

Package ‘PepsNMR’

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Type Package

Title Pre-process 1H-NMR FID signals

Version 1.27.0

Description

This package provides R functions for common pre-processing steps that are applied on 1H-NMR data. It also provides a function to read the FID signals directly in the Bruker format.

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URL <https://github.com/ManonMartin/PepsNMR>

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methods, graphics, stats

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Note This package originates from a previous work of Eli Lilly together with Paul Eilers that have developed an automated Matlab library with innovating methods for 1H NMR pre-treatment that was called ‘Bubble’. (J. Vanwinsberghe. Bubble: development of a matlab tool for automated 1H-NMR data processing in metabonomics. Master's thesis Strasbourg University, 2005.)

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Description

This package provides R functions for classic and advanced pre-processing steps that are applied on ^1H NMR data. It also provides the function [ReadFids](#) to read the FID directly from the Bruker format. Those pre-processing are cited below in the advised order of their application:

[GroupDelayCorrection](#) Correct for the first order phase correction.

[SolventSuppression](#) Remove solvent signal from the FIDs.

[Apodization](#) Increase the sensitivity/resolution of the FIDs.

[ZeroFilling](#) Improve the visual representation of the spectra.

[FourierTransform](#) Transform the FID into a spectrum and convert the frequency scale (Hertz -> ppm).

[ZeroOrderPhaseCorrection](#) Correct for the zero order phase correction.

[InternalReferencing](#) Calibrate the spectra with internal compound referencing.

[BaselineCorrection](#) Remove the spectral baseline.

[NegativeValuesZeroing](#) Set negatives values to 0.

[Warping](#) Warp the samples according to a reference spectrum.

[WindowSelection](#) Select the informative part of the spectrum.

[Bucketing](#) Data reduction by integration.

[RegionRemoval](#) Set intensities of a desired region to 0.

[ZoneAggregation](#) Aggregate a region to a single peak.

[Normalization](#) Normalize the spectra.

Details

Package:	PepsNMR
Type:	Package
Version:	0.99.0
License:	GPLv2

The FIDs are read using [ReadFids](#) which also gives a matrix with meta-information about each FID. The other functions apply different pre-processing steps on these signals, and some need the info matrix as outputted from [ReadFids](#). During this pre-processing, the signal is transformed through fourier transformation and the frequency scale is expressed in ppm. For more details and illustrated explanations about those pre-treatment steps, see the documentation of each function and/or the chapter 1 of the reference below.

Author(s)

Benoît Legat, Bernadette Govaerts & Manon Martin

Maintainer: Manon Martin <manon.martin@uclouvain.be>

References

- Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ^1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.
- Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in ^1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
path <- system.file("extdata", package = "PepsNMRData")
dir(path)

fidList <- ReadFids(file.path(path, "HumanSerum"))
Fid_data <- fidList[["Fid_data"]]
Fid_info <- fidList[["Fid_info"]]
Fid_data <- GroupDelayCorrection(Fid_data, Fid_info)
Fid_data <- SolventSuppression(Fid_data)
Fid_data <- Apodization(Fid_data, Fid_info)
Fid_data <- ZeroFilling(Fid_data)
Spectrum_data <- FourierTransform(Fid_data, Fid_info)
Spectrum_data <- ZeroOrderPhaseCorrection(Spectrum_data)
Spectrum_data <- InternalReferencing(Spectrum_data, Fid_info)
Spectrum_data <- BaselineCorrection(Spectrum_data)
Spectrum_data <- NegativeValuesZeroing(Spectrum_data)
Spectrum_data <- Warping(Spectrum_data)
Spectrum_data <- WindowSelection(Spectrum_data)
Spectrum_data <- Bucketing(Spectrum_data)
Spectrum_data <- RegionRemoval(Spectrum_data, typeofspectra = "serum")
# Spectrum_data <- ZoneAggregation(Spectrum_data)
Spectrum_data <- Normalization(Spectrum_data, type.norm = "mean")
```

Apodization

Apodization of the FID

Description

The function multiplies the FID by a defined factor to increase the sensibility and/or resolution of the spectra.

Usage

```
Apodization(Fid_data, Fid_info = NULL, DT = NULL, type.apod = c("exp", "cos2",
  "blockexp", "blockcos2", "gauss", "hanning", "hamming"), phase = 0,
  rectRatio = 1/2, gaussLB = 1, expLB = 0.3, plotWindow = FALSE,
  returnFactor = FALSE, verbose=FALSE)
```

Arguments

Fid_data	Matrix containing the FIDs, one row per signal, as outputted by ReadFids .
Fid_info	Matrix containing the info about the FIDs, one row per signal, as outputted by ReadFids .
DT	If given, used instead of Fid_info to give the Dwell Time, the time between 2 points of the FID.
type.apod	Type of apodization, see details.
phase	Phase at which the apodization window is maximum for cos2, hanning and hamming types. For example, if phase is 0.2, the maximum is at 20% of the signal.
rectRatio	If there is a rectangular window, ratio between the width of the window and the width of the signal.

gaussLB	Line Broadening for the gaussian window, see details.
expLB	Line Broadening for the exponential window, see details.
plotWindow	If TRUE, a plot of the signal applied to the FID is displayed.
returnFactor	If TRUE, returns a list with the final FIDs and the apodization function.
verbose	If "TRUE", will print processing information.

Details

The apodization is usually performed in order to increase the sensitivity, *i.e.* the Signal-to-Noise Ratio (SNR) of the spectra. This is based on the fact that the signal intensity is decreasing over time unlike the noise that keeps a constant amplitude, leaving a noisy tail at the end of the FID. Multiplying the FID with a decaying signal will then increase the SNR. Since the area under the spectral peak remains unchanged, a faster decay will also result in a reduced peak height in spectra, lowering the spectral resolution. Optimal trade-off parameters for the apodization signal are thus needed to prevent high losses in sensitivity/resolution.

A FID of the form $s_0 \exp(i2\pi\nu t) \exp(-t/T)$ has a peak in its spectrum at the frequency ν of width that is inversely proportional to T . This peak is called a *spectral line* and its width a *spectral width*.

In the case of the exponential multiplication ("exp"), which is the default apodization, the decaying exponential becomes:

$$\exp(-t(1/T + LB))$$

The new decay T^* which satisfies $1/T^* = 1/T + LB$ is therefore smaller so the spectral line is *broadened*. That is why we call this parameter the Line Broadening.

If LB increases, the SNR increases but at the expense of the spectral resolution. Usual values in proton NMR for "LB" found in the literature are 0.3 for the NOESY presat pulse sequence and -0.01 for the CPMG presat pulse sequence. It should not exceed the value of 1 to avoid information loss.

The different types of apodization are:

exp The signal is multiplied by a decreasing exponential $\exp(-t/\text{expLB})$.

cos2 The signal is multiplied by the value of a \cos^2 from 0 (where its value is 1) until $\pi/2$ (where its value is 0).

blockexp The first part of the signal (defined by rectRatio) is left unchanged and the second is multiplied by $\exp(-t/\text{expLB})$ starting at value 1.

blockcos2 the first part is left unchanged as with blockexp and the second part is multiplied by a \cos^2 where its value starts at 1 at the end of the block and ends at 0 at the end of the signal.

gauss The signal is multiplied by a gaussian window centered at the beginning of the FID and with $\sigma = 1/\text{gaussLB}$.

hanning The signal is multiplied by a hanning window : $0.5 + 0.5 \cos \cos$.

hamming The signal is multiplied by a hamming window : $0.54 + 0.46 \cos \cos$.

Value

If returnFactor is TRUE, will return a list with the following elements: Fid_data and Factor. Otherwise, the function will just return Fid_data.

Fid_data	The apodized FIDs.
Factor	The apodization signal.

Author(s)

Benoît Legat & Manon Martin

References

Inspired from the matNMR library.

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ¹H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Apod_res <- Apodization(Data_HS_sp$FidData_HS_2,
                        FidInfo_HS, plotWindow=FALSE)

#or
Apod_res <- Apodization(Data_HS_sp$FidData_HS_2,
                        FidInfo_HS, plotWindow=FALSE, returnFactor=TRUE)
Apod_fid = Apod_res[["Fid_data"]]
plot(Apod_res[["Factor"]], type="l")
```

BaselineCorrection	<i>Set the baseline to a uniform zero signal.</i>
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Description

The function estimates and removes the smoothed baseline from the spectra.

Usage

```
BaselineCorrection(Spectrum_data, ptw.bc = TRUE, maxIter = 42,
                  lambda.bc = 1e7, p.bc = 0.05, eps = 1e-8,
                  ppm.bc = TRUE, exclude.bc = list(c(5.1,4.5)),
                  returnBaseline = FALSE, verbose = FALSE)
```

Arguments

Spectrum_data	Matrix containing the spectra, one row per spectrum.
ptw.bc	If TRUE, calculates the baseline in C using the ptw library which is a lot faster. The R version is only kept because it is easier to understand than C and in case of problems with the installation of the ptw package.
maxIter	Maximum number of iterations for the R version (if ptw.bc is set to FALSE).
lambda.bc	Smoothing parameter (generally 1e5 – 1e8). See details.
p.bc	Asymmetry parameter. See details.
eps	Numerical precision for convergence when estimating the baseline.

ppm.bc	If TRUE, the values in <code>exclude.zopc</code> represent frequencies in ppm value (column names of spectra), if FALSE these values are column indices.
exclude.bc	If not NULL and <code>ptw.bc == FALSE</code> , a list containing the extremities of the intervals excluded for the baseline estimation, either expressed in ppm (decreasing values) OR in column indices (increasing values), e.g. <code>exclude.bc = list(c(0, 10000))</code> if <code>ppm.bc == FALSE</code> or <code>exclude.bc = list(c(1, -1))</code> if <code>ppm.bc == TRUE</code> .
returnBaseline	If TRUE, returns the estimated baselines.
verbose	If "TRUE", will print processing information.

Details

The signal should be an addition of positive peaks which represent metabolites from the samples. These peaks are added to the baseline which is the signal representing the absence of any metabolite and should therefore be uniformly zero. For each spectrum, its baseline is thus estimated and removed. Let F be our initial spectrum and Z be its baseline. Once Z is approximated, the corrected spectrum is $F - Z$.

A negative signal doesn't make sense and creates problems with the statistical analysis. The estimated baseline should then not be such that $F - Z < 0$. Hence, in the objective function to be minimized, the squared difference $F - Z$ are weighted by p if $F - Z > 0$ or $1 - p$ if $F - Z < 0$. p is indeed taken very small, e.g. 0.05, to avoid negative intensities. The function [NegativeValuesZeroing](#) is used thereafter to set the remaining negative intensities to zero after the baseline correction.

With this function to minimize, we would simply have $F = Z$ as a solution which would make $F - Z$ uniformly zero. Therefore, a roughness penalty term on Z is applied so that it does not match exactly the peaks. The importance of this smoothness constraint in the objective function is tuned by λ which is typically equal to $1e7$.

In summary, usefull parameters are:

`p.bc` The default value is 0.05. The smaller it is, the less Z will try to follow peaks when it is under the function and the more it will try to be under the function.

`lambda.bc` The default value is $1e7$. The larger it is, the smoother Z will be. With `lambda = 0`, the baseline will be equal to the signal and the corrected signal will be zero.

The algorithm used to find the baseline is iterative. In `ptw`, the iteration is done until the baseline is found but if `ptw.bc` is set to FALSE, we stop after `maxIter` iterations.

More details and motivations are given in the articles mentionned in the References.

Value

If `returnBaseline` is TRUE, will return a list with the following elements: `Spectrum_data` and `Baseline`. Otherwise, the function will just return `Spectrum_data`.

`Spectrum_data` The matrix of spectra with the baseline removed.

`Baseline` Estimation of the baseline.

Author(s)

Benoît Legat, Manon Martin & Paul H. C. Eilers

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ¹H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Eilers, PHC. and Boelens, HFM. (2005). *Baseline correction with asymmetric least squares smoothing*. Leiden University Medical Centre report, 2005.

See Also

See also [SolventSuppression](#) which also uses the Whittaker smoother.

Examples

```
require(PepsNMRData)
BC_res <- BaselineCorrection(Data_HS_sp$Spectrum_data_HS_5,
                             lambda.bc=5e+06, p.bc=0.05)

#or
BC_res <- BaselineCorrection(Data_HS_sp$Spectrum_data_HS_5,
                             lambda.bc=5e+06, p.bc=0.05, returnBaseline=TRUE)
BC_spec = BC_res[["Spectrum_data"]]
plot(BC_res[["Baseline"]], type="l")
```

Bucketing	<i>Spectral data reduction</i>
-----------	--------------------------------

Description

Reduces the number of data points by aggregating intensities into buckets.

Usage

```
Bucketing(Spectrum_data, width = FALSE, mb = 500, boundary = NULL,
           intmeth = c("r", "t"), tol buck = 10^-4, verbose = FALSE)
```

Arguments

Spectrum_data	Matrix containing the spectra in ppm, one row per spectrum.
width	If width is TRUE, then m represents the buckets width, otherwise, it represents the number of buckets.
mb	The number of buckets OR the buckets' width. If mb represents the number of buckets, it should be an integer smaller or equal to the number of frequencies in Spectrum_data.
boundary	Numeric vector of left and right boundaries for ppm integration.
intmeth	Type of bucketing: rectangular ("r") or trapezoidal ("t"). See details below.
tol buck	Tolerance threshold to check if the buckets of the original spectra are of constant length.
verbose	If "TRUE", will print processing information.

Details

It is important to note that the input spectrum can have its ppm axis in increasing or decreasing order and it does not have to be equispaced.

Bucketing has two main interests:

- Ease the statistical analysis
- Decrease the impact of peaks misalignments between different spectra that should be aligned; assuming we are in the ideal case where they fall in the same bucket. Of course, the better the prior warping is, the larger m can be without major misalignment and the more informative the spectra will be.

The ppm interval of `Spectrum_data`, let's say $[a, b]$ where $a > b$, is divided into mb buckets of size $(a - b)/mb$. The new ppm scale contains the m centers of these intervals. The spectral intensity at these centers is the integral of the initial spectral intensity on this bucket using either trapezoidal or rectangular integration.

Value

`Spectrum_data` The matrix of spectra with their new ppm axis.

Author(s)

Benoît Legat, Bernadette Govaerts & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ^1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in ^1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Bucket.spec <- Bucketing(Data_HS_sp$Spectrum_data_HS_10, mb = 500)
```

Draw

Draw signals or their PCA scores/loadings.

Description

Draws FIDs, spectra or their PCA scores/loadings.

Usage

```
Draw(Signal_data, type.draw = c("signal", "pca"),
     output = c("default", "window", "png", "pdf"),
     dirpath = ".", filename = "%003d", height = 480,
     width = 640, pdf.onefile = TRUE, ...)
```

Arguments

<code>Signal_data</code>	Matrix containing the FIDs or spectra, one line per FID/spectrum.
<code>type.draw</code>	Either "signal" or "pca", which calls respectively DrawSignal or DrawPCA to do the drawing.
<code>output</code>	Specifies how to display the drawings: <code>default</code> The output is the default one. <code>window</code> Create a new window for each page. <code>png</code> Create and save a new png image for each image. <code>pdf</code> Create and save a new pdf image for each image.
<code>dirpath</code>	The path to the directory where the png or pdf are outputted.
<code>filename</code>	The filenames of the png and pdf, see argument <code>filename</code> in <code>grDevices::png</code> for more details.
<code>height</code>	Height of the png and pdf in pixels.
<code>width</code>	Width of the png and pdf in pixels.
<code>pdf.onefile</code>	When output is set to "pdf" and there are multiples pages, if <code>pdf.onefile</code> is TRUE, all the pages are in the same file and if it is FALSE all the pages are in a different pdf file.
<code>...</code>	The remaining arguments are passed either to DrawSignal or DrawPCA .

Details

Depending on the `type.draw` value, it can draw each row of `Signal_data` in a way described by subtype or the PCA scores or loadings (depending on the `type.pca` value) of all the FIDs/spectra in `Signal_data`.

Author(s)

Benoît Legat & Manon Martin

See Also

See Also [DrawSignal](#) and [DrawPCA](#).

Examples

```
# Draw each signal Real part and Mod in separate png with name end001 end002, ...
# Draw the spectra
require(PepsNMRData)
Draw(FinalSpectra_HS, type.draw = "signal",
     output="window", subtype="together")

# Draw a PCA
Draw(FinalSpectra_HS, type.draw="pca", output="window")
```

DrawPCA

Draw the PCA scores or loadings of the signals

Description

The function draws the PCA scores or loadings of the FIDs/spectra given in the matrix `Signal_data`. Do not call this function directly but rather call [Draw](#) to specify how the plot will be returned.

Usage

```
DrawPCA(Signal_data, drawNames = TRUE, main = "PCA score plot", Class = NULL,
        axes = c(1,2), type.pca = c("scores", "loadings"),
        loadingstype=c("l", "p"), num.stacked = 4, xlab = "rowname",
        createWindow)
```

Arguments

<code>Signal_data</code>	Matrix containing the FIDs or spectra, one line per FID/spectrum.
<code>drawNames</code>	If TRUE, the names of the spectra have to be shown alongside the points on the scores plot.
<code>main</code>	Plot title.
<code>Class</code>	Vector (numeric or character) indicating the class of each spectra. Used for scores plot only.
<code>axes</code>	Vector of score or loading numbers to be plotted. If it represents the score's numbers, only the first two elements are used.
<code>type.pca</code>	The type of plot, either "scores" or "loadings"
<code>loadingstype</code>	The type of loadings plot, either a line plot ("l") or points with histogram-like vertical lines ("p").
<code>num.stacked</code>	Number of stacked plots for the loadings plots.
<code>xlab</code>	Label of the x-axis of loadings plots.
<code>createWindow</code>	If TRUE, will open a new window to display the graphs.

Author(s)

Benoît Legat & Manon Martin

See Also

See also [Draw](#) and [DrawSignal](#).

Examples

```
require(PepsNMRData)
# Draw loadings
DrawPCA(FinalSpectra_HS, main = "PCA loadings plot",
        Class = NULL, axes =c(1,3, 5), type ="loadings", loadingstype="l",
        num.stacked=4, xlab="ppm", createWindow = TRUE)
```

```
# Draw scores
class = substr(rownames(FinalSpectra_HS),5,5)
DrawPCA(FinalSpectra_HS, drawNames = TRUE, main = "PCA scores plot",
        Class = class, axes = c(1,2), type = "scores", createWindow = TRUE)
```

DrawSignal

Draw Signals

Description

Depending on the subtype, will draw the different parts of the complex FIDs/spectra.

Usage

```
DrawSignal(Signal_data, subtype = c("stacked", "together", "separate",
    "diffmean", "diffmedian", "diffwith"), ReImModArg = c(TRUE,
    FALSE, FALSE, FALSE), vertical = TRUE, xlab = "index",
    RowNames = NULL, row = 1, num.stacked = 4, main = NULL,
    createWindow)
```

Arguments

Signal_data	Matrix containing the FIDs or spectra, one line per FID/spectrum.
subtype	Specifies the drawing array: together Plots all the signals in the same plot. separate Plots each signal on a different page. stacked Plots num.stacked signals on stacked plots with the same x-axis. diffmean Plots all the signals in the same plot but subtracted by their mean at each point. diffmedian Plots all the signals in the same plot but subtracted by their median at each point. diffwith Plots all the signals in the same plot but subtracted by the row th signal at each point.
ReImModArg	Specifies which of the real, imaginary, modulus, or argument part of the complex signal has to be plotted. Those plots are on the same page.
vertical	Specifies whether the parts of the complex signal have to be put vertically or horizontally on the page if there are only 2 parts. If more, there will be 2 horizontally and 2 vertically anyway.
xlab	Label of the x-axis.
RowNames	Strings to use instead of the rownames as labels for the plots if subtype = "separate". It should be a vector of the same length than the number of FIDs.
row	row to be compared to if the subtype is "diffwith".
num.stacked	Number of stacked plots if subtype is "stacked".
main	If not NULL, the main title when subtype is different from "separate".
createWindow	If TRUE, will open a new window.

Details

Don't call this function directly but rather call [Draw](#) to specify how the plot will be outputted.

Author(s)

Benoît Legat & Manon Martin

See Also

See also [Draw](#) and [DrawPCA](#).

Examples

```
require(PepsNMRData)
plots <- DrawSignal(FinalSpectra_HS[1:4,], subtype = "together",
  ReImModArg = c(TRUE, TRUE, FALSE, FALSE), createWindow = TRUE)

grid::grid.draw(plots)
```

FirstOrderPhaseCorrection

Perform a first order phase correction.

Description

The function removes the group delay at the beginning of the FIDs.

Usage

```
FirstOrderPhaseCorrection(Fid_data, Fid_info = NULL, group_delay = NULL, verbose = FALSE)
```

Arguments

Fid_data	Matrix containing the FIDs, one row per signal, as outputted by ReadFids .
Fid_info	Matrix containing the info about the FIDs, one row per signal, as outputted by ReadFids .
group_delay	If given, it is used instead of Fid_info to decide how much the FIDs must be shifted to the left. It can be non-integer, in that case the values are interpolated. However it has to be non-negative since in our practical case, it would make no sense to add a part of the end of the FID at the beginning.
verbose	If "TRUE", will print processing information.

Details

First Order Phase Correction step could also called "removal of Bruker digital filter".

Due to Bruker's digital filter and to other technical reasons a first order phase shift caused by a group delay is present in the FID and needs to be removed. Luckily, information about this delay is available when loading the FID with [ReadFids](#) and is written in Fid_info.

This function shifts circularly each FID in order to cancel this delay. By circularly, we mean that the starting portion of the FID becomes its ending portion when applied.

Each FID is shifted by the same amount since it can be non-integer and the columns names which are the time coordinates are shared between all the FIDs.

Value

`Fid_data` The matrix of FIDs corrected for the first order phase shift.

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ^1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in ^1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Fopc.fid <- FirstOrderPhaseCorrection(Data_HS_sp$FidData_HS_0,FidInfo_HS)
```

FourierTransform	<i>Applies the fourier transformation to the FIDs.</i>
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Description

The function takes the FIDs in the time domain and translate it into the frequency domain. It also converts the frequency scale from hertz to part per million (ppm).

Usage

```
FourierTransform(Fid_data, Fid_info = NULL, SW_h = NULL, SW = NULL,
  O1 = NULL, reverse.axis = TRUE, verbose = FALSE)
```

Arguments

<code>Fid_data</code>	Matrix containing the FIDs, one row per signal, as outputted by ReadFids .
<code>Fid_info</code>	Matrix containing the info about the FIDs, one row per signal, as outputted by ReadFids .
<code>SW_h</code>	Sweep Width in hertz. If given, the value in <code>Fid_info</code> is ignored.
<code>SW</code>	Sweep width in ppm. If given, the value in <code>Fid_info</code> is ignored.
<code>O1</code>	Spectrometer frequency offset. If given, the value in <code>Fid_info</code> is ignored.
<code>reverse.axis</code>	If TRUE, the frequency scale is reversed.
<code>verbose</code>	If "TRUE", will print processing information.

Details

The number of points m doesn't change and the frequency interval is from $-SW/2$ to $SW/2 - SW/m$ (the $-SW/m$ is due to the fact that we only have m points, not $m + 1$ and the fourier transform is periodic with period SW so it is the same at $-SW/2$ and $SW/2$ anyway).

SW , SW_h and $O1$ are usually taken from the `Fid_info` matrix. SW and SW_h are assumed to be the same for every FID since their column names are shared.

The frequency scale is dependent on the kind of spectrometer used, more precisely on its external magnetic field. We therefore translate it to a ppm (part per million) scale which is independent of this external magnetic field thanks to the recovered transmitter frequency offset value ($O1$).

Value

`RawSpect_data` The matrix of spectra in ppm.

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for 1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
FT.spec <- FourierTransform(Data_HS_sp$FidData_HS_3,FidInfo_HS_sp, SW_h = 12019.23)
```

GroupDelayCorrection *Perform a first order phase correction.*

Description

The function removes the group delay at the beginning of the FIDs.

Usage

```
GroupDelayCorrection(Fid_data, Fid_info = NULL, group_delay = NULL, verbose = FALSE)
```

Arguments

`Fid_data` Matrix containing the FIDs, one row per signal, as outputted by [ReadFids](#).
`Fid_info` Matrix containing the info about the FIDs, one row per signal, as outputted by [ReadFids](#).

group_delay	If given, it is used instead of Fid_info to decide how much the FIDs must be shifted to the left. It can be non-integer, in that case the values are interpolated. However it has to be non-negative since in our practical case, it would make no sense to add a part of the end of the FID at the beginning.
verbose	If "TRUE", will print processing information.

Details

First Order Phase Correction step could also called "removal of Bruker digital filter".

Due to Bruker's digital filter and to other technical reasons a first order phase shift caused by a group delay is present in the FID and needs to be removed. Luckily, information about this delay is available when loading the FID with [ReadFids](#) and is written in Fid_info.

This function shifts circularly each FID in order to cancel this delay. By circularly, we mean that the starting portion of the FID becomes its ending portion when applied.

Each FID is shifted by the same amount since it can be non-integer and the columns names which are the time coordinates are shared between all the FIDs.

Value

Fid_data	The matrix of FIDs corrected for the first order phase shift.
----------	---

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for 1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Fopc.fid <- GroupDelayCorrection(Data_HS_sp$FidData_HS_0, FidInfo_HS)
```

InternalReferencing *Chemical shift referencing.*

Description

Chemical shifts are referenced against a Reference Compound (RC, *e.g.* TMSP).

Usage

```
InternalReferencing(Spectrum_data, Fid_info, method = c("max",
  "thres"), range = c("nearvalue", "all", "window"),
  ppm.value = 0, direction = "left",
  shiftHandling = c("zerofilling", "cut", "NAfilling",
  "circular"), c = 2, pc = 0.02, fromto.RC = NULL,
  ppm.ir = TRUE, rowindex_graph = NULL, verbose = FALSE)
```

Arguments

Spectrum_data	Matrix containing the spectra in ppm, one row per spectrum.
Fid_info	Matrix containing the information for each spectrum, one row per spectrum, as returned by ReadFids .
method	Method used to find the RC peak in the spectra, See the details section.
range	How the search zone is defined. Either accross the whole ppm axis ("all"), near the 0 ppm location (nearvalue) with parameter pc, or in a manually specified area of the ppm axis ("window") with the non-null parameter fromto.RC.
ppm.value	By default, the ppm value of the reference compound is set to 0, but any arbitrary value in the ppm interval of spectra can be used instead.
direction	If method = "thres", the direction towards which to search for the RC peak.
shiftHandling	See the details section.
c	If method = "thres", parameter used to fix the threshold for the RC peak.
pc	If range = "nearvalue", percentage of the ppm axis around the ppm.value ppm value to look for the RC peak (e.g. for pc = 0.02, intensities whose index values are 0.01% below and above 0 ppm are investigated).
fromto.RC	If range = "window", a list containing numerical vectors indicating the extremities of the intervals within which to search for the RC peak. These extremities are either frequencies in ppm (decreasing values) OR in column indices (increasing values) depending on the ppm.ir value (e.g. fromto.RC = list(c(0, 10000)) if ppm.ir == FALSE or fromto.RC = list(c(1, -1)) if ppm.ir == TRUE).
ppm.ir	If TRUE, the values in fromto.RC represent frequencies in ppm (column names of spectra), if FALSE these values are column indices.
rowindex_graph	If not NULL, a numeric vector with the row numbers of spectra that need to be plotted for inspection.
verbose	If "TRUE", will print processing information.

Details

Once the search zone is defined with range, the RC is found depending on the method. If method = "thres", RC is the first peak in the spectrum higher than a predefined threshold which is computed as: $c * (\text{cumulated_mean} / \text{cumulated_sd})$. If method = "max", the maximum intensity in the search zone is defined as the RC.

Since the spectra can be shifted differently, we need to handle misalignment of the left and right of the spectrum.

This can be illustrated here:

| : TMSP peak

before

```
1 2 3 | 5 6 7 8 9
1 2 3 4 5 | 7 8 9
1 2 3 4 | 6 7 8 9
```

shifted

```
-5 -4 -3 -2 -1 0 1 2 3 4 5 : ppm scale
      1 2 3 | 5 6 7 8 9
1 2 3 4 5 | 7 8 9
      1 2 3 4 | 6 7 8 9
```

The different **shift handlings** (shiftHandling) are the following:

NAfilling The extremities at which a spectrum is not defined are replaced by NA. It is detected by [WindowSelection](#) which produces a warning if there are NAs in the selected window.

```
-5 -4 -3 -2 -1 0 1 2 3 4 5 ppm scale
NA NA 1 2 3 | 5 6 7 8 9
1 2 3 4 5 | 7 8 9 NA NA
NA 1 2 3 4 | 6 7 8 9 NA
```

zerofilling The extremities at which a spectrum is not defined are replaced by 0. It makes sense since in practice the spectrum is close to zero at the extremities.

```
-5 -4 -3 -2 -1 0 1 2 3 4 5 ppm scale
0 0 1 2 3 | 5 6 7 8 9
1 2 3 4 5 | 7 8 9 0 0
0 1 2 3 4 | 6 7 8 9 0
```

circular The spectra are shifted circularly which means that the end of a spectrum is reproduced at the beginning. It makes sense since the spectrum is periodic since it is the result of FFT.

```
-5 -4 -3 -2 -1 0 1 2 3 ppm scale
8 9 1 2 3 | 5 6 7
1 2 3 4 5 | 7 8 9
9 1 2 3 4 | 6 7 8
```

cut The ppm values for which some spectra are not defined are removed.

```
-3 -2 -1 0 1 2 3 ppm scale
1 2 3 | 5 6 7
3 4 5 | 7 8 9
2 3 4 | 6 7 8
```

The difference between these shift handlings should not be critical in practice since the extremities of the spectra are not used most of the time and are removed in [WindowSelection](#).

Value

if rowindex_graph is NULL:

Spectrum_data The matrix of the spectral value in the ppm scale.

if rowindex_graph is not NULL:

Spectrum_data The matrix of the spectral value in the ppm scale.

plots The spectra that need to be plotted for inspection.

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ¹H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
PpmConv.spec <- InternalReferencing(Data_HS_sp$Spectrum_data_HS_5,
                                     FidInfo_HS, shiftHandling = "zerofilling")
```

NegativeValuesZeroing *Zeroing of negative values.*

Description

The function sets negative intensities to zero.

Usage

```
NegativeValuesZeroing(Spectrum_data, verbose = FALSE)
```

Arguments

Spectrum_data Matrix containing the spectra in ppm, one row per spectrum.
verbose If "TRUE", will print processing information.

Details

As explained in [BaselineCorrection](#), negative values does not make sense and can have bad impacts on our statistical analyses. [BaselineCorrection](#) do its best to avoid negative intensity values but there might be some remaining.

This filter simply sets them to zero. After the [BaselineCorrection](#) they should be close to zero anyway because of the high penalty given to negative values of the signal after the correction.

Value

Spectrum_data The matrix of spectrums with the negative values set to zero.

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ^1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in ^1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Nvz.spec <- NegativeValuesZeroing(Data_HS_sp$Spectrum_data_HS_7)
```

Normalization	<i>Normalizes the spectra</i>
---------------	-------------------------------

Description

Spectra normalization to correct for the dilution factor common to all biofluid samples.

Usage

```
Normalization(Spectrum_data, type.norm, fromto.norm = c(3.05, 4.05), ref.norm = "median",
  returnFactor = FALSE, verbose = FALSE)
```

Arguments

Spectrum_data	Matrix containing the spectra in ppm, one row per spectrum.
type.norm	Different types of normalization are available: "mean", "pqn", "median", "firstquartile" or "peak". No default value is provided. See the details section for more info.
fromto.norm	Used if type.norm is "peak". See details.
ref.norm	The reference spectrum if type.norm is "pqn". See details.
returnFactor	If TRUE, returns a vector with the normalization factors.
verbose	If "TRUE", will print processing information.

Details

Normalization of spectra before their warping or their statistical analysis is necessary in order to be able to efficiently compare their relative peak intensities.

It is therefore appropriate to call this filter at the end of the preprocessing workflow.

Normalization types can be:

mean Each spectrum is divided by its mean so that its mean becomes 1.

median Each spectrum is divided by its median so that its median becomes 1.

firstquartile Each spectrum is divided by its first quartile so that its first quartile becomes 1.

peak Each spectrum is divided by the value of the peak of the spectrum contained between "fromto.norm" inclusive (*i.e.* the maximum value of spectral intensities in that interval).

pqn Probabilistic Quotient Normalization from Dieterle et al. (2006). If ref.norm is "median" or "mean", will use the median or the mean spectrum as the reference spectrum ; if it is a single number, will use the spectrum located at that row in the spectral matrix; if ref.norm is a numeric vector of length equal to the number of spectral variables, it defines manually the reference spectrum.

The choice of a proper normalisation method is a crucial although not straightforward step in a metabolomic analysis.

Applying CSN is accurate in the following situations:

- when working on human/animal sera in the case of not serious pathology, given the homeostasis principle and since no dilution effect is present.
- When working on biopsies, the "metabolome quantity" is set constant across the samples by adding a varying volume of a buffer and the same applies when working with cell media, where the quantity of cells is made constant.

To counteract all the dilution effects and the excretion differences between urine samples, the PQN approach is often recommended in the literature (Dieterle et al., 2006).

For any other situation (large difference between the groups, other kind of sample, etc.), the choice of the normalisation method is not straightforward. A solution is to refer to endogenous stable metabolites that are present in a constant quantity across samples and use them as standards to normalize all spectral profiles. For the urine samples, the creatinine has been considered as such standard (this option is also implemented in PepsNMR), even though it has been shown that the creatinine concentration could fluctuate given specific parameters (Tang et al., 2015). A review on normalization techniques for mass spectroscopy metabolomics from Wu & Li (2015) provides some guidance in the choice on the normalization approach regarding the type of sample analysed and can be transposed to the NMR spectra normalisation.

Value

Spectrum_data The matrix of normalized spectra.

Author(s)

Benoît Legat & Manon Martin

References

- Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ¹H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.
- Yiman Wu, Liang Li. (2016). *Sample normalization methods in quantitative metabolomics*, Journal of Chromatography A, Volume 1430, Pages 80-95, ISSN 0021-9673
- Tang KWA, Toh QC, Teo BW. (2015). *Normalisation of urinary biomarkers to creatinine for clinical practice and research – when and why*. Singapore Medical Journal. 56(1):7-10.
- Rousseau, R. (2011). *Statistical contribution to the analysis of metabolomics data in ¹H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).
- Dieterle, F., Ross, A., Schlotterbeck, G., and Senn, H (2006). Probabilistic Quotient Normalization as Robust Method to Account for Dilution of Complex Biological Mixtures. *Analytical Chemistry* 78 (13), 4281-4290

Examples

```
require(PepsNMRData)
Norm.spec <- Normalization(Data_HS_sp$Spectrum_data_HS_12,
                           type.norm = "mean")
```

PepsNMR-internal	<i>Internal PepsNMR Functions</i>
------------------	-----------------------------------

Description

Internal PepsNMR Functions

Details

These are not to be called by the user (or in some cases are just waiting for proper documentation to be written ...).

PreprocessingChain	<i>Preprocessing workflow for 1H-NMR data</i>
--------------------	---

Description

The function is a wrapper for all the preprocessing steps available in PepsNMR.

Usage

```
PreprocessingChain(Fid_data = NULL, Fid_info = NULL, data.path = NULL, readFids = TRUE,
  groupDelayCorr = TRUE, solventSuppression = TRUE, apodization = TRUE,
  zerofilling = TRUE, fourierTransform = TRUE, zeroOrderPhaseCorr = TRUE,
  internalReferencing = TRUE, baselineCorrection = TRUE, negativeValues0 = TRUE,
  warping = TRUE, windowSelection = TRUE, bucketing = TRUE, regionRemoval = TRUE,
  zoneAggregation = TRUE, normalization = TRUE, ..., export = FALSE,
  format = c("Rdata", "csv", "txt"), out.path = ".", filename = "filename",
  writeArg = c("none", "return", "txt"), verbose = FALSE)
```

Arguments

Fid_data	If non NULL, matrix containing the complex FIDs, one row per FID.
Fid_info	If non NULL, matrix containing the information for each spectrum, one row per spectrum, as returned by ReadFids .
data.path	A character string specifying the directory where the FIDs are searched.
readFids	If TRUE, applies the ReadFids function to the data.
groupDelayCorr	If TRUE, applies the GroupDelayCorrection function to the data.
solventSuppression	If TRUE, applies the SolventSuppression function to the data.
apodization	If TRUE, applies the Apodization function to the data.
zerofilling	If TRUE, applies the ZeroFilling function to the data.

fourierTransform	If TRUE, applies the FourierTransform function to the data.
zeroOrderPhaseCorr	If TRUE, applies the ZeroOrderPhaseCorrection function to the data.
internalReferencing	If TRUE, applies the InternalReferencing function to the data.
baselineCorrection	If TRUE, applies the BaselineCorrection function to the data.
negativeValues0	If TRUE, applies the NegativeValuesZeroing function to the data.
warping	If TRUE, applies the Warping function to the data.
windowSelection	If TRUE, applies the WindowSelection function to the data.
bucketing	If TRUE, applies the Bucketing function to the data.
regionRemoval	If TRUE, applies the RegionRemoval function to the data.
zoneAggregation	If TRUE, applies the ZoneAggregation function to the data.
normalization	If TRUE, applies the Normalization function to the data.
...	Other optionnal arguments of the above pre-processing functions.
export	If TRUE, will export the spectral intensities and the aquisition parameters matrices.
format	Format chosen to export the spectral intensities and the aquisition parameters matrices.
out.path	Path used to export the spectral intensities and the aquisition parameters matrices if export == TRUE and the function argument if writeArg == "txt".
filename	Name given to exported files.
writeArg	If not "none", will export the function arguments, either in the return of the function ("return") or as a text file ("txt").
verbose	If "TRUE", will print processing information.

Value

The function will return a list with the spectral intensities and the aquisition parameters matrices. If writeArg == "return", an additionnal list element is returned (arguments).

Spectrum_data	The pre-processed spectra.
Fid_info	The acquisition parameters.
arguments	The function arguments.

Author(s)

Manon Martin

References

- Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for 1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.
- Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
path <- system.file("extdata", package = "PepsNMRData")
data.path <- file.path(path, "HumanSerum")
res <- PreprocessingChain(Fid_data = NULL, Fid_info = NULL, data.path = data.path,
  ReadFids = TRUE, type.norm = "mean", export = FALSE, writeArg = "return")
```

ReadFids

Read FIDs in Bruker format from a directory

Description

Finds all directories of path which contain a valid FID (*i.e.* contain the files fid, acqu and acquS) and loads them in a matrix.

Usage

```
ReadFids(path, l = 1, subdirs = FALSE, dirs.names = FALSE, verbose = FALSE)
```

Arguments

path	A character string specifying the directory where the FIDs are searched.
l	A positive number indicating which line of the title file to use as spectra names.
subdirs	If TRUE, will search inside subdirectories for FIDs and will merge them to have unique FID and info matrices.
dirs.names	If TRUE, the FID names are recovered from the (sub)directories names, provided one subdirectory corresponds to one FID.
verbose	If "TRUE", will print processing information.

Details

The row names are the first line of the file "pdata/1/title" in the directory or the directory name(and subdirectory if subdirs == TRUE) if the title file doesn't exists or the line 1 is blank. The column names are the time coordinates of the FID. All the FIDs therefore need to have the same length and time interval between points.

Case 1: subdirs = FALSE

DIR1 => 1, 2, 3, ...

Case 2a: subdirs = TRUE

DIR1 => 1 ; DIR2 => 1 ; DIR3 => 1 ; ...

Case 2b: subdirs = TRUE

DIR1 => 1, 2, ... ; DIR2 => 1, 2, ... ; ...

Value

Returns a list with the FIDs and their related information.

Fid_data	The matrix containing the FIDs.
Fid_info	<p>A matrix containing the information about the FIDs. The naming of the row is the same than for Fid_data.</p> <p>The columns are:</p> <p>TD Time domain size</p> <p>BYTORDA Determine the endianness of stored data. If 0 -> Little Endian; if 1 -> Big Endian</p> <p>DIGMOD Digitization mode</p> <p>DECIM Decimation rate of digital filter</p> <p>DSPFVS DSP firmware version</p> <p>SW_h Sweep width in Hz</p> <p>SW Sweep width in ppm</p> <p>O1 Spectrometer frequency offset</p> <p>GPRDLY Group Delay</p> <p>DT Dwell time in microseconds</p>

Author(s)

Benoît Legat & Manon Martin

Examples

```
path <- system.file("extdata", package = "PepsNMRData")
dir(path)

fidList_HS <- ReadFids(file.path(path, "HumanSerum"))
FidData_HS_0 <- fidList_HS[["Fid_data"]]
FidInfo_HS <- fidList_HS[["Fid_info"]]
```

RegionRemoval

Removal of non-informative regions

Description

Removes the non-informative regions by setting the values of the spectra in these intervals to zero.

Usage

```
RegionRemoval(Spectrum_data, typeofspectra = c("manual", "serum", "urine"),
              type.rr = c("zero", "NA"),
              fromto.rr = list(Water = c(4.5, 5.1)), verbose = FALSE)
```

Arguments

<code>Spectrum_data</code>	Matrix containing the spectra in ppm, one row per spectrum.
<code>typeofspectra</code>	Type of spectra, if not "manual", will automatically remove unwanted regions depending on the nature of spectra.
<code>type.rr</code>	Type of region removal method. If <code>type.rr = "zero"</code> , intensities are set to 0; if <code>type.rr = "NA"</code> , intensities are set to NA.
<code>fromto.rr</code>	List containing the extremities of the intervals to be removed.
<code>verbose</code>	If "TRUE", will print processing information.

Details

The presence of non-informative regions can strongly bias the subsequent statistical analysis.

The inclusive ppm interval `fromto.rr` is set to zero or completed with NAs for every spectrum. The ppm scale can be increasing or decreasing (i.e. `from < to` or `from > to`).

The type of spectra can be NULL to manually specify the area to be removed otherwise it is specified as `typeofspectra = "serum"` or `typeofspectra = "urine"` and the removed area are for `typeofspectra = "serum"`: water (4.5 - 5.1 ppm) and for `typeofspectra = "urine"`: water, uree and maleic acid (4.5 - 6.1 ppm).

Value

`Spectrum_data` The matrix of spectra with the removed regions.

Author(s)

Benoît Legat & Manon Martin

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for 1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
# Remove the lactate and water regions for serum spectra
require(PepsNMRData)
fromto <- list(Water =c(4.5, 5.1), Lactate=c(1.32, 1.36))
Rr.spec <- RegionRemoval(Data_HS_sp$Spectrum_data_HS_11,fromto.rr = fromto)
```

SolventSuppression	<i>Suppress the Solvent signal present in each FID.</i>
--------------------	---

Description

Signal smooting for water residuals resonance removal.

Usage

```
SolventSuppression(Fid_data, lambda.ss = 1e6, ptw.ss = TRUE,
  returnSolvent = FALSE, verbose = FALSE)
```

Arguments

Fid_data	Matrix containing the FIDs, one row per signal, as outputted by ReadFids .
lambda.ss	Penalty on roughness used to calculate the smoothed version of the FID. The higher lambda is, the smoother the estimated solvent signal will be.
ptw.ss	If TRUE, calculates the solvent signal in C using the ptw package which is a lot faster. The R version is only kept in case of problems with the installation of ptw.
returnSolvent	If TRUE, returns a list with the resulting FIDs, the real and imaginary parts of the estimated solvent signal, see the examples.
verbose	If "TRUE", will print processing information.

Details

FIDs usually present a wavy shape. Under the assumption that water is the main compound of the analyzed samples, its signal can be modelled by the smoothing of the FIDs. We then subtract this wave, *i.e.* the solvent residuals resonance signal, from the original FIDs.

The smoothing is done with a Whittaker smoother which is obtained by the minimization of

$$V + \lambda R$$

where

- V is the sum of the squared differences between the original and the smoothed signal.
- R measures the roughness of the estimated signal.

The larger λ is, the smoother the solvent residuals resonance signal. Eilers (2003) and Frasso & Eilers (2015) suggest different ways to tune λ in order to optimise the smoothing: either visually, by cross-validation or using the V-curve procedure.

Value

If returnSolvent = TRUE, will return a list with the following elements: Fid_data, SolventRe and SolventIm. Otherwise, the function will just return Fid_data.

Fid_data	The matrix of FIDs with the solvent residuals signal removed.
SolventRe	The real part of the solvent signal.
SolventIm	The imaginary part of the solvent signal.

Author(s)

Benoît Legat, Manon Martin & Paul H. C. Eilers

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for 1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Frasso, G., & Eilers, P.H.C. (2015). L-and V-curves for optimal smoothing. *Statistical Modelling*, 15(1), 91-111.

Rousseau, R. (2011). Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy. PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium.

Eilers, P.H.C. (2003). A perfect smoother. *Analytical Chemistry*, 75(14), 3631-3636.

See Also

See also [BaselineCorrection](#) which also uses the Whittaker smoother.

Examples

```
require(PepsNMRData)
Ss.fid <- SolventSuppression(Data_HS_sp$FidData_HS_1, returnSolvent=FALSE)

#or
Ss.res <- SolventSuppression(Data_HS_sp$FidData_HS_1, returnSolvent=TRUE)
Ss.fid = Ss.res[["Fid_data"]]
SolventRe = Ss.res[["SolventRe"]]
plot(SolventRe[1,], type="l")
```

Warping

Warping of the spectra

Description

Warp the frequency x -axis to minimize the pairwise distance between a sample spectrum and a reference spectrum.

Usage

```
Warping(Spectrum_data, normalization.type = c("median", "mean",
  "firstquartile", "peak", "none"), fromto.normW = c(3.05, 4.05),
  reference.choice = c("fixed", "before",
  "after", "manual"), reference = 1, optim.crit = c("RMS", "WCC"),
  ptw.wp = FALSE, K = 3, L = 40, lambda.smooth = 0, deg = 3,
  lambda.bspline = 0.01, kappa = 0.0001, max_it_Bspline = 10,
  returnReference = FALSE, returnWarpFunc = FALSE, verbose = FALSE)
```

Arguments

<code>Spectrum_data</code>	Matrix containing the spectra in ppm, one row per spectrum.
<code>normalization.type</code>	Type of normalization applied to the spectra prior to warping. See Normalization for details about the different types. <code>none</code> means that no normalization is applied. It is advised to use <code>median</code> instead of the default <code>mean</code> normalization.
<code>fromto.normW</code>	Used by Normalization when <code>normalization.type</code> is <code>peak</code> .
<code>reference.choice</code>	Specifies how the reference will be chosen: <code>"fixed"</code> The reference is specified by the rowname given in <code>reference</code> . <code>"before"</code> The reference is taken as the spectrum with the minimum sum of square difference with the other spectra. <code>"after"</code> Each spectrum is taken as the reference and the sum of square difference with the other spectra is calculated after the warping. See details below. <code>"manual"</code> The reference spectrum is specified in the <code>reference</code> argument.
<code>reference</code>	The row number or name of the reference spectrum when <code>reference.choice</code> is <code>"fixed"</code> or a numeric vector with the reference spectrum when <code>reference.choice</code> is <code>"manual"</code> .
<code>optim.crit</code>	If <code>ptw.wp</code> is set to <code>TRUE</code> , <code>WCC</code> can also be considered as a criterion for optimization, see <code>ptw: :ptw</code> for details.
<code>ptw.wp</code>	If set to <code>TRUE</code> , it applies the Parametric Time Warping with the <code>ptw: :ptw</code> function to the data. In this case, the warping does not use B-splines and the arguments <code>L</code> , <code>deg</code> , <code>lambda.bspline</code> , <code>kappa</code> and <code>max_it_Bspline</code> are ignored.
<code>K</code>	It is the degree of the polynomial used for the warping (see details).
<code>L</code>	This is the number of B-splines that are used for the warping. It should be either 0 or greater than <code>deg</code> .
<code>lambda.smooth</code>	Nonnegative coefficient for the smoothing <code>lambda.smooth = 0</code> means no smoothing. See <code>ptw: :difsm</code> for more details.
<code>deg</code>	Degree of the B-splines.
<code>lambda.bspline</code>	Nonnegative second-order smoothness penalty coefficient for the B-splines warping. See the reference for more details.
<code>kappa</code>	Nonnegative ridge (zero-order) penalty coefficient for the B-splines warping. See the reference for more details.
<code>max_it_Bspline</code>	Maximum number of iterations for the B-splines warping.
<code>returnReference</code>	If <code>TRUE</code> , will return the name of the reference spectrum.
<code>returnWarpFunc</code>	If <code>TRUE</code> , will return the warping functions.
<code>verbose</code>	If <code>"TRUE"</code> , will print processing information.

Details

When `reference.choice` is `"after"`, the reference with the minimum sum is taken as the reference and the warped spectra according to this reference (that have already been calculated at this stage) are returned. This is n times slower than the 2 others where n is the number of spectra.

Principle:

We try to find a warping function between a reference spectrum and a sample. This function is a sum of polynomial of degree K and L B-splines of degree deg . The unknowns are the polynomial and B-splines coefficients.

No warping is equivalent to warping with a , the polynomial identity and all the coefficients of the B-splines with value 0. See the reference for details.

First, the polynomial is estimated on the reference and the sample both smoothed with parameter `lambda.smooth`. The B-splines are estimated on the non-smoothed reference and sample using the polynomial just found.

The higher `lambda.bspline` and `kappa` are, the less flexible the warping function will be.

Value

If `returnReference = TRUE`, the function will return the name of the reference spectrum and if `returnWarpingfunc = TRUE`, it will also return the warping functions.

<code>Spectrum_data</code>	The warped spectra.
<code>Reference</code>	The name of the reference spectrum.
<code>Warpingfunc</code>	The warping functions.

Author(s)

Benoît Legat, Manon Martin & Paul H. C. Eilers

References

Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ^1H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.

Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in ^1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Warp.spec <- Warping(Data_HS_sp$Spectrum_data_HS_8, reference.choice="fixed",
                    reference = row.names(Data_HS_sp$Spectrum_data_HS_8)[1],
                    returnReference = FALSE)

#or
Warp.res <- Warping(Data_HS_sp$Spectrum_data_HS_8, reference.choice="fixed",
                  reference = row.names(Data_HS_sp$Spectrum_data_HS_8)[1],
                  returnReference = TRUE)

Warp.spec <- Warp.res[["Spectrum_data"]]
Warp.res[["Reference"]]
```

WindowSelection	<i>Spectral window selection</i>
-----------------	----------------------------------

Description

Selects an interval in the ppm scale and returns the value of the spectra in that interval.

Usage

```
WindowSelection(Spectrum_data, from.ws = 10, to.ws = 0.2, verbose = FALSE)
```

Arguments

Spectrum_data	Matrix containing the spectra in ppm, one row per spectrum.
from.ws	The left ppm value of the interval. A typical value is 10. If NULL, default value is the first index without NA.
to.ws	The right ppm value of the interval. A typical value is 0.2. If NULL, default value is the last index without NA.
verbose	If "TRUE", will print processing information.

Details

If from.ws and/or to.ws are not specified we calculate it so that we have the largest window without NA. Those NAs are typically produced by the InternalReferencing function.

Value

Spectrum_data The matrix of the value of the spectra in the specified interval.

Author(s)

Benoît Legat & Manon Martin

Examples

```
require(PepsNMRData)
# The interval is chosen so that we have the largest interval without NA
Ws.spec <- WindowSelection(Data_HS_sp$Spectrum_data_HS_9)

# or
Ws.spec <- WindowSelection(Data_HS_sp$Spectrum_data_HS_9, from.ws=10, to.ws=0.2)
```

ZeroFilling

*Zero Filling***Description**

The function applies zero filling to the FIDs.

Usage

```
ZeroFilling(Fid_data, fn = ncol(Fid_data), verbose = FALSE)
```

Arguments

Fid_data	Matrix containing the FIDs, one row per signal, as outputted by ReadFids .
fn	Number of 0 to be added.
verbose	If "TRUE", will print processing information.

Details

Zero filling does not improve the spectral resolution but lead to better visually defined lines in the spectra. During zero filling, fn zeros are appended at the end of the FIDs. This number is rounded to the nearest 2^x value to ease the upcoming Fourier Transform of the FIDs.

Value

Fid_data	The zero-filled FIDs.
----------	-----------------------

Author(s)

Manon Martin

Examples

```
require(PepsNMRData)
ZF_fid <- ZeroFilling(Data_HS_sp$FidData_HS_3, fn = ncol(Data_HS_sp$FidData_HS_3))
```

ZeroOrderPhaseCorrection

*Zero Order Phase Correction***Description**

The function corrects the spectra in order to have their real part in an absorptive mode.

Usage

```
ZeroOrderPhaseCorrection(Spectrum_data, type.zopc = c("rms", "manual", "max"),
  plot_rms = NULL, returnAngle = FALSE,
  createWindow = TRUE, angle = NULL, plot_spectra = FALSE,
  ppm.zopc = TRUE, exclude.zopc = list(c(5.1,4.5)), verbose = FALSE)
```


Arguments

<code>Spectrum_data</code>	Matrix containing the spectra in ppm, one row per spectrum.
<code>type.zopc</code>	Method used to select the angles to rotate the spectra. See details.
<code>plot_rms</code>	Contains a vector of row names for which a debug plot should be made showing the value of the function we try to minimize as a function of the phase.
<code>returnAngle</code>	If TRUE, will return the rotation angle used for phase correction.
<code>createWindow</code>	If TRUE, will open a new window to draw the rms or spectra plots, if FALSE, plots are drawn in the current device.
<code>angle</code>	If not NULL, a numeric vector with angles specified in radian to manually rotate the spectra, one angle per spectrum. By convention, the spectra are rotated with the correction angle - angle.
<code>plot_spectra</code>	If TRUE, will draw real and imaginary parts of the rotated spectra.
<code>ppm.zopc</code>	If TRUE, the values in <code>exclude.zopc</code> represent frequencies in ppm value (column names of spectra), if FALSE these values are column indices.
<code>exclude.zopc</code>	If not NULL, a list containing the extremities of the intervals excluded for the computation of the positiveness criterion, either expressed in ppm (decreasing values) OR in column indices (increasing values), e.g. <code>exclude.zopc = list(c(0,10000))</code> if <code>ppm.zopc == FALSE</code> or <code>exclude.zopc = list(c(1,-1))</code> if <code>ppm.zopc == TRUE</code> .
<code>verbose</code>	If "TRUE", will print processing information.

Details

We focus our optimization on the positiveness of the real part which should be in an absorptive mode.

When `type.zopc` is "rms", a positiveness criterion is measured for each spectrum. "manual" is used when a vector of angles are specified in `angle` and "max" will optimize the maximum spectral intensity in the non-excluded window(s). Beware that if `exclude.zopc` is not NULL, the optimization will only consider the non-excluded spectral window(s).

By default the water region (5.1 - 4.5) is ignored.

[BaselineCorrection](#) and [NegativeValuesZeroing](#) will take care of the last negative values of the real part of the spectra. See the reference for more details.

Value

`Spectrum_data` The matrix of rotated spectra.

Author(s)

Benoît Legat & Manon Martin

References

- Martin, M., Legat, B., Leenders, J., Vanwinsberghe, J., Rousseau, R., Boulanger, B., & Govaerts, B. (2018). PepsNMR for ¹H NMR metabolomic data pre-processing. *Analytica chimica acta*, 1019, 1-13.
- Rousseau, R. (2011). *Statistical contribution to the analysis of metabonomics data in 1H NMR spectroscopy* (Doctoral dissertation, PhD thesis. Institut de statistique, biostatistique et sciences actuarielles, Université catholique de Louvain, Belgium).

Examples

```
require(PepsNMRData)
Zopc.res <- ZeroOrderPhaseCorrection(Data_HS_sp$Spectrum_data_HS_4,
  ppm.zopc = FALSE, exclude.zopc = list(c(5000,15000)))
```

ZoneAggregation

Aggregates the values in a given ppm interval.

Description

The function replaces the values given in specified intervals by triangular shaped peaks with the same area than the original peaks.

Usage

```
ZoneAggregation(Spectrum_data, fromto.za = list(Citrate = c(2.5, 2.7)), verbose = FALSE)
```

Arguments

Spectrum_data Matrix containing the spectra in ppm, one row per spectrum.
 fromto.za List containing the borders in ppm of the intervals to aggregate.
 verbose If "TRUE", will print processing information.

Details

The interval is specified in the unit of the column names (which should be ppm). This aggregation is usually performed with urine samples that contains citrate.

Value

Spectrum_data The matrix of spectra with their zone aggregated.

Author(s)

Benoît Legat & Manon Martin

Examples

```
require(PepsNMRData)
Spectrum_data <- ZoneAggregation(Data_HU_sp$Spectrum_data_HU_12,
  fromto.za = list(Citrate = c(2.5, 2.7)))
```

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