

TurboNorm

October 25, 2011

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

van Iterson et al. (2010) *in preparation*.

Examples

```
data(methylation)
```

normalize.pspline *Functions for single-colour microarray data normalization using the*

Description

Modified version of `normalize.loess` and `normalize.AffyBatch.pspline` from the `affy` package uses the P-spline smoother in stead 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

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

Laurent Gautier, Leslie Cope, Benjamin M. Bolstad and Rafael A. Irizarry (2004). `affy` -analysis of Affymetrix GeneChip data at the probe level. *Bioinformatics*, Vol. 20, no. 3, 307-315.

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. *Statistical Science*, Vol 11, No. 2, 89-121.

See Also

[normalize.loess](#)

Examples

```
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")
```

panel.pspline

Panel function for adding a P-spline smoothed curves to a lattice

Description

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

Usage

```
panel.pspline(x, y, weights = rep(1, length(y)), nintervals = 100, type, horizontal
```

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. |
| ... | see panel.loess |

Details`?panel.loess`**Author(s)**

Maarten van Iterson and Chantal van Leeuwen

References

Deepayan Sarkar (2009). `lattice`: Lattice Graphics. R package version 0.17-26. <http://CRAN.R-project.org/package=lattice> Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. *Statistical Science*, Vol 11, No. 2, 89-121.

See Also[panel.loess](#)**Examples**

```
library(marray)
library(lattice)
data(swirl)
data <- data.frame(M=as.vector(maM(swirl)), A=as.vector(maA(swirl)), Sample=rep(paste("A", 1:100)))

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*

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", "subtract"), weights = NULL,
        nintervals = 100, subset=NULL, showArrays = 0, verbose=FALSE,
        line.col=2, line.lty=1, line.lwd=2, ...)
```

Arguments

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

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

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")
```

TurboNorm-package *A fast scatterplot smoother with applications for microarray*

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: | 1.0 |
| Date: | 2010-09-15 |
| License: | LGPL |
| LazyLoad: | yes |

This package contains a 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<M.van_Iterson.HG@lumc.nl>

References

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. Statistical Science, Vol 11, No. 2, 89-121.

See Also

[turbotrend](#), [pspline](#), [normalize.pspline](#), [normalize.AffyBatch.pspline](#), [panel.pspline](#)

turbotrend

*turbotrend: a fast scatterplot smoother***Description**

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),
           method=c("original", "demmler"))
```

Arguments

| | |
|---------------------|---|
| <code>x, y</code> | vectors giving the coordinates of the points in the scatter plot. |
| <code>w</code> | vector of weights of with same length as the data for a weighted smoothing. Default all weights are 1. |
| <code>n</code> | an integer indicating the number of intervals equal to 1 + number of knots. Currently the intervals must be larger than 10. |
| <code>lambda</code> | Optionally a user-defined penalty parameter can be provided, if not generalized cross-validation is used to find the optimal penalty parameter. |
| <code>method</code> | 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:

| | |
|---------------------|--|
| <code>x</code> | original data vector <code>x</code> |
| <code>y</code> | fitted <code>y</code> -values with same length as vector <code>x</code> |
| <code>w</code> | vector of weights |
| <code>n</code> | number of bins |
| <code>ytrend</code> | binned fitted <code>y</code> -values |
| <code>xtrend</code> | binned <code>x</code> -values |
| <code>lambda</code> | if scalar penalty parameter used else if vector of two lower and upper bound of the grid |
| <code>gcv</code> | generalized cross-validation |
| <code>edf</code> | effective degrees of freedom (trace of the smoother matrix) |
| <code>call</code> | function call which produced this output |

Author(s)

Maarten van Iterson, Chantal van Leeuwen

References

Paul .H.C. Eilers and Brain D. Marx (1996). Flexible smoothing with B-splines and Penalties. *Statistical Science*, Vol 11, No. 2, 89-121.

See Also

[loess](#), [lowess](#), [smooth](#), [smooth.spline](#) and [smooth.Pspline](#)

Examples

```
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.co
```


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