

# Package ‘TurboNorm’

October 16, 2018

**Type** Package

**Title** A fast scatterplot smoother suitable for microarray normalization

**Version** 1.28.0

**Date** 2014-18-08

**Author** Maarten van Iterson and Chantal van Leeuwen

**Maintainer** Maarten van Iterson <[mviterson@gmail.com](mailto: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

**Suggests** BiocStyle, affydata

**biocViews** Microarray, OneChannel, TwoChannel, Preprocessing, DNAMethylation, CpGISland, MethylationArray, Normalization

**URL** <http://www.humgen.nl/MicroarrayAnalysisGroup.html>

**git\_url** <https://git.bioconductor.org/packages/TurboNorm>

**git\_branch** RELEASE\_3\_7

**git\_last\_commit** 7582b92

**git\_last\_commit\_date** 2018-04-30

**Date/Publication** 2018-10-15

## R topics documented:

TurboNorm-package . . . . .	2
methylation . . . . .	3
normalize.pspline . . . . .	3
panel.pspline . . . . .	5
pspline . . . . .	6
turbotrend . . . . .	8

<b>Index</b>	<b>10</b>
--------------	-----------

---

TurboNorm-package	<i>A fast scatterplot smoother with applications for microarray normalization</i>
-------------------	---

---

## 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
Date:	2013-29-01
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>

## References

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

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](#)

---

methylation	<i>CpG island DNA methylation array data</i>
-------------	--

---

**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 M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

**Examples**

```
data(methylation)
```

---

normalize.pspline	<i>Functions for single-colour microarray data normalization using the P-splines</i>
-------------------	--

---

**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**

mat	a matrix with columns containing the values of the chips to normalize.
abatch	an <a href="#">AffyBatch</a> 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**

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.

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. *SAGMB*, 11(4).

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")

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

```

---

panel.pspline	<i>Panel function for adding a P-spline smoothed curves to a lattice graphics panel</i>
---------------	---

---

### 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 = FALSE, col.l
```

### 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 langer than 10.
type	see <a href="#">panel.loess</a>
horizontal	see <a href="#">panel.loess</a>
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 <a href="#">panel.loess</a>

### 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>

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. SAGMB, 11(4).

Paul .H.C. Eilers and Brian 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("Array", 1:4), each=nr))

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", "subtract"), weights = NULL, nintervals = 100, subset=NULL)
```

## Arguments

object	either a RGList or an MarrayRaw-object.
background	for background subtraction use 'subtract'. Default is no background subtraction.
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.

<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 <code>col=2</code> , <code>lty=1</code> and <code>lwd=2</code> .
<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**

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. *SAGMB*, 11(4).

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")
```

---

turbotrend	<i>turbotrend: a fast scatterplot smoother</i>
------------	--

---

**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), iter=0, meth
```

**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 larger 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.
iter	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
ytrend	binned fitted y-values
xtrend	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

van Iterson M, Duijkers FA, Meijerink JP, Admiraal P, van Ommen GJ, Boer JM, van Noesel MM, Menezes RX (2012). A novel and fast normalization method for high-density arrays. *SAGMB*, 11(4).

Paul .H.C. Eilers and Brian 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.col=c("red", "green", "purple"))
```

# Index

- \*Topic **datasets**
  - methylation, 3
- \*Topic **hplot**
  - panel.pspline, 5
- \*Topic **package**
  - TurboNorm-package, 2
- \*Topic **regression**
  - turbotrend, 8
- \*Topic **smooth**
  - normalize.pspline, 3
  - pspline, 6
  - turbotrend, 8
  
- AffyBatch, 4
  
- loess, 9
- lowess, 9
  
- maNormMain, 7
- methylation, 3
  
- normalize.AffyBatch.pspline, 2
- normalize.AffyBatch.pspline  
(normalize.pspline), 3
- normalize.loess, 4
- normalize.pspline, 2, 3
- normalizeWithinArrays, 7
  
- panel.loess, 5, 6
- panel.pspline, 2, 5
- pspline, 2, 6
  
- smooth, 9
- smooth.Pspline, 9
- smooth.spline, 9
  
- TurboNorm-package, 2
- turbotrend, 2, 8