Package ‘baseline’

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Title Baseline Correction of Spectra
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Description Collection of baseline correction algorithms, along with a framework and a GUI for optimising baseline algorithm parameters.
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R topics documented:

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A common framework with implementations of several baseline correction methods
Use function `baseline` for baseline correction. This function takes matrices of spectra, a method name and parameters needed for the specific method. See helpfiles for details.

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik

Maintainer: Kristian Hovde Liland <kristian.liland@nmbu.no>

References


Examples

```r
data(milk)
b.irls <- baseline(milk$spectra[,1, drop=FALSE])
## Not run:
plot(b.irls)

## End(Not run)
```

 Extraction methods specifically for objects of class `baselineAlgTest`
Usage

    baseline(object)
    extraArgs(object)

Arguments

    object Object of class baselineAlgTest

Value

    The corresponding slot

Author(s)

    Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

    baselineAlgTest

---

Baseline correction

Description

Common framework for baseline correction

Usage

    baseline(spectra, method = "irls", ...)

Arguments

    spectra Matrix with spectra in rows
    method Baseline correction method
    ... Additional parameters, sent to the method

Details

    Estimates baselines for the spectra, using the algorithm named in method.

Value

    An object of class baseline.

Author(s)

    Kristian Hovde Liland and Bjørn-Helge Mevik
See Also

The functions implementing the baseline algorithms: baseline.als, baseline.fillPeaks, baseline.irls, baseline.lowpass, baseline.medianWindow, baseline.modpolyfit, baseline.peakDetection, baseline.rfbaseline, baseline.rollingBall, baseline.shirley

Examples

data(milk)
b.c.irls <- baseline(milk$spectra[, , drop=FALSE])
  ## Not run:
  plot(bc.irls)

  ## End(Not run)

baseline-class  Class "baseline"

Description

Stores the result of estimating baselines for one or more spectra.

Objects from the Class

The normal way to create objects is with the function baseline. Several baseline algorithms are available. See baseline for details. There is a plot method for the class; see plot, baseline-method.

Slots

baseline: A matrix with the estimated baselines
corrected: A matrix with the corrected spectra
spectra: A matrix with the original spectra
call: The call to baseline

Methods

getBaseline signature(object = "baseline"): Extract the estimated baselines
getCall signature(object = "baseline"): Extract the call to baseline used to create the object
getCorrected signature(object = "baseline"): Extract the corrected spectra
getSpectra signature(object = "baseline"): Extract the original spectra

Warning

In a future version, one of the slots might be removed from the class definition and calculated on the fly instead, in order to save space. Therefore, do use the extractor functions (getSpectra, getBaseline and getCorrected) instead of accessing the slots directly.
Author(s)
Bjørn-Helge Mevik and Kristian Hovde Liland

See Also
baseline, getBaseline, getSpectra, getCorrected, getCall

Examples
showClass("baseline")

baseline.als  Asymmetric Least Squares

Description
Baseline correction by 2nd derivative constrained weighted regression. Original algorithm proposed by Paul H. C. Eilers and Hans F.M. Boelens

Usage
baseline.als(spectraL lambda \] VL p \] PNPUL maxit \] RPI

Arguments
spectra  Matrix with spectra in rows
lambda  2nd derivative constraint
p  Weighting of positive residuals
maxit  Maximum number of iterations

Details
Iterative algorithm applying 2nd derivative constraints. Weights from previous iteration is p for positive residuals and 1−p for negative residuals.

Value
baseline  Matrix of baselines corresponding to spectra spectra
corrected  Matrix of baseline corrected spectra
wgts  Matrix of final regression weights

Author(s)
Kristian Hovde Liland and Bjørn-Helge Mevik
baseline.fillPeaks

References

Paul H. C. Eilers and Hans F.M. Boelens: Baseline Correction with Asymmetric Least Squares Smoothing

Examples

data(milk)
bc.als <- baseline(milk$spectra[1,, drop=FALSE], lambda=10, method='als')
## Not run:
plot(bc.als)
## End(Not run)

baseline.fillPeaks  Fill peaks

Description

An iterative algorithm using suppression of baseline by means in local windows

Usage

baseline.fillPeaks(spectra, lambda, hwi, it, int)

Arguments

  spectra          Matrix with spectra in rows
  lambda           2nd derivative penalty for primary smoothing
  hwi              Half width of local windows
  it               Number of iterations in suppression loop
  int              Number of buckets to divide spectra into

Details

In local windows of buckets the minimum of the mean and the previous iteration is chosen as the new baseline

Value

  baseline         Matrix of baselines corresponding to spectra spectra
  corrected        Matrix of baseline corrected spectra

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik
**Examples**

data(milk)
brc.fillPeaks <- baseline(milk$spectra[, drop=FALSE], lambda=6,
hwi=50, it=10, int=2000, method='fillPeaks')
## Not run:
plot(bc.fillPeaks)

## End(Not run)

---

**baseline.irls**  
*Iterative Restricted Least Squares*

**Description**

An algorithm with primary smoothing and repeated baseline suppressions and regressions with 2nd derivative constraint

**Usage**

baseline.irls(spectra, lambda1 = 5, lambda2 = 9, maxit = 200, wi = 0.05)

**Arguments**

- `spectra`: Matrix with spectra in rows
- `lambda1`: 2nd derivative constraint for primary smoothing
- `lambda2`: 2nd derivative constraint for secondary smoothing
- `maxit`: Maximum number of iterations
- `wi`: Weighting of positive residuals

**Value**

- `baseline`: Matrix of baselines corresponding to spectra `spectra`
- `corrected`: Matrix of baseline corrected spectra
- `smoothed`: Matrix of primary smoothed spectra

**Author(s)**

Kristian Hovde Liland and Bjørn-Helge Mevik

**Examples**

data(milk)
brc.irls <- baseline(milk$spectra[, drop=FALSE], method='irls')
## Not run:
plot(bc.irls)

## End(Not run)
Description

An algorithm for removing baselines based on Fast Fourier Transform filtering

Usage

baseline.lowpass(spectra, steep = 2, half = 5)

Arguments

spectra Matrix with spectra in rows
steep Steepness of filter curve
half Half-way point of filter curve

Details

Since the scale of the spectra will be different after filtering, baselines will not be returned by the algorithm

Value

baseline Matrix of baselines corresponding to spectra spectra
corrected Matrix of baseline corrected spectra

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik

References

AHMET K. ATAKAN, W. E. BLASS, and D. E. JENNINGS: Elimination of Baseline Variations from a Recorded Spectrum by Ultra-low Frequency Filtering

Examples

data(milk)
bcl.lowpass <- baseline(milk$spectra[, , drop=FALSE], method='lowpass')
## Not run:
plot(bcl.lowpass)

## End(Not run)
baseline.medianWindow  
Median window

Description
An implementation and extention of Mark S. Friedrichs’ model-free algorithm

Usage
baseline.medianWindow(spectra, hwm, hws, end)

Arguments
spectra  
Matrix with spectra in rows
hwm  
Window half width for local medians
hws  
Window half width for local smoothing (optional)
end  
Original endpoint handling (optional boolean)

Details
An algorithm finding medians in local windows and smoothing with gaussian weighting

Value
baseline  
Matrix of baselines corresponding to spectra spectra
corrected  
Matrix of baseline corrected spectra

Author(s)
Kristian Hovde Liland and Bjørn-Helge Mevik

References
Mark S. Friedrichs: A model-free algorithm for the removal of baseline artifacts

Examples
data(milk)
bc.medianWindow <- baseline(milk$spectra[1,, drop=FALSE], hwm=300, method='medianWindow')
## Not run:
plot(bc.medianWindow)
## End(Not run)
baseline.modpolyfit

Modified polynomial fitting

Description

An implementation of CHAD A. LIEBER and ANITA MAHADEV-JANSENs algorithm for polynomial fitting.

Usage

baseline.modpolyfit(spectra, t, degree = 4, tol = 0.001, rep = 100)

Arguments

- spectra: Matrix with spectra in rows
- t: Optional vector of spectrum abcissa
- degree: Degree of polynomial
- tol: Tolerance of difference between iterations
- rep: Maximum number of iterations

Details

Polynomial fitting with baseline suppression relative to original spectrum.

Value

- baseline: Matrix of baselines corresponding to spectra spectra
- corrected: Matrix of baseline corrected spectra

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik

References

CHAD A. LIEBER and ANITA MAHADEV-JANSEN: Automated Method for Subtraction of Fluorescence from Biological Raman Spectra

Examples

data(milk)
bc.modpolyfit <- baseline(milk$spectra[, drop=FALSE], method='modpolyfit', deg=6)
## Not run:
plot(bc.modpolyfit)

## End(Not run)
Simultaneous Peak Detection and Baseline Correction

Description

A translation from Kevin R. Coombes et al.’s MATLAB code for detecting peaks and removing baselines

Usage

baseline.peakDetection(spectra, left, right, lwin, rwin, snminimum, mono=0, multiplier=5, left.right, lwin.rwin)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>spectra</td>
<td>Matrix with spectra in rows</td>
</tr>
<tr>
<td>left</td>
<td>Smallest window size for peak widths</td>
</tr>
<tr>
<td>right</td>
<td>Largest window size for peak widths</td>
</tr>
<tr>
<td>lwin</td>
<td>Smallest window size for minimums and medians in peak removed spectra</td>
</tr>
<tr>
<td>rwin</td>
<td>Largest window size for minimums and medians in peak removed spectra</td>
</tr>
<tr>
<td>snminimum</td>
<td>Minimum signal to noise ratio for accepting peaks</td>
</tr>
<tr>
<td>mono</td>
<td>Monotonically decreasing baseline if mono&gt;0</td>
</tr>
<tr>
<td>multiplier</td>
<td>Internal window size multiplier</td>
</tr>
<tr>
<td>left.right</td>
<td>Sets eflt and right to value of left.right</td>
</tr>
<tr>
<td>lwin.rwin</td>
<td>Sets lwin and rwin to value of lwin.rwin</td>
</tr>
</tbody>
</table>

Details

Peak detection is done in several steps sorting out real peaks through different criteria. Peaks are removed from spectra and minimums and medians are used to smooth the remaining parts of the spectra. If snminimum is omitted, y3, midspec, y and y2 are not returned (faster)

Value

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>baseline</td>
<td>Matrix of baselines corresponding to spectra spectra</td>
</tr>
<tr>
<td>corrected</td>
<td>Matrix of baseline corrected spectra</td>
</tr>
<tr>
<td>peaks</td>
<td>Final list of selected peaks</td>
</tr>
<tr>
<td>sn</td>
<td>List signal to noise ratios for peaks</td>
</tr>
<tr>
<td>y3</td>
<td>List of peaks prior to singal to noise selection</td>
</tr>
<tr>
<td>midspec</td>
<td>Mid-way baseline estimation</td>
</tr>
<tr>
<td>y</td>
<td>First estimate of peaks</td>
</tr>
<tr>
<td>y2</td>
<td>Second estimate of peaks</td>
</tr>
</tbody>
</table>
**Author(s)**

Kristian Hovde Liland and Bjørn-Helge Mevik

**References**

KEVIN R. COOMBES et al.: Quality control and peak finding for proteomics data collected from nipple aspirate fluid by surface-enhanced laser desorption and ionization.

**Examples**

```r
data(milk)
bc.peakDetection <- baseline(milk$spectra[, drop=FALSE], method='peakDetection',
left=300, right=300, lwin=50, rwin=50)
## Not run:
plot(bc.peakDetection)
## End(Not run)
```

---

**baseline.rfbaseline**  
*Robust Baseline Estimation*

**Description**

Wrapper for Andreas F. Ruckstuhl, Matthew P. Jacobson, Robert W. Field, James A. Dodd’s algorithm based on LOWESS and weighted regression

**Usage**

```r
baseline.rfbaseline(spectra, span = 2/3, NoXP = NULL, maxit = c(2, 2),
b = 3.5, weight = NULL, Scale = function(r) median(abs(r))/0.6745,
delta = NULL, SORT = FALSE, DOT = FALSE, init = NULL)
```

**Arguments**

- **spectra**: Matrix with spectra in rows
- **span**: Amount of smoothing (by fraction of points)
- **NoXP**: Amount of smoothing (by number of points)
- **maxit**: Maximum number of iterations in robust fit
- **b**: Tuning constant in the biweight function
- **weight**: Optional weights to be given to individual observations
- **Scale**: S function specifying how to calculate the scale of the residuals
- **delta**: Nonnegative parameter which may be used to save computation. (See `rfbaseline`
- **SORT**: Boolean variable indicating whether x data must be sorted.
- **DOT**: Disregard outliers totally (boolean)
- **init**: Values of initial fit
Details
Most of the code is the original code as given by the authors. The ability to sort by X-values has been removed and ability to handle multiple spectra has been added.

Value
baseline Matrix of baselines corresponding to spectra
corrected Matrix of baseline corrected spectra

Author(s)
Kristian Hovde Liland and Bjørn-Helge Mevik

References
Andreas F. Ruckstuhl, Matthew P. Jacobson, Robert W. Field, James A. Dodd: Baseline subtraction using robust local regression estimation

Examples
data(milk)
bc.rbe <- baseline(milk$spectra[,1,, drop=FALSE], method='rfbaseline',
span=NULL, NoXP=1000)
## Not run:
plot(bc.rbe)

## End(Not run)

Description
Ideas from Rolling Ball algorithm for X-ray spectra by M.A.Kneen and H.J. Annegarn. Variable window width has been left out

Usage
baseline.rollingBall(spectra, wm, ws)

Arguments
spectra Matrix with spectra in rows
wm Width of local window for minimization/maximization
ws Width of local window for smoothing
baseline.shirley

Value

baseline Matrix of baselines corresponding to spectra spectra
corrected Matrix of baseline corrected spectra

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik

References

M.A. Kneen, H.J. Annegarn: Algorithm for fitting XRF, SEM and PIXE X-ray spectra backgrounds

Examples

data(milk)
bc.rollingBall <- baseline(milk$spectra[, drop=FALSE], wm=200, ws=200, method='rollingBall')
## Not run:
plot(bc.rollingBall)
## End(Not run)

baseline.shirley Shirley Background Estimation

Description

Shirley Background correction for X-ray Photoelectron Spectroscopy.

Usage

baseline.shirley(spectra, t = NULL, limits = NULL, maxit = 50, err = 1e-6)

Arguments

spectra matrix with only 1 y-coordinates by rows (i.e.: y = spectra[1,])
t Optional vector of spectrum abscissa
limits list with the y coordinates between calculation of background. Usually these are the extreme point of the data range.
maxit max number of iteration
err Tolerance of difference between iterations
The shape of the spectrum background or baseline is affected by inelastic energy loss processes, secondary electrons and nearby peaks. A reasonable approximation is essential for a qualitative and quantitative analysis of XPS data especially if several components interfere in one spectrum. The choice of an adequate background model is determined by the physical and chemical conditions of the measurements and the significance of the background to the information to be obtained. The subtraction of the baseline before entering the fit iterations or the calculation of the peak area can be an acceptable approximation for simple analytical problems. In order to obtain chemical and physical parameters in detail, however, it is absolutely necessary to include the background function in the iterative peak fit procedure. The primary function F(E) results from the experimentally obtained function M(E) and the background function U(E) as

\[ F(E) = M(E) - U(E) \]

The kinetic energy E of the spectra can be described as

\[ E = SE + SW \times (i - 1) \]

SE means the start energy in eV, SW is the step width in eV and i the channel number. i can assume values between 1 and N with N as the number of data points.

In case of baseline calculation before initiating the fit procedure, the background is set to the averaged experimental function M(E) in a sector around the chosen start and end channels. With \( i_1 \) as left channel (\( E_1 \): low energy side) and \( i_2 \) as right channel (\( E_2 \): high energy side) the simulation of the baseline is obtained as

\[ U(E_1) = M(E_1) \]

and

\[ U(E_2) = M(E_2) \]

If ZAP is the number of points used for averaging (can be set in the preferences), the intensity of the averaged measuring function at the low energy side is calculated by

\[ M(i_1) = \frac{\sum_{i=0}^{ZAP-1} M(i_1 + i)}{ZAP} \]

and at the high energy side by

\[ M(i_2) = \frac{\sum_{i=0}^{ZAP-1} M(i_2 + i)}{ZAP} \]

In many cases the Shirley model turned out to be a successful approximation for the inelastic background of core level peaks of buried species, which suffered significantly from inelastic losses of the emitted photoelectrons. The calculation of the baseline is an iterative procedure. The number of iteration cycles should be chosen high enough so that the shape of the obtained background function does not change anymore. The analytical expression for the Shirley background is
\[ U(E) = \int_{E}^{\infty} F(E')dE' + c \]

The algorithm of Proctor and Sherwood ([1] A. Proctor, P.M.A. Sherwood, Anal. Chem. 54 (1982) 13) is based on the assumption that for every point of the spectrum the background intensity generated by a photoelectron line is proportional to the number of all photoelectrons with higher kinetic energy. The intensity of the background \( U(i) \) in channel \( i \) is given by

\[ U(i) = \frac{(a - b)Q(i)}{P(i) + Q(i)} + b \]

where \( a \) and \( b \) are the measured intensities in channel \( i_1 \) and \( i_2 \), respectively, and \( P(i) \) and \( Q(i) \) represent the effective peak areas to lower and higher kinetic energies relative to the channel under consideration. An iterative procedure is necessary because \( P \), \( Q \), and \( U(i) \) are unknown. In first approximation \( U(i) = b \) is used.

The function baseline.shirley implements the shirley baseline. It is an iterative algorithm. The iteration stops when the deviation between two consequent iteration is lower than \( err \) or when the max number of iterations \( maxit \) is reached.

**Value**

The baseline function return an object of class baseline.

**References**


**See Also**

baseline

**Examples**

data("01s")
Data <- 01s

## The same example with C1s data
# data("C1s")
# Data <- C1s

Y <- Data[2, , drop = FALSE]
X <- Data[1,]

corrected <- baseline(Y, method = "shirley", t = X)
plot(corrected, rev.x = TRUE, labels = X)

## Not run:
# Dependent on external software
baselineGUI(Y, labels=X, method="shirley")
## baselineAlg-class

### Description

A class that describes a baseline correction algorithm. The idea is that it contains all information needed to use an algorithm with the optimisation framework and the graphical user interface (but see Notes below).

### Objects from the Class

Objects can be created by calls of the form `new("baselineAlg", ...)`. 

### Slots

- **name**: Short-name of the algorithm. This must match the name of the object in the `baselineAlgorithms` list of algorithms, and is used throughout the code to identify the algorithm. It should thus start with a letter and contain only letters, digits, underscores ("_") or dots (".").
- **description**: Description of the algorithm, typically the full name. This will be used in the code to describe the algorithm, so it should not be too long, and not contain newline characters.
- **funcName**: The name of the function used to estimate the baseline. The function must take an argument `spectra`, and return a list with the estimated baselines (`baseline`) original spectra (`spectra`) and the corrected spectra (`corrected`). It can also take other arguments (typically parameters) and return additional components in the list.
- **param**: A data frame with information about the parameters of the algorithm. It should contain the following columns: name - the name of the parameter; integer - TRUE if the parameter only takes integer values, otherwise FALSE; min - the lower limit of allowed values; incl.Min - TRUE if the lower limit is an allowed value, otherwise FALSE; default - the default value; max - the upper limit of allowed values; incl.Max - TRUE if the upper limit is an allowed value, otherwise FALSE.

### Methods

- **description** signature(object = "baselineAlg"): Extract the description slot
- **funcName** signature(object = "baselineAlg"): Extract the funcName slot
- **name** signature(object = "baselineAlg"): Extract the name slot
- **param** signature(object = "baselineAlg"): Extract the param slot

### Note

The goal is that the optimisation framework and the GUI code should get all information about available baseline algorithms through a list of `baselineAlg` objects. This will make it relatively simple to add new baseline algorithms.

Currently, there is information about the algorithms spread around in the code. We plan to move that information into the `baselineAlg` objects, and expand the class accordingly.
Description

A list with descriptions of all baseline algorithms available through the optimisation framework and graphical user interface. The elements of the list are `baselineAlg` objects. The list is used by the code to extract names and information about the baseline algorithms.

Details

The list is not meant for usage by end-users, but is extendable and customizable, allowing for extra algorithms or removal of algorithms.

The names of the list must match the name slot of the elements.

Examples

```r
## Get a list of all algorithms:
names(baselineAlgorithms)
## Show the descriptions
sapply(baselineAlgorithms, description)
## Add new algorithm
baseline.my.alg <- function(spectra, kappa=1, gamma=1){
  baseline <- spectra-kappa+gamma
  corrected <- spectra-baseline
  list(baseline=baseline,corrected=corrected)
}

baselineAlgorithms$my.alg = new("baselineAlg",
  name = "my.alg",
  description = "A new baseline correction algorithm",
  funcName = "baseline.my.alg",
  param = data.frame(
    name = c("kappa","gamma"), # maxit
    integer = c(FALSE, FALSE),
    min = c(0, 0),
    incl.min = c(TRUE, TRUE),
    default = c(1, 1),
    max = c(Inf, 1),
    incl.max = c(FALSE, TRUE)
  )
)
```
baselineAlgorithmsGUI  List of available baseline algorithms for GUI function

Description

A list with data.frames containing parameters, minimum and maximum values for GUIs, step lengths for sliders, default values and currently selected values, plus a short description of each parameter. The list is used by the GUIs, and is user customizable.

Details

The list is not meant for usage by end-users, but is extendable and customizable, allowing for extra algorithms, removal of algorithms or changing of parameter sets.

Examples

```r
## Get a list of all algorithms:
names(baselineAlgorithmsGUI)
## Add new algorithm:
baselineAlgorithmsGUI$my_alg <- as.data.frame(matrix(c(0,20,1,1,0,20,1,1),2,4,byrow=TRUE))
dimnames(baselineAlgorithmsGUI$my_alg) <- list(par=c("kappa", "gamma"),
val=c("min", "max", "step", "default"))
baselineAlgorithmsGUI$my_alg$current <- c(1,1)
baselineAlgorithmsGUI$my_alg$name <- c("Subtractive constant", "Additive constant")
```
minQualMeas: The minimum quality measure value
param.ind.min: A vector of indices into the elements of param of the parameter values corresponding to the minimum quality measure value
param.min: A list of the parameter values corresponding to the minimum quality measure value
qualMeasName: The name of the quality measure

Methods

minQualMeas signature(object = "baselineAlgResult"): Extract the minQualMeas slot
param signature(object = "baselineAlgResult"): Extract the param slot
param.ind.min signature(object = "baselineAlgResult"): Extract the param.ind.min slot
param.min signature(object = "baselineAlgResult"): Extract the param.min slot
qualMeas signature(object = "baselineAlgResult"): Extract the qualMeas slot
qualMeas.ind.min signature(object = "baselineAlgResult"): Extract the qualMeas.ind.min slot
qualMeasName signature(object = "baselineAlgResult"): Extract the qualMeasName slot

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

Class baselineAlgTest, function runTest.

Examples

showClass("baselineAlgResult")
Methods

- **algorithm** signature(object = "baselineAlgTest"): Extract the algorithm slot
- **extraArgs** signature(object = "baselineAlgTest"): Extract the extraArgs slot...
- **funcName** signature(object = "baselineAlgTest"): Extract the funcName slot...
- **param** signature(object = "baselineAlgTest"): Extract the param slot
- **runTest** signature(object = "baselineAlgTest"): Run the test.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

Classes `baselineAlg`, `baselineAlgResult`. Function `runTest`.

Examples

```
showClass("baselineAlgTest")
```

---

**baselineEnv**  
*Baseline environment*

Description

Methods to access the baseline environment.

Usage

```r
baselineEnv()
getBaselineEnv(x, mode="any")
putBaselineEnv(x, value)
```

Arguments

- **x**  
  Name of object to put/get.
- **mode**  
  Mode of object to get.
- **value**  
  Object to put.

Value

getBaseline retrieves an object.

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik
See Also

The functions implementing the baseline algorithms: baseline.als, baseline.fillPeaks, baseline.irls, baseline.lowpass, baseline.medianWindow, baseline.modpolyfit, baseline.peakDetection, baseline.rfbaseline, baseline.rollingBall

Examples

putBaselineEnv('fish', '<=x<-')
getBaselineEnv('fish')

baselineGUI Interactive plotting tool

Description

An interactive plotting tool for dynamic visualization of baselines and their effect using the gWidgets package with GTK+ or Tcl/Tk.

Usage

baselineGUI(spectra, method='irls', labels, rev.x = FALSE)

Arguments

spectra Matrix with spectra in rows
method Baseline correction method (optional)
labels Labels for X-axis (optional)
rev.x Reverse X-axis (optional, default=FALSE)

Details

Creates and updates a list containing current baseline and spectrum (baseline.result). Make sure a gWidget implementation is available, e.g gWidgetsRGtk2 or gWidgetscltk and a corresponding backend like GTK+ or Tcl/Tk. The GUI was developed using GTK which is an external dependency in Windows ans OS X.

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik

Examples

data(milk)
## Not run:
# Dependent on external software
baselineGUI(milk$spectra)
## End(Not run)
custom.baseline  

Customized baseline correction

Description

This function rescales spectrum abscissa by use of breaks and gaps before baseline correction. The effect is that the chosen baseline correction algorithm and parameters will have varying effects along the spectra, effectively giving local control of the amount of rigidity/flexibility of the estimated baseline.

Usage

```r
custom.baseline(spectra, breaks, gaps, trans.win = NULL, just.plot = FALSE, method, ...)
```

Arguments

- `spectra`: Matrix with spectra in rows.
- `breaks`: Vector of locations of break points between sections of varying baseline flexibility (given as abscissa numbers).
- `gaps`: Vector giving the abscissa spacing between each instance of `breaks` (and end-points if not specified in `breaks`).
- `trans.win`: Optional width of transition window around break points used for smoothing rough breaks by LOWESS (default = NULL).
- `just.plot`: Plot the rescaled spectra instead of applying the customized baseline correction if `just.plot` = TRUE (default = FALSE).
- `method`: Baseline correction method to use (class character).
- `...`: Additional named arguments to be passed to the baseline correction method.

Details

This is an implementation of the customized baseline correction suggested by Liland et al. 2011 for local changes in baseline flexibility.

Value

- `baseline`: Estimated custom baselines.
- `corrected`: Spectra corrected by custom baselines.
- `spectra.scaled`: Re-scaled spectra.
- `baseline.scaled`: Estimated baselines of re-scaled spectra.

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik
**doOptim**  

*Optimise several baseline algorithms on a data set*

**Description**

Tests several baseline algorithms with one predictor for a given data set. The baseline algorithms are represented as a list of `baselineAlgTest` objects, and the predictor as a `predictionTest` object.

**Usage**

```r
doOptim(baselineTests, X, y, predictionTest, postproc = NULL,  
tmpfile = "tmp.baseline", verbose = FALSE, cleanTmp = FALSE)
```

**Arguments**

- `baselineTests`: a list of `baselineAlgTest` objects. The baseline algorithms and parameter values to test.
- `X`: A matrix. The spectra to use in the test.
- `y`: A vector or matrix. The response(s) to use in the test.
- `predictionTest`: A `predictionTest` object. The predictor and parameter values to use in the test.
- `postproc`: A function, used to postprocess the baseline corrected spectra prior to prediction testing. The function should take a matrix of spectra as its only argument, and return a matrix of postprocessed spectra.
- `tmpfile`: The basename of the files used to store intermediate calculations for checkpointing. Defaults to "tmp.baseline".
- `verbose`: Logical, specifying whether the test should print out progress information. Default is `FALSE`.
- `cleanTmp`: Logical, specifying whether the intermediate files should be deleted when the optimisation has finished. Default is `FALSE`.

**Examples**

```r
data(milk)  
spectrum1 <- milk$spectra[1,1:10000,drop=FALSE]  
ordinary <- baseline(spectrum1, method="als", lambda=6, p=0.01)  
customized <- custom.baseline(spectrum1, 2900, c(1,20), trans.win=100,  
    just.plot=FALSE, method="als", lambda=6, p=0.01)  
## Not run:
plot(1:10000, spectrum1, type='l')  
lines(1:10000, getBaseline(ordinary), lty=2, col=2, lwd=2)  
lines(1:10000, customized$baseline, lty=3, col=3, lwd=2)  
## End(Not run)
```
Details

The function loops through the baseline algorithm tests in `baselinetests`, testing each of them with the given data and prediction test, and collects the results. The results of each baseline algorithm test is saved in a temporary file so that if the optimisation is interrupted, it can be re-run and will use the pre-calculated results. If `cleantmp` is TRUE, the temporary files are deleted when the whole optimisation has finished.

Value

A list with components

- `baselinetests` The `baselinetests` argument
- `results` A list with the `baselineAlgResult` objects for each baseline test
- `minQualMeas` The minimum quality measure value
- `baselineAlg.min` The name of the baseline algorithm giving the minimum quality measure value
- `param.min` A list with the parameter values corresponding to the minimum quality measure value

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

`baselineAlgTest`, `predictionTest`

Description

Extract the "funcName" slot.

Usage

`funcName(object)`

Arguments

- `object` An object of class `baselineAlg` or `baselineAlgTest`

Value

The `funcName` slot of the object.
getBaseline

Author(s)
Bjørn-Helge Mevik and Kristian Hovde Liland

See Also
baselineAlg, baselineAlgTest

getBaseline
Functions to extract the components of a "baseline" object

Description
The functions extract the baseline, spectra, corrected or call slot of a baseline object; usually the result of a call to baseline.

Usage
getBaseline(object)
getSpectra(object)
getCorrected(object)
getCall(object)

Arguments
object A baseline object

Value
getCall returns the baseline call used to create the object. The other functions return a matrix with the original spectra, estimated baselines or corrected spectra.

Warning
In a future version, one of the slots might be removed from the class definition and calculated on the fly instead, in order to save space. Therefore, do use the extractor functions (getSpectra, getBaseline and getCorrected) instead of accessing the slots directly.

Author(s)
Bjørn-Helge Mevik and Kristian Hovde Liland

See Also
The function baseline, the class baseline
Examples

data(milk)
bl <- baseline(milk$spectra[1:2,])
getBaseline(bl)
getSpectra(bl)
getCorrected(bl)
getCall(bl)

----

ind.min Extraction methods specific for "predictionResult" objects

Description

Extract information from objects of class predictionResult.

Usage

ind.min(object)
paramName(object)

Arguments

object Object of class predictionResult

Value

The corresponding slot of the object.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

predictionResult
**milk**

*MALDI-TOF mass spectra*

**Description**

Matrix of 45 spectra of 21451 m/z values from MALDI-TOF on mixed milk samples.

**Usage**

```r
data(milk)
```

**Format**

A data frame with 45 observations on the following 2 variables.

- `cow` a numeric vector
- `spectra` a matrix with 21451 columns

**Details**

`cow` is the concentration of cow milk in mixed samples of cow, goat, and ewe milk.

**References**


**Examples**

```r
data(milk)
## Not run:
plot(milk$spectra[1,], type = "l")
## End(Not run)
```

**name**

*Extraction methods for "baselineAlg" objects*

**Description**

Extraction methods specifically for objects of class `baselineAlg`

**Usage**

```r
name(object)
description(object)
```
optimWizard

Arguments

object Object of class baselineAlg

Value

The methods return the corresponding slot of the object.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

baselineAlg, funcName.

Description

Set up optimization through a graphical user interface. Optionally collecting values directly from 'baselineGUI'. Retrieve optimisation parameters and results with getOptim and getOptimRes, respectively.

Usage

optimWizard(xL yL postprocL predictionTestL cvsegmentsI getoptimI getoptimresI

Arguments

x Matrix with spectra in rows
y Response vector or matrix in analysis
postproc Custom function for post processing of spectra (optional)
predictionTest Custom prediction object (optional)
cvsegments Cross-validation segments (optional)

Author(s)

Kristian Hovde Liland and Bjørn-Helge Mevik
Examples

```r
## Not run:
data(milk)
X <- milk$spectra[,1]
y <- milk$spectra[,2]
optimWizard(X,y)

# After optimisation is complete
plotOptim(myResults)

## End(Not run)
```

---

`overall.min`  
*Extract the minimum from a baseline optimisation*

Description

Takes the result of an optimisation (a call to `doOptim`) and extracts the minimum quality measure value along with the parameters giving rise to the value.

Usage

`overall.min(results)`

Arguments

- `results`  
  Result of call to `doOptim`

Value

A list with components

- `qualMeas`  
  The minimum quality measure value
- `algorithm`  
  The name of the baseline algorithm corresponding to the minimum
- `param`  
  A list with the parameter values corresponding to the minimum quality measure value

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

- `doOptim`
param

Extract the "param" slot

Description

Extracts the param slot of the object.

Usage

param(object)

Arguments

object An object of class baselineAlg, baselineAlgTest, baselineAlgResult or predictionResult.

Value

The param slot of the object. Usually a data frame, list or numeric.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

Classes baselineAlg, baselineAlgTest, baselineAlgResult, predictionResult

param.ind.min

Extraction methods for "baselineAlgResult" objects

Description

Extraction methods that are specific for objects of class baselineAlgResult

Usage

param.ind.min(object)
qualMeas.ind.min(object)

Arguments

object Object of class baselineAlgResult

Value

The corresponding slot
plotBaseline

Author(s)
Bjørn-Helge Mevik and Kristian Hovde Liland

See Also
Class baselineAlgResult

plotBaseline
Plot method for "baseline" objects

Description
Plot the original spectrum, the estimated baseline, and the corrected spectrum. Optionally zoom and pan plot, either with arguments or interactively.

Usage
## S4 method for signature 'baseline'
plot(x, y, specNo = 1, grid = FALSE, labels = 1:n, rev.x = FALSE, zoom = NULL, ...)
plotBaseline(x, y, specNo = 1, grid = FALSE, labels = 1:n, rev.x = FALSE, zoom = list(xz = 1, yz = 1, xc = 0, yc = 0), ...)

Arguments
- x: The baseline object to be plotted
- y: Unused. Ignored with a warning
- specNo: The row number of the spectrum and baseline to plot. Defaults to 1
- grid: Logical. Whether to show a grid or not. Defaults to FALSE
- labels: Vector. Labels for the x tick marks. Defaults to 1:n
- rev.x: Logical. Whether the spectrum should be reversed. Defaults to FALSE
- zoom: Either TRUE (only for the plot method), which turns on the interactive zoom controls, or a list with components xz, xc, yz and yc, which specifies the desired zoom and pan. Defaults to no zoom or pan
- ...: Other arguments. Currently ignored

Details
The normal way to plot baseline objects is to use the plot method. The plotBaseline function is the underlying work-horse function, and is not meant for interactive use.

Note
Because the argument list of any plot method must start with x, y, and the plot method for the baseline class does not use the y argument, all arguments except x must be named explicitly. Positional matching will not work.
Author(s)
Kristian Hovde Liland and Bjørn-Helge Mevik

See Also
baseline, baseline, baselineGUI

Examples

data(milk)
bl <- baseline(milk$spectra[,1], drop=FALSE)
## Not run:
plot(bl)
plot(bl, zoom = TRUE)
## End(Not run)

plotOptim

Plotting tool for result objects from optimization

Description
A graphical user interface for plotting optimisation results, either one algorithm at the time or comparing algorithms.

Usage
plotOptim(results)

Arguments
results Result list from optimization

Details
plotOptim creates a user interface based on the supplied results. Curve and level plots from single algorithms or comparison of algorithms is avilable.

For single algorithms subsets, levels corresponding to local or global minima, and averages can be extracted for plotting. For comparison of algorithms levels corresponding to local or global minima can be used, or levels corresponding to the minimum when averaging over selected values of the regression parameter, e.g. selected components in PLSR.

Author(s)
Kristian Hovde Liland and Bjørn-Helge Mevik
Class "PLSRTest"

Description

A class describing a PLSR prediction test. To run the test, the "pls" package must be installed.

Objects from the Class

Objects can be created by calls of the form new("PLSRTest", ...).

Slots

- `ncomp`: Integer vector. The number of PLSR components to test
- `cvsegments`: A list of the segments to use in the cross-validation

Extends

Class `predictionTest`, directly.

Methods

- `runTest` signature(object = "PLSRTest"): Run the test

Author(s)

Bjørn-Helge Mevik and Krisitan Hovde Liland

See Also

The base class `predictionTest`. The `runTest` function. The `plsr` function from the "pls" package.

Examples

showClass("PLSRTest")
predictionResult-class

Class "predictionResult"

Description

A class containing the result of running a predictionTest.

Objects from the Class

The normal way to create objects is by calling the method runTest for any object of subclass of predictionTest.

Slots

- **param**: Numeric vector. The regression parameter values tested.
- **qualMeas**: Numeric vector. The quality measure values for each of the values of the `param` slot
- **ind.min**: The index (into `qualMeas`) of the minimum quality measure value
- **minQualMeas**: The minimum quality measure value
- **param.min**: The value of the parameter value corresponding to the minimum quality measure value
- **qualMeasName**: The name of the quality measure
- **paramName**: The name of the regression parameter

Methods

- `ind.min` signature(object = "predictionResult"): Extract the `ind.min` slot
- `minQualMeas` signature(object = "predictionResult"): Extract the `minQualMeas` slot
- `param` signature(object = "predictionResult"): Extract the `param` slot
- `param.min` signature(object = "predictionResult"): Extract the `param.min` slot
- `paramName` signature(object = "predictionResult"): Extract the `paramName` slot
- `qualMeas` signature(object = "predictionResult"): Extract the `qualMeas` slot
- `qualMeasName` signature(object = "predictionResult"): Extract the `qualMeasName` slot

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

Function `runTest`, class `predictionTest`, subclasses `PLSRTTest` and `ridgeRegressionTest`

Examples

```
showClass("predictionResult")
```
**predictionTest-class**  
*Class "predictionTest"*

---

**Description**

A virtual class for all predictor test subclasses. Currently subclasses `PLSRTest` and `ridgeRegressionTest` are defined.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Methods**

No methods defined with class "predictionTest" in the signature.

**Author(s)**

Bjørn-Helge Mevik and Kristian Hovde Liland

**See Also**

Subclasses `PLSRTest` and `ridgeRegressionTest`.

---

**qualMeas**  
*Extraction functions for "predictionResult" or "baselineAlgResult" objects*

---

**Description**

Extract slots from objects of class `predictionResult` or `baselineAlgResult`.

**Usage**

```r
qualMeas(object, ...)
## S4 method for signature 'predictionResult'
qualMeas(object, ...)
## S4 method for signature 'baselineAlgResult'
qualMeas(object, ..., MIN, AVG,
    DEFAULT = c("all", "cond.min", "overall.min", "avg"))
minQualMeas(object)
param.min(object)
qualMeasName(object)
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>object</code></td>
<td>An object of class <code>predictionResult</code> or <code>baselineAlgResult</code></td>
</tr>
<tr>
<td><code>MIN</code></td>
<td>List or vector of parameter names to take the minimum over. Not used if <code>DEFAULT</code> is &quot;cond.min&quot;. See Details</td>
</tr>
<tr>
<td><code>AVG</code></td>
<td>List or vector of parameter names to take the average over. Not used if <code>DEFAULT</code> is &quot;avg&quot;. See Details</td>
</tr>
<tr>
<td><code>DEFAULT</code></td>
<td>Character string. The default way to calculate the minimum (or average) for all parameters. See Details</td>
</tr>
<tr>
<td><code>...</code></td>
<td>Other arguments. Selection of subsets of parameter levels. See Details</td>
</tr>
</tbody>
</table>

Details

The arguments to the `baselineAlgResult` method are interpreted in the following way:

Subsets of parameters levels can be selected by supplying their names and specifying the level indices as vectors. Substituting a vector with "all" will return all levels of the corresponding parameter, and substituting it with "overall" will return the level corresponding to the overall minimum. Minimum and average values for selected parameters can be chosen using `MIN` and `AVG`, respectively, together with a vector of parameter names.

`DEFAULT` specifies the action for each remaining parameters: If "all" (default): returns all levels. If "cond.min": take minimum for each remaining parameter (MIN is not used). If "overall.min": set any remaining parameters to their value corresponding to the overall min. If "avg": take average for each remaining parameter (AVG is not used).

Value

The `qualMeas` method for `baselineAlgResult` objects returns the subsets or minimum values of the `qualMeas` slot of the object as specified above. All other methods simply return the corresponding slot.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

Function `runTest`, classes `baselineAlgResult` and `predictionResult`

Description

A class describing a ridge regression test.
Objects from the Class

Objects can be created by calls of the form `new("ridgeRegressionTest", ...)`.

Slots

  1) lambda: Numeric vector. The smoothing parameter values to test

Extends

  Class `predictionTest`, directly.

Methods

  `runTest` signature(object = "ridgeRegressionTest"): Run the test

Author(s)

  Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

  The base class `predictionTest`. The `runTest` function.

Examples

  `showClass("ridgeRegressionTest")`

---

`runTest`  
Run a `predictionTest` or `baselineAlgTest`  

Description

  Runs the test defined in a `predictionTest` or `baselineAlgTest` object

Usage

  `runTest(object, X, y, ...)`  
  `## S4 method for signature 'PLSRTest'`  
  `runTest(object, X, y)`  
  `## S4 method for signature 'ridgeRegressionTest'`  
  `runTest(object, X, y)`  
  `## S4 method for signature 'baselineAlgTest'`  
  `runTest(object, X, y, predictionTest, postproc, verbose = FALSE)`
Arguments

- **object**: An object of class `baselineAlgTest` or subclass of `predictionTest` (currently `PLSRTTest` or `ridgeRegressionTest`). The object specify the test to be run.
- **X**: A matrix. The spectra to use in the test.
- **y**: A vector or matrix. The response(s) to use in the test.
- **predictionTest**: A `predictionTest` object, describing the prediction test to use for this baseline algorithm test.
- **postproc**: A function, used to postprocess the baseline corrected spectra prior to prediction testing. The function should take a matrix of spectra as its only argument, and return a matrix of postprocessed spectra.
- **verbose**: Logical, specifying whether the test should print out progress information. Default is `FALSE`.
- **...**: Other arguments. Currently only used by the `baselineAlgTest` method.

Value

`runTest` returns an object of class `predictionResult` or `baselineAlgResult`.

Methods

- `signature(object = "baselineAlgTest")`: Baseline corrects the spectra, optionally postprocesses them, and runs a prediction test on the corrected spectra.
- `signature(object = "PLSRTTest")`: Runs PLSR on the data and calculates the cross-validated RMSEP.
- `signature(object = "ridgeRegressionTest")`: Runs ridge regression on the data and calculates the GCV.

Author(s)

Bjørn-Helge Mevik and Kristian Hovde Liland

See Also

`baselineAlgTest, predictionTest, PLSRTTest, ridgeRegressionTest`

---

**XPSdata**

*XPS core line data*

Description

Matrix of x,y values from X-Ray Photoelectron Spectroscopy on test sample. The data are about the Carbon and Oxygen element for 1s shell.
**Usage**

```r
data(C1s)
data(01s)
```

**Format**

A matrix with the following 2 variables (rows).

- **first row** is the abscissa, (Binding Energy [eV])
- **second row** is the Intensity, (a.u.)

**See Also**

`baseline.shirley`

**Examples**

```r
data(C1s)
data(01s)
plot(C1s[,1], C1s[,2], type = "l")
plot(01s[,1], 01s[,2], type = "l")
```
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