

# Package ‘ptairMS’

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**Title** Pre-processing PTR-TOF-MS Data

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**Description** This package implements a suite of methods to preprocess data from PTR-TOF-MS instruments (HDF5 format) and generates the 'sample by features' table of peak intensities in addition to the sample and feature metadata (as a single ExpressionSet object for subsequent statistical analysis). This package also permit usefull tools for cohorts management as analyzing data progressively, visualization tools and quality control. The steps include calibration, expiration detection, peak detection and quantification, feature alignment, missing value imputation and feature annotation. Applications to exhaled air and cell culture in headspace are described in the vignettes and examples. This package was used for data analysis of Gassin Delyle study on adults undergoing invasive mechanical ventilation in the intensive care unit due to severe COVID-19 or non-COVID-19 acute respiratory distress syndrome (ARDS), and permit to identify four potentiel biomarquers of the infection.

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## Contents

ptairMS-package . . . . .	3
aggregate . . . . .	4
align . . . . .	4
alignSamples . . . . .	5
annotateVOC . . . . .	6
calibration . . . . .	8
calibrationFun . . . . .	10
changeTimeLimits . . . . .	10
convert_to_mzML . . . . .	11
createPtrSet . . . . .	11
cumulative_fit_function . . . . .	13
deadTimeCorr . . . . .	14
defineKnots . . . . .	14
detectPeak . . . . .	16
determinePeakShape . . . . .	18
exportSampleMetada . . . . .	19
extractEIC . . . . .	19
fit_averagePeak . . . . .	20
fit_averagePeak_function . . . . .	20
formula2mass . . . . .	21
getDirectory . . . . .	21
getFileNames . . . . .	22
getPeakList . . . . .	22
getSampleMetadata . . . . .	23
importSampleMetadata . . . . .	24
impute . . . . .	24
imputeMat . . . . .	25
initializeFit . . . . .	26
LocalMaximaSG . . . . .	27
makeSubGroup . . . . .	27
OptimalWindowsSG . . . . .	28
PeakList . . . . .	28
plot,ptrSet,ANY-method . . . . .	30
plotCalib . . . . .	31
plotFeatures . . . . .	32
plotPeakShape . . . . .	33
plotRaw . . . . .	33
plotTIC . . . . .	35

ptrRaw-class . . . . .	36
ptrSet-class . . . . .	37
readRaw . . . . .	38
resetSampleMetadata . . . . .	39
rmPeakList . . . . .	39
RunShinnyApp . . . . .	40
setSampleMetadata . . . . .	40
show,ptrRaw-method . . . . .	41
show,ptrSet-method . . . . .	41
snipBase . . . . .	42
timeLimits . . . . .	42
TransmissionCurve . . . . .	44
updatePtrSet . . . . .	44
width . . . . .	45
writeEset . . . . .	45
<b>Index</b>	<b>47</b>

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ptairMS-package

*ptairMS: Pre-processing PTR-TOF-MS Data*


---

## Description

This package implements a suite of methods to preprocess data from PTR-TOF-MS instruments (HDF5 format) and generates the 'sample by features' table of peak intensities in addition to the sample and feature metadata (as a single ExpressionSet object for subsequent statistical analysis). This package also permit usefull tools for cohorts management as analyzing data progressively, visualization tools and quality control. The steps include calibration, expiration detection, peak detection and quantification, feature alignment, missing value imputation and feature annotation. Applications to exhaled air and cell culture in headspace are described in the vignettes and examples. This package was used for data analysis of Gassin Delyle study on adults undergoing invasive mechanical ventilation in the intensive care unit due to severe COVID-19 or non-COVID-19 acute respiratory distress syndrome (ARDS), and permit to identify four potentiel biomarkers of the infection.

## Author(s)

**Maintainer:** camille Roquencourt <camille.roquencourt@hotmail.fr>

## See Also

Useful links:

- Report bugs at <https://github.com/camilleroquencourt/ptairMS/issues>

---

aggregate	<i>aggregate peakgroup for align function</i>
-----------	---

---

**Description**

aggregate peakgroup for align function

**Usage**

```
aggregate(subGroupPeak, n.exp)
```

**Arguments**

subGroupPeak	teh group tp aggregate
n.exp	number of expiration done in the file

**Value**

a matrix with the median of mz, mean of ppb, ppb in background, and percentage of expiration where the peak is detected @keywords internal

---

align	<i>Alignment with kernel gaussian density</i>
-------	---

---

**Description**

Alignment with kernel gaussian density

**Usage**

```
align(peakTab, ppmGroup = 70, dmzGroup = 0.001)
```

**Arguments**

peakTab	table with comlumn : mass, quantification, and groups number to aligned
ppmGroup	width of sub group created beafore density estimation in ppm
dmzGroup	width of sub group created beafore density estimation in Da

**Value**

A list containing groups formed by alignment.

---

`alignSamples`*Alignment between samples*

---

### Description

`AlignSamples` performs alignment between samples (i.e. the matching of variables between the peak lists within the `ptrSet` object) by using a kernel gaussian density (Delabriere et al, 2017). This function returns an `ExpressionSet`, which contains the matrix of peak intensities, the sample metadata (borrowed from the input `ptrSet`) and the variable metadata which contains the peak intensities in the background. Two filters may be applied to:

- keep only variables with a significant higher intensity in the expirations compared to the background (i.e., a p-value less than `pValGreaterThres`) for at least `fracExp`
- keep only variables which are detected in more than `fracGroup` percent of the samples (or group)

If you do not want to apply those filters, set `fracGroup` to 0 and `pValGreaterThres` to 1.

### Usage

```
alignSamples(  
  X,  
  ppmGroup = 70,  
  fracGroup = 0.8,  
  group = NULL,  
  fracExp = 0.3,  
  pValGreaterThres = 0.001,  
  pValLessThres = 0,  
  quantiUnit = c("ppb", "ncps", "cps")[1],  
  bgCorrected = TRUE,  
  dmzGroup = 0.001  
)
```

```
## S4 method for signature 'ptrSet'  
alignSamples(  
  X,  
  ppmGroup = 70,  
  fracGroup = 0.8,  
  group = NULL,  
  fracExp = 0.3,  
  pValGreaterThres = 0.001,  
  pValLessThres = 0,  
  quantiUnit = c("ppb", "ncps", "cps")[1],  
  bgCorrected = TRUE,  
  dmzGroup = 0.001  
)
```

### Arguments

<code>X</code>	<code>ptrSet</code> already processed by the <code>detectPeak</code> function
<code>ppmGroup</code>	ppm maximal width for an <code>mzGroup</code>

fracGroup	only variables present in fracGroup percent of at least one group will be kept (if 0 the filter is not applied)
group	character: sampleMetadata data column name. If NULL, variables not present in fracGroup percent of samples will be deleted. Else, variables not present in fracGroup percent in in at least one group group will be removed.
fracExp	fraction of samples which must have their p-value less than pValGreaterThres and pValLessThres
pValGreaterThres	threshold of the p-value for the unilateral testing that quantification (in cps) of expiration points are greater than the intensities in the background.
pValLessThres	threshold of the p-value for the unilateral testing that quantification (in cps) of expiration points are less than the intensities of the background.
quantiUnit	ppb, ncps or cps
bgCorrected	logical: should the peak table contain the background corrected values?
dmzGroup	minimum mz width to be used for grouping the features (required for low masses)

**Value**

an [ExpressionSet](#) (Biobase object)

**References**

Delabriere et al., 2017

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw,
setName="exhaledPtrset", mzCalibRef = c(21.022, 60.0525),
fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mzNominal=c(21,60,79))
eset <- alignSamples(exhaledPtrset,pValGreaterThres=0.05)
Biobase::exprs(eset)
Biobase::fData(eset)
Biobase::pData(eset)
```

---

annotateVOC

*Putative annotation of VOC mz by using the reference compilation from the literature*

---

**Description**

Putatively annotate VOC mz by using the reference compilation from the literature, and propose an isotope detection.

**Usage**

```

annotateVOC(
  x,
  ionMassColname = "ion_mass",
  ppm = 20,
  prefix = "vocDB_",
  fields = c("ion_mass", "ion_formula", "formula", "mass_monoiso", "name_iupac",
             "pubchem_cid", "inchi", "inchikey", "ref_year", "ref_pmid", "disease_name",
             "disease_meshid")[c(1, 2, 5)]
)

## S4 method for signature 'ExpressionSet'
annotateVOC(
  x,
  ionMassColname = "ion_mass",
  ppm = 50,
  prefix = "vocDB_",
  fields = c("ion_mass", "ion_formula", "formula", "mass_monoiso", "name_iupac",
             "pubchem_cid", "inchi", "inchikey", "ref_year", "ref_pmid", "disease_name",
             "disease_meshid")[c(1, 2, 5)]
)

## S4 method for signature 'data.frame'
annotateVOC(
  x,
  ionMassColname = "ion_mass",
  ppm = 50,
  prefix = "vocDB_",
  fields = c("ion_mass", "ion_formula", "formula", "mass_monoiso", "name_iupac",
             "pubchem_cid", "inchi", "inchikey", "ref_year", "ref_pmid", "disease_name",
             "disease_meshid")[c(1, 2, 5)]
)

## S4 method for signature 'numeric'
annotateVOC(
  x,
  ionMassColname = "",
  ppm = 50,
  prefix = "vocDB_",
  fields = c("ion_mass", "ion_formula", "formula", "mass_monoiso", "name_iupac",
             "pubchem_cid", "inchi", "inchikey", "ref_year", "ref_pmid", "disease_name",
             "disease_meshid")[c(1, 2, 5)]
)

```

**Arguments**

- x** Expression set object (resp. data.frame) (resp. numeric vector) containing the PTR-MS processed data (resp. containing a column with the ion mass values) (resp. containing the ion mass values)
- ionMassColname** Character: column name from the fData (resp. from the data.frame) containing the ion mass values; [default: 'ion\_mass']; this argument is not used when x is a numeric vector

ppm	Numeric: tolerance
prefix	Character: prefix for the new 'annotation' columns [default: 'vocDB_']
fields	Character vector: fields of the 'vocDB' database to be queried among: 'ion_mass' [default], 'ion_formula' [default], 'formula', 'mass_monoiso', 'name_iupac' [default], 'pubchem_cid', 'inchi', 'inchikey', 'ref_year', 'ref_pmid', 'disease_name', 'disease_meshid'

**Value**

Returns the data.frame with additional columns containing the vocDB informations for the matched ion\_mass values as well as the detected isotopes

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw,
  setName="exhaledPtrset", mzCalibRef = c(21.022, 60.0525),
  fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mz=c(21,59,77))
exhaled.eset <-alignSamples(exhaledPtrset ,pValGreaterThres=0.05)
# Expression Set
exhaled.eset <- annotateVOC(exhaled.eset)
head(Biobase::fData(exhaled.eset))
# Data frame
exhaled_fdata.df <- Biobase::fData(exhaled.eset)
exhaled_fdata.df <- annotateVOC(exhaled_fdata.df)
head(exhaled_fdata.df)
# Numeric
ionMass.vn <- as.numeric(Biobase::featureNames(exhaled.eset))
annotated_ions.df <- annotateVOC(ionMass.vn)
head(annotated_ions.df)
```

---

 calibration

---

*Calibrates the mass axis with references masses*


---

**Description**

To convert Time Of Flight (TOF) axis to mass axis, we use the formula:  $mz = ((tof-b)/a)^2$  (Muller et al. 2013) To estimate those parameters, references peaks with accurate know masses and without overlapping peak are needed. The best is that the references masses covers a maximum of the mass range.

**Usage**

```
calibration(
  x,
  mzCalibRef = c(21.022, 29.013424, 41.03858, 60.0525, 203.943, 330.8495),
  calibrationPeriod = 60,
  tol = 70,
  ...
)
```

```

## S4 method for signature 'ptrRaw'
calibration(
  x,
  mzCalibRef = c(21.022, 29.013424, 41.03858, 59.049141, 75.04406, 203.943, 330.8495),
  calibrationPeriod = 60,
  tol = 70,
  ...
)

## S4 method for signature 'ptrSet'
calibration(
  x,
  mzCalibRef = c(21.022, 29.013424, 41.03858, 75.04406, 203.943, 330.8495),
  calibrationPeriod = 60,
  tol = 70,
  fileNames = getParameters(x)$listFile
)

```

### Arguments

x	a <a href="#">ptrRaw-class</a> or <a href="#">ptrSet-class</a> object
mzCalibRef	Vector of accurate mass values of intensive peaks and 'unique' in a nominal mass interval (without overlapping)
calibrationPeriod	in second, coefficient calibration are estimated for each sum spectrum of calibrationPeriod seconds
tol	the maximum error tolerated in ppm. If more than tol warnings.
...	" "
fileNames	file to recalibrate

### Value

the same ptrRaw or ptrSet as in input, with the following modified element:

- mz: the new mz axis calibrated
- rawM: same raw matrix with the new mz axis in rownames
- calibMassRef: reference masses used for the calibration
- calibMzToToF and calibToFToMz: function to convert TOF to mz
- calibError: the calibration error to the reference masses in ppm
- calibrationIndex: index time of each calibration period

### Examples

```

### ptrRaw object

library(ptairData)
filePath <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
  package = 'ptairData')
raw <- readRaw(filePath, calib = FALSE)
rawCalibrated <- calibration(raw)

```

---

calibrationFun	<i>calibration function</i>
----------------	-----------------------------

---

**Description**

Performs calibration on `sp` with `mzCalibRef` reference masses and `mzToToFFunc` as previous calibration function

**Usage**

```
calibrationFun(sp, mz, mzCalibRef, calibCoef, peakShape, tol)
```

**Arguments**

<code>sp</code>	spectrum
<code>mz</code>	mass axis
<code>mzCalibRef</code>	masses of know reference peaks
<code>calibCoef</code>	coeficient of the previous calibration
<code>peakShape</code>	a list with reference axis and a reference peak shape centered in zero
<code>tol</code>	maximum error tolarated in ppm

**Value**

list

---

changeTimeLimits	<i>Shinny application to modify and view expiration limits This function run a shiny app, where you can check the automatic expiration detection, knots location, and modify it.</i>
------------------	--

---

**Description**

Shinny application to modify and view expiration limits

This function run a shiny app, where you can check the automatic expiration detection, knots location, and modify it.

**Usage**

```
changeTimeLimits(ptrSet)
```

**Arguments**

<code>ptrSet</code>	a ptrSet object
---------------------	-----------------

**Value**

the ptrSet object modified

**Examples**

```
library(ptairData)
directory <- system.file("extdata/exhaledAir", package = "ptairData")
ptrSet <- createPtrSet(directory, setName="ptrSet", mzCalibRef=c(21.022, 59.049),
  fracMaxTIC=0.8)
## Not run: ptrSet <- changeTimeLimits(ptrSet)
```

---

convert_to_mzML	<i>Convert a h5 file to mzML</i>
-----------------	----------------------------------

---

**Description**

convert\_to\_mzML create a mzML file from a h5 file in the same directory with the writeMLData of the MSnbase package

**Usage**

```
convert_to_mzML(file)
```

**Arguments**

file                    A .h5 file path

**Value**

create a mzML file in the same directory of the h5 input file

**Examples**

```
library(ptairData)
filePathRaw <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
  package = 'ptairData')
# write a mzml file in the same directory
convert_to_mzML(filePathRaw)
file_mzML <- gsub(".h5", ".mzML", filePathRaw)
file.remove(file_mzML)
```

---

createPtrSet	<i>Creates a ptrSet object form a directory</i>
--------------	---

---

**Description**

This function creates a [ptrSet-class](#) S4 object. It opens each file and:

- performs an external calibration by using the mzCalibRef reference masses on the sum spectra every calibrationPeriod second
- quantifies the primary ion (H3O+ isotope by default) on the average total ion spectrum.
- calculates expiration on the mzBreathTracer trace. The part of the trace where the intensity is higher than fracMaxTIC \* max(trace) is considered as expiration. If fracMaxTIC is different to zero, this step is skipped

- defines the set of knots for the peak analysis (see [detectPeak](#))
- provides a default sampleMetadata based on the tree structure of the directory and the acquisition date (a data.frame with file names as row names)
- If saveDir is not NULL, the returned object will be saved as a .Rdata in saveDir with the setName as name

### Usage

```
createPtrSet(
  dir,
  setName,
  mzCalibRef = c(21.022, 29.013424, 41.03858, 60.0525, 203.943, 330.8495),
  calibrationPeriod = 60,
  fracMaxTIC = 0.8,
  mzBreathTracer = NULL,
  knotsPeriod = 3,
  mzPrimaryIon = 21.022,
  saveDir = NULL
)
```

### Arguments

dir	character. a directory path which contains several h5 files, possibly organized in subfolder
setName	character. name of the ptrSet object. If 'saveDir' is not null, the object will be saved with this name.
mzCalibRef	vector of the reference mass values; those masses should be accurate, and the corresponding peaks should be of high intensity and 'unique' in a nominal mass interval (without overlapping peaks) to performs calibration. See ?calibration.
calibrationPeriod	in second, coefficient calibration are estimated for each sum spectrum of calibrationPeriod seconds
fracMaxTIC	Fraction (between 0 and 1) of the maximum of the Total Ion Current (TIC) amplitude after baseline removal. Only the part of the spectrum where the TIC intensity is higher than 'fracMaxTIC * max(TIC)' will be analyzed. If you want to analyze the entire spectrum, set this parameter to 0.
mzBreathTracer	integer: nominal mass of the Extracted Ion Current (EIC) used to compute the expiration time limits. If NULL, the limits will be computed on the Total Ion Current (TIC).
knotsPeriod	period in second (time scale) between two knots for the two dimensional modeling
mzPrimaryIon	Exact mass of the primary ion isotope
saveDir	Directory where the ptrSet object will be saved as .RData. If NULL, nothing will be saved.

### Value

a ptrSet object with slots :

- Parameter: list containing the parameters used for createPtrSet, detectPeak and alignTimePeriods functions.

- `sampleMetadata`: data frame containing information about the data, with file names in row names
- `mzCalibRef`: list containing for each file the masses used for the calibration (see `?ptairMS::calibration` for more details)
- `signalCalibRef`: m/z and intensity  $\pm 0.4$ Da around the calibration masses
- `errorCalibPpm`: list containing for each file the accuracy error in ppm at each calibration masses
- `coefCalib`: list containing the calibration coefficients 'a' and 'b' which enable to convert to m/z for each file (see `calibration` function for more details).
- `resolution`: estimated resolution  $m/\Delta m$  for each calibration masses within each file
- `TIC`: The Total Ion Current for each file
- `timeLlimit`: list containing, for each file, a list of two element: the matrix of time limit for each file (if `fracMaxTIC` is different to zero), and the background index. See `timeLimits` for more details
- `peakList`: list containing for each file an expression set `eSet`, with m/z peak center, quantification for background and exhaled air in cps, ppb and ncps, and quantity for each time points. See `getPeakList` for more details.

## Examples

```
library(ptairData)
directory <- system.file('extdata/mycobacteria', package = 'ptairData')
ptrSet<-createPtrSet(dir=directory, setName='ptrSet'
, mzCalibRef=c(21.022, 59.049),
fracMaxTIC=0.9, saveDir= NULL)
```

---

cumulative\_fit\_function

*Create cumulative function fit*

---

## Description

Create cumulative function fit

## Usage

```
cumulative_fit_function(fit_function_str, par_var_str, par_fix_str, n.peak)
```

## Arguments

<code>fit_function_str</code>	fit function who will be use in character
<code>par_var_str</code>	parameters of fit function who change with the peak in a vector of character
<code>par_fix_str</code>	parameters of fit function independent of the peak in a vector of character
<code>n.peak</code>	number of peak

## Value

a list:  
`init.names`: names of paramters for the initialization  
`func.eval`: function who will be fitted

---

deadTimeCorr                      *Dead time correction on raw data*

---

### Description

Dead time correction on raw data

### Usage

```
deadTimeCorr(raw, ve, vne, r, threshold = 0.1)
```

### Arguments

raw	ptrRaw object
ve	extending dead time
vne	non extending dead time
r	number of extraction
threshold	only bin of intensity more then threshold*r which be corrected

### Value

a ptrRaw object with the raw matrix corrected

---

defineKnots                      *Define the knots location*

---

### Description

defineKnots function determine the knots location for a ptrSet or ptrRaw object. There is three possibilities :

- method = expiration in the expiration periods, a knots is placed every knotsPeriod seconds, and 1 knots in the middle of two expiration, one at begin and at the end
- method= uniforme, the knots are placed uniformly every knotsPeriod time points
- give in knotsList a list of knot, with all base name file in name of the list element. All file must be informed. The knots location must be contained in the time axis

### Usage

```
defineKnots(
  object,
  knotsPeriod = 3,
  method = c("expiration", "uniform", "manual")[1],
  knotsList = NULL,
  ...
)

## S4 method for signature 'ptrRaw'
```

```

defineKnots(
  object,
  knotsPeriod = 3,
  method = c("expiration", "uniform")[1],
  knotsList = NULL,
  timeLimit = list(NULL)
)

## S4 method for signature 'ptrSet'
defineKnots(
  object,
  knotsPeriod = 3,
  method = c("expiration", "uniform")[1],
  knotsList = NULL
)

```

### Arguments

object	ptrSet object
knotsPeriod	the period in second (times scale) between two knots for the two dimensional modelization
method	expiration or uniform
knotsList	a list of knot location for each files, with all base name file in name of the list element
...	not used
timeLimit	index time of the expiration limits and background

### Value

numeric vector of knots  
a list with numeric vector of knots for each file

### Examples

```

library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )

#### placed knots every 2 times points
exhaledPtrset <- defineKnots(exhaledPtrset ,knotsPeriod=2,method='uniform')

#### placed knots every 3 times points in the expiration (default)
exhaledPtrset <- defineKnots(exhaledPtrset ,knotsPeriod=3,method='expiration')

```

---

 detectPeak

*Detection and quantification of peaks for a ptrSet object.*


---

## Description

The detectPeak function detects peaks on the average total spectrum around nominal masses, for all files present in ptrSet which have not already been processed. The temporal evolution of each peak is then evaluated by using a two-dimensional penalized spline regression. Finally, the expiration points (if defined in the ptrSet) are averaged, and a t-test is performed between expiration and ambient air. The peakList can be accessed with the [getPeakList](#) function, which returns the information about the detected peaks in each file as a list of ExpressionSet objects. The peak detection steps within each file are as follows:  
for each nominal mass:

- correction of the calibration drift
- peak detection on the average spectrum
- estimation of temporal evolution
- t-test between expiration and ambient air

## Usage

```
detectPeak(
  x,
  ppm = 130,
  minIntensity = 10,
  minIntensityRate = 0.01,
  mzNominal = NULL,
  resolutionRange = NULL,
  fctFit = NULL,
  smoothPenalty = NULL,
  parallelize = FALSE,
  nbCores = 2,
  saving = TRUE,
  saveDir = getParameters(x)$saveDir,
  ...
)

## S4 method for signature 'ptrRaw'
detectPeak(
  x,
  ppm = 130,
  minIntensity = 10,
  minIntensityRate = 0.01,
  mzNominal = NULL,
  resolutionRange = NULL,
  fctFit = NULL,
  smoothPenalty = NULL,
  timeLimit,
  knots = NULL,
  mzPrimaryIon = 21.022,
```

```

    ...
)

## S4 method for signature 'ptrSet'
detectPeak(
  x,
  ppm = 130,
  minIntensity = 10,
  minIntensityRate = 0.01,
  mzNominal = NULL,
  resolutionRange = NULL,
  fctFit = NULL,
  smoothPenalty = 0,
  parallelize = FALSE,
  nbCores = 2,
  saving = TRUE,
  saveDir = getParameters(x)$saveDir,
  ...
)

```

### Arguments

x	a <a href="#">ptrSet</a> object
ppm	minimum distance in ppm between two peaks
minIntensity	minimum intensity for peak detection. The final threshold for peak detection will be: $\max(\text{minIntensity}, \text{threshold noise})$ . The threshold noise corresponds to $\max(\max(\text{noise around the nominal mass}), \text{minIntensityRate} * \max(\text{intensity within the nominal mass}))$
minIntensityRate	Fraction of the maximum intensity to be used for noise thresholding
mzNominal	nominal masses at which peaks will be detected; if NULL, all nominal masses of the mass axis
resolutionRange	vector with the minimum, average, and maximum resolution of the PTR instrument. If NULL, the values are estimated by using the calibration peaks.
fctFit	function for the peak quantification: should be <code>sech2</code> or <code>averagePeak</code> . If NULL, the best function is selected by using the calibration peaks
smoothPenalty	second order penalty coefficient of the p-spline used for two-dimensional regression. If NULL, the coefficient is estimated by generalized cross validation (GCV) criteria
parallelize	Boolean. If TRUE, loops over files are parallelized
nbCores	number of cluster to use for parallel computation.
saving	boolean. If TRUE, the object will be saved in <code>saveDir</code> with the <code>setName</code> parameter of the <code>createPtrSet</code> function
saveDir	The directory where the <code>ptrSet</code> object will be saved as <code>.RData</code> . If NULL, nothing will be saved
...	may be used to pass parameters to the <code>processFileTemporal</code> function
timeLimit	index time of the expiration limits and background. Should be provided by <a href="#">timeLimits</a> function

**knots** numeric vector corresponding to the knot values, which used for the two dimensional regression for each file. Should be provided by `defineKnots` function

**mzPrimaryIon** the exact mass of the primary ion isotope

### Value

an S4 ptrSet object, that contains the input ptrSet completed with the peakLists.

### References

Muller et al 2014, Holzinger et al 2015, Marx and Eilers 1992

### Examples

```
## For ptrRaw object
library(ptairData)
filePath <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
package = 'ptairData')
raw <- readRaw(filePath,mzCalibRef=c(21.022,59.049),calib=TRUE)
timeLimit<-timeLimits(raw,fracMaxTIC=0.7)
knots<-defineKnots(object = raw,timeLimit=timeLimit)
raw <- detectPeak(raw, timeLimit=timeLimit, mzNominal = c(21,59),
smoothPenalty=0,knots=knots,resolutionRange=c(2000,5000,8000))

## For a ptrSet object
library(ptairData)
directory <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset<-createPtrSet(dir=directory,setName="exhaledPtrset",
mzCalibRef=c(21.022,59.049),
fracMaxTIC=0.9,saveDir= NULL)
exhaledPtrset <- detectPeak(exhaledPtrset)
peakListEset<-getPeakList(exhaledPtrset)
Biobase::fData(peakListEset[[1]])
Biobase::exprs(peakListEset[[1]])
```

---

determinePeakShape      *Determine peak shape from raw data in tof*

---

### Description

This function use the method describe by average and al 2013, for determine a peak shape from the raw data :

$\$peak\_i(\Delta\_i, A\_i, t\_i) = \text{interpolation}(x = \text{tof.ref} * \Delta\_i + t\_i, y = A\_i * \text{peak.ref}, xout = \text{TOF\_i})$  where peak.ref and tof.ref are peaks reference use for mass calibration.

### Usage

```
determinePeakShape(raw, plotShape = FALSE)
```

### Arguments

**raw** a ptrRaw-class object

**plotShape** if true plot each reference peak and the average peak (the peak shape)

**Value**

A list of two vectors which are the reference peak normalized tof and intensity.

---

exportSampleMetada	<i>export sampleMetadata</i>
--------------------	------------------------------

---

**Description**

export sampleMetadata

**Usage**

```
exportSampleMetada(set, saveFile)
```

**Arguments**

set	a ptrSet object
saveFile	a file path in tsv extension where the data.frame will be exported

**Value**

nothing

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
saveFile<-file.path(getwd(), 'sampleMetadata.tsv')
#exportSampleMetada(exhaledPtrset ,saveFile)
```

---

extractEIC	<i>extract all raw EIC from a pre-defined peak List</i>
------------	---

---

**Description**

extract all raw EIC from a pre-defined peak List

**Usage**

```
extractEIC(raw, peak, peakQuantil = 0.01, fctFit = "sech2")
```

**Arguments**

raw	ptrRaw object
peak	a data.frame with a column named 'Mz'. The Mz of the VOC detected
peakQuantil	the quantile of the peak shape to determine the borne of the EIC
fctFit	function used to fit peak

**Value**

list containing all EIC and the mz borne for all peak

---

fit_averagePeak	<i>Fit peak with average function</i>
-----------------	---------------------------------------

---

**Description**

Fit peak with average function

**Usage**

```
fit_averagePeak(initTof, l.shape, sp, bin, lower.cons, upper.cons)
```

**Arguments**

initTof	list of initialisation in tof
l.shape	peak shape average
sp	spectrum
bin	tof axis
lower.cons	lower constrain for fit
upper.cons	upper constrain for fit

**Value**

list with fit information

---

fit_averagePeak_function	<i>fit function average</i>
--------------------------	-----------------------------

---

**Description**

fit function average

**Usage**

```
fit_averagePeak_function(t, delta, h, intervRef, peakShape, bin)
```

**Arguments**

t	tof center of peak
delta	FWHM of peak
h	peak height
intervRef	reference interval for peak shape
peakShape	peak shape estimated on intervalRef
bin	bin interval of peak will be fitted

**Value**

peak function made on an average of reference peaks normalized

---

formula2mass	<i>Compute exact mass.</i>
--------------	----------------------------

---

**Description**

Compute exact mass from an elemental formula

**Usage**

```
formula2mass(formula.vc, protonate.l = TRUE)
```

**Arguments**

formula.vc      Vector of molecular formulas.  
protonate.l      Should a proton be added to the formula?

**Value**

Vector of the corresponding (protonated) masses.

**Examples**

```
formula2mass("CO2")
```

---

getDirectory	<i>get the files directory of a ptrSet</i>
--------------	--

---

**Description**

get the files directory of a ptrSet

**Usage**

```
getDirectory(ptrSet)
```

**Arguments**

ptrSet            ptrSet object

**Value**

the directory in absolute path as character

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
getDirectory(exhaledPtrset )
```

---

getFileNames	<i>get the file names containing in the directory of a ptrSet or ptrRaw</i>
--------------	---

---

**Description**

get the file names containing in the directory of a ptrSet or ptrRaw  
 get the file names containing in the directory of a ptrSet

**Usage**

```
getFileNames(object, fullNames = FALSE)

## S4 method for signature 'ptrSet'
getFileNames(object, fullNames = FALSE)

## S4 method for signature 'ptrRaw'
getFileNames(object, fullNames = FALSE)
```

**Arguments**

object	ptrSet object
fullNames	logical: if TRUE, it return the the directory path is prepended to the file names.

**Value**

a vector of character that contains all file names

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
getFileNames(exhaledPtrset )
```

---

getPeakList	<i>get the peak list of a ptrSet object</i>
-------------	---

---

**Description**

get the peak list of a ptrSet object

**Usage**

```
getPeakList(set)
```

**Arguments**

set	ptrSet object
-----	---------------

**Value**

a list of expressionSet, where:

- assay Data contains the matrix with m/z peak center in row names, and the quantification in cps at each time point
- feature Data the matrix with m/z peak center in row names, and the following columns:
  - quanti\_unit: the mean of the quantification over the expiration/headspace time limits defined
  - background\_unit: the mean of the quantification over the background time limits defined
  - diffAbs\_unit: the mean of the quantification over the expiration/headspace time limits defined after subtracting the baseline estimated from the background points defined
  - pValLess/ pValGreater: the p-value of the unilateral t-test, who test that quantification (in cps) of expiration points are less/greater than the intensity of the background.
  - lower/upper: integration boundaries
  - parameter peak: estimated peak parameter

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mz=c(21,59))
peakList<- getPeakList(exhaledPtrset )
X<-Biobase::exprs(peakList[[1]])
Y<- Biobase::fData(peakList[[1]])
head(Y)
```

---

<code>getSampleMetadata</code>	<i>get sampleMetadata of a ptrSet</i>
--------------------------------	---------------------------------------

---

**Description**

get sampleMetadata of a ptrSet

**Usage**

```
getSampleMetadata(set)
```

**Arguments**

set                      a ptrSet object

**Value**

a data.frame

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL)
SMD<-getSampleMetadata(exhaledPtrset)
```

---

```
importSampleMetadata import a sampleMetadata from a tsv file to a ptrSet object
```

---

**Description**

import a sampleMetadata from a tsv file to a ptrSet object

**Usage**

```
importSampleMetadata(set, file)
```

**Arguments**

set	a ptrSet object
file	a tsv file contains the sample metadata to import, with all file names in row name (the first column on the excel).

**Value**

a ptrSet with the new sample Metadata

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
saveFile<-file.path(getwd(), 'sampleMetadata.tsv')
#exportSampleMetadata(exhaledPtrset ,saveFile)
#exhaledPtrset<-importSampleMetadata(exhaledPtrset ,saveFile)
```

---

```
impute Imputes the missing values
```

---

**Description**

Imputes missing values by returning back to the raw data and fitting the peak shape function on the noise (or on the residuals signals if peaks have already been detected).

**Usage**

```
impute(eSet, ptrSet, parallelize = FALSE, nbCores = 2)
```

**Arguments**

eSet	ExpressionSet returned by the <a href="#">alignSamples</a> function
ptrSet	<a href="#">ptrSet-class</a> object processed by the <a href="#">detectPeak</a> function
parallelize	boolean. If TRUE, the loop over all files will be parallelized
nbCores	number of clusters to use for parallel computation.

**Value**

the same ExpressionSet as in input, with the imputed missing values in the assayData slot

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw,
setName="exhaledPtrset", mzCalibRef = c(21.022, 60.0525),
fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mz=c(21,52))
eSet <- alignSamples(exhaledPtrset,pValGreaterThres=0.05,fracGroup=0)
Biobase::exprs(eSet)
eSet <- impute(eSet,exhaledPtrset)
Biobase::exprs(eSet)
```

---

imputeMat

*Impute missing values on an matrix set from an ptrSet*


---

**Description**

Imputing missing values by returning back to the raw data and fitting the peak shape function on the noise / residuals

**Usage**

```
imputeMat(X, ptrSet, quantiUnit)
```

**Arguments**

X	the peak table matrix with missing values
ptrSet	processed by detectPeak function
quantiUnit	the unit of the quantities in the matrix X (ppb, cps or ncps)

**Value**

the same matrix as in input, with missing values imputing

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw,
setName="exhaledPtrset", mzCalibRef = c(21.022, 60.0525),
fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mz=c(21,52))
eSet <- alignSamples(exhaledPtrset,pValGreaterThres=0.05,fracGroup=0)
X <-Biobase::exprs(eSet)
X <- imputeMat(X,exhaledPtrset,quantiUnit='ppb')
plotFeatures(exhaledPtrset,mz = 52.047,typePlot = "ggplot",colorBy = "subfolder")
```

---

initializeFit                      *initialization for apply fit function in the spectrum*

---

### Description

initialization for apply fit function in the spectrum

### Usage

```
initializeFit(
  i,
  sp.i.fit,
  sp.i,
  mz.i,
  calibCoef,
  resmean,
  minpeakheight,
  noiseacf,
  ppmPeakMinSep,
  daSeparation,
  d,
  plotAll,
  c
)
```

### Arguments

i	the nominal mass
sp.i.fit	the vector who will be fettet (spectrum pf residual)
sp.i	the spectrum around a nominal mass
mz.i	the mass vector around a nominal mass
calibCoef	calibration coeficient
resmean	resolution m/delta(m) mean
minpeakheight	the minimum peak intensity
noiseacf	aytorelation of the noise
ppmPeakMinSep	the minimum distance between two peeks in ppm
daSeparation	the minimum distance between two peeks in da
d	the degree of savitzky golay filter
plotAll	bollean if TRUE, it plot all the initialiation step
c	the number of current itteration

### Value

a list with fit input

---

LocalMaximaSG                      *Find local maxima with Savitzky Golay filter*

---

**Description**

Apply Savitzky Golay filter to the spectrum and find local maxima such that : second derivate Savitzky Golay filter < 0 and first derivate = 0 and intensity > minPeakHeight

**Usage**

```
LocalMaximaSG(sp, minPeakHeight = -Inf, noiseacf = 0.1, d = 3)
```

**Arguments**

sp	the array of spectrum values
minPeakHeight	minimum intensity of a peak
noiseacf	autocorrelation of the noise
d	the degree of Savitzky Golay filter, defalut 3

**Value**

array with peak's index in the spectrum

**Examples**

```
spectrum<-dnorm(x=seq(-5,5,length.out = 100))
index.max<-LocalMaximaSG(spectrum)
```

---

makeSubGroup                      *Use in align function. return a peak group thanks to kernel gaussian density in a peak matrix.*

---

**Description**

Use in align function. return a peak group thanks to kernel gaussian density in a peak matrix.

**Usage**

```
makeSubGroup(subpeakl, den, plim)
```

**Arguments**

subpeakl	a matrix with mz, ppb, background and group column.
den	the kernel gaussian density estimated on subpeakl
plim	the limit of a peak in the density of the group who will be formed

**Value**

the sub peakgroup

---

OptimalWindowsSG      *Find optimal window's size for Savitzky Golay filter*

---

**Description**

Find optimal window's size for Savitzky Golay filter

**Usage**

```
OptimalWindowsSG(sp, noiseacf, d = 3)
```

**Arguments**

sp	the array of spectrum values
noiseacf	autocorrelation of the noise
d	the degree of Savitzky Golay filter

**Value**

the optimal size of Savitzky Golay filter's windows

---

PeakList      *Detection and quantification of peaks on a sum spectrum.*

---

**Description**

Detection and quantification of peaks on a sum spectrum.

**Usage**

```
PeakList(
  raw,
  mzNominal = unique(round(getRawInfo(raw)$mz)),
  ppm = 130,
  resolutionRange = c(3000, 5000, 8000),
  minIntensity = 5,
  fctFit = c("sech2", "averagePeak")[1],
  peakShape = NULL,
  maxIter = 1,
  R2min = 0.995,
  autocorNoiseMax = 0.3,
  plotFinal = FALSE,
  plotAll = FALSE,
  thNoiseRate = 1.1,
  minIntensityRate = 0.01,
  countFacFWHM = 10,
  daSeparation = 0.005,
  d = 3,
  windowSize = 0.4
```

```

)

## S4 method for signature 'ptrRaw'
PeakList(
  raw,
  mzNominal = unique(round(getRawInfo(raw)$mz)),
  ppm = 130,
  resolutionRange = c(300, 5000, 8000),
  minIntensity = 5,
  fctFit = c("sech2", "averagePeak")[1],
  peakShape = NULL,
  maxIter = 3,
  R2min = 0.995,
  autocorNoiseMax = 0.3,
  plotFinal = FALSE,
  plotAll = FALSE,
  thNoiseRate = 1.1,
  minIntensityRate = 0.01,
  countFacFWHM = 10,
  daSeparation = 0.005,
  d = 3,
  windowSize = 0.4
)

```

### Arguments

raw	<a href="#">ptrRaw-class</a> object
mzNominal	the vector of nominal mass where peaks will be detected
ppm	the minimum distance between two peaks in ppm
resolutionRange	vector with resolution min, resolution Mean, and resolution max of the PTR
minIntensity	the minimum intensity for peaks detection. The final threshold for peak detection will be : $\max(\text{minPeakDetect}, \text{thresholdNoise})$ . The threshold-Noise correspond to $\max(\text{thNoiseRate} * \max(\text{noise around the nominal mass}), \text{minIntensityRate} * \max(\text{intensity in the nominal mass}))$ . The noise around the nominal mass correspond : $[m-\text{windowSize}-0.2, m-\text{windowSize}] \cup [m+\text{windowSize}, m+\text{windowSize}+$
fctFit	the function for the quantification of Peak, should be average or Sech2
peakShape	a list with reference axis and a reference peak shape centered in zero
maxIter	maximum iteration of residual analysis
R2min	R2 minimum to stop the iterative residual analysis
autocorNoiseMax	the autocorrelation threshold for Optimal windows Savitzky Golay filter in <code>OptimalWindowSG</code> <code>ptairMS</code> function. See <code>?OptimalWindowSG</code>
plotFinal	boolean. If TRUE, plot the spectrum for all nominal masses, with the final fitted peaks
plotAll	boolean. If TRUE, plot all step to get the final fitted peaks
thNoiseRate	The rate which multiplies the max noise intensity
minIntensityRate	The rate which multiplies the max signal intensity

countFacFWHM	integer. We will sum the fitted peaks on a window's size of countFacFWHM * FWHM, centered in the mass peak center.
daSeparation	the minimum distance between two peaks in Da for nominal mass < 17.
d	the degree for the Savitzky Golay filter
windowSize	peaks will be detected only around $m - \text{windowSize}$ ; $m + \text{windowSize}$ , for all $m$ in <code>mzNominal</code>

**Value**

a list containing:

- `peak`: a data.frame, with for all peak detected: the mass center, the intensity count in cps, the peak width (`delta_mz`), correspond to the Full Width Half Maximum (FWHM), the resolution `m/delta_m`, the other parameters values estimated of `fitFunc`.
- `warnings`: warnings generated by the peak detection algorithm per nominal masses
- `infoPlot`: elements needed to plot the fitted peak per nominal masses

**Examples**

```
library(ptairData)
filePath <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
package = 'ptairData')
file <- readRaw(filePath)

peakList <- PeakList(file, mzNominal = c(21,63))
peakList$peak
```

---

`plot,ptrSet,ANY-method`

*Plot a ptrSet object*

---

**Description**

plot a ptrSet object

**Usage**

```
## S4 method for signature 'ptrSet,ANY'
plot(x, y, typePlot = "")
```

**Arguments**

<code>x</code>	a ptrSet object
<code>y</code>	not use
<code>typePlot</code>	could be : <code>calibError</code> , <code>resolution</code> , <code>peakShape</code> , or a empty character if you want all.

**Value**

plot

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
plot(exhaledPtrset )
plot(exhaledPtrset ,typePlot='calibError')
plot(exhaledPtrset ,typePlot='resolution')
plot(exhaledPtrset ,typePlot='peakShape')
```

plotCalib

*Plot the calibration peaks after calibration***Description**

Plot the calibration peaks after calibration

**Usage**

```
plotCalib(object, ppm = 2000, ...)

## S4 method for signature 'ptrRaw'
plotCalib(object, ppm = 2000, ...)

## S4 method for signature 'ptrSet'
plotCalib(object, ppm = 2000, pdfFile = NULL, fileNames = NULL, ...)
```

**Arguments**

object	a ptrSet or ptrRaw object
ppm	the width of plot windows
...	not used
pdfFile	is different of NULL, the file path to save the plots in pdf
fileNames	the name of the files in the ptrSet object to plot. If NULL, all files will be plotted

**Value**

plot

**Examples**

```
## ptrSet
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
plotCalib(exhaledPtrset ,fileNames=getFileNames(exhaledPtrset )[1])

## ptrRaw
filePath<-system.file('extdata/exhaledAir/ind1/ind1-1.h5',
package = 'ptairData')
raw <- readRaw(filePath,mzCalibRef=c(21.022,59.049))
plotCalib(raw)
```

---

plotFeatures

*Plot raw average spectrum around a mzRange*


---

### Description

Plot the raw data spectrum for several files in a ptrSet object around the mz masses. The expiration average spectrum is in full lines, and background in dashed lines.

### Usage

```
plotFeatures(
  set,
  mz,
  typePlot = "plotly",
  addFeatureLine = TRUE,
  ppm = 2000,
  pdfFile = NULL,
  fileNames = NULL,
  colorBy = "rownames"
)

## S4 method for signature 'ptrSet'
plotFeatures(
  set,
  mz,
  typePlot = "plotly",
  addFeatureLine = TRUE,
  ppm = 2000,
  pdfFile = NULL,
  fileNames = NULL,
  colorBy = "rownames"
)
```

### Arguments

set	a <a href="#">ptrSet-class</a> object
mz	the mz values to plot
typePlot	set "plotly" to get an interactive plot, or "ggplot"
addFeatureLine	boolean. If TRUE a vertical line at the mz masses is plotted
ppm	windows size of the plot round mz in ppm
pdfFile	a file path to save a pdf with a individual plot per file
fileNames	vector of character. The file names you want to plot. If NULL, it plot all files
colorBy	character. A column name of sample metadata by which the line are colored.

### Value

a plotly or ggplot2 object

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw,
  setName="exhaledPtrset", mzCalibRef = c(21.022, 60.0525),
  fracMaxTIC = 0.7, saveDir = NULL )
plotF<-plotFeatures(exhaledPtrset ,mz=59.049,type="ggplot",colorBy="subfolder")
print(plotF)
```

---

plotPeakShape	<i>plot the average peak shape of reference calibration masses for a ptrSet</i>
---------------	---

---

**Description**

plot the average peak shape of reference calibration masses for a ptrSet

**Usage**

```
plotPeakShape(set, showAverage = FALSE)
```

**Arguments**

set	ptrSet object
showAverage	boolean

**Value**

ggplot object

---

plotRaw	<i>Plot method for 'ptrRaw' objects</i>
---------	---

---

**Description**

Displays the image of the matrix of intensities, the TIC and the TIS, for the selected m/z and time ranges

**Usage**

```
plotRaw(
  object,
  mzRange,
  timeRange = c(NA, NA),
  type = c("classical", "plotly")[1],
  ppm = 2000,
  palette = c("heat", "revHeat", "grey", "revGrey", "ramp")[1],
  showVocDB = TRUE,
  figure.pdf = "interactive",
  ...
)
```

```

)

## S4 method for signature 'ptrRaw'
plotRaw(
  object,
  mzRange,
  timeRange = c(NA, NA),
  type = c("classical", "plotly")[1],
  ppm = 2000,
  palette = c("heat", "revHeat", "grey", "revGrey", "ramp")[1],
  showVocDB = TRUE,
  figure.pdf = "interactive",
  ...
)

## S4 method for signature 'ptrSet'
plotRaw(
  object,
  mzRange,
  timeRange = c(NA, NA),
  type = c("classical", "plotly")[1],
  ppm = 2000,
  palette = c("heat", "revHeat", "grey", "revGrey", "ramp")[1],
  showVocDB = TRUE,
  figure.pdf = "interactive",
  fileNames = NULL,
  ...
)

```

### Arguments

object	An S4 object of class ptrRaw-class or ptrSet
mzRange	Either a vector of 2 numerics indicating the m/z limits or an integer giving a nominal m/z
timeRange	Vector of 2 numerics giving the time limits
type	Character: plot type; either 'classical' [default] or 'plotly'
ppm	Integer: Half size of the m/z window when mzRange is set to a nominal mass
palette	Character: Color palette for the 'classical' plot; either 'heat' [default], 'revHeat', 'grey', 'revGrey' or 'ramp'
showVocDB	Logical: Should putative m/z annotations from the internal package database be displayed (default is TRUE)
figure.pdf	Character: Either 'interactive' [default], or the filename of the figure to be saved (with the 'pdf' extension); only available for the 'classical' display
...	not used
fileNames	vector of character. The file names of the ptrSer that you want to plot. Could be in basename or fullname.

### Value

Invisibly returns a list of the raw (sub)matrix 'rawsubM' and the voc (sub)database 'vocsubDB'

**Examples**

```

dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
ptairMS::plotRaw(exhaledPtrset ,mzRange=59,fileNames='ind1-1.h5')

patientRaw <- ptairMS::readRaw(system.file('extdata/exhaledAir/ind1/ind1-1.h5',
package = 'ptairData'), mzCalibRef=c(21.022,59.049,75.05))
ptairMS::plotRaw(patientRaw, mzRange = 59)
ptairMS::plotRaw(patientRaw, mzRange = 59, type = 'plotly')

```

---

plotTIC

*plot the Total Ion spectrum (TIC) for one or several files.*


---

**Description**

plot the Total Ion spectrum (TIC) for one or several files.

**Usage**

```

plotTIC(
  object,
  type = c("plotly", "ggplot")[1],
  baselineRm = FALSE,
  showLimits = FALSE,
  ...
)

## S4 method for signature 'ptrRaw'
plotTIC(object, type, baselineRm, showLimits, fracMaxTIC = 0.8, ...)

## S4 method for signature 'ptrSet'
plotTIC(
  object,
  type,
  baselineRm,
  showLimits,
  pdfFile = NULL,
  fileNames = NULL,
  colorBy = "rownames",
  normalizePrimariIon = FALSE,
  ...
)

```

**Arguments**

object	ptrSet or ptrRaw S4 object
type	set 'plotly' to get an interactive plot, and 'ggplot' for classical plot.
baselineRm	logical. If TRUE, remove the baseline of the TIC

showLimits	logical. If TRUE, add the time limits to the plot (obtain with the 'fracMaxTIC' argument or 'createPtrSet' function)
...	not used
fracMaxTIC	Percentage (between 0 and 1) of the maximum of the Total Ion Current (TIC) amplitude with baseline removal. We will analyze only the part of the spectrum where the TIC intensity is higher than 'fracMaxTIC * max(TIC)'. If you want to analyze the entire spectrum, set this parameter to 0.
pdfFile	a absolute file path. A pdf will be generated with a plot for each file, caints TIC and time limits.
fileNames	vector of character. The file names of the ptrSer that you want to plot. Could be in basename or fullname.
colorBy	character. A name of the ptrSet's sampleMetaData column, to display with the same color files of same attributes.
normalizePrimariIon	should the TIC be normalized by the primary ion

### Value

a plotly of ggplot2 object.

### Examples

```
### ptrRaw object

library(ptairData)
filePath <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
package = 'ptairData')
raw <- readRaw(filePath)
p <- plotTIC(raw)
p
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
plotTIC(exhaledPtrset ,type='ggplot')
```

---

ptrRaw-class

*PTR-TOF-MS raw data from a rhdf5 file*

---

### Description

A ptrRaw object contains PTR-TOF-MS raw data from one rhdf5 file. It is created with the [readRaw](#) function.

### Slots

name the file name  
rawM the raw intensities matrix  
mz array of the m/z axis  
time numeric vector of acquisition time (in seconds)  
calibMzToTof function to convert m/z to ToF

calibToftoMz function to convert tof to m/z  
 calibCoef calibration coefficients (a,b) such that:  $mz = ((tof-b)/a)^2$  for each calibration period  
 indexTimeCalib index time of each calibration period  
 calibMassRef the reference masses used for the calibration  
 calibError the shift error in ppm at the reference masses  
 calibSpectr the spectrum of calibration reference masses  
 peakShape average normalized peak shape of the calibration peak  
 ptrTransmisison matrix with transmission values  
 ptrReaction a list containing PTR reaction information: drift temperature, pressure and voltage  
 date acquisition date and hour  
 peakList individual peak list in [eSet](#)  
 fctFit the peak function used for peak deconvolution for each file  
 resolution estimation of the resolution for each file based on the calibration reference masses  
 primaryIon the quantity in count per acquisition time of the isotope of primary ion for each file

## References

<https://www.hdfgroup.org>

---

ptrSet-class

*A set of PTR-TOF-MS raw data informations*

---

## Description

A ptrSet object is related to a directory that contains several PTR-TOF-MS raw data in rhdf5 format. It is created with the [createPtrSet](#) function. This object could be updated when new files are added with the [updatePtrSet](#) function.

## Slots

parameter the input parameters value of the function [createPtrSet](#) and [detectPeak](#)  
 sampleMetadata dataframe of sample metadata, with file names in row names, suborders names and acquisition date in columns  
 date acquisition date for each file  
 mzCalibRef the masses used for calibration for each file  
 signalCalibRef the spectrum of mass calibration for each file  
 errorCalibPpm the calibration error for each file  
 coefCalib the coefficients of mass axis calibration of each calibration periods for each file  
 indexTimeCalib index time of each calibration period for each file  
 primaryIon the quantity in count per acquisition time of the isotope of primary ion for each file  
 resolution estimation of the resolution for each file based on the calibration reference masses  
 ptrReaction drift information (temperature, pressure and voltage)  
 ptrTransmisison transmission curve for each file

TIC the total ion current (TIC) for each file  
 breathTracer the tracer for expiration/head spaces detection  
 timeLimit the index of time limit for each file  
 knots numeric vector correspond to the knot that will be used for the two dimensional regression for each file  
 fctFit the peak function used for peak deconvolution for each file  
 peakShape average normalized peak shape of the calibration peak for each file  
 peakList individual peak list in [eSet](#)

---

readRaw *Read a h5 file of PTR-TOF-MS data*

---

### Description

readRaw reads a h5 file with rhdf5 library, and calibrates the mass axis with mzCalibRef masses each calibrationPeriod seconds. It returns a [ptrRaw-class](#) S4 object, that contains raw data.

### Usage

```
readRaw(
  filePath,
  calib = TRUE,
  mzCalibRef = c(21.022, 29.013424, 41.03858, 60.0525, 203.943, 330.8495),
  calibrationPeriod = 60,
  tolCalibPpm = 70,
  maxTimePoint = 900
)
```

### Arguments

filePath	h5 absolute file path full name.
calib	boolean. If true, an external calibration is performed on the calibrationPeriod sum spectrum with mzCalibRef reference masses.
mzCalibRef	calibration parameter. Vector of exact theoretical masses values of an intensive peak without overlapping.
calibrationPeriod	in second, coefficient calibration are estimated for each sum spectrum of calibrationPeriod seconds
tolCalibPpm	calibration parameter. The maximum error tolerated in ppm. A warning appears for error greater than tolCalibPpm.
maxTimePoint	number maximal of time point to read

### Value

a ptrRaw object, including slot

- rawM the data raw matrix, in count of ions
- mz the mz axis
- time time acquisition in second

**Examples**

```
library(ptairData)
filePathRaw <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
package = 'ptairData')
raw <- readRaw(filePath=filePathRaw, mzCalibRef=c(21.022, 60.0525), calib=FALSE)
```

---

resetSampleMetadata	<i>reset the default sampleMetadata, containing the suborders names and the acquisition dates as columns.</i>
---------------------	---

---

**Description**

reset the default sampleMetadata, containing the suborders names and the acquisition dates as columns.

**Usage**

```
resetSampleMetadata(ptrset)
```

**Arguments**

ptrset            a ptrser object

**Value**

a data.frame

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
SMD<- resetSampleMetadata(exhaledPtrset)
```

---

rmPeakList	<i>remove the peakList of an ptrSet object</i>
------------	--

---

**Description**

This function is useful when you want to change the parameters of the detect peak function. First delete the peakList with rmPeakList, and apply detectPeakwith the new parameters.

**Usage**

```
rmPeakList(object)
```

**Arguments**

object            ptrSet object

**Value**

a ptrSet

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset <-rmPeakList(exhaledPtrset )
```

---

RunShinnyApp

*Graphical interface of ptairMS workflow*

---

**Description**

The whole workflow of ptairMS can be run interactively through a graphical user interface, which provides visualizations (expiration phases, peaks in the raw data, peak table, individual VOCs), quality controls (calibration, resolution, peak shape and evolution of reagent ions depending on time), and exploratory data analysis.

**Usage**

RunShinnyApp()

**Value**

Shinny app

**Examples**

```
## Not run: RunShinnyApp()
```

---

setSampleMetadata

*set sampleMetadata in a ptrSet*

---

**Description**

Insert a samplemetada data.frame in a ptrSet object. The dataframe must have all file names in rownames.

**Usage**

```
setSampleMetadata(set, sampleMetadata)
```

**Arguments**

set                    a ptrSet object

sampleMetadata    a data.frame with all file names of the ptrSet in row names

**Value**

the ptrSet object in argument with the sampleMetadata modified

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
SMD<-getSampleMetadata(exhaledPtrset )
colnames(SMD)[1]<-'individual'
exhaledPtrset<-setSampleMetadata(exhaledPtrset ,SMD)
```

---

show,ptrRaw-method      *show a ptrRaw object*

---

**Description**

It indicates the files, the mz range, time acquisition range, and calibration error.

**Usage**

```
## S4 method for signature 'ptrRaw'
show(object)
```

**Arguments**

object                  a ptrRaw object

**Value**

nothing

---

show,ptrSet-method      *show a ptrSet object*

---

**Description**

It indicates the directory, the number of files that contain the directory at the moment, and the number of processed files. The two numbers are different, use updatePtrSet function.

**Usage**

```
## S4 method for signature 'ptrSet'
show(object)
```

**Arguments**

object                  a ptrSet object

**Value**

nothing

---

snipBase	<i>Baseline estimation</i>
----------	----------------------------

---

**Description**

Baseline estimation

**Usage**

```
snipBase(sp, widthI = 11, iteI = 5)
```

**Arguments**

sp	an array with spectrum values
widthI	width of interval
iteI	number of iteration

**Value**

baseline estimation of the spectrum

---

timeLimits	<i>Calculates time limits on the breath tracer</i>
------------	--

---

**Description**

This function derives limits on the breath tracer indicated, where the intensity is greater than  $\text{fracMaxTIC} \times \max(\text{tracer})$ . By setting  $\text{fracMaxTIC}$  close to 1, the size of the limits will be restricted. This function also determine the index corresponding to the background, where variation between two successive point can be control with  $\text{derivThreshold}$  parameter.

**Usage**

```
timeLimits(
  object,
  fracMaxTIC = 0.5,
  fracMaxTICBg = 0.2,
  derivThresholdExp = 1,
  derivThresholdBg = 0.05,
  mzBreathTracer = NULL,
  minPoints = 2,
  degreeBaseline = 1,
  baseline = TRUE,
  redefineKnots = TRUE,
  plotDel = FALSE
)

## S4 method for signature 'ptrRaw'
timeLimits(
```

```

object,
fracMaxTIC = 0.6,
fracMaxTICBg = 0.2,
derivThresholdExp = 0.5,
derivThresholdBg = 0.05,
mzBreathTracer = NULL,
minPoints = 2,
degreeBaseline = 1,
baseline = TRUE,
redefineKnots = TRUE,
plotDel = FALSE
)

## S4 method for signature 'ptrSet'
timeLimits(
  object,
  fracMaxTIC = 0.5,
  fracMaxTICBg = 0.2,
  derivThresholdExp = 1,
  derivThresholdBg = 0.05,
  minPoints = 2,
  degreeBaseline = 1,
  baseline = TRUE,
  redefineKnots = TRUE,
  plotDel = FALSE
)

```

### Arguments

object	a ptrRaw or ptrSet object
fracMaxTIC	between 0 and 1. Percentage of the maximum of the tracer amplitude with baseline removal. If you want a finer limitation, increase fracMaxTIC, indeed decrease
fracMaxTICBg	same as fracMaxTIC but for background detection (lower than fracMaxTIC*max(TIC))
derivThresholdExp	the threshold of the difference between two successive points of the expiration
derivThresholdBg	the threshold of the difference between two successive points of the background
mzBreathTracer	NULL or a integer. Correspond to a nominal masses of Extract Ion Current (EIC) whose limits you want to compute. If NULL, the limits are calculated on the Total Ion Current (TIC).
minPoints	minimum duration of an expiration (in index).
degreeBaseline	the degree of polynomial baseline function
baseline	logical, should the trace be baseline corrected?
redefineKnots	logical, should the knot location must be redefined with the new times limits ?
plotDel	boolean. If TRUE, the trace is plotted with limits and threshold.

### Value

a list with expiration limits (a matrix of index, where each column correspond to one expiration, the first row it is the beginning and the second the end, or NA if no limits are detected) and index of the

background.

### Examples

```
## ptrRaw object

library(ptairData)
filePath <- system.file('extdata/exhaledAir/ind1', 'ind1-1.h5',
  package = 'ptairData')
raw <- readRaw(filePath)

timLim <- timeLimits(raw, fracMaxTIC=0.9, plotDel=TRUE)
timLim_acetone <- timeLimits(raw, fracMaxTIC=0.5, mzBreathTracer = 59,
  plotDel=TRUE)
```

---

TransmissionCurve	<i>Estimation of the transmissison curve</i>
-------------------	--

---

### Description

Estimation of the transmissison curve

### Usage

```
TransmissionCurve(x, y)
```

### Arguments

x	masses
y	transmission data

### Value

a numeric vector

---

updatePtrSet	<i>update a ptrSet object</i>
--------------	-------------------------------

---

### Description

When new files are added to a directory which has already a ptrSet object associated, run updatePtrSet to add the new files in the object. The information on the new files are added to object with the same parameter used for the function createPtrSet who has created the object. updatePtrSet also delete from the ptrSet deleted files in the directory.

### Usage

```
updatePtrSet(ptrset)
```

**Arguments**

ptrset            a ptrset object

**Value**

the same ptrset object than ininput, but completed with new files and without deleted files in the directory

**Examples**

```
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
##add or delete files in the directory
# exhaledPtrset<- updatePtrSet(exhaledPtrset)
```

---

width	<i>Calculate the FWHM (Full Width at Half Maximum) in raw data</i>
-------	--

---

**Description**

Calculate the FWHM (Full Width at Half Maximum) in raw data

**Usage**

```
width(tof, peak, fracMaxTIC = 0.5)
```

**Arguments**

tof                A vector of tof interval  
peak               A vector of peak Intensity  
fracMaxTIC        the fraction of the maximum intensity to compute the width

**Value**

the delta FWHM in tof

---

writeEset	<i>Exporting an ExpressionSet instance into 3 tabulated files 'dataMatrix.tsv', 'sampleMetadata.tsv', and 'variableMetadata.tsv'</i>
-----------	--

---

**Description**

Note that the dataMatrix is transposed before export (e.g., the samples are written column wise in the 'dataMatrix.tsv' exported file).

**Usage**

```
writeEset(x, dirName, overwrite = FALSE, verbose = TRUE)

## S4 method for signature 'ExpressionSet'
writeEset(x, dirName, overwrite = FALSE, verbose = TRUE)
```

**Arguments**

x	An S4 object of class ExpressionSet
dirName	Character: directory where the tables should be written
overwrite	Logical: should existing files be overwritten?
verbose	Logical: should messages be printed?

**Value**

No object returned.

**Examples**

```
library(ptairData)
dirRaw <- system.file("extdata/exhaledAir", package = "ptairData")
exhaledPtrset <- createPtrSet(dir=dirRaw, setName="exhaledPtrset",
mzCalibRef = c(21.022, 60.0525), fracMaxTIC = 0.7, saveDir = NULL )
exhaledPtrset<-detectPeak(exhaledPtrset,mz=c(21,59,77))
eset <- ptairMS::alignSamples(exhaledPtrset )
writeEset(eset, dirName = file.path(getwd(), "processed_dataset"))
unlink(file.path(getwd(), "processed_dataset"),recursive = TRUE)
```

# Index

## \* internal

- align, [4](#)
  - calibrationFun, [10](#)
  - cumulative\_fit\_function, [13](#)
  - deadTimeCorr, [14](#)
  - determinePeakShape, [18](#)
  - extractEIC, [19](#)
  - fit\_averagePeak, [20](#)
  - fit\_averagePeak\_function, [20](#)
  - initializeFit, [26](#)
  - makeSubGroup, [27](#)
  - OptimalWindowsSG, [28](#)
  - plotPeakShape, [33](#)
  - ptairMS-package, [3](#)
  - snipBase, [42](#)
  - TransmissionCurve, [44](#)
  - width, [45](#)
- aggregate, [4](#)
- align, [4](#)
- alignSamples, [5](#), [24](#)
- alignSamples, ptrSet-method  
(alignSamples), [5](#)
- annotateVOC, [6](#)
- annotateVOC, data.frame-method  
(annotateVOC), [6](#)
- annotateVOC, ExpressionSet-method  
(annotateVOC), [6](#)
- annotateVOC, numeric-method  
(annotateVOC), [6](#)
- calibration, [8](#), [13](#)
- calibration, ptrRaw-method  
(calibration), [8](#)
- calibration, ptrSet-method  
(calibration), [8](#)
- calibrationFun, [10](#)
- changeTimeLimits, [10](#)
- convert\_to\_mzML, [11](#)
- createPtrSet, [11](#), [37](#)
- cumulative\_fit\_function, [13](#)
- deadTimeCorr, [14](#)
- defineKnots, [14](#), [18](#)
- defineKnots, ptrRaw-method  
(defineKnots), [14](#)
- defineKnots, ptrSet-method  
(defineKnots), [14](#)
- detectPeak, [5](#), [12](#), [16](#), [24](#), [37](#)
- detectPeak, ptrRaw-method (detectPeak),  
[16](#)
- detectPeak, ptrSet-method (detectPeak),  
[16](#)
- determinePeakShape, [18](#)
- eSet, [13](#), [37](#), [38](#)
- exportSampleMetada, [19](#)
- ExpressionSet, [5](#), [6](#)
- extractEIC, [19](#)
- fit\_averagePeak, [20](#)
- fit\_averagePeak\_function, [20](#)
- formula2mass, [21](#)
- getDirectory, [21](#)
- getFileNames, [22](#)
- getFileNames, ptrRaw-method  
(getFileNames), [22](#)
- getFileNames, ptrSet-method  
(getFileNames), [22](#)
- getPeakList, [13](#), [16](#), [22](#)
- getSampleMetadata, [23](#)
- importSampleMetadata, [24](#)
- impute, [24](#)
- imputeMat, [25](#)
- initializeFit, [26](#)
- LocalMaximaSG, [27](#)
- makeSubGroup, [27](#)
- OptimalWindowsSG, [28](#)
- PeakList, [28](#)
- PeakList, ptrRaw-method (PeakList), [28](#)
- plot, ptrSet, ANY-method, [30](#)
- plot, ptrSet-method  
(plot, ptrSet, ANY-method), [30](#)

plot.ptrSet (plot,ptrSet,ANY-method), 30  
plotCalib, 31  
plotCalib,ptrRaw-method (plotCalib), 31  
plotCalib,ptrSet-method (plotCalib), 31  
plotFeatures, 32  
plotFeatures,ptrSet-method  
    (plotFeatures), 32  
plotPeakShape, 33  
plotRaw, 33  
plotRaw,ptrRaw-method (plotRaw), 33  
plotRaw,ptrSet-method (plotRaw), 33  
plotTIC, 35  
plotTIC,ptrRaw-method (plotTIC), 35  
plotTIC,ptrSet-method (plotTIC), 35  
ptairMS (ptairMS-package), 3  
ptairMS-package, 3  
ptrRaw-class, 36  
ptrSet, 17  
ptrSet-class, 37  
  
readRaw, 36, 38  
resetSampleMetadata, 39  
rmPeakList, 39  
RunShinyApp, 40  
  
setSampleMetadata, 40  
show,ptrRaw-method, 41  
show,ptrSet-method, 41  
snipBase, 42  
  
timeLimits, 13, 17, 42  
timeLimits,ptrRaw-method (timeLimits),  
    42  
timeLimits,ptrSet-method (timeLimits),  
    42  
TransmissionCurve, 44  
  
updatePtrSet, 37, 44  
  
width, 45  
writeEset, 45  
writeEset,ExpressionSet-method  
    (writeEset), 45