integer vector. In most cases, leave it as NULL. This parameter is used to configure the column names or positions of RI text files. See the documentation on the <a href="#">text2bin</a> function for further details. |
| showProgressBar | Logical. Should the progress bar be displayed?  |

## Value

A tsLib object. It will update the slot med\_RI which contains the median RI of every searched metabolite.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[ImportSamples](#), [ImportLibrary](#), [tsLib-class](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
# update RI file path
RIpath(sampleDescription) <- RI.path
# Import Library
refLibrary <- ImportLibrary(file.path(RI.path, 'library.txt'))
# update median RI
refLibrary <- medianRILib(sampleDescription, refLibrary)

# perhaps you need to adjust the library RI of one metabolite and the allowed time
# deviation (first time deviation window)
libRI(refLibrary)[5] <- 306500
RIdev(refLibrary)[5,1] <- 2000

refLibrary <- medianRILib(sampleDescription, refLibrary)
```

---

ncdf4Convert, tsSample-method

*Method for converting CDF-3 files to CDF-4*

---

**Description**

ncdf4Convert is a high level method used to convert from CDF-3 to 'TargetSearch' new CDF-4 custom file format.

**Usage**

```
ncdf4Convert(obj, path, ...)
```

**Arguments**

|      |   |
|------|---|
| obj  | A <a href="#">tsSample</a> object   |
| path | A character vector representing file path in which the newly created CDF-4 files will be stored. If missing, the files will be save in the same directory as the source CDF-3 files |
| ...  | Extra arguments passed to <a href="#">ncdf4_convert</a> , such as baseline correction options.  |

## Details

This is a high level interface to [ncdf4\\_convert](#) which uses a [tsSample](#) as input. The advantage of using this function is that it updates the paths to the CDF-4 files for downstream analysis.

The parameter `path` can be used to change the original paths, which may be necessary if those files are on a read-only file-system. If this parameter is missing, the same paths are used. Note that the path are re-cycled to match the length of the samples.

The `...` can be used to pass extra arguments to [ncdf4\\_convert](#) and to [baseline](#). Refer to those man pages for details.

## Value

A new [tsSample](#) object with updated CDF-4 file paths. The files are converted in the background.

## Author(s)

Alvaro Cuadros-Inostroza

## See Also

[ncdf4\\_convert](#)

## Examples

```
require(TargetSearchData)
data(TSExample)
# get the CDF files
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# update the CDF path
CDFpath(sampleDescription) <- cdfpath

# tranform the CDF (the files are copied in the current directoru)
newSamples <- ncdf4Convert(sampleDescription, path=".")
```

---

ncdf4\_convert

*Convert from a NetCDF file format 3 to format 4*

---

## Description

Convert from NetCDF format 3 into a custom TargetSearch NetCDF format 4. The new NetCDF just contains the raw data in a matrix format in order to allow easier and faster data manipulation.

## Usage

```
ncdf4_convert(cdfFile, outFile = NULL, force = FALSE,
             baseline = FALSE, ...)
```



## Arguments

|                       |  |
|-----------------------|--|
| <code>cdfFile</code>  | The NetCDF file to be converted  |
| <code>outFile</code>  | The new output file. If NULL, it replaces the <code>cdfFile</code> 's file extension (which should be <code>.cdf</code> ) by <code>.nc4</code> . If the file extension is not <code>.cdf</code> , then <code>.nc4</code> is just appended. If the path to the file does not exist, it will be created automatically. |
| <code>force</code>    | Logical. Set to TRUE to allow file overwrites, for example if the destination file still exists, in which case a warning is thrown. Default to FALSE.  |
| <code>baseline</code> | Logical. Whether or not baseline correct the input file.   |
| <code>...</code>      | extra options passed to <code>baseline()</code> .  |

## Details

Starting from version 1.42.0, TargetSearch introduces a custom NetCDF file which is used for faster and easier data manipulation. This means, ion traces within a retention time can be quickly extracted, which is often required before plotting. Formerly, this process required parsing the whole file before the data could be extracted.

Note that this function only takes one file at the time. To convert many files at the same time, see the function `ncdf4_convert_from_path()` or the high level method `ncdf4Convert()`. Alternatively, you can call this function in a loop or using the `lapply` family of functions.

Keep in mind this function is intended for internal use (or advanced users); it is exported for convenience. Using the method `ncdf4Convert()` is recommended.

## Value

A string. The path to the converted file or invisible.

## File structure

The structure of the NetCDF format 4 is straightforward and the variables and attributes are self-evident. The following variables are defined.

- `retention_time` is a vector representing the retention time in seconds (double).
- `retention_index` is a vector representing the retention time indices (double). If missing, then the variable contains zeros. Its length is equal to the length of `retention_time`.
- `mass_range` is vector of length two containing the minimum and maximum *m/z* values (integer).
- `intensity` is matrix of intensity values (integer) where columns represent ion traces and rows are scans. The dimensions are length of "retention time" times the number of ions, ie, `mass max - mass min + 1`.

In addition, the following attributes are defined. Note that only `creator` and `version` are mandatory.

- `creator` a string equal to "TargetSearch" (for identification purposes).
- `version` file format version (string). Currently "1.1".
- `time_corrected` (optional) a flag (short integer) to indicate RI correction. If missing it defaults to false.

- `baseline_corrected` (optional) a flag (short integer) to indicate that the file was baseline corrected by TargetSearch. If missing it defaults to `false`.

### Note

Currently, it is not possible to reconstruct the original NetCDF file from the converted file, especially if nominal mass or baseline correction was applied. On the other hand, if the NetCDF files are exported from custom chromatogram files (such as thermo raw files or LECO peg files), then the NetCDF 3 files can be deleted safely as there is always a way to recover them.

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

[ncdf4Convert\(\)](#), [ncdf4\\_convert\\_from\\_path\(\)](#), [baseline\(\)](#)

### Examples

```
require(TargetSearchData)

# get files from package TargetSearchData
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# choose any file
cdf <- file.path(cdfpath, '7235eg04.cdf')
nc4 <- '7235eg04.nc4' # save file in current path

# run the function
ret <- ncdf4_convert(cdf, nc4)

# the output should match the output file
stopifnot(ret == nc4)

# Use mapply to convert many files at the same time.
cdf <- paste0('7235eg0', 6:8, '.cdf')
nc4 <- paste0('7235eg0', 6:8, '.nc4')
ret <- mapply(ncdf4_convert, file.path(cdfpath, cdf), nc4)
stopifnot(ret == nc4)
```

---

ncdf4\_convert\_from\_path

*Convert CDF files to CDF4 from a path automatically*

---

### Description

Scan and convert NetCDF format 3 files into a custom TargetSearch NetCDF format 4 automatically. The function scans the given input path(s) for files with "cdf" extension. This function simply wraps around [ncdf4\\_convert\(\)](#), so that function will then convert each detected file.

## Usage

```
ncdf4_convert_from_path(cdf_path = ".", out_path = cdf_path, recursive = FALSE, ignore.case = TRUE, ...)
```

## Arguments

|                          |   |
|--------------------------|---|
| <code>cdf_path</code>    | Character string. The path(s) to scan for CDF files.  |
| <code>out_path</code>    | Character string. The output path(s) in which the converted files will be saved.                                |
| <code>recursive</code>   | Logical. Should the search recurse into directories?  |
| <code>ignore.case</code> | Logical. Should the file extension matching be case insensitive?  |
| <code>...</code>         | Extra options passed to <code>ncdf4_convert()</code> , which in turn can be passed to <code>baseline()</code> . |

## Details

This function simply searches for CDF-3 files and converts them to CDF-4 (custom format). By default the current path is scanned and files are converted and save in the same place.

Multiple input directories can be given. If this is the case, the output path `out_path` must be either a single path (in which case all files will be copied to the same directory) or an equal number of paths, such that there is a corresponding match between input and output directories. If not, an assertion error will be raised.

By default the search is case insensitive (see parameter `ignore.case`). For sensitive case matching, the function looks for all lowercase extension `cdf`. At the moment, it is not possible to change this pattern.

If `recursive` is `TRUE`, the search will also descend into subdirectories and the converted files will follow a similar directory structure. Output directories will be created on demand if required (this is actually done by `ncdf4_convert()` internally).

## Value

A character vector of generated files or invisible.

## Author(s)

Alvaro Cuadros-Inostroza

## See Also

[ncdf4\\_convert\(\)](#), [baseline\(\)](#)

## Examples

```
## Not run:
# get files from package TargetSearchData
require(TargetSearchData)
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
ncdf4_convert_from_path(cdfpath, ".")

# recursive search. note that output files will be saved under "gc-ms-data"
cdfpath <- find.package("TargetSearchData")
```

```
ncdf4_convert_from_path(cdfpath, ".", recursive=TRUE)

## End(Not run)
```

---

ncdf4\_data\_extract      *Extract data ranges from a NetCDF file format 4*

---

### Description

A flexible and convenient function to extract raw data from a NetCDF file format 4 using time ranges and m/z ranges or values. This is a better (and faster) alternative to the old [peakCDFextraction\(\)](#) function, which reads the whole CDF into memory, specially when only sections of the CDF are needed.

### Usage

```
ncdf4_data_extract(cdfFile, massValues, timeRange, useRT = FALSE)
```

### Arguments

|            |   |
|------------|---|
| cdfFile    | A path to a NetCDF file format 4.   |
| massValues | A numeric vector representing m/z values.   |
| timeRange  | A numeric vector of length 2 representing the lower and upper time limits.  |
| useRT      | Logical. If TRUE, the time range is in seconds, otherwise if FALSE (default), the time range is in retention time index units (TRUE). |

### Details

The function takes a NetCDF format 4 generated by "TargetSearch" and extracts raw intensity values from given m/z ion traces within a given time range. The time range can be in seconds or arbitrary retention time index units. For the latter case, the function expects a time corrected CDF file.

If the given time range is out of range, a NULL value will be returned. In contrast, if the m/z values are out of range, then zeros will be returned for out of range masses (provided that the time range is not out of range). If timeRange is missing, then the whole time range. Similarly, if massRange is missing, then all the masses are extracted. If both are missing, the function behaves as [peakCDFextraction\(\)](#), but the output (a named list) uses slightly different names.

The NetCDF must have been previously converted to the custom "TargetSearch" format, otherwise an error will be raised. See [ncdf4\\_convert\(\)](#) for the conversion.

**Value**

A named list with the following components.

- Time Numeric vector: the retention time in seconds
- Index Numeric vector: the retention time index (or zero if the file was not retention time corrected)
- Intensity Matrix: Rows are the retention times (or scans) and columns are masses.
- massRange Numeric vector of length 2: the mass range of the CDF

**Note**

An error will be produced for invalid files. Also, this function is intended to be used internally, but it is exposed for convenience, for example, to create custom plots.

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[ncdf4\\_convert\(\)](#), [peakCDFextraction\(\)](#)

**Examples**

```
## Not run:
# set a NCDF-4 file
nc4file <- "/path/to/netcdf4.nc4"

# extract all data (behaves like peakCDFextraction)
data <- ncdf4_data_extract(nc4file)

# extract only certain m/z values
data <- ncdf4_data_extract(nc4file, massValues=c(116, 192))

# to use mass ranges, use the colon (:) operator for example
data <- ncdf4_data_extract(nc4file, massValues=c(120:130, 200, 203:209))

# restrict extraction to a retention index interval
data <- ncdf4_data_extract(nc4file, massValues=c(116, 192),
                          timeRange=c(200000, 220000))

# same, but using retention time in seconds.
data <- ncdf4_data_extract(nc4file, massValues=c(116, 192),
                          timeRange=c(200, 300), useRT=TRUE)

## End(Not run)
```

---

ncdf4\_plot\_peak      *Plot peaks from ncdf4 files*

---

### Description

A simple function to plot  $m/z$  ion traces from a CDF-4 file. This new interface supersedes the function [plotPeakSimple](#) (but that can be used for CDF-3 files).

### Usage

```
ncdf4_plot_peak(obj, massValues, timeRange, useRT = TRUE, showRT = useRT, plot = TRUE, ...)
```

### Arguments

|            |  |
|------------|--|
| obj        | Either a <a href="#">tsSample</a> object or a path to NetCDF format 4 files.   |
| massValues | A numeric vector representing $m/z$ values.  |
| timeRange  | A numeric vector of length 2 representing the lower and upper time limits.   |
| useRT      | Logical. If TRUE (default), the time range is expressed in seconds, otherwise if FALSE, the time range is in retention time index units. This requires retention time corrected CDF files or an error will be raised.      |
| showRT     | Logical. Whether the $x$ -axis of the resulting plot should represent seconds (TRUE) or retention index units (FALSE). This allows, for example, to search for a time range in seconds and display a graph in index units. |
| plot       | Logical. if FALSE nothing is plotted. This option may be used to simply extract the data from the CDF files, but see also <a href="#">ncdf4_data_extract</a> .   |
| ...        | Extra arguments, such as pch, col, ..., to be passed to the plotting functions. See details below.   |

### Details

The function takes a list of path to CDF-4 files or an object of class [tsSample](#) as input; a list a  $m/z$  values to select for; and a time range, which can be in seconds (default) or retention time index (RI) units. For the RI units to work, the CDF files must have been previously time corrected (See [RIcorrect](#), [updateRI](#)).

The selection of the time range units depends on the parameter useRT. If TRUE, then the search will be restricted to the specified range in seconds, otherwise RI units will be used. However, the displayed time units are defined by the parameter showRT. The default behavior is to use the same time units that were search for, but using seconds to search and RI units to display is possible by setting showRT = !useRT (or the reverse). This is useful if the retention time correction was not performed correctly and you want to verify what retention time correspond to what retention index.

The logical parameter plot controls whether a plot is drawn. This might be useful for simply extracting the data used for the plot and not caring about the plot itself. The function [ncdf4\\_data\\_extract](#) can be used for that purpose as well (in fact that function is run under the hood).

Plot styling can be achieved by passing plotting extra parameters such as col, pch, lty, and others (see [par](#) and [plot](#)). There is however a caveat due to how this function is implemented: the function

calls `matlines` once per each file (or sample), so parameters such as `col`, `lty`, etc., apply only to the  $m/z$  values, not to the samples.

If you want to display different color lines for different samples (for example), add a 's' to the respective parameter name as a prefix. Currently, these parameters are allowed: `scol`, `stype`, `slty`, `slwd`, `spch`, `sbg`, `scex`. See the examples below for details.

Finally, all plotting parameters are cycled over and in case of conflicts, the 's' parameters take precedence.

### Value

Either a named list, one element per sample or CDF file, or `invisible`. Each element is in itself a list with the following components (same as the output of `ncdf4_data_extract`).

- Time Numeric vector: the retention time in seconds
- Index Numeric vector: the retention time index (or zero if the file was not retention time corrected)
- Intensity Matrix: Rows are the retention times (or scans) and columns are masses.
- massRange Numeric vector of length 2: the mass range of the CDF

### Note

This function is only for CDF-4 files. Use the method `ncdf4Convert` or the function `ncdf4_convert` for conversion of CDF-3 files. You may also use function `plotPeakSimple` if you don't want to convert the files.

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

[plotPeak](#), [plotPeakSimple](#), [ncdf4\\_data\\_extract](#), [Rlcorrect](#), [updateRI](#)

### Examples

```
require(TargetSearchData)

# load CDF files, convert them and save them in a temporary directory
path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
dest <- tempdir()
cdf <- dir(path, pattern='*.cdf', full=TRUE)[1:3]
cdf <- sapply(cdf, function(x) ncdf4_convert(x, outFile=file.path(dest, basename(x))))

# plot single m/z on many cdf files
ncdf4_plot_peak(cdf, massValues=c(144), timeRange=c(255, 265))
# add some style (note the usage of `slty` and `scol`)
ncdf4_plot_peak(cdf, massValues=c(144), timeRange=c(255, 265), scol=1:3, slty=1:3,
                main='Example Plot')

# plot many m/z on single cdf file (colors are set by matlines)
```

```
ncdf4_plot_peak(cdf[1], massValues=c(144, 145, 100, 218), timeRange=c(255, 265))
# add some styling (here simply use `lty` and `col`)
ncdf4_plot_peak(cdf[1], massValues=c(144, 145, 100, 218), timeRange=c(255, 265),
                col=1:4, lty=1, main='Example Plot')

# multiple m/z and files is possible but it gets messy
ncdf4_plot_peak(cdf, massValues=c(144, 145, 218), timeRange=c(255, 265),
                scol=1:3, main='Example Plot')

# do not plot anything and just get the data
z <- ncdf4_plot_peak(cdf, massValues=c(144, 145, 218), timeRange=c(255, 265), plot=FALSE)
str(z)

# using a tsSample object can achieve the same results
smp <- ImportSamplesFromDir(dest)
ncdf4_plot_peak(smp, massValues=c(144), timeRange=c(255, 265))
```

---

ncdf4\_update\_ri

*Update retention time index on a NCDF4 file*

---

## Description

Performs retention time index (RI) correction on a CDF file, using the retention markers found by [RIcorrect\(\)](#), or to force the markers time if, for example, the RI markers were not co-injected with the biological samples. It wraps around [rt2ri\(\)](#)

## Usage

```
ncdf4_update_ri(cdfFile, observed, standard)
```

## Arguments

|          |   |
|----------|---|
| cdfFile  | Path to the CDF file                      |
| observed | The observed RI markers retention times'. |
| standard | The RI of said markers.                   |

## Details

This function is similar to [fixRI\(\)](#), with the difference that it acts upon a single file, whereas [fixRI\(\)](#) requires a [tsSample](#) object.

## Value

Returns invisible

## Note

This function is meant to be used internally. It is exposed for convenience.



**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**[fixRI\(\)](#), [RIcorrect\(\)](#)


---

 NetCDFPeakFinding      *Peak picking algorithm from CDF files*


---

**Description**

This function reads a netcdf chromatogram file, finds the apex intensities and returns a list containing the retention time and the intensity matrices.

**Usage**

```
NetCDFPeakFinding(ncdf, massRange = NULL, Window = 15, IntThreshold = 10,
                  pp.method = "ppc", baseline = FALSE, ...)
```

**Arguments**

|              |   |
|--------------|---|
| ncdf         | A character string naming a netcdf file or a list generated by the function <a href="#">peakCDFextraction</a> . |
| massRange    | Deprecated. It is completely ignored but it is kept for compatibility with old scripts.                         |
| Window       | The window used by peak picking method. The number of points actually used is $2 * \text{Window} + 1$ .         |
| IntThreshold | Apex intensities lower than this value will be removed from the RI files.                                       |
| pp.method    | The pick picking method to be used. Options are "smoothing", "gaussian" and "ppc".                              |
| baseline     | Logical. Should baseline correction be performed?   |
| ...          | Extra options passed to <a href="#">baseline</a> .  |

**Details**

The parameter `ncdf` should be either a path to a NetCDF file or a list generated by the function [peakCDFextraction](#). This list contains elements named "Time", "Peaks", "massRange", "Index", and "baselineCorrected". Refer to the function's man page for details.

Formerly, the `massRange` parameter was a numeric vector with two components: lower and higher masses. Now, the mass range is detected automatically and it has no effect if it is set. It is kept only for compatibility reasons.

There are three peak picking algorithms that can be used. The "smoothing" method smooths the  $m/z$  curves by a moving average and then looks for a change of sign of the intensity difference between two consecutive points. The "gaussian" is exactly the same, but it uses a gaussian smoother instead of a moving average.

The "ppc" uses a sliding window and looks for the local maxima. This method is based on the R-package `ppc` (now unavailable).

**Value**

A three component list.

|           |  |
|-----------|--|
| Time      | The retention time vector.   |
| Peaks     | The intensity matrix. Rows are the retention times and columns are masses. The first column is the lower mass value and the last one is the higher mass. |
| massRange | The mass range.  |

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[peakCDFextraction](#)

**Examples**

```
require(TargetSearchData)
CDFpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
CDFfiles <- dir(CDFpath, pattern = ".cdf$", full.names = TRUE)
CDFfiles

# extrac peaks of first chromatogram
peaks.1 <- NetCDFPeakFinding(CDFfiles[1], Window = 15, IntThreshold = 10, pp.method = "ppc")
# scan acquisition times
head(peaks.1$Time)
# peaks in matrix form. first column is mass 85, last one is mass 320.
head(peaks.1$Peaks)
```

---

peakCDFextraction      *NetCDF to R*

---

**Description**

This function reads a netcdf chromatogram (format 3 or 4) file and returns a list containing raw data (retention time, intensity matrix) for easy manipulation.

**Usage**

```
peakCDFextraction(cdfFile, massRange)
```

**Arguments**

|           |  |
|-----------|--|
| cdfFile   | A character string naming a netcdf file.               |
| massRange | Deprecated. The mass range is extracted automatically. |

### Details

The `cdfFile` is a path to a CDF-3 or a CDF-4 format file. The CDF-4 format file is a custom file used on [TargetSearch](#).

The `massRange` parameter is deprecated but kept for compatibility. The actual m/z range is detected automatically and returned to the user.

### Value

A list with the following components:

|                   |  |
|-------------------|--|
| Time              | The retention time vector.   |
| Index             | The retention time index vector or NULL if unavailable.  |
| Peaks             | The intensity matrix. Rows are the retention times and columns are masses. The first column is the lower mass value and the last one is the higher mass. |
| massRange         | The mass range.  |
| baselineCorrected | Logical. It is TRUE if the file was baseline corrected by the function <a href="#">baseline</a> . See note below.  |

### Note

This function does not look for peaks, just extracts all the raw intensity values of the chromatogram file. Use [NetCDFPeakFinding](#) instead.

The function does not know whether a CDF file was baseline corrected (for example by the GC-MS software vendor), unless it was performed by the function [baseline](#). It is perfectly possible to have a baseline corrected file and the element `baselineCorrected` be FALSE.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

### See Also

[NetCDFPeakFinding](#), [baseline](#).

---

peakFind

*Intensities and RI matrices*

---

### Description

This function returns a list of the intensities and RI matrices that were searched.

### Usage

```
peakFind(samples, Lib, cor_RI, columns = NULL, showProgressBar = FALSE)
```

**Arguments**

|                 |   |
|-----------------|---|
| samples         | A tsSample object created by ImportSamples function.  |
| Lib             | A tsLib object created by ImportLibrary function with corrected RI values. See medianRILib.   |
| cor_RI          | A matrix of correlating selective masses RI for every sample. See sampleRI.   |
| columns         | Either NULL, a character vector, or an integer vector. In most cases, leave it as NULL. This parameter is used to configure the column names or positions of RI text files. See the documentation on the <a href="#">text2bin</a> function for further details. |
| showProgressBar | Logical. Should the progress bar be displayed?  |

**Value**

A tsMSdata object.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[ImportSamples](#), [ImportLibrary](#), [medianRILib](#), [sampleRI](#), [tsMSdata](#), [tsLib](#), [tsSample](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
refLibrary <- ImportLibrary(file.path(RI.path,"library.txt"))

# update RI file path
RIpath(sampleDescription) <- RI.path

peakData <- peakFind(sampleDescription, refLibrary, corRI)
# show peak Intensities.
head(Intensity(peakData), 2)

# How to get intensities for a particular metabolite
# just select the identifier. Here extract the intensities
# for the first metabolite in the library
IntMatrix <- Intensity(peakData)[[1]]
```

---

|          |                               |
|----------|-------------------------------|
| plotFAME | <i>Plot a standard marker</i> |
|----------|-------------------------------|

---

**Description**

Plots a given standard marker.

**Usage**

```
plotFAME(samples, RImatrix, whichFAME)
```

**Arguments**

|           |   |
|-----------|---|
| samples   | A tsSample object created by ImportSamples function.                                |
| RImatrix  | A retention time matrix of the found retention time markers.                        |
| whichFAME | The retention marker to plot. Must be a number between 1 and the number of markers. |

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[Rlcorrect](#), [FAMEoutliers](#), [tsSample](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)
# plot Retention index standards 1 to 3
plotFAME(sampleDescription, RImatrix, 1)
plotFAME(sampleDescription, RImatrix, 2)
plotFAME(sampleDescription, RImatrix, 3)
```

---

|          |                   |
|----------|-------------------|
| plotPeak | <i>Plot peaks</i> |
|----------|-------------------|

---

**Description**

Plot a peak of a given metabolite in a given sample showing the search windows.

**Usage**

```
plotPeak(samples, Lib, metProf, rawpeaks, which.smp=1, which.met=1,
massRange=NULL, corMass=FALSE)
```

**Arguments**

|           |  |
|-----------|--|
| samples   | A tsSample object created by ImportSamples function.   |
| Lib       | A tsLib object created by ImportLibrary function.  |
| metProf   | A metabolite profile object. See Profile   |
| rawpeaks  | A three component list containing the retention time, the intensity matrix, and the mass range. See peakCDFextraction. |
| which.smp | A numeric value indicating the sample.   |
| which.met | A numeric value indicating the metabolite.   |
| massRange | A two component numeric vector with the scan mass range to extract. Use NULL for automatic detection.                  |
| corMass   | Logical. If TRUE, show only correlating masses for the selected metabolite. Show all masses otherwise.                 |

**Value**

A two component list containing the retention time and the intensity matrices. This list can be recycled as the 'rawpeaks' parameter for further plots (for example in a loop), so the CDF file doesn't need to be read again.

**Note**

This function was completely rewritten. For the old function, see [plotPeakSimple](#).

In case the RI files are in text format and their column names are not standard (for example, when the files were generated with another software), use the global option 'TS\_RI\_columns' or transform the RI files to [TargetSearch](#) binary format. See the documentation in function [text2bin](#).

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[plotPeakSimple](#), [RIcorrect](#), [tsMSdata](#), [tsRim](#), [peakCDFextraction](#), [matplot](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# update CDF and RI paths
CDFpath(sampleDescription) <- file.path(find.package("TargetSearchData"), "gc-ms-data")
RIpath(sampleDescription) <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# Plot the peak "Valine" for sample number 1
grep("Valine", libName(refLibrary)) # answer: 3

# plot peak from the cdf file. The rawpeaks object can be recycled in order to plot
```

```
# other metabolites.
rawpeaks <- plotPeak(sampleDescription, refLibrary, metabProfile, which.smp=1,
  which.met=3, massRange=c(85,500), corMass=FALSE)
```

---

plotPeakRI

*Plot peak RI across samples*


---

## Description

Plot peak RI of the quant mass of a given metabolite across samples. This function can be used to visualize the elution time of a metabolite in the RI and RT dimension, and in combination with the function [sampleRI](#) for fine tuning.

## Usage

```
plotPeakRI(samples, Lib, libID, dev=NULL, mz=NULL, RI=NULL,
  method=c('RI', 'Intensity'), useRI=TRUE, main=NULL,
  col=NULL, int_range=c(2,6), cex_range=c(.7,6), key_width=2)
```

## Arguments

|           |  |
|-----------|--|
| samples   | A tsSample object created by <a href="#">ImportSamples</a> function.   |
| Lib       | A tsLib object created by <a href="#">ImportLibrary</a> function.  |
| libID     | An index (integer or character) value representing the respective metabolite in the reference library Lib.   |
| dev       | The allowed retention index (RI) deviation or NULL.  |
| mz        | A list of m/z values to search or NULL.  |
| RI        | The expected retention index or NULL.  |
| method    | A character vector used to decided what peak should be chosen in case there are ambiguous peaks. If 'RI', then the closest peak to the expected RI is chosen. If 'Intensity', then the highest is taken. |
| useRI     | Logical. Should the RI or RT be displayed in the y-axis?   |
| main      | The title for the plot. If NULL, then the metabolite name is displayed.  |
| col       | A color vector (length > 2) to show different levels of peak intensity.  |
| int_range | A length-two vector. The limits of the intensity for the color key. Note the the intensity is expressed in log10. Eg, a value of 2 represents a intensity of 100.  |
| cex_range | The 'cex' range value of the points. lower-intense peaks are represented as points of smaller size.  |
| key_width | The width in cm of the area allocated for the color key.   |

**Details**

This function uses internally [FindAllPeaks](#), so the same rules apply, i.e., the parameters dev, mz, and RI have preference over the settings of the metabolite indexed by libID.

In the plot, the x-axis are samples as defined by the object samples. The y-axis is retention index (RI) as shown on the left-hand-side. On the right-hand-side y-axis the approximate retention time (RT) is shown. This is because the RT varies across samples, therefore it is averaged for displays purposes. If useRI==FALSE, then the RT is displayed on the left hand size and the RI is averaged and shown on the left. Note that in either case, the RI is used for searching.

The point size is proportional to the log10 of the peak intensity. Their size is controlled by the parameters int\_range and cex\_range. By default, intensities of 100 (log10 => 2) or lower are shown with cex=0.7, while intensities greater than 1000000 (log10 => 6) as displayed with cex=6. This also affects the scaling of the color key.

The best peaks, selected according to method, are shown with a black border, while the other are shown with no border and slightly transparent.

The output is the RI of the best peaks or invisible. Note that if no peak is found, then no plot is drawn.

**Value**

Returns invisible or a numeric vector with the corresponding RI of the best peak chosen by method.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[FindAllPeaks](#), [sampleRI](#), [ImportSamples](#), [ImportLibrary](#)

**Examples**

```
def.par <- par(no.readonly = TRUE) # save parameters for resetting

# load pre-calculated example data files and objects
require(TargetSearchData)
data(TSExample)

# get and set the RI file path
RIpath(sampleDescription) <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# search all peaks of Valine (GC.3) and selective masses. Retention index
ri <- plotPeakRI(sampleDescription, refLibrary, 'GC.3')

# increase deviation, change m/z to search, change colors and title
main <- 'Valine'
cols <- c('red', 'blue', 'green')
ri <- plotPeakRI(sampleDescription, refLibrary, 'GC.3', dev=4000, mz=144,
                 main=main, col=cols)
```



```
# plot by RT instead. Note the RI is still returned
ri <- plotPeakRI(sampleDescription, refLibrary, 'GC.3', useRI=FALSE)

par(def.par) # reset to default
```

---

plotPeakSimple                    *Plot peaks - simple (old) interface*

---

## Description

Plot selected ions in a given time range. This is the old plot peak interface. *Note:* This function is considered **deprecated** and its usage is discouraged.

## Usage

```
plotPeakSimple(rawpeaks, time.range, masses, cdfFile = NULL, useRI = FALSE,
  rimTime = NULL, standard = NULL, massRange = NULL, ...)
```

## Arguments

|            |   |
|------------|---|
| rawpeaks   | A three component list containing the retention time, the intensity matrix, and the mass range. See <a href="#">peakCDFextraction</a> . |
| time.range | The time range to plot in retention time or retention time index units to plot.   |
| masses     | A vector containing the ions or masses to plot.   |
| cdfFile    | The name of a CDF file. If a file name is specified, the ions will be extracted from there instead of using rawpeaks.                   |
| useRI      | Logical. Whether to use Retention Time Indices or not.  |
| rimTime    | A retention time matrix of the found retention time markers. It is only used when useRI is TRUE.  |
| standard   | A numeric vector with RI values of retention time markers. It is only used when useRI is TRUE.  |
| massRange  | A two component numeric vector with the scan mass range to extract or NULL for automatic detection.                                     |
| ...        | Further options passed to <a href="#">matplot</a> .   |

## Note

This function used to be named 'plotPeak'. This function was completely rewritten so we kept the old version and renamed it 'plotPeakSimple'.

*Important:* This function is considered **deprecated**, though it is not yet labeled as such. This function can still be used to plot peaks for CDF files version 3 without the need to convert them to CDF format 4.

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[plotPeak](#), [RICorrect](#), [tsMSdata](#), [tsRim](#), [peakCDFextraction](#), [matplot](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# update CDF path
CDFpath(sampleDescription) <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# Plot the peak "Valine" for sample number 1
grep("Valine", libName(refLibrary)) # answer: 3
# select the first file
cdfFile <- CDFfiles(sampleDescription)[1]

# select "Valine" top masses
top.masses <- topMass(refLibrary)[[3]]

# plot peak from the cdf file
plotPeakSimple(cdfFile = cdfFile, time.range = libRI(refLibrary)[3] + c(-2000,2000),
  masses = top.masses, useRI = TRUE, rimTime = RImatrix[,1],
  standard = rimStandard(rimLimits), massRange = c(85, 500))

# the same, but extracting the peaks into a list first. This may be better if
# you intend to loop through several peaks.
rawpeaks <- peakCDFextraction(cdfFile, massRange = c(85,500))
plotPeakSimple(rawpeaks, time.range = libRI(refLibrary)[3] + c(-2000,2000),
  masses = top.masses, useRI = TRUE, rimTime = RImatrix[,1],
  standard = rimStandard(rimLimits), massRange = c(85, 500))
```

---

plotRIdev

*Plot Retention Time Index Deviation*

---

**Description**

plotRIdev plots the Retention Time Index Deviation of a given set of metabolites. plotAllRIdev saves the plots of the RI deviations of all the metabolites in the library object into a PDF file.

**Usage**

```
plotRIdev(Lib, peaks, libId = 1)
```

```
plotAllRIdev(Lib, peaks, pdfFile, width = 8, height = 8, ...)
```

**Arguments**

|               |  |
|---------------|--|
| Lib           | A tsLib object created by <a href="#">ImportLibrary</a> function.  |
| peaks         | A tsMSdata object. See <a href="#">peakFind</a> .                  |
| libId         | A numeric vector providing the indices of the metabolites to plot. |
| pdfFile       | A file name where the plot will be saved. Only plotAllRIdev.       |
| width, height | The width and height of the plots in inches. Only plotAllRIdev.    |
| ...           | Further options passed to <a href="#">pdf</a> .                    |

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[ImportLibrary](#), [tsLib](#), [tsMSdata](#), [pdf](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
# update RI file path
RIpath(sampleDescription) <- RI.path

peakData <- peakFind(sampleDescription, refLibrary, corRI)

# Plot RI deviation of metabolite "Valine"
grep("Valine", libName(refLibrary)) # answer: 3
plotRIdev(refLibrary, peakData, libId = 3)

# Plot an RI deviation overview of the first nine metabolites
plotRIdev(refLibrary, peakData, libId = 1:9)

# Save all RI deviation into a pdf file
plotAllRIdev(refLibrary, peakData, pdfFile = "RIdeviations.pdf")
```

---

plotSpectra

*Plot a Spectra Comparison*

---

**Description**

plotSpectra plots a contrast between the reference spectra and the median spectra of a given metabolite in the library. plotAllRIdev saves the plots of the median-reference spectra comparisons of all the metabolites in the reference library into a PDF file.

**Usage**

```
plotSpectra(Lib, peaks, libId = 1, type = "ht")

plotAllSpectra(Lib, peaks, type = "ht", pdfFile, width = 8, height = 8, ...)
```

**Arguments**

|               |  |
|---------------|--|
| Lib           | A tsLib object created by <a href="#">ImportLibrary</a> function.  |
| peaks         | A tsMSdata object. See <a href="#">peakFind</a> .  |
| libId         | A numeric vector providing the indices of the metabolites to plot.   |
| type          | The type of the plot. Options are "ht", head-tail plot, "ss", side by side plot, and "diff", spectrum difference plot. |
| pdfFile       | A file name where the plot will be saved. Only plotAllRIdev.   |
| width, height | The width and height of the plots in inches. Only plotAllRIdev.  |
| ...           | Further options passed to pdf.   |

**Details**

The median spectra is obtained by computing the median intensity of every ion across the samples. The median and the reference spectra values are scaled to vary between 0 and 999 in order to make them comparable.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[tsLib](#), [tsMSdata](#), [pdf](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
# update RI file path
RIpath(sampleDescription) <- RI.path

peakData <- peakFind(sampleDescription, refLibrary, corRI)

# Plot a comparison RI deviation of metabolite "Valine"
grep("Valine", libName(refLibrary)) # answer: 3
plotSpectra(refLibrary, peakData, libId = 3, type = "ht")

# Plot the spectra "side by side"
plotSpectra(refLibrary, peakData, libId = 3, type = "ss")
```

```
# Plot the spectra difference
plotSpectra(refLibrary, peakData, libId = 3, type = "diff")
```

---

|         |   |
|---------|---|
| Profile | <i>Average the correlating masses for each metabolite</i> |
|---------|---|

---

## Description

This function makes a profile from the masses that correlate for each metabolite.

## Usage

```
Profile(samples, Lib, peakData, r_thres = 0.95, method = "dayNorm", minPairObs = 5)
```

## Arguments

|            |  |
|------------|--|
| samples    | A tsSample object created by ImportSamples function.   |
| Lib        | A tsLib object created by ImportLibrary function with corrected RI values. See <a href="#">medianRILib</a> .   |
| peakData   | A tsMSdata object. See <a href="#">peakFind</a> .  |
| r_thres    | A correlation threshold.   |
| method     | Normalisation method. Options are "dayNorm", a day based median normalisation, "medianNorm", normalisation using the median of all the intensities of a given mass, and "none", no normalisation at all.   |
| minPairObs | Minimum number of pair observations. Correlations between two variables are computed using all complete pairs of observations in those variables. If the number of observations is too small, you may get high correlations values just by chance, so this parameters is used to avoid that. Cannot be set lower than 5. |

## Value

A tsProfile object. The slots are:

|           |   |
|-----------|---|
| Info      | A data frame with a profile of all masses that correlate.             |
| Intensity | A list containing peak-intensity matrices, one matrix per metabolite. |
| RI        | A list containing RI matrices, one matrix per metabolite.             |
| profInt   | A matrix with the averaged intensities of the correlating masses.     |
| profRI    | A matrix with the averaged RI of the correlating masses.              |

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[ImportSamples](#), [ImportLibrary](#), [medianRILib](#), [peakFind](#), [tsProfile](#)

**Examples**

```

require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
# update RI file path
RIpath(sampleDescription) <- RI.path
# Import Library
refLibrary <- ImportLibrary(file.path(RI.path, 'library.txt'))
# update median RI
refLibrary <- medianRILib(sampleDescription, refLibrary)
# get the sample RI
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.95)
# obtain the peak Intensities of all the masses in the library
peakData <- peakFind(sampleDescription, refLibrary, corRI)
# make a profile of the metabolite data
metabProfile <- Profile(sampleDescription, refLibrary, peakData, r_thres = 0.95)

# same as above, but with different thresholds.
metabProfile <- Profile(sampleDescription, refLibrary, peakData,
                       r_thres = 0.9, minPairObs = 5)

```

---

|                |   |
|----------------|---|
| ProfileCleanUp | <i>Reduce redundancy of the profile</i> |
|----------------|---|

---

**Description**

This function reduces/removes redundancy in a profile.

**Usage**

```

ProfileCleanUp(Profile, timeSplit=500, r_thres=0.95, minPairObs=5,
               prioritization=c('mass', 'score'), corMass=1, score=0,
               show=c('unidentified', 'knowns', 'full'))

```

**Arguments**

|                |  |
|----------------|--|
| Profile        | A tsProfile object. See <a href="#">Profile</a> .  |
| timeSplit      | A RI window.   |
| r_thres        | A correlation threshold.   |
| minPairObs     | Minimum number of pair observations. Correlations between two variables are computed using all complete pairs of observations in those variables. If the number of observations is too small, you may get high correlations values just by chance, so this parameters is used to avoid that. Cannot be set lower than 5. |
| prioritization | Selects whether the metabolite suggestion should be based on the number of correlation masses (mass) or the score (score).   |

|         |   |
|---------|---|
| corMass | Metabolites with a number of correlation masses lower than score will be marked as 'Unidentified RI'  |
| score   | Metabolites with a score lower than score will be marked as unidentified.   |
| show    | A character vector. If <code>unidentified</code> , all non-redundant metabolites will be returned; if <code>knowns</code> , only returns those metabolites with correlation masses and score greater than the given values; and if <code>full</code> , it shows all redundant metabolites, which may be useful to retrieve the data from misidentified metabolites. |

### Details

Metabolites that are inside a `timeSplit` window will be correlated to see whether the metabolites are potentially the same or not, by using `r_thres` as a cutoff. If so, the best candidate will be chosen according to the value of `prioritization`: If `'mass'`, then metabolites will be suggested based on number of correlating masses, and if `'score'`, then the score will be used. Metabolites that don't have at least `corMass` correlating masses and `score` will be marked as `'unidentified'` and not will be suggested, unless all the metabolites in group are unidentified.

For example, suppose that three metabolites A (CM=3, S=900), B (CM=6, S=700), C (CM=5, S=800) correlate within the same time group, where CM is the number of correlating masses and S is the score.

- If `prioritization='mass'`, `corMass=3`, `score=650`, then the suggested order is B, C, A.
- If `prioritization='mass'`, `corMass=3`, `score=750`, then the suggested order is C, A, B.
- If `prioritization='mass'`, `corMass=3`, `score=850`, then the suggested order is A, B, C.
- If `prioritization='score'`, `corMass=3`, `score=650`, then the suggested order is A, C, B.
- If `prioritization='score'`, `corMass=4`, `score=650`, then the suggested order is C, B, A.
- If `prioritization='score'`, `corMass=4`, `score=850`, then the suggested order is C, A, B.

Note that by choosing `prioritization='mass'`, `score=0`, and `corMass=1` you will get the former behavior (`TargetSearch <= 1.6`).

### Value

A `tsProfile` object with a non-redundant profile of the masses that were searched and correlated, and intensity and RI matrices of the correlating masses.

|                  |   |
|------------------|---|
| slot "Info"      | A data frame with a profile of all masses that correlate and the metabolites that correlate in a <code>timeSplit</code> window. |
| slot "profInt"   | A matrix with the averaged intensities of the correlating masses.   |
| slot "profRI"    | A matrix with the averaged RI of the correlating masses.  |
| slot "Intensity" | A list containing peak-intensity matrices, one matrix per metabolite.   |
| slot "RI"        | A list containing RI matrices, one matrix per metabolite.   |

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[Profile](#), [tsProfile](#)

**Examples**

```
# load example data
require(TargetSearchData)
data(TSExample)

RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
refLibrary <- ImportLibrary(file.path(RI.path,"library.txt"))
# update RI file path
RIpath(sampleDescription) <- RI.path
# Import Library
refLibrary <- ImportLibrary(file.path(RI.path,'library.txt'))
# update median RI
refLibrary <- medianRILib(sampleDescription, refLibrary)
# get the sample RI
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.95)
# obtain the peak Intensities of all the masses in the library
peakData <- peakFind(sampleDescription, refLibrary, corRI)
metabProfile <- Profile(sampleDescription, refLibrary, peakData, r_thres = 0.95)

# here we use the metabProfile previously calculated and return a "cleaned" profile.
metabProfile.clean <- ProfileCleanUp(metabProfile, timeSplit = 500,
                                     r_thres = 0.95)

# Different cutoffs could be specified
metabProfile.clean <- ProfileCleanUp(metabProfile, timeSplit = 1000,
                                     r_thres = 0.9)
```

---

quantMatrix

*Create an intensity matrix using quantification masses*

---

**Description**

Create an intensity matrix using quantification masses. The quantification masses can be specified when importing the library file or by manually setting its values (see example).

**Usage**

```
quantMatrix(Lib, metabProfile, value = "maxint")
```

**Arguments**

|              |   |
|--------------|---|
| Lib          | A tsLib object created by <a href="#">ImportLibrary</a> function.   |
| metabProfile | A tsProfile object. The final result of the package. This object is generated by either <a href="#">Profile</a> or <a href="#">ProfileCleanUp</a> . |



value            The default method to select automatically the quantification mass, in case it is not given by the user. 'maxint' selects the selective mass with the highest intensity. 'maxobs' selects the most observed mass, i.e., the one with less missing values.

### Value

An intensity matrix with metabolites as rows and samples as columns. The matrix has two attributes: 'quantMass' a numeric vector that contains the quantification masses that were selected; 'isSelMass' a logical vector that indicates whether a quantification mass is also a selected mass.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

### See Also

[tsLib](#), [tsMSdata](#)

### Examples

```
require(TargetSearchData)
data(TSExample)

# process chromatograms and get a profile
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
RIpath(sampleDescription) <- RI.path
refLibrary <- ImportLibrary(file.path(RI.path,"library.txt"))
refLibrary <- medianRILib(sampleDescription, refLibrary)
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.95)
peakData <- peakFind(sampleDescription, refLibrary, corRI)
metabProfile <- Profile(sampleDescription, refLibrary, peakData, r_thres = 0.95)

# show quant Matrix
quantMass(refLibrary)
# no quantMass have been defined yet, so are all zeros
# 0 0 0 0 0 0 0 0 0 0 0 0

# get a Matrix using use default values, ie, select the masses
# with the highest intensity
quantMat <- quantMatrix(refLibrary, metabProfile)
quantMat

# set the quantification Masses
quantMass(refLibrary)[1:3] <- c(89,86,100)
quantMat <- quantMatrix(refLibrary, metabProfile)
quantMat
```

---

`ri2rt`*Retention Time Index to Retention Time conversion*

---

**Description**

Convert retention time indices to retention times indices based on observed FAME RI and their standard values.

**Usage**

```
ri2rt(riTime, rt.observed, ri.standard)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>riTime</code>      | And RI vector or matrix to convert to Retention Time.     |
| <code>rt.observed</code> | The observed FAME RT's. It could be a vector or a matrix. |
| <code>ri.standard</code> | The standard RI for each FAME                             |

**Details**

This function is the inverse of [rt2ri](#).

**Value**

The converted RT

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[RIcorrect](#), [FAMEoutliers](#)

**Examples**

```
# RI standards
standard <- c(100, 200, 300, 400, 500)
# observed standard retention times
observed <- c(10.4, 19.3, 32.4, 40.2, 50.3)
# a random set of retention times
RI <- runif(100,90,600)
# the corrected RIs
RT <- ri2rt(RI, observed, standard)
```

RIcorrect

*Peak picking from CDF files and RI correction***Description**

This function reads from CDF files, finds the apex intensities, converts the retention time to retention time index (RI), and writes RI corrected text files (a.k.a. RI files). In addition, it can perform baseline correction and also convert files to the new NetCDF-4 TargetSearch format.

**Usage**

```
RIcorrect(samples, rimLimits = NULL, massRange=NULL, Window, IntThreshold,
          pp.method="ppc", showProgressBar=FALSE, baseline=FALSE,
          writeCDF4path=TRUE, ...)
```

**Arguments**

|                 |  |
|-----------------|--|
| samples         | A <a href="#">tsSample</a> object usually created by <a href="#">ImportSamples</a> function.   |
| rimLimits       | A <a href="#">tsRim</a> object. If set to NULL, no retention time will be performed. See <a href="#">ImportFameSettings</a> .              |
| massRange       | Deprecated. It is completely ignored but it is kept for compatibility with old scripts.  |
| Window          | The window used for smoothing. The number of points actually used is $2 * \text{Window} + 1$ . It must be an integer. See details.         |
| IntThreshold    | Apex intensities lower than this value will be removed from the RI files.  |
| pp.method       | Peak picking method. Options are "smoothing", "gaussian" and "ppc". See details.   |
| showProgressBar | Logical. Should the progress bar be displayed?   |
| baseline        | Logical. Should baseline correction be performed?  |
| writeCDF4path   | Whether or not convert a CDF-3 into a CDF-4. It can take a logical value or a character vector representing file paths. See details below. |
| ...             | A list of options passed to <a href="#">baseline</a> .   |

**Details**

There are three pick picking methods available: "ppc", "smoothing", "gaussian".

The "ppc" method (default) implements the peak detection method described in the ppc package. It looks for the local maxima within a  $2 * \text{Window} + 1$  scans for every mass trace.

The "smoothing" method calculates a moving average of  $2 * \text{Window} + 1$  points for every mass trace. Then it looks for a change of sign (from positive to negative) of the difference between two consecutive points. Those points will be returned as detected peaks.

The "gaussian" method behaves similar to the "smoothing" method, but instead a gaussian smoother is used instead of the moving average.

To work out a suitable Window value, the following might be useful:  $\text{Window} = (\text{SR} * \text{PW} - 1) / 2$ , where SR is the scan rate of the MS instrument and PW is the peak width. Because Window is an integer, the resulting value must be rounded. For example, for SR = 20 scans per second, a PW = 1.5 seconds, then Window = 14.5, which can be rounded to 15.

The RI file type is determined by the output of `fileFormat` method applied to the `tsSample` input object. To choose between the available formats ("binary" and "text"), select it with `fileFormat` method before calling `RIcorrect`.

The parameter `writeCDF4path` is used to convert CDF-3 files into a custom CDF-4 format. It can be logical or a character vector. If TRUE, the default, the CDF-3 files will be converted automatically to CDF-4 format. The files will be saved in the same directory as the original CDF-3. If it is character vector representing file paths, then the CDF-4 will be saved in those paths instead (re-cycled to the length of samples). Finally, if FALSE, then no CDF conversion will be performed. This is not recommended, but if possible if you want to match the old `TargetSearch` behaviour. Note that also the baseline correction or the retention time indices will not be updated as well.

If `baseline` is TRUE, the CDF files will be baseline corrected by passing the extra parameters to `baseline`. See that manpage for details.

### Value

A retention time matrix of the found retention time markers. Every column represents a sample and rows RT markers.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

### See Also

[ImportSamples](#), [ImportFameSettings](#), [NetCDFPeakFinding](#), [FAMEoutliers](#), [tsSample](#), [tsRim](#).

### Examples

```
require(TargetSearchData)
# import refLibrary, rimLimits and sampleDescription.
data(TSExample)
# get the CDF files
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
cdfpath
list.files(cdfpath)
# update the CDF path
CDFpath(sampleDescription) <- cdfpath

# change file format of RI files as bin
fileFormat(sampleDescription) <- 'binary'

# Parameters: Intensity Threshold = 50 peak detection method = "ppc", window = 15
# To match the old behavior, the do not create CDF-4 Files (not recommended)
RImatrix <- Rlcorrect(sampleDescription, rimLimits, writeCDF4path=FALSE,
                      Window = 15, pp.method = "ppc", IntThreshold = 50)
```

```
# Convert to CDF-4 (recommended) with same parameters
# Note: save files in same directory (as
RIMatrix <- RIMcorrect(sampleDescription, rimLimits, writeCDF4path=".",
                      Window = 15, pp.method = "ppc", IntThreshold = 50)

# we need to update the sampleDescription to use the new files
# this is not done automatically
sampleDescription <- ncdf4Convert(sampleDescription, ".")

# you can try other parameters and other peak picking algorithm
RIMatrix <- RIMcorrect(sampleDescription, rimLimits,
                      Window = 15, pp.method = "smoothing", IntThreshold = 10)

RIMatrix <- RIMcorrect(sampleDescription, rimLimits,
                      Window = 15, pp.method = "ppc", IntThreshold = 100)
```

---

riMatrix

*Retention Time Index Matrix*

---

## Description

A function to search for retention index RI markers.

## Usage

```
riMatrix(samples, rim)
```

## Arguments

|         |  |
|---------|--|
| samples | A tsSample object created by <a href="#">ImportSamples</a> function. |
| rim     | A tsRim object. See <a href="#">ImportFameSettings</a> .             |

## Details

This function works similar to [RIMcorrect](#), but searches for RI markers in RI files (not in CDF files). Can be used to retrieve the retention times of RI markers in already processed files.

Note that it does not perform any RI adjustment. See [fixRI](#).

## Value

A retention time matrix of the found retention time markers. Every column represents a sample and rows RT markers.

## Note

In case the RI files are in text format and their column names are not standard (for example, when the files were generated with another software), use the global option 'TS\_RI\_columns' or transform the RI files to [TargetSearch](#) binary format. See the documentation in function [text2bin](#).

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[RlCorrect](#), [FAMEoutliers](#), [ImportSamples](#), [ImportFameSettings](#), [fixRI](#)

**Examples**

```
require(TargetSearchData)
# import refLibrary, rimLimits and sampleDescription.
data(TSEexample)
# get the CDF files
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")

# select a subset of samples
smp <- sampleDescription[1:4]

# update the CDF path
CDFpath(smp) <- cdfpath

# make a copy of the RI markers object
rim <- rimLimits

# run RlCorrect
Rlmat <- RlCorrect(smp, rim, massRange = c(85,320), writeCDF4path=FALSE,
                  Window = 15, pp.method = "ppc", IntThreshold = 50)

# extract the retention times of the markers
Rlmat2 <- rlMatrix(smp, rim)

# both matrices should be equal
stopifnot( all.equal(Rlmat, Rlmat2, tolerance=1e-8) )
```

---

ri\_data\_extract

*Extract peak data from a RI file*

---

**Description**

A convenient function to extract peak data from a RI file. This function is mostly intended for debugging purposes, for example, when a given peak is not found within a expected time range (which could be because a faulty retention time correction). The arguments of this function are similar as those of the [ncdf4\\_data\\_extract](#) function.

**Usage**

```
ri_data_extract(RIfile, massValues, timeRange, useRT = FALSE, ...)
```

### Arguments

|            |   |
|------------|---|
| RIfile     | A path to a RI file format (binary or text).  |
| massValues | A numeric vector representing $m/z$ values. The values will be converted to integers internally.  |
| timeRange  | A numeric vector of even length, or, a two-column matrix. This parameter represents the lower and upper time limits. See details below.   |
| useRT      | Logical. If TRUE, the time range is in seconds, otherwise if FALSE (default), the time range is in retention time index units (TRUE).   |
| ...        | Extra parameters passed to internal functions. Currently, only the columns parameter is used for text-format RI files. This, however, should <b>not</b> be necessary. See also <a href="#">text2bin</a> . |

### Details

The function takes a RI file generated by [TargetSearch](#) (binary or text works) and extracts all the peaks detected of given  $m/z$  ion traces in a given time range. The time range can be in seconds or arbitrary retention time index units.

The parameter `timeRange` can be either a numeric vector of even length or a two-column matrix. If it is a matrix, the first column represent the lower bounds while the second the upper ones. If it is a vector, it must have at least two elements, which in this case represent the lower and upper limits, or if longer, it will be coerced to matrix internally (**Important**: the values are filled by *columns*). In any case, the number of rows of the (coerced) matrix must divide the length of the `massValues` parameter, such that each row corresponds to a time range for each  $m/z$  value. This is done so the ranges can be recycled.

The output is simply a four column matrix in which a row is a peak of a given ion trace at a retention time (index). The output is always a matrix even if no peaks are found, in which case the number of rows is zero.

### Value

A four column matrix with column names described below. Each row represents a peak in the specified time range. Potentially, there could be zero rows if no peaks are found.

- RI retention time index of the peak.
- RT retention time.
- Intensity peak height intensity
- $m/z$  the  $m/z$  of the peak

### Note

This function is intended to be used internally or by advanced users. It can be used for debugging when [TargetSearch](#) fails to find a peak.

See also the function [FindAllPeaks](#) which offers a similar functionality but with different input parameters.

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[text2bin](#), [ncdf4\\_data\\_extract](#), [FindAllPeaks](#), [FindPeaks](#)

**Examples**

```
require(TargetSearchData)
path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
rifile <- dir(path, pattern="RI_", full=TRUE)[1]

# extract peak data for m/z 116 and 117 in time range 180 - 220 seconds
data <- ri_data_extract(rifile, c(116, 117), c(180, 220), useRT=TRUE)

# same but using Retention Time Index
data <- ri_data_extract(rifile, c(116, 117), c(205000, 228000), useRT=FALSE)

# different time ranges for each m/z
trange <- c(180, 240, 280, 190, 250, 290)
data <- ri_data_extract(rifile, c(116, 144, 147), trange, useRT=TRUE)

# Note: the range definition above is equivalent to
trange <- cbind(c(180,240,280), c(190, 250, 290))
```

---

ri\_plot\_peak

*Plot peak RI across samples - low level interface*

---

**Description**

Plot retention index or time of peaks from RI files or samples. This is a low level interface to [plotPeakRI](#) that not relies on a metabolite library. This function is useful for quick peak data visualization.

**Usage**

```
ri_plot_peak(obj, massValues, timeRange, useRT = TRUE, showRT = useRT, sizefun = NULL, plot = TRUE, ...)
```

**Arguments**

|            |  |
|------------|--|
| obj        | Either a <a href="#">tsSample</a> object or a character vector of paths to RI files.   |
| massValues | A numeric vector representing <i>m/z</i> values.   |
| timeRange  | A numeric vector of length 2 representing the lower and upper time limits.   |
| useRT      | Logical. If TRUE (default), the time range is expressed in seconds, otherwise if FALSE, the time range is in retention time index units. |



|         |   |
|---------|---|
| showRT  | Logical. Whether the <i>x</i> -axis of the resulting plot should represent seconds (TRUE) or retention index units (FALSE). This allows, for example, to search for a time range in seconds and display a graph in index units.   |
| sizefun | A function that could be used to scale the point size of the plot via the parameter ‘cex’, for example, to scale the peak intensity. This function should take a numeric vector as input and return a positive value. If NULL, then a default function will be used. This function is called using the peak intensity as input. |
| plot    | Logical. If FALSE nothing is plotted. This option may be used to simply extract the data from the RI files, but see also <a href="#">ri_data_extract</a> .  |
| ...     | Extra arguments, such as pch, col, ..., to be passed to the plotting functions. See details below.  |

### Details

The function uses internally [ri\\_data\\_extract](#) wrapped with a call to [lapply](#). Because the output of [lapply](#) is a list, the list is transformed to a matrix by calling [rbind](#). A column of sample indices called `sample` is added so each row can be traced back to a sample.

The *x*-axis of the plot are indexed samples (or RI files), i.e., first sample is 1, second 2, and so on. The *y*-axis is retention time (RT) or retention index (RI) depending on the value of `showRT`. Note that you can search by RT and plot by RI depending on the value of `useRT`.

Plot styling can be achieved by passing plotting extra parameters such as `col`, `pch`, `lty`, and others (see [par](#) and [plot](#)). Because the styles can be applied per sample or per *m/z* value, it is possible to prefix a ‘s’ to those parameters to specify that the style applies to samples and no masses. The available parameters are `scol`, `spch`, `sbg` and `scex`. See examples below.

The parameter `sizefun` is a function that takes a numeric vector as input and returns a positive value which correspond to the point size (parameter `cex`). This function will be applied on the peak intensities and the result will be used as `cex`. If NULL, the scaling function is implemented as  $(\log_{10}(x/100)) * (9/8) + (1/2)$ , where *x* is the peak intensity. Note that if either `cex` or `scex` is passed to the function, then `sizefun` will have no effect.

The logical parameter `plot` controls whether a plot is drawn. This might be useful for simply extracting the data for custom plotting with other packages such as `ggplot2`.

### Value

Returns [invisible](#) or a five-column matrix (see below), where the number of rows correspond to the number of peaks (or points) in the searched range. If no peaks are found in the given range, then it returns NULL.

- RI retention time index or the peak.
- RT retention time.
- Intensity peak height intensity.
- *mz* the *m/z* of the peak.
- `sample` an integer representing the sample index.

Compare this list with [ri\\_data\\_extract](#).

**Note**

This function is intended for advanced users and for debugging purposes when `TargetSearch` fails to detect a peak.

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[plotPeakRI](#), [ri\\_data\\_extract](#)

**Examples**

```
require(TargetSearchData)

# get RI files from TargetSearchData
path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
rifiles <- dir(path, pattern='RI_*', full=TRUE)

# simple plot no style
z <- ri_plot_peak(rifiles, massValues=c(144, 145, 100, 218), timeRange=c(255, 265))
# watch output data
head(z)

# add some style
ri_plot_peak(rifiles, massValues=c(144, 145, 100, 218), timeRange=c(255, 265),
             pch=1:4, col=1:4)
# display the Retention Index instead
ri_plot_peak(rifiles, massValues=c(144, 145, 100, 218), timeRange=c(255, 265),
             pch=1:4, col=1:4, showRT=FALSE)
# use RI index for the time range
ri_plot_peak(rifiles, massValues=c(144, 145, 100, 218), timeRange=c(267000, 275000),
             useRT=FALSE, pch=1:4, col=1:4)
# use styling per sample
scol <- rep(1:5, each=3)
ri_plot_peak(rifiles, massValues=c(144), timeRange=c(255, 265), pch=19, scol=scol)

# using a tsSample object can achieve the same results (RI files are in text format)
smp <- ImportSamplesFromDir(path, ftype = "text")
ri_plot_peak(smp, massValues=c(144), timeRange=c(255, 265), pch=19, scol=scol)
```

---

rt2ri

*Retention Time to Retention Time Index conversion*

---

**Description**

Convert retention times to retention indices based on observed FAME RI and their standard values.

**Usage**

```
rt2ri(rtTime, observed, standard)
```

**Arguments**

|          |                               |
|----------|-------------------------------|
| rtTime   | The extracted RT's to convert |
| observed | The observed FAME RT's        |
| standard | The standard RI for each FAME |

**Details**

Linear interpolation, interpolation outside bounds are done with continued linear interpolation from the last two FAME's

**Value**

The converted RI

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[RIcorrect](#), [FAMEoutliers](#)

**Examples**

```
# RI standards
standard <- c(100, 200, 300, 400, 500)
# observed standard retention times
observed <- c(10.4, 19.3, 32.4, 40.2, 50.3)
# a random set of retention times
RT <- runif(100,1,60)
# the corrected RIs
RI <- rt2ri(RT, observed, standard)
```

---

sampleRI

*Sample specific RI detection*

---

**Description**

Return a matrix of the sample specific retention indices (RI) based on the correlating selective masses.

**Usage**

```
sampleRI(samples, Lib, r_thres = 0.95, columns = NULL,
         method = "dayNorm", minPairObs = 5, showProgressBar = FALSE,
         makeReport = FALSE, pdfFile = "medianLibRep.pdf")
```

**Arguments**

|                 |  |
|-----------------|--|
| samples         | A tsSample object created by ImportSamples function.   |
| Lib             | A tsLib object created by <a href="#">ImportLibrary</a> function with corrected RI values. See medianRILib.  |
| r_thres         | A correlation threshold.   |
| columns         | Either NULL, a character vector, or an integer vector. In most cases, leave it as NULL. This parameter is used to configure the column names or positions of RI text files. See the documentation on the <a href="#">text2bin</a> function for further details.  |
| method          | Normalization method. Options are "dayNorm", a day based median normalization, "medianNorm", normalization using the median of all the intensities of a given mass, and "none", no normalization at all.   |
| minPairObs      | Minimum number of pair observations. Correlations between two variables are computed using all complete pairs of observations in those variables. If the number of observations is too small, you may get high correlations values just by chance, so this parameters is used to avoid that. Cannot be set lower than 5. |
| showProgressBar | Logical. Should the progress bar be displayed?   |
| makeReport      | Logical. If TRUE will report the RI deviations for every metabolite in the library.  |
| pdfFile         | The file name where the report will be saved.  |

**Value**

A matrix of correlating selective masses RI. Columns represent samples and rows the median RI of the selective masses.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[ImportSamples](#), [ImportLibrary](#), [medianRILib](#), [tsLib](#), [tsSample](#)

**Examples**

```
require(TargetSearchData)
data(TSExample)

# get RI file path
RI.path <- file.path(find.package("TargetSearchData"), "gc-ms-data")
```

```
# update RI file path
RIpath(sampleDescription) <- RI.path
# Import Library
refLibrary      <- ImportLibrary(file.path(RI.path, 'library.txt'))

# get the sample RI
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.95)

# same as above, but changing the correlation threshold and the minimum number
# of observations
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.9,
minPairObs = 10)
```

---

TargetSearch-defunct    *Defunct functions in package 'TargetSearch'*

---

## Description

Functions listed here are defunct and no longer available.

## Details

These function have been removed from 'TargetSearch' and no longer available. Use the replacement if any.

- fixRIcorrection has been replaced by [fixRI](#).
- TargetSearchGUI has been removed. Please use regular 'TargetSearch' functions. The old source code is archived at <https://github.com/acinostroza/TargetSearchGUI>.

---

text2bin                      *Convert RI files from text to binary format and vice versa*

---

## Description

This function converts a list of RI files (also known as peak list files) in text or binary format to binary or text format.

## Usage

```
text2bin(in.files, out.files=NULL, columns=NULL)
```

```
bin2text(in.files, out.files=NULL)
```

**Arguments**

|           |  |
|-----------|--|
| in.files  | A character vector of file paths to the input RI files.  |
| out.files | A character vector of file paths. If NULL, the input file extensions will be changed accordingly ("txt" to "dat" and vice versa).  |
| columns   | Either a numeric vector with the positions of the columns for SPECTRUM, RETENTION_TIME_INDEX, and RETENTION_TIME; or a character vector with the respective names of those columns. If NULL, then default (hard-coded) values will be used. If an integer vector, the column position must start at zero. In addition, the column names can be set by a global option (see details below). |

**Details**

These functions transform a list of RI files from and to binary to text representation. The format of the input files is detected dynamically and an error will be issued on invalid files.

Transforming a binary file to text might be useful if you need to inspect what a RI file looks in the inside (for example, you need to check that the peak detection was correct). On the other hand, a text file to binary is highly recommended as it is faster to parse than a text file.

For text files, the order of the columns is important (see option columns above). The first entry is the spectrum list, followed by the retention time index and the retention time. If the column names are other than SPECTRUM, RETENTION\_TIME\_INDEX, and RETENTION\_TIME, use the respective column names or the column names positions starting at zero (first column is zero, second is one, and so on).

Many functions rely on those column names and having to pass them as arguments on each function is tedious, so the global option TS\_RI\_columns can be set at the beginning, for example:

```
options(TS_RI_columns=c('spec_column', 'RI_column', 'RT_column'))
```

where "spec\_column", "RI\_column", and "RT\_columns" are the names of the spectrum, retention index and retention time columns.

This command is useful if your RI files were generated by another software. However, it is highly recommended to simply convert those custom RI files into [TargetSearch](#)'s binary format and do not worry about column names.

**Value**

A character vector of the created files paths or invisible.

**File Format**

The so-called RI files contain lists of m/z peaks detected for every ion trace measured in the samples. Historically, the file format was a simple tab-delimited text file in the format described below. Note that the column order could differ and additional columns could be present, but they are ignored.

| RETENTION_TIME | SPECTRUM             | RETENTION_TIME_INDEX |
|----------------|----------------------|----------------------|
| 212.46         | 250:26 256:26 316:27 | 221029.7             |
| 212.51         | 114:46 162:30 251:27 | 221081.3             |

|        |                                   |          |
|--------|-----------------------------------|----------|
| 212.56 | 319:25                            | 221132.9 |
| 212.61 | 95:38 108:30 262:32 266:27 292:25 | 221184.5 |

The retention time is usually represented in seconds, while the retention time in arbitrary units, which depends on the retention time correction standard method (in the table above it is in milliseconds, but other units can be used).

The spectrum column is represented by pairs of  $m/z$  and raw intensity (peak height), similarly as the representation of a metabolite library (see [ImportLibrary](#)). Thus each pair correspond to a peak of the respective ion trace.

The disadvantage of using text files is they are slow to parse, so a binary format was created which represents the peak data as binary vectors so they are fast to parse. These files contain the extension `dat`.

### Note

Beware that the respective `tsSample` object may need to be updated by using the method `fileFormat`.

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

[ImportSamples](#), [tsSample](#), [RIcorrect](#)

### Examples

```
require(TargetSearchData)
# take three example files from package TargetSearchData
in.files <- dir(file.path(find.package("TargetSearchData"), "gc-ms-data"), pattern="RI_", full=TRUE)[1:3]
# out files to current directory
out.files <- sub(".txt", ".dat", basename(in.files))
# convert to binary format
res <- text2bin(in.files, out.files)
stopifnot(res == out.files)

# convert back to text
res <- bin2text(out.files)
stopifnot(res == basename(in.files))

# Demonstrate how to use the `columns` option
# make dummy RI file with arbitrary column names and save it
tmp <- data.frame(RT=c(101.5,102.5), SPEC=c('12:100 23:100', '114:46 162:30'), RI=c(300, 400) + .75)

# file must be tab-delimited, unquoted strings and no row names
write.table(tmp, file="RI_test.txt", sep="\t", quote=FALSE, row.names=FALSE)

# convert this text file to binary format
## wrong! It fails because of invalid columns
# text2bin("RI_test.txt")
```

```
# correct! The columns are correct
text2bin("RI_test.txt", columns=c('SPEC', 'RI', 'RT'))

# same example but using integers (not recommended)
text2bin("RI_test.txt", columns=c(1, 2, 0)) # note they start from zero.

# Alternative, set a global option (so it can be used in a session)
opt <- options(TS_RI_columns=c('SPEC', 'RI', 'RT'))
text2bin("RI_test.txt")

# unset options
options(opt)
```

---

TSExample

*Example GC-MS data for TargetSearch Package*

---

## Description

A TargetSearch example GC-MS data. This datasets contains TargetSearch object examples generated from a E.coli salt stress experiment (See package TargetSearchData).

## Usage

```
data(TSExample)
```

## Format

The data contains the following objects:

**sampleDescription** a tsSample object. The sample description.

**refLibrary** a tsLib object. The reference library.

**rimLimits** a tsRim object. The RI markers definition.

**RImatrix** a matrix object. The retention time of the RI markers.

**corRI** a matrix object. The sample RI.

**peakData** a tsMSdata object. The intensities and RIs of all the masses that were searched for.

**metabProfile** a tsProfile object. The metabolite profile.

## Details

This dataset contain only the objects. The actual source files are provided by the package TargetSearchData.

## See Also

[ImportLibrary](#), [ImportSamples](#), [ImportFameSettings](#),



**Examples**

```

# this run an example pipeline
require(TargetSearchData)

## The directory with the NetCDF GC-MS files
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
cdfpath
list.files(cdfpath)
samp.file <- file.path(cdfpath, "samples.txt")
rim.file <- file.path(cdfpath, "rimLimits.txt")
lib.file <- file.path(cdfpath, "library.txt")

# import files from package
sampleDescription <- ImportSamples(samp.file, CDFpath = cdfpath, RIpath = ".")
refLibrary <- ImportLibrary(lib.file)
rimLimits <- ImportFameSettings(rim.file, mass = 87)

# update NCDF4
sampleDescription <- ncdf4Convert(sampleDescription, path=".")

# perform RI correction
RImatrix <- Rlcorrect(sampleDescription, rimLimits, massRange = c(85,320),
  IntThreshold = 25, pp.method = "ppc", Window = 15)
# update median RI
refLibrary <- medianRILib(sampleDescription, refLibrary)
# get the sample RI
corRI <- sampleRI(sampleDescription, refLibrary, r_thres = 0.95)
# obtain the peak Intensities of all the masses in the library
peakData <- peakFind(sampleDescription, refLibrary, corRI)
# make a profile of the metabolite data
metabProfile <- Profile(sampleDescription, refLibrary, peakData, r_thres = 0.95)

# show the metabolite profile
profileInfo(metabProfile)
# show the matrix intensities
Intensity(metabProfile)

```

---

tsLib-class

*Class for representing a reference library*


---

**Description**

This is a class representation of a reference library.

**Objects from the Class**

Objects can be created by the function [ImportLibrary](#).

**Slots**

Name: "character", the metabolite or analyte names.  
 RI: "numeric", the expected retention time indices (RI) of the metabolites/analytes.  
 medRI: "numeric", the median RI calculated from the samples.  
 RIdev: "matrix", the RI deviation windows,  $k = 1,2,3$ . A three column matrix  
 selMass: "list", every component is a numeric vector containing the selective masses.  
 topMass: "list", every component is a numeric vector containing the top masses.  
 quantMass: "numeric", the mass used for quantification.  
 libData: "data.frame", additional library information.  
 spectra: "list", the metabolite spectra. Each component is a two column matrix: m/z and intensity.

**Methods**

[ signature(x = "tsLib"): Selects a subset of metabolites from the library.  
 \$name signature(x = "tsLib"): Access column name of libData slot.  
 libId signature(obj = "tsLib"): Returns a vector of indices.  
 length signature(x = "tsLib"): returns the length of the library. i.e., number of metabolites.  
 libData signature(obj = "tsLib"): gets/sets the libData slot.  
 libName signature(obj = "tsLib"): gets the Name slot.  
 libRI signature(obj = "tsLib"): gets the RI slot.  
 medRI signature(obj = "tsLib"): gets the medRI slot.  
 refLib signature(obj = "tsLib"): Low level method to create a matrix representation of the library.  
 RIdev signature(obj = "tsLib"): gets the RI deviations.  
 RIdev<- signature(obj = "tsLib"): sets the RI deviations.  
 quantMass signature(obj = "tsLib"): gets the quantification mass.  
 quantMass<- signature(obj = "tsLib"): sets the quantification mass.  
 selMass signature(obj = "tsLib"): gets the selective masses.  
 show signature(object = "tsLib"): show method.  
 spectra signature(obj = "tsLib"): gets the spectra.  
 topMass signature(obj = "tsLib"): gets the top masses.

**Note**

Some care is needed when using the methods `quantMass<-`, `selMass<-`, `topMass<-`. In order to be consistent, the first m/z value of the slot `topMass` and `selMass` are equal to `quantMass`, and the values of `selMass` are equal to the first couple of values of `topMass`. In other words, the following constrain is applied.

```

quantMass : x[0]
selMass   : x[0], x[1], ..., x[k]
topMass   : x[0], x[1], ..., x[k], x[k+1], ..., x[n]

```

where  $1 \leq k \leq n$  and  $x[i]$  is a  $m/z$  value. Thus, using one these methods will change the values of the other slots. In the future, these methods will be deprecated, so it is better to not rely on them.

See the last example on how this can lead to unexpected results.

### Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

### See Also

[ImportLibrary](#)

### Examples

```

showClass("tsLib")

# define some metabolite names
libNames <- c("Metab1", "Metab2", "Metab3")
# the expected retention index
RI <- c(100,200,300)
# selective masses to search for. A list of vectors.
selMasses <- list(c(95,204,361), c(87,116,190), c(158,201,219))
# define the retention time windows to look for the given selective masses.
RIdev <- matrix(rep(c(10,5,2), length(libNames)), ncol = 3, byrow = TRUE)
# Set the mass spectra. A list object of two-column matrices, or set to
# NULL if the spectra is not available
spectra <- NULL
# some extra information about the library
libData <- data.frame(Name = libNames, Lib_RI = RI)
# create a reference library object
refLibrary <- new("tsLib", Name = libNames, RI = RI, medRI = RI, RIdev = RIdev,
                 selMass = selMasses, topMass = selMasses, spectra = spectra, libData = libData)

# get the metabolite names
libName(refLibrary)
# set new names
libName(refLibrary) <- c("Metab01", "Metab02", "Metab03")

# get the expected retention times
libRI(refLibrary)
# set the retention time index for metabolite 3 to 310 seconds
libRI(refLibrary)[3] <- 310
# change the selection and top masses of metabolite 3
selMass(refLibrary)[[3]] <- c(158,201,219,220,323)
topMass(refLibrary)[[3]] <- c(158,201,219,220,323)
# change the retention time deviations
RIdev(refLibrary)[3,] <- c(8,4,1)

```

```
#####
#####
# These examples show how changing a quantitative or selective mass
# could lead to unexpected results.

# show quantMasses
quantMass(refLibrary)

# suppose that we want to change the quant mass of metabolite 1 to 96 due
# to a typo in the library. We could do just
quantMass(refLibrary)[1] <- 96

# however, we still see the mass 95 in the selective and top masses.
selMass(refLibrary)[[1]]
topMass(refLibrary)[[1]]

# to remove the mass 95, set the topMass and selMass explicitly, noting that
# the first masses coincides with 96 (the quantMass)
selMass(refLibrary)[[1]] <- c(96, 204, 361)
topMass(refLibrary)[[1]] <- c(96, 204, 361)
```

---

tsMSdata-class

*Class for representing MS data*


---

## Description

This is a class to represent MS data obtained from the sample.

## Details

The method `as.list` converts every slot (RI, RT, and Intensity) of a `tsMSdata` object into a matrix. The converted matrices are stored in a list. Each converted matrix has an attribute called `'index'` that relates the metabolite index with the respective rows. The components of the resulting list are named as the slots. If the slot RT is not defined or empty, then the output list will have only two components. (`'RT'` and `'Intensity'`).

## Objects from the Class

Objects be created by calls of the form

## Slots

RI: "list", a list containing an RI matrix, one matrix per metabolite

RT: "list", a list containing an RT matrix, one matrix per metabolite

Intensity: "list", a list containing a peak intensity matrix, one matrix per metabolite

## Methods

**Intensity** signature(obj = "tsMSdata"): gets the peak intensity list.  
**Intensity<-** signature(obj = "tsMSdata"): gets the peak intensity list.  
**retIndex** signature(obj = "tsMSdata"): gets RT list.  
**retIndex<-** signature(obj = "tsMSdata"): sets the RI list.  
**retTime** signature(obj = "tsMSdata"): gets the RT list.  
**retTime<-** signature(obj = "tsMSdata"): sets the RT list.  
**show** signature(object = "tsMSdata"): show function.  
**as.list** signature(object = "tsMSdata"): coerce a list object. See details

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[FindPeaks](#), [peakFind](#)

## Examples

```
showClass("tsMSdata")
```

---

|                 |  |
|-----------------|--|
| tsProfile-class | <i>Class for representing a MS profile</i> |
|-----------------|--|

---

## Description

This class is to represent a MS profile

## Objects from the Class

Objects can be created by the function [Profile](#) or by

```
new("tsMSdata", RI = [retention time index matrix], RT = [retention time matrix], Intensity  
= [peak intensity])
```

## Slots

**info:** "data.frame", the profile information.  
**RI:** "list", a list containing RI matrices, one matrix per metabolite  
**RT:** "list", a list containing RT matrices, one matrix per metabolite  
**Intensity:** "list", a list containing peak-intensity matrices, one matrix per metabolite  
**profRI:** "matrix", the profile RI matrix.  
**profRT:** "matrix", the profile RT matrix.  
**profInt:** "matrix", the profile Intensity matrix.

**Extends**

Class [tsMSdata](#), directly.

**Methods**

**profileInfo** signature(obj = "tsProfile"): get the profile information.  
**profileInfo<-** signature(obj = "tsProfile"): set the profile information.  
**profileInt** signature(obj = "tsProfile"): get the profile intensity matrix.  
**profileInt<-** signature(obj = "tsProfile"): set the profile intensity matrix.  
**profileRI** signature(obj = "tsProfile"): get the profile RI matrix.  
**profileRI<-** signature(obj = "tsProfile"): set the profile RI matrix.  
**profileRT** signature(obj = "tsProfile"): get the profile RT matrix.  
**profileRT<-** signature(obj = "tsProfile"): set the profile RT matrix.  
**show** signature(object = "tsProfile"): the show function.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[Profile](#), [ProfileCleanUp](#), [tsMSdata](#)

**Examples**

```
showClass("tsProfile")
```

---

 tsRim-class

*Class for representing retention index markers*

---

**Description**

This is a class to represent retention index markers.

**Objects from the Class**

Objects can be created by the function [ImportFameSettings](#) or by calls of the form `new("tsRim", limits = [two column matrix with time limits], standard = [a vector with RI standards], mass = [m/z marker])`.

**Slots**

**limits:** "matrix", two column matrix with lower and upper limits where the standards will be search. One row per standard.  
**standard:** "numeric", the marker RI values.  
**mass:** "numeric", the m/z marker.

## Methods

```
[ signature(x = "tsRim"): Selects a subset of markers.  
rimLimits signature(obj = "tsRim"): gets the time limits.  
rimLimits<- signature(obj = "tsRim"): sets the time limits.  
rimMass signature(obj = "tsRim"): gets the m/z marker.  
rimMass<- signature(obj = "tsRim"): sets the m/z marker.  
rimStandard signature(obj = "tsRim"): gets the standards.  
rimStandard<- signature(obj = "tsRim"): sets the standards.
```

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[ImportFameSettings](#)

## Examples

```
showClass("tsRim")  
  
# create a rimLimit object:  
# - set the lower (first column) and upper (second column) time limites to  
#   search for standards.  
Lim <- rbind(c(200, 300), c(400,450), c(600,650))  
# - set the retention indices of the standard  
Std <- c(250000, 420000, 630000)  
# - set the mass marker  
mass <- 87  
# - create the object  
rimLimits <- new("tsRim", limits = Lim, standard = Std, mass = mass)  
  
# sometimes you need to change the limits of a particular standard  
rimLimits(rimLimits)[2,] <- c(410, 450)  
  
# to change the mass value  
rimMass(rimLimits) <- 85  
  
# to select a subset  
rim <- rimLimits[1:2]  
  
# remove a marker (number 3 in this case)  
rim <- rimLimits[-3]
```

---

|                |                                       |
|----------------|---------------------------------------|
| tsSample-class | <i>Class for representing samples</i> |
|----------------|---------------------------------------|

---

### Description

This is a class to represent a set of samples.

### Objects from the Class

Objects can be created by the function [ImportSamples](#) or by calling the object generator function.

```
new("tsSample", Names = [sample names], CDFfiles = [list of CDF file names], RIfiles = [list
of RI file names], CDFpath = [CDF files path], RIpath = [RI files path], days = [measurement
days], data = [additional sample information], ftype = [RI file format])
```

### Slots

Names: "character", the sample names.

CDFfiles: "character", the list of CDF file names.

RIfiles: "character", the list of RI file names.

CDFpath: "character", CDF files path. Deprecated. See Notes.

RIpath: "character", RI file path. Deprecated. See Notes.

days: "character", measurement days.

data: "data.frame", additional sample information.

### Methods

[ signature(x = "tsSample"): Selects a subset of samples.

\$name signature(x = "tsSample"): Access column name of sampleData slot.

CDFfiles signature(obj = "tsSample"): list of CDF files.

RIfiles signature(obj = "tsSample"): list of RI files.

RIpath signature(obj = "tsSample"): The RI file path.

CDFpath signature(obj = "tsSample"): The CDF file path.

length signature(x = "tsSample"): number of samples.

sampleData signature(obj = "tsSample"): additional sample information.

sampleDays signature(obj = "tsSample"): measurement days.

sampleNames signature(obj = "tsSample"): sample names. The names must be unique

show signature(object = "tsSample"): the show funtion.

fileFormat signatureobj = "tsSample": Sets or gets the RI file format. Options are either "binary" or "text". See note below.



**Notes**

The method `fileFormat` only changes the internal information of the file type and not the files themselves. To actually change the files, use the functions `bin2text` and `text2bin`.

Note that the slot Names (i.e., the sample names/identifiers) must be unique. This allows sample selection by using sample identifiers as well as indices. Also, if columns are selected, the output will be either a vector or a `data.frame` depending on whether one or more columns were selected. More over, it is required that the rownames of the data slot are equal to the sample names slots. This is handled internally. If the Names are not provided, then the CDF files are used instead (directories and extension are removed). In this case the file names must be unique.

The slots `CDFpath` and `RIpath` are deprecated and not used. However, the methods to set or get the paths will still work. The file paths is stored on the `CDFfiles` and `RIfiles` slots.

**Author(s)**

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

**See Also**

[ImportSamples](#)

**Examples**

```
showClass("tsSample")

# get a list of CDF files from a directory
require(TargetSearchData)
CDFpath <- system.file("gc-ms-data", package = "TargetSearchData")
cdffiles <- dir(CDFpath, "cdf", full=TRUE)

# define the RI file path
RIpath <- "."

# create a tsSample object with minimal info
sampleDescription <- new("tsSample", CDFfiles = cdffiles, RIpath = RIpath)

## ## ## ## ##

# Alternatively, the CDF path and CDF file names can be given separately
# (this was the old TargetSearch behavior)
cdffiles <- basename(cdffiles)

# create the sample object
sampleDescription <- new("tsSample", CDFfiles = cdffiles, CDFpath = CDFpath, RIpath = RIpath)

## ## ## ## ##

# More parameters could be defined:
# define the RI files and the RI path
RIfiles <- sub("cdf$", "txt", paste("RI_", cdffiles, sep = ""))
RIpath <- "."
```

```

# get the measurement days (the four first numbers of the cdf files, in this
# example)
days <- substring(cdffiles, 1, 4)

# sample names (must be unique)
smp_names <- paste("Sample", 1:length(sampleDescription), sep = "_")

# add some sample info
smp_data <- data.frame(CDF_FILE =cdffiles, GROUP = gl(5,3))

# create the sample object
sampleDescription <- new("tsSample", Names = smp_names, CDFfiles = cdffiles, CDFpath = CDFpath,
  RIpath = RIpath, days = days, RIfiles = RIfiles, data = smp_data)

# chang the file paths (relative to the working path)
CDFpath(sampleDescription) <- "my_cdfs"
RIpath(sampleDescription) <- "my_RIs"

# change sample Names
sampleNames(sampleDescription) <- sprintf("S%03d", 1:length(sampleDescription))

## sample subsetting.
# select samples 1, 3 and 5
(sampleset <- sampleDescription[c(1, 3, 5)])

# or use sample IDs
(sampleset <- sampleDescription[c("S001", "S003", "S005")])

## extract columns
# select column 'GROUP'
(group <- sampleDescription$GROUP)
# or
(group <- sampleDescription[, 'GROUP'])

## change the measurement days (sets the same day for all samples)
sampleDays(sampleDescription) <- "1"

## Note: the length of `measurement days` variable must be 1 or equal
## to the number of samples, otherwise an error will be thrown

```

---

tsUpdate,tsSample-method

*Methods for Updating TargetSearch objects tsUpdate*


---

## Description

tsUpdate is a generic function which can be used to update and old 'TargetSearch' class definition. Currently, this function is only implemented for [tsSample](#) objects.

**Methods**

signature(obj = "tsSample") Method to update an old `tsSample` object. A change was introduced starting from 'TargetSearch' version 1.42.0.

**Author(s)**

Alvaro Cuadros-Inostroza

**Examples**

```
## Not run:
newObject <- tsUpdate(oldObject)

## End(Not run)
```

---

updateRI

*Updating Time Index correction*

---

**Description**

This function can be used to correct or adjust the detected retention time index (RI) markers or their location to specific retention times. This function adds on `fixRI()` as it also corrects the RI of the CDF files

**Usage**

```
updateRI(samples, rimLimits, RImatrix = NULL, quiet = TRUE)
```

**Arguments**

|                        |   |
|------------------------|---|
| <code>samples</code>   | A <code>tsSample</code> object created by <code>ImportSamples</code> .  |
| <code>rimLimits</code> | A <code>tsRim</code> object. See <code>ImportFameSettings</code> .  |
| <code>RImatrix</code>  | An optional matrix. It represents a retention time matrix of the detected retention time markers that was obtained after running <code>RIcorrect</code> |
| <code>quiet</code>     | Logical. Do not print a list of converted files.  |

**Details**

Sometimes the retention time of the RI markers are not detected correctly, either because there was a problem with the standard, or the time limits of the `tsRim` object were not set correctly, or simply because the markers are not injected with the samples.

In any case, the retention time correction can be fixed by calling this function. This function works almost exactly like `fixRI()`, in fact, it is called internally, and allows correction of RIfiles and CDFfiles at the same time. Check also the documentation of `fixRI()` for extra details.

The parameters are the `tsSample` and the `tsRim` object, with optionally a `RImatrix` to force the location of the markers. The parameter `quiet` can be unset to show what samples are corrected.

If only a subset of samples require correction, then they can be chosen by subsetting the object `sample`.

Needless to say, this function expect that the CDF files exists and are in the TargetSearch format. If this is not the case, then use the function `fixRI()`, as this function deals only with RI files.

### Value

The retention index matrix. If `RImatrix` is not NULL, then the output is the same matrix.

### Note

It is required that all the sample names of `samples` are contained in the colnames of `RImatrix`, but the reverse is not necessary. The number of columns of the output matrix will match the number of samples. Extra columns in `RImatrix` will be ignored and not returned.

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

`fixRI()`, `RIcorrect()`, `ImportSamples()`, `ImportFameSettings()`

### Examples

```
require(TargetSearchData)
# import refLibrary, rimLimits and sampleDescription.
data(TSEexample)
CDFpath(sampleDescription) <-
  file.path(find.package("TargetSearchData"), "gc-ms-data")

# convert a subset of files to netCDF4
smp <- ncdf4Convert(sampleDescription[1:6], path=".")

# make a copy of the RI markers object
fames <- rimLimits

# mess up the limits of marker 3 (real value is 369 seconds app.)
rimLimits(fames)[3,] <- c(375, 400)

# run RImcorrect (skip CDF-4 conversion)
RImat <- RImcorrect(smp, fames, Window = 15, IntThreshold = 200)

# fix the limits of marker 3
rimLimits(fames)[3,] <- c(360, 380)

# update RI files and CDF files
RImat <- updateRI(smp, fames)

# Pass a RI matrix for manual adjustment
RImat[, 3] <- c(252, 311, 369)
```

```
RImat <- updateRI(smp, fames, RImat)

# To select specific samples, simply use sample subsetting
# Note, RImat2 has only one column in this case.
( RImat2 <- updateRI(smp[3], fames, RImat) )
```

---

Write.Results

*Save TargetSearch result objects into files*

---

## Description

This is a convenient function to save the TargetSearch result into text files.

## Usage

```
Write.Results(Lib, metabProfile, quantMatrix=c('maxint','maxobs','none'),
  prefix = NA)
```

## Arguments

|              |  |
|--------------|--|
| Lib          | A tsLib object.  |
| metabProfile | A tsProfile object. The final result of the package. This object is generated by either Profile or ProfileCleanUp.   |
| quantMatrix  | Should an intensity matrix using quantification masses be created? This parameter will be passed to <a href="#">quantMatrix</a> and indicates whether the quantification mass should be chosen based on intensity or observations. The file will have the extension '.profile.quantmatrix.txt'. If none, then the file is not created. |
| prefix       | A character string. This is used as a name prefix for the written files. "TargetSearch-" is used by default.   |

## Value

This function doesn't return anything. Just print a message with the saved files.

## Author(s)

Alvaro Cuadros-Inostroza, Matthew Hannah, Henning Redestig

## See Also

[peakFind](#), [Profile](#), [ProfileCleanUp](#), [tsLib](#), [tsMSdata](#), [tsProfile](#), [quantMatrix](#)

---

|              |   |
|--------------|---|
| writeLibText | <i>Save a library object in text format</i> |
|--------------|---|

---

### Description

This function creates tab delimited text file with library information. The created file can be re-imported with the [ImportLibrary](#) function.

### Usage

```
writeLibText(lib, file)
```

### Arguments

|      |                                       |
|------|---------------------------------------|
| lib  | A tsLib object. A metabolite library. |
| file | A string naming the output file.      |

### Author(s)

Alvaro Cuadros-Inostroza

### See Also

[tsLib](#), [ImportLibrary](#)

### Examples

```
# get the reference library file
cdfpath <- file.path(find.package("TargetSearchData"), "gc-ms-data")
lib.file <- file.path(cdfpath, "library.txt")

# Import the reference library
refLibrary <- ImportLibrary(lib.file)

# save it to a file
writeLibText(refLibrary, file="libraryCopy.txt")
```

---

|          |  |
|----------|--|
| writeMSP | <i>Save spectra in MSP format to be visualized in NIST</i> |
|----------|--|

---

**Description**

This function creates MSP format file from peak intensities that can be viewed with NIST.

**Usage**

```
writeMSP(metlib, metprof, file, append = FALSE)
```

**Arguments**

|         |  |
|---------|--|
| metlib  | A tsLib object. A metabolite library.  |
| metprof | A tsProfile object. Usually the output of <a href="#">Profile</a> or <a href="#">ProfileCleanUp</a> functions. |
| file    | A string naming the output file.   |
| append  | Logical. If TRUE the results will be appended to file. Otherwise, it will overwrite the contents of file.      |

**Author(s)**

Alvaro Cuadros-Inostroza

**See Also**

[peakFind](#), [Profile](#), [ProfileCleanUp](#), [tsLib](#), [tsMSdata](#), [tsProfile](#)

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