
`boxplot.pg`

Boxplot intensities per group

Description

Plots intensities M of an array, per subarray.

Usage

```
boxplot.pg(madat,zerocurve=FALSE,...)
```

Arguments

<code>madat</code>	The name of the madat to be plotted.
<code>zerocurve</code>	If true, plots an x-axis in blue.
<code>...</code>	Miscellaneous graphical paramaters passed down to the <code>plot</code> function.

Examples

```
data(rats)
boxplot.pg(rat22.raw)
```

`brc`

Description of the brc (block,row,column) class

Description

`brc` is a class used to store information about sets of individual spots. Functions like `setexpr` can be applied to `brc` objects to collect further information about them. Functions like `setfinder` usually return `brc` objects.

See Also

`setfinder`,`setexpr`

`craw`

craw

Description

Creates an object of class `madat` (raw intensities).

Usage

```
craw(lamina)
```

Arguments

`lamina` The name of the array we want to analyse.

Examples

```
## Not run: rat22 <- craw('rat22')
```

`cspot`

cspot

Description

Create an object of class `spot`.

Usage

```
cspot(lamina,block,row,column)
```

Arguments

`lamina` The name of the array the spot belongs to.

`block` Block number of the spot.

`row` Row of the spot.

`column` Column of the spot.

Examples

```
spot1 <- cspot('rat22',32,1,2)
```

`global.lowess`

Global lowess normalization

Description

Normalize a microarray intensities file using the global lowess technique.

Usage

```
global.lowess(madat,lowess.f=2/3,flaglevel=-200)
```

Arguments

`madat` a `madat` array intensities file.
`lowess.f` the bandwidth (f), used in the `lowess` robust regression fit.
`flaglevel` spots below this flaglevel will be silently discarded.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
## Not run: rat22.raw <- craw('rat22')  
rat22.glowess <- global.lowess(rat22.raw,flaglevel=-51)
```

`global.norm`

Subarray total normalization

Description

Normalize a microarray intensities file using the total intensity technique.

Usage

```
global.norm(madat,flaglevel=-200)
```

Arguments

`madat` a `madat` array intensities file.
`flaglevel` spots below this flaglevel will be silently discarded.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
## Not run: rat22.raw <- crawl('rat22')
rat22.gnorm <- global.norm(rat22.raw,flaglevel=-51)
```

<code>global.splines</code>	<i>Global splines normalization</i>
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Description

Normalize a microarray intensities file using the global splines technique.

Usage

```
global.splines(madat, cv=FALSE, flaglevel=-200)
```

Arguments

<code>madat</code>	a madat array intensities file.
<code>cv</code>	specifies whether ordinary ('TRUE') or generalized cross-validation ('FALSE') should be used. Note that it's risky to use ordinary cross-validation on most large microarrays experiments.
<code>flaglevel</code>	spots below this flaglevel will be silently discarded.

References

Wahba G. and Craven P. (1979). *Smoothing noisy data with spline functions*. Numerische Mathematik, no. 31 p337-403.

Examples

```
## Not run: rat22.raw <- crawl('rat22')
rat22.gsplines <- global.splines(rat22.raw,flaglevel=-51)
```

intersectEXPR

Intersection of Expression Levels

Description

Applies to two intensities components of madat objects. It returns a brc object, result of the intersection of the two madats, concerning spots whose M had a signal-reversal. In plain english: it filters out the spots which aren't concordant between the two madats.

Usage

```
intersectEXPR(expr1,expr2)
```

Arguments

expr1 Intensity component of the first madat object. Something like madat1\$intensities.
expr2 Intensity component of the second madat object. Something like madat2\$intensities.

madat

Description of the madat class

Description

madat is a class used to store microarrays experiments intensities data. It should be used for raw data as well as normalized and filtered data. It is the default object type handled by all normalization functions, and also the one returned by most of the functions dealing with microarrays data intensities.

See Also

[craw,intersectEXPR,maplot,boxplot.pg](#)

Examples

```
# create the two raw madat files
## Not run: rat22.raw <- craw('rat22')
## Not run: rat23.raw <- craw('rat23')
# self normalize them with the default settings
rat2223.self <- self.normalization(rat22.raw,rat23.raw)
```

maplot

MAPlot: M vs. A Plot

Description

Plots an M vs. A plot of the madat file.

Usage

```
maplot(madat, ..., lowess=TRUE, lowess.f=2/3, lowess.col='red', zerocurve=TRUE, main, reverse=F)
```

Arguments

<code>madat</code>	The name of the madat to be plotted.
<code>...</code>	Miscellaneous graphical paramaters passed down to the <code>plot</code> function.
<code>lowess</code>	If TRUE the lowess robust regression of M vs. A is plotted with the data points.
<code>lowess.f</code>	Lowess bandwidth selection, in case of <code>lowess == TRUE</code> .
<code>lowess.col</code>	Color of the lowess line, in case of <code>lowess == TRUE</code> .
<code>zerocurve</code>	If true, plots an x-axis in blue.
<code>main</code>	Optional custom main title for the plot.
<code>reverse</code>	If true, M is reversed to -M before plotting.
<code>flaglevel</code>	Determines the minimum allowed flaglevel. Spots below this level are silently discarded.
<code>highlight</code>	An optional <code>brc</code> file indicating a set of spots to be highlighte.

Examples

```
data(rats)
maplot(rat22.raw)
```

`rats`

Sample microarray experiments with rats

Description

This is a randomly generated micro madat raw intensity file. It provides `rat22.raw` and `rat23.raw`, to test the normalization functions.

Usage

```
data(rats)
```

reciproca

Dye Swap

Description

Returns the dye-swap of the provided spot.

Usage

```
reciproca(spot)
```

Arguments

spot A spot object file.

replica

Replicate

Description

Returns the in-block replicate of the spot, when available.

Usage

```
replica(spot)
```

Arguments

spot A spot object file.

self.normalization

Dye-swap self normalization

Description

Normalize two microarrays intensities data files against each other, assuming one is a dye-swap of the other.

Usage

```
self.normalization(madat, madat.swap, lowess.f=2/3, flaglevel=-200)
```

Arguments

`madat` a `madat` array intensities file.
`madat.swap` the dye-swap of `madat`.
`lowess.f` the bandwidth (f), used in the `lowess` robust regression fit.
`flaglevel` spots below this `flaglevel` will be silently discarded.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
# create the two raw madat files
## Not run: rat22.raw <- crawl('rat22')
## Not run: rat23.raw <- crawl('rat23')
# self normalize them with the default settings
rat2223.self <- self.normalization(rat22.raw,rat23.raw)
```

`setdesc`

Setdesc

Description

Applies to `brc` objects. It returns information on the identification tags of the spots identified by the `brc`, relating to the supplied `madat` object.

Usage

```
setdesc(brc, madat)
```

Arguments

`brc` A set of spots, namely an object of `brc` class.
`madat` A `madat` object file (used to identify to which array the `brc` pertains).

`setexpr`

Setexpr

Description

Applies to `brc` objects. It returns information on the expression levels of the spots identified by the `brc`, relating to the supplied `madat` object.

Usage

```
setexpr(brc, madat)
```

Arguments

<code>brc</code>	A set of spots, namely an object of <code>brc</code> class.
<code>madat</code>	A <code>madat</code> object file (used to identify to which array the <code>brc</code> pertains).

`setfinder`

Setfinder

Description

May be used after an `maplot` of the `madat` to identify a set of spots and save them into a `brc` object.

Usage

```
setfinder(madat)
```

After having issued a `maplot(madat)` the mouse cursor will turn into an '+', and you can

Arguments

<code>madat</code>	A <code>madat</code> object file.
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setview

Setviewer

Description

Applies to brc objects. It issues a **viewspot** on each element of the brc file. Use with caution, may take a lot of memory.

Usage

```
setview(brc, madat, limit=10, ...)
```

Arguments

brc	A set of spots, namely an object of brc class.
madat	A madat object file (used to identify to which array the brc pertains).
limit	Maximum limit of the spots to show.
...	Additional arguments which will be passed to viewspot .

spot

Description of the spot class

Description

madat is a class used to store information about individual spots. Functions like **summary** and **replica** can be applied to spot objects to collect further information about them.

See Also

cspot, **viewspot**

Examples

```
spot1 <- cspot('rat22', 32, 1, 2)
```

subarray.lowess *Subarray lowess normalization*

Description

Normalize a microarray intensities file using the lowess per subgrid technique.

Usage

```
subarray.lowess(madat,lowess.f=2/3,flaglevel=-200)
```

Arguments

madat a **madat** array intensities file.
lowess.f the bandwidth (f), used in the **lowess** robust regression fit.
flaglevel spots below this flaglevel will be silently discarded.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
## Not run: rat22.raw <- craw('rat22')  
rat22.slowess <- subarray.lowess(rat22.raw,flaglevel=-51)
```

subarray.norm *Subarray total normalization*

Description

Normalize a microarray intensities file using the total intensity per subgrid technique.

Usage

```
subarray.norm(madat,flaglevel=-200)
```

Arguments

madat a **madat** array intensities file.
flaglevel spots below this flaglevel will be silently discarded.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
## Not run: rat22.raw <- crawl('rat22')
rat22.snorm <- subarray.norm(rat22.raw,flaglevel=-51)
```

<code>subarray.splines</code>	<i>Subarray splines normalization</i>
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Description

Normalize a microarray intensities file using the subarray splines technique.

Usage

```
subarray.splines(madat,cv=FALSE,flaglevel=-200)
```

Arguments

<code>madat</code>	a <code>madat</code> array intensities file.
<code>cv</code>	specifies whether ordinary ('TRUE') or generalized cross-validation ('FALSE') should be used. Note that it's risky to use ordinary cross-validation on most large microarrays experiments.
<code>flaglevel</code>	spots below this flaglevel will be silently discarded.

References

Wahba G. and Craven P. (1979). *Smoothing noisy data with spline functions*. Numerische Mathematik, no. 31 p337-403.

Examples

```
## Not run: rat22.raw <- crawl('rat22')
rat22.ssplines <- subarray.splines(rat22.raw,flaglevel=-51)
```

viewspot

Viewspot

Description

Shows (when available) the image of the spot, cropped from the array raw image file.

Usage

```
viewspot(spot,surrounds=FALSE)
```

Arguments

spot A spot object file.
surrounds If true, shows not only the spot but also its surroundings.

within.slide.scale

Within Slide Scale

Description

Scale the variance of a microarray intensities madat object among its subarrays.

Usage

```
within.slide.scale(madat)
```

Arguments

madat a **madat** array intensities file.

References

Yang H. Y., Dudoit S., Luu P. and Speed. T. P. (2001). *Normalization for cDNA microarray data*. <http://www.stat.berkeley.edu/users/terry/zarray/Html/normspie.html>

Examples

```
# Let's first do a smoothing splines global normalization
rat22.gsplines <- global.splines(rat22.raw)
# Take a look at the variances between subarrays
boxplot.pg(rat22.gsplines)
# Not good, lets then scale them
rat22.gsplines <- within.slide.scale(rat22.gsplines)
boxplot.pg(rat22.gsplines)
```