

Package ‘mrbin’

April 27, 2022

Title Magnetic Resonance Binning, Integration and Normalization

Version 1.6.4

Description Nuclear Magnetic Resonance is widely used for metabolite analysis. This package is a collection of functions for processing and analyzing metabolite data. (<[doi:10.1021/acs.jproteome.0c00684](https://doi.org/10.1021/acs.jproteome.0c00684)>). The namesake function converts 1D or 2D data into a matrix of values suitable for further data analysis and performs basic processing steps in a reproducible way. Negative values, a common issue in such data, are replaced by positive values. All used parameters are stored in a readable text file and can be restored from that file to enable exact reproduction of the data at a later time.

Imports grDevices, graphics, stats, utils

Depends R (>= 2.10)

License GPL-3

Encoding UTF-8

RoxygenNote 7.1.1

Suggests parallel

VignetteBuilder utils

URL <http://www.kleinomicslab.com/software/>,
<https://github.com/kleinomicslab/mrbin>

NeedsCompilation no

Author Matthias Klein [aut, cre] (<<https://orcid.org/0000-0001-7455-5381>>)

Maintainer Matthias Klein <klein.663@osu.edu>

Repository CRAN

Date/Publication 2022-04-27 13:30:14 UTC

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addToPlot	<i>A function for adding NMR spectra to the plot list.</i>
-----------	--

Description

This function adds a spectrum to the plot list.

Usage

```

addToPlot(
  folder = NULL,
  dimension = "1D",
  NMRvendor = "Bruker",
  useAsNames = "Folder names",
  add = TRUE
)

```

Arguments

folder	Defines the exact NMR data folder. If NULL, mrbin parameter set is used
dimension	Defines the data dimension, "1D" or "2D". Only used if not NULL
NMRvendor	Defines the NMR manufacturer, default is "Bruker"
useAsNames	How should sample names be generated
add	Add spectra to existing list, or replace existing spectra. Default is TRUE

Value

none

Examples

```
addToPlot()
```

atnv

A function replacing negative values.

Description

This function replaces (column-wise) negative values by a small positive number. The number is calculated as an affine transformation to the range of the lowest positive number to 0,01*the lowest positive number (of this column). Ranks stay unchanged. Positive numbers are not altered. If sample-wise noise levels are available, the median noise level of samples with negative values is calculated and replaces the lowest positive number in case it is smaller. If no noise data is available, the 1 positive values in the data set is used as an estimate. It is recommended to use this function AFTER noise removal and other data clean-up methods, as it may alter (reduce) the noise level. If no NMR data and noise levels are provided as arguments, the function will use NMR data and noise levels from the global variables mrbin.env\$bins and mrbin.env\$mrbinTMP.

Usage

```
atnv(NMRdata = NULL, noiseLevels = NULL)
```

Arguments

NMRdata A matrix containing NMR data. Columns=frequencies,rows=samples
 noiseLevels A vector

Value

NMRdata An invisible matrix containing NMR data without negative values.

Examples

```

resetEnv()
Example<-mrbin(silent=TRUE,
               parameters=list(verbose=TRUE,dimension="1D",PQNScaling="No",
                               binwidth1D=0.005,signal_to_noise1D=1,PCA="No",binRegion=c(9.5,7.5,10,156),
                               saveFiles="No",referenceScaling="No",noiseRemoval="No",
                               fixNegatives="No",logTrafo="No",noiseThreshold=.05,
                               NMRfolders=c(system.file("extdata/2/10/pdata/10",package="mrbin"),
                                             system.file("extdata/3/10/pdata/10",package="mrbin")))
               ))
sum(Example$bins<=0)
exampleNMRpositive<-atnv(NMRdata=Example$bins, noiseLevels=Example$parameters$noise_level)
sum(exampleNMRpositive<=0)

```

 contMin

A function for changing plotNMR plots.

Description

This function decreases the minimum contour level of the current 2D NMR spectrum plot.

Usage

```
contMin(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()
mrbin(silent=TRUE,parameters=list(dimension="2D",binwidth2D=0.5,
    binheight=3,PQNScaling="No",referenceScaling="No",binRegion=c(4,3,60,65),
    noiseRemoval="No",trimZeros="No",cropHSQC="No",
    fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,saveFiles="No",
    NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin"))))
plotNMR()
contMin()
```

contPlus	<i>A function for changing plotNMR plots.</i>
----------	---

Description

This function increases the minimum contour level of the current 2D NMR spectrum plot.

Usage

```
contPlus(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()
readBruker(folder=system.file("extdata/1/12/pdata/10",package="mrbin"),dimension="2D")
plotNMR()
contPlus()
```

cropNMR	<i>A function for cropping HSQC spectra.</i>
---------	--

Description

This function crops HSQC spectra to the region along the diagonal to remove uninformative signals. Will work only for 1H-13C HSQC spectra.

Usage

```
cropNMR(plot = FALSE)
```

Arguments

plot Should a plot of the bins before and after cropping be shown? Defaults to FALSE.

Value

None

Examples

```
resetEnv()
Example<-mrbin(silent=TRUE,
  parameters=list(dimension="2D",binwidth2D=1,binheight=4,cropHSQC="No",PCA="No",
  PQNScaling="No",noiseRemoval="No",removeSolvent="No",verbose=TRUE,
  NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin")))
cropNMR()
```

down *A function for changing plotNMR plots.*

Description

This function moves down the plot region of the current NMR plot (only 2D).

Usage

```
down(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()
mrbin(silent=TRUE,parameters=list(dimension="2D",binwidth2D=0.5,
  binheight=3,PQNScaling="No",referenceScaling="No",binRegion=c(4,3,60,65),
  noiseRemoval="No",trimZeros="No",cropHSQC="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,saveFiles="No",
  NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin")))
plotNMR()
zoomIn()
down()
```

fia *A function identifying features of importance.*

Description

This function finds features that can change the outcomes of a model's prediction. Example: fia=1.00 means single compound found in all but 0 percent of samples. fia=2.45 indicates this compound is found in pairs in all but 45 percent of tested samples A function named predict needs to be present for this to work. If the function name of the prediction function is different, the function name has to be provided in the parameter functionNamePredict.

Usage

```
fia(  
  model,  
  dataSet,  
  factors,  
  nSeed = 6,  
  numberOfSamples = 100,  
  maxFeatures = 10000,  
  innerLoop = 100,  
  verbose = TRUE,  
  maxNumberAllTests = 5,  
  firstLevel = 1,  
  saveMemory = FALSE,  
  functionNamePredict = "predict",  
  parameterNameObject = "object",  
  parameterNameData = "x",  
  ...  
)
```

Arguments

model	A predictive model. Make sure to have loaded all required packages before starting this function
dataSet	An object containing data, columns=features, rows=samples. This should be either a matrix or a dataframe, depending on which of these two the specific prediction function requires
factors	A factor vector with group membership of each sample in the data set. Order of levels must correspond to the number predicted by the model
nSeed	Number of times that the test will be repeated, selecting different random features
numberOfSamples	Number of samples that will be randomly chosen from each group
maxFeatures	Maximum number of features that will be tested. Larger numbers will be split into child nodes without testing to increase speed

innerLoop	Number of repeated loops to test additional child nodes
verbose	A logical vector to turn messages on or off
maxNumberAllTests	Combinations of features of this length or shorter will not be split in half to create two children, but into multiple children with one feature left out each. This is done make sure no combination is missed.
firstLevel	Numeric value of first level or group. Usually 1 but for glm such as in the example this needs to be 0.
saveMemory	Save memory by performing predictions one by one, which will be slower.
functionNamePredict	The name of the prediction function. This only needs to be changed if the prediction function is not called predict
parameterNameObject	The name of the parameter for passing the model to the prediction function
parameterNameData	The name of the parameter for passing the data to the prediction function
...	Optional, additional parameters that will be passed to the prediction function.

Value

A list of results: scores contains vectors of fia scores for each predicted group; scoresSummary A vector of fia scores for all predicted sample; fiaListPerSample A list of important combinations of features for each predicted sample; fiaMatrix A list of fia scores for each predicted group.

Examples

```
#First, define group membership and create the example feature data
group<-factor(c(rep("Group1",4),rep("Group2",5)))
names(group)<-paste("Sample",1:9,sep="")
dataset<-data.frame(
  Feature1=c(5.1,5.0,6.0,2.9,4.8,4.6,4.9,3.8,5.1),
  Feature2=c(2.6,4.0,3.2,1.2,3.1,2.1,4.5,6.1,1.3),
  Feature3=c(3.1,6.1,5.8,5.1,3.8,6.1,3.4,4.0,4.4),
  Feature4=c(5.3,5.2,3.1,2.7,3.2,2.8,5.9,5.8,3.1),
  Feature5=c(3.2,4.4,4.8,4.9,6.0,3.6,6.1,3.9,3.5)
)
rownames(dataset)<-names(group)
#train a model - here we use a logit model instead of ANN as a demonstration
mod<-glm(group~Feature1+Feature2+Feature3+Feature4+Feature5,
  data=data.frame(group=group,dataset),family="binomial")
fiaResults<-fia(model=mod,dataSet=dataset,factors=group,parameterNameData="newdata",
  firstLevel=0,type="response")
fiaResults$scores
```

getEnv	<i>A function for saving the package environment.</i>
--------	---

Description

This function returns a list of all objects of the current package environment. This may be helpful for debugging or for accessing NMR spectral data and the raw bin data.

Usage

```
getEnv()
```

Value

A list containing all objects from the local package environment.

Examples

```
tempList<-getEnv()
```

intMin	<i>A function for changing plotNMR plots.</i>
--------	---

Description

This function decreases the intensity of the current NMR spectrum plot.

Usage

```
intMin(dimension = "1D", refreshPlot = TRUE, value = NULL)
```

Arguments

dimension	Dimension to use. Defaults to "1D"
refreshPlot	Refresh plot automatically. Defaults to TRUE
value	Set exact value. Defaults to NULL

Value

None

Examples

```
mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
intMin()
```

intPlus

A function for changing plotNMR plots.

Description

This function increases the intensity of the current NMR spectrum plot.

Usage

```
intPlus(dimension = "1D", refreshPlot = TRUE)
```

Arguments

dimension	Dimension to use. Defaults to "1D"
refreshPlot	Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
intPlus()
```

left	<i>A function for changing plotNMR plots.</i>
------	---

Description

This function moves left the plot region of the current NMR plot.

Usage

```
left(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()
mrbin(silent=TRUE,parameters=list(dimension="1D",binwidth1D=.5,
  noiseRemoval="No",trimZeros="No",
  PQNScaling="No",saveFiles="No",referenceScaling="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
zoomIn()
left()
```

logTrafo	<i>A function for log transforming data.</i>
----------	--

Description

This function simply log transforms. Will not work with negative data.

Usage

```
logTrafo()
```

Value

None

Examples

```

resetEnv()
mrbinExample<-mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D", logTrafo="No",
  binwidth1D=0.05,signal_to_noise1D=50, verbose=TRUE, PCA="No",
  NMRfolders=c(system.file("extdata/1/10/pdata/10",package="mrbin"),
    system.file("extdata/2/10/pdata/10",package="mrbin"))))
logTrafo()

```

mrbin	<i>A function setting the parameters and performing binning and data processing</i>
-------	---

Description

This function guides the user through the set-up of parameters, starts binning and performs the chosen data processing steps. If a list of parameters is provided and silent is set to TRUE, no user input is requested and binning and data processing are performed silently.

Usage

```
mrbin(silent = FALSE, setDefault = FALSE, parameters = NULL)
```

Arguments

silent	If TRUE, the user will be asked no questions and binning and data analysis will run according to the current parameters. Defaults to FALSE.
setDefault	If TRUE, all current parameters will be replaced by the default parameters (before loading any provided parameters sets). Defaults to FALSE.
parameters	Optional: A list of parameters, see examples for details. If omitted, the user will be asked through a series of question to set the parameters.

Value

An invisible list containing bins (data after processing), parameters, and factors

Examples

```

# Set parameters in command line.
mrbinExample<-mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",
  binwidth1D=0.01,signal_to_noise1D=25,
  NMRfolders=c(system.file("extdata/1/10/pdata/10",package="mrbin"),
    system.file("extdata/2/10/pdata/10",package="mrbin"),
    system.file("extdata/3/10/pdata/10",package="mrbin")),
  Factors=factor(c("Group A","Group A","Group B"))))

```

mrbinrun *A function performing all data read and processing steps.*

Description

This function reads parameters from the global variable `mrbin.env$mrbinparam` and performs the following operations: Reading NMR files, creating bins, removing solvent area, removing additional user-defined areas, summing up bins that contain unstable peaks such as citric acid, removes noise bins, crops HSQC spectra to the diagonal area, performs PQN scaling, replaces negative values, log transforms and displays a PCA plot. Parameters are then saved in a text file. These can be recreated using `recreatemrbin()`.

Usage

```
mrbinrun()
```

Value

None

Examples

```
resetEnv()
setParam(parameters=list(dimension="2D",binwidth2D=0.1,binheight=4,
  binRegion=c(8,1,15,140),PQNScaling="No",
  fixNegatives="No",logTrafo="No",signal_to_noise2D=10,solventRegion=c(5.5,4.2),
  NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin"),
    system.file("extdata/2/12/pdata/10",package="mrbin"))))
mrbinrun()
```

mrplot *A function for plotting NMR spectra.*

Description

This function plots NMR spectra. A menu of commands is displayed to edit the plot view and add spectra. Multiple spectra will be overlaid, and if both 1D and 2D spectra are selected, they are shown in two plots with matched ranges.

Usage

```
mrplot(
  hideMenu = FALSE,
  folders = NULL,
  dimensions = NULL,
  intensity1D = NULL,
  zoom = NULL
)
```

Arguments

hideMenu	Do not show the menu. Defaults to FALSE
folders	Optional vector of folder names of spectra to load. Defaults to NULL
dimensions	Optional vector dimensions of spectra to load. Defaults to NULL
intensity1D	Optional value of initial 1D intensity. Defaults to NULL
zoom	Optional vector of initial zoom area. Defaults to NULL

Value

None

Examples

```

resetEnv()
mrplot(folders=c(system.file("extdata/1/12/pdata/10", package="mrbin"),
                        system.file("extdata/1/10/pdata/10", package="mrbin"),
                        system.file("extdata/2/10/pdata/10", package="mrbin"),
                        system.file("extdata/3/10/pdata/10", package="mrbin")),
        dimensions=c("2D", "1D", "1D", "1D"), zoom=c(2.8, 2.3, 20, 55),
        intensity1D=32, hideMenu=TRUE)

```

plotMultiNMR

A function for plotting NMR spectra.

Description

This function plots the current NMR spectrum. If no parameters are provided, parameters are read from the mrbin.env environment variables, set by mrbin. To change the plot, use zoom(), zoomIn(), zoomOut(), intPlus(), intMin(), left(), right(). For 2D data use additionally: contMin(), contPlus(), up(), down()

Usage

```

plotMultiNMR(
  region = NULL,
  rectangleRegions = NULL,
  rectangleColors = c("green", "orange", "blue", "red", "yellow", "gray", "purple"),
  rectangleFront = FALSE,
  polygonRegion = NULL,
  color = NULL,
  add = FALSE,
  showGrid = FALSE,
  manualScale = TRUE,
  plotTitle = "",
  restrictToRange = FALSE
)

```

Arguments

region	A vector defining the plot region (left, right, top, bottom)
rectangleRegions	A 4-column matrix defining areas where to plot rectangles
rectangleColors	Define colors for the rectangles
rectangleFront	Plot rectangles in front of spectrum rather than in background (only 2D)
polygonRegion	Defines 4 corners of a polygon to be plotted
color	Defines the color of the spectrum plot. If NULL, a rainbow theme is used for 2D NMR
add	If TRUE, additional spectrum plots are overlaid with the current plot
showGrid	Shows a grid of data points. Defaults to FALSE
manualScale	If TRUE, scaling factor is taken from environment variables
plotTitle	Defines the main title of the plot
restrictToRange	Restrict plot area to range of available data points. Defaults to FALSE

Value

None

Examples

```

mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotMultiNMR()

```

plotNMR

A function for plotting NMR spectra.

Description

This function plots the current NMR spectrum. If no parameters are provided, parameters are read from the `mrbin.env` environment variables, set by `mrbin`. To change the plot, use `zoom()`, `zoomIn()`, `zoomOut()`, `intPlus()`, `intMin()`, `left()`, `right()`. For 2D data use additionally: `contMin()`, `contPlus()`, `up()`, `down()`

Usage

```
plotNMR(
  region = NULL,
  rectangleRegions = NULL,
  rectangleColors = c("green", "orange", "blue", "red", "yellow", "gray", "purple"),
  rectangleFront = FALSE,
  polygonRegion = NULL,
  color = NULL,
  add = FALSE,
  showGrid = FALSE,
  manualScale = TRUE,
  plotTitle = "",
  restrictToRange = FALSE,
  currentSpectrumOriginal = NULL
)
```

Arguments

region	A vector defining the plot region (left, right, top, bottom)
rectangleRegions	A 4-column matrix defining areas where to plot rectangles
rectangleColors	Define colors for the rectangles
rectangleFront	Plot rectangles in front of spectrum rather than in background (only 2D)
polygonRegion	Defines 4 corners of a polygon to be plotted
color	Defines the color of the spectrum plot. If NULL, a rainbow theme is used for 2D NMR
add	If TRUE, additional spectrum plots are overlaid with the current plot
showGrid	Shows a grid of data points. Defaults to FALSE
manualScale	If TRUE, scaling factor is taken from environment variables
plotTitle	Defines the main title of the plot
restrictToRange	Restrict plot area to range of available data points. Defaults to FALSE
currentSpectrumOriginal	Optional spectral data. If omitted, data from the environment variables is used

Value

None

Examples

```
mrbin(silent=TRUE, setDefault=TRUE, parameters=list(dimension="1D", binwidth1D=.1,
  PQNScaling="No", noiseRemoval="No", trimZeros="No",
  fixNegatives="No", logTrafo="No", PCA="No", verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10", package="mrbin")))
plotNMR()
```

`plotResults`*A function for plotting quality indicators, including PCA plots.*

Description

This function plots boxplots (bin-wise and sample-wise) as visual quality indicators. It also performs PCA, then plots PC1 and PC2 and loading plots.

Usage

```
plotResults()
```

Value

None

Examples

```
mrbinExample<-mrbin(silent=TRUE,setDefault=FALSE,parameters=list(dimension="2D",
  binRegion=c(8,1,15,140),binwidth2D=0.1,binheight=4,solventRegion=c(5.5,4.2),
  PQNScaling="No",noiseRemoval="Yes",trimZeros="Yes",
  fixNegatives="No",logTrafo="No",PCA="No",signal_to_noise2D=10,
  NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin"),
    system.file("extdata/2/12/pdata/10",package="mrbin")))
plotResults()
```

`PQNScaling`*A function for PQN scaling.*

Description

This function performs PQN scaling. To further exclude unreliable noise, only the most intense signals are used. For 1H and 1H-13C HSQC spectra, most of the sugar regions can be excluded to avoid a dominating effect of the multiple glucose signals.

Usage

```
PQNScaling(
  NMRdata = NULL,
  ignoreGlucose = "Yes",
  dimension = "1D",
  ppmNames = "borders",
  sugarArea = c(5.4, 3.35, 72, 100),
  minimumFeatures = 40,
  showHist = FALSE
)
```

Arguments

NMRdata	A matrix containing NMR data. Columns=frequencies,rows=samples
ignoreGlucose	A character value ("Yes" or "No")
dimension	A character value ("1D" or "2D")
ppmNames	A character value ("borders" or "mean")
sugarArea	A numeric vector defining the the borders of glucose area
minimumFeatures	A numeric value defining minimum feature number used
showHist	A logical value, default is FALSE

Value

NMRdata An invisible matrix containing scaled NMR data.

Examples

```
mrbinExample<-mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",
  binwidth1D=0.05,PQNScaling="No",PCA="No",
  NMRfolders=c(system.file("extdata/1/10/pdata/10",package="mrbin"),
    system.file("extdata/2/10/pdata/10",package="mrbin"),
    system.file("extdata/3/10/pdata/10",package="mrbin"))))
PQNScaling()
```

predictWrapper

A function returning predicted values for use with the fia function.

Description

This function predicts group membership and returns a numeric vector with results.

Usage

```
predictWrapper(
  model,
  dataSet,
  functionNamePredict = "predict",
  firstLevel = 1,
  parameterNameObject = "object",
  parameterNameData = "x",
  dataFrameFlag = FALSE,
  ...
)
```

Arguments

model	A predictive model. Make sure to have loaded all required packages before starting this function
dataSet	A matrix or dataframe containing data, depending on what your predict function requires. Columns=features, rows=samples
functionNamePredict	The name of the prediction function. This only needs to be changed if the prediction function is not called predict
firstLevel	Numeric value of first level or group. Usually 1 but for glm such as in the example this needs to be 0.
parameterNameObject	The name of the parameter for passing the model to the prediction function
parameterNameData	The name of the parameter for passing the data to the prediction function
dataFrameFlag	Logical value indicating whether the data object is a data frame rather than a matrix.
...	Optional, additional parameters that will be passed to the prediction function.

Value

A numeric (integer) vector of predicted group memberships.

Examples

```
#First, define group membership and create the example feature data
group<-factor(c(rep("Group1",4),rep("Group2",5)))
names(group)<-paste("Sample",1:9,sep="")
dataset<-data.frame(
  Feature1=c(5.1,5.0,6.0,2.9,4.8,4.6,4.9,3.8,5.1),
  Feature2=c(2.6,4.0,3.2,1.2,3.1,2.1,4.5,6.1,1.3),
  Feature3=c(3.1,6.1,5.8,5.1,3.8,6.1,3.4,4.0,4.4),
  Feature4=c(5.3,5.2,3.1,2.7,3.2,2.8,5.9,5.8,3.1),
  Feature5=c(3.2,4.4,4.8,4.9,6.0,3.6,6.1,3.9,3.5)
)
rownames(dataset)<-names(group)
#train a model - here we use a logit model instead of ANN as a demonstration
mod<-glm(group~Feature1+Feature2+Feature3+Feature4+Feature5,
  data=data.frame(group=group,dataset),family="binomial")
predictWrapper(model=mod,dataSet=dataset,firstLevel=0,type="response")
```

printParameters *A function for printing parameters to the screen.*

Description

This function reads parameters from the global variable `mrbin.env$mrbinparam` and prints the required R code for creating a data set to the screen.

Usage

```
printParameters()
```

Value

None

Examples

```
printParameters()
```

putToEnv

A function for changing and adding variables in the package environment.

Description

This function can change variables in the current package environment. This may be helpful for debugging or for some plotting functions.

Usage

```
putToEnv(variableList)
```

Arguments

`variableList` A list containing all objects to be saved in the local package environment.

Value

None

Examples

```
putToEnv(list(bins=NULL))
```

readBruker	<i>A function for reading Bruker NMR spectra.</i>
------------	---

Description

This function reads Bruker NMR data. 1D and 2D data are supported.

Usage

```
readBruker(  
  folder = NULL,  
  dimension = NULL,  
  onlyTitles = FALSE,  
  useAsNames = "Spectrum titles",  
  checkFiles = FALSE  
)
```

Arguments

folder	Defines the exact NMR data folder. If NULL, mrbin parameter set is used
dimension	Defines the data dimension, "1D" or "2D". Only used if not NULL
onlyTitles	Read only spectrum titles, but no data. Defaults to FALSE
useAsNames	How should sample names be generated
checkFiles	Only check if the folder exists or contains NMR data. Defaults to FALSE

Value

An (invisible) list containing spectral data and the spectrum name

Examples

```
exampleData<-readBruker(folder=system.file("extdata/1/10/pdata/10",package="mrbin"),  
  dimension="1D")
```

recreatemrbin	<i>A function recreating parameters from previous runs.</i>
---------------	---

Description

This function reads parameters from a text file that was created during a previous run or mrbin(). After reading, the data can be recreated using mrbin(). File names in mrbin\$param might need to be updated. using recreatemrbin().

Usage

```
recreatemrbin(filename = NULL)
```

Arguments

filename File path/name of the mrbin parameter file to be loaded

Value

None

Examples

```
# Insert full folder path and file name
recreatemrbin(system.file("extdata/mrbin.txt", package="mrbin"))
```

removeFromPlot *A function for removing NMR spectra from the plot list.*

Description

This function removes a spectrum from the plot list.

Usage

```
removeFromPlot(folder = NULL, dimension = "1D")
```

Arguments

folder Defines the exact NMR data folder.
dimension Defines the data dimension, "1D" or "2D".

Value

none

Examples

```
removeFromPlot()
```

removeNoise	<i>A function for removing bins below noise level.</i>
-------------	--

Description

This function checks for each bin (column) whether its level is below the individual noise level times the signal-to-noise ratio. If less than the defined threshold level are above noise*SNR, the whole bin is removed.

Usage

```
removeNoise()
```

Value

None

Examples

```
mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",
  binwidth1D=0.05,noiseRemoval="No",PQNScaling="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=c(system.file("extdata/1/10/pdata/10",package="mrbin"),
    system.file("extdata/2/10/pdata/10",package="mrbin"),
    system.file("extdata/3/10/pdata/10",package="mrbin"))))
removeNoise()
```

resetEnv	<i>A parameter resetting function</i>
----------	---------------------------------------

Description

This function resets the parameter variables.

Usage

```
resetEnv()
```

Value

None

Examples

```
resetEnv()
```

right *A function for changing plotNMR plots.*

Description

This function moves right the plot region of the current NMR plot.

Usage

```
right(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()
mrbin(silent=TRUE,parameters=list(dimension="1D",binwidth1D=.5,
    noiseRemoval="No",trimZeros="No",
    PQNScaling="No",saveFiles="No",referenceScaling="No",
    fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
    NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
zoomIn()
right()
```

setCurrentSpectrum *A function for interactively setting the current spectrum.*

Description

This function lets the user pick a spectrum from the list of spectra analysis. This function is meant only for use within the mrbin function.

Usage

```
setCurrentSpectrum(spectrumNumber = NULL)
```

Arguments

spectrumNumber If provided, this number will be used; defaults to NULL

Value

None

Examples

```
setCurrentSpectrum(spectrumNumber=1)
```

setOffset	<i>A function for changing plotNMR plots.</i>
-----------	---

Description

This function moves up or down the 1D plot region of the current NMR plot.

Usage

```
setOffset(offsetValue = NULL)
```

Arguments

offsetValue The new offset value. Defaults to NULL

Value

None

Examples

```
setOffset(0)
```

setParam	<i>A function setting parameters and checking for consistency.</i>
----------	--

Description

This function set parameters and checks parameters for consistency.

Usage

```
setParam(parameters = NULL)
```

Arguments

parameters List of parameters to be set

Value

None

Examples

```
setParam(parameters=list(dimension="1D"))
```

up

A function for changing plotNMR plots.

Description

This function moves up the plot region of the current NMR plot (only 2D).

Usage

```
up(refreshPlot = TRUE)
```

Arguments

refreshPlot Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
resetEnv()  
mrbin(silent=TRUE,parameters=list(dimension="2D",binwidth2D=0.5,  
  binheight=3,PQNScaling="No",referenceScaling="No",binRegion=c(4,3,60,65),  
  noiseRemoval="No",trimZeros="No",cropHSQC="No",  
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,saveFiles="No",  
  NMRfolders=c(system.file("extdata/1/12/pdata/10",package="mrbin"))))  
plotNMR()  
zoomIn()  
up()
```

zoom *A function for changing plotNMR plots.*

Description

This function changes the plot region of the current NMR plot. Can be called with no arguments: zoom(). In this case the user will be asked for manual input.

Usage

```
zoom(left = NULL, right = NULL, top = NULL, bottom = NULL, refreshPlot = TRUE)
```

Arguments

left	New left boundary
right	New right boundary
top	New top boundary
bottom	New bottom boundary
refreshPlot	Refresh plot automatically. Defaults to TRUE

Value

None

Examples

```
mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
zoom(left=4.6,right=2,top=10,bottom=150)
```

zoomIn *A function for changing plotNMR plots.*

Description

This function zooms into the plot region of the current NMR plot.

Usage

```
zoomIn(refreshPlot = TRUE, x = TRUE, y = TRUE)
```

Arguments

refreshPlot	Refresh plot automatically. Defaults to TRUE
x	Change x axis? Defaults to TRUE
y	Change y axis? Defaults to TRUE

Value

None

Examples

```

mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
zoomIn()

```

zoomOut	<i>A function for changing plotNMR plots.</i>
---------	---

Description

This function zooms out from the plot region of the current NMR plot.

Usage

```
zoomOut(refreshPlot = TRUE, x = TRUE, y = TRUE)
```

Arguments

refreshPlot	Refresh plot automatically. Defaults to TRUE
x	Change x axis? Defaults to TRUE
y	Change y axis? Defaults to TRUE

Value

None

Examples

```

mrbin(silent=TRUE,setDefault=TRUE,parameters=list(dimension="1D",binwidth1D=.1,
  PQNScaling="No",noiseRemoval="No",trimZeros="No",
  fixNegatives="No",logTrafo="No",PCA="No",verbose=TRUE,
  NMRfolders=system.file("extdata/1/10/pdata/10",package="mrbin")))
plotNMR()
zoomIn()
zoomOut()

```

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