Package ‘TurboNorm’

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Type Package

Title A fast scatterplot smoother suitable for microarray normalization

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Author Maarten van Iterson and Chantal van Leeuwen

Maintainer Maarten van Iterson <mviterson@gmail.com>

Description A fast scatterplot smoother based on B-splines with second-order difference penalty. Functions for microarray normalization of single-colour data i.e. Affymetrix/Illumina and two-colour data supplied as marray MarrayRaw-objects or limma RGList-objects are available.

License LGPL

LazyLoad yes

Depends R (>= 2.12.0), convert, limma (>= 1.7.0), marray

Imports stats, grDevices, affy, lattice

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Description

A fast scatterplot smoother based on B-splines with second order difference penalty. Functions for microarray normalization of single-colour data i.e. Affymetrix/Illumina and two-colour data supplied as marray MarrayRaw-objects or limma RGList-objects are available.

Details

Package: TurboNorm
Type: Package
Version: 1.7.2
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License: LGPL
LazyLoad: yes

This package contains an implementation of piecewise constant P-splines of Eilers and Marx (1996) that can be used for normalization of either single- or two-colour data. For two-colour data objects of type RGList from the limma package and MarrayRaw from the package marray can be normalized using the function pspline(). For single colour microarray data wrapper functions are written based on the affy package functions normalize.loess() and normalize.AffyBatch.loess() namely normalize.pspline() and normalize.AffyBatch.pspline(). Also a panel.pspline() is available for adding the smoothed curve to lattice graphics panels.

Note

The package pspline (S original by Jim Ramsey, R port by Brian Ripley) implements the B-spline/Natural Cubic Spline smoother

Author(s)

Chantal van Leeuwen and Maarten van Iterson Maintainer: Maarten van Iterson<mviterson@gmail.com>
methylmethylationation

References


See Also
turbotrend, pspline, normalize.pspline, normalize.AffyBatch.pspline, panel.pspline

---
methylation  

CpG island DNA methylation array data

Description
CpG island DNA methylation array data of a neuro-ectodermal cell line that was treated with a demethylating agent

Usage
data(methylation)

Format
"RGList" as defined in the package limma containing data from CpG island DNA methylation array data of a neuro-ectodermal cell line that was treated with a demethylating agent. The element "weights" of the "RGList" contains the subset of invariant fragments, those without methylation-sensitive restriction sites, as a logical vector.

Details
The data is extracted from a larger experiment described in van Iterson et al. Because the data is from a high-dense tiling array a random subset of the data was chosen for convenience in making the vignette.

References

Examples
data(methylation)
normalize.pspline

Functions for single-colour microarray data normalization using the P-splines

Description

Modified version of normalize.loess and normalize.AffyBatch.pspline from the affy package uses the P-spline smoother instead of the loess algorithm

Usage

normalize.pspline(mat, epsilon = 10^-2, maxit = 1, log.it = TRUE, verbose = TRUE, weights = rep(1, nrow(mat)), ...)

normalize.AffyBatch.pspline(abatch, type=c("together","pmonly","mmonly","separate"), ...)

Arguments

- **mat**: a matrix with columns containing the values of the chips to normalize.
- **abatch**: an AffyBatch object.
- **epsilon**: a tolerance value (supposed to be a small value - used as a stopping criterion).
- **maxit**: maximum number of iterations.
- **log.it**: logical. If TRUE it takes the log2 of mat.
- **verbose**: logical. If TRUE displays current pair of chip being worked on.
- **weights**: For weighted normalization. The default is NULL, so there are no weights used.
- **type**: A string specifying how the normalization should be applied. See details for more.
- **...**: Graphical parameters can be supplied.

Details

This function is a modified version of the function normalize.loess from the affy package. In stead of the loess algorithm the function uses the P-spline algorithm. The type argument should be one of "separate","pmonly","mmonly","together" which indicates whether to normalize only one probe type(PM,MM) or both together or separately.

Value

Normalized AffyBatch

Author(s)

Maarten van Iterson and Chantal van Leeuwen
**References**


**See Also**

normalize.loess

**Examples**

```r
library(affydata)
data(Dilution)
PM <- log2(pm(Dilution[,c(1,3)]))
M <- PM[,1]-PM[,2]
A <- 0.5*(PM[,1]+PM[,2])
nPM <- log2(normalize.pspline(pm(Dilution[,c(1,3)])))
nM <- nPM[,1]-nPM[,2]
nA <- 0.5*(nPM[,1]+nPM[,2])

par(mfcol=c(2,1))
plot(M~A)
plot(nM~nA)

norm <- normalize.AffyBatch.pspline(Dilution, type="pmonly")
weights <- rep(1, nrow(exprs(Dilution)))
normw <- normalize.AffyBatch.pspline(Dilution, type="pmonly", weights=weights)
```

---

**Description**

The function `panel.pspline` is similar to `panel.loess` but show the P-spline smoothed curve.

**Usage**

```r
panel.pspline(x, y, weights = rep(1, length(y)), nintervals = 100, type, horizontal = FALSE, col.line=1
```
Arguments

- **x, y**: vectors giving the coordinates of the points in the scatter plot.
- **weights**: vector of weights of with same length as the data for a weighted smoothing. Default all weights are 1.
- **nintervals**: an integer indicating the number of intervals equal to 1 + number of knots. Currently the intervals must be larger than 10.
- **type**: see `panel.loess`.
- **horizontal**: see `panel.loess`.
- **col.line, lty, lwd**: line colour, type and width that will be used in the plots, defaults are col=1, lty=1 and lwd=1.

Details

`?panel.loess`

Author(s)

Maarten van Iterson and Chantal van Leeuwen

References


See Also

`panel.loess`

Examples

```r
library(marray)
library(lattice)
data(swirl)
data <- data.frame(M=as.vector(maM(swirl)), A=as.vector(maA(swirl)), Sample=rep(paste("Array", 1:4), each=nrow(swirl)))

xyplot(M~A|Sample, data=data, panel = function(x, y) {
  panel.grid(h=-1, v= 2)
  panel.xyplot(x, y)
  panel.loess(x, y, span=0.25, col="black")
  panel.pspline(x, y, col="red", lwd=2))
```
pspline

Function for two-colour microarray data normalization using the P-splines

Description

Wrapper function for two colour microarray data normalization using the P-spline smoother suitable for a RGList- or MarrayRaw-objects.

Usage

pspline(object, background = c("none", "substract"), weights = NULL, nintervals = 100, subset=NULL, showArrays = 0, verbose=FALSE, line.col=2, line.lty=1, line.lwd=2, ...)

Arguments

- **object**: either a RGList or an MarrayRaw-object.
- **background**: for background substraction use 'substract'. Default is no background substraction.
- **weights**: vector of weights that will be used a for a weighted normalization. The default NULL assume equal weight 1 for all data points.
- **nintervals**: number of bins in which the data will be divided. The default is 100 bins.
- **showArrays**: either a integer( > 0) or a vector of integers indicating the arrays for which a MA-plot will be produced.
- **subset**: subset of the data on which the normalization will be based. A special case of weighted normalization.
- **verbose**: if TRUE gives additional information on the fit.
- **line.col, line.lty, line.lwd**: line colour, type and width that will be used in the plots, defaults are col=2, lty=1 and lwd=2.
- **...**: additional graphical arguments for plotting.

Details

if necessary?

Value

The value that will be returned is either a MAList or MarrayNorm-object depending on the input type.

Author(s)

Chantal van Leeuwen and Maarten van Iterson
References


See Also

normalizeWithinArrays, maNormMain

Examples

library(marray)
data(swirl)

x <- pspline(swirl, showArrays=2, pch=20, col="grey")
x <- pspline(swirl, showArrays=2:4, line.col="green")

Descriptio

A fast scatterplot smoother based on B-splines with second order difference penalty

Usage

turbotrend(x, y, w = rep(1, length(y)), n = 100, lambda=10^seq(-10, 10, length=1000), iter=0, method=c("original", "demmler"))

Arguments

x, y: vectors giving the coordinates of the points in the scatter plot.
w: vector of weights of with same length as the data for a weighted smoothing. Default all weights are 1.
n: an integer indicating the number of intervals equal to 1 + number of knots. Currently the intervals must be longer than 10.
lambda: Optionally a user-defined penalty parameter can be provided, if not generalized cross-validation is used to find the optimal penalty parameter.
iters: Number of robustifying iterations similar as lowess.
method: method for solving the system of linear equations either using the data in the original space or transformed to the Demmler-Reinsch basis.

Details

some details about implementation
Value

An object of type pspline is returned as a list with the following items:

- **x**: original data vector \( x \)
- **y**: fitted y-values with same length as vector \( x \)
- **w**: vector of weights
- **n**: number of bins
- **y_trend**: binnend fitted y-values
- **x_trend**: binned x-values
- **lambda**: if scalar penalty parameter used else if vector of two lower and upper bound of the grid
- **iter**: number of robustifying iterations
- **gcv**: generalized cross-validation
- **edf**: effective degrees of freedom (trace of the smoother matrix)
- **call**: function call which produced this output

Author(s)

Maarten van Iterson, Chantal van Leeuwen

References


See Also

- `loess`, `lowess`, `smooth`, `smooth.spline` and `smooth.Pspline`

Examples

```r
library(marray)
data(swirl)

x <- maA(swirl)[,1]
y <- maM(swirl)[,1]
xord <- x[order(x)]
yord <- y[order(x)]
plot(xord, yord, main = "data(swirl) & smoothing splines + lowess")
lines(turbotrend(xord, yord), col = "red", lwd=2)
lines(smooth.spline(xord, yord), col = "green", lwd=2)
lines(lowess(xord, yord), col = "purple", lwd=2)
legend("topleft", c("piecewise constant P-splines", "Cubic B-splines", "lowess"), text.col=c("red","green","purple"))
```
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