Introduction to OLIN package

Matthias E. Futschik

SysBioLab, Universidade do Algarve

URL: *http://olin.sysbiolab.eu*

April 27, 2020

Contents

1 Overview

Microarray measurements are affected by a variety of systematic experimental errors limiting the accuracy of data produced. Two well-known systematic errors for two-colour arrays are the so-called intensity-dependent and spatial (location-dependent) dye bias. Normalisation aims to correct for systematic errors in microarray data.

The common linear (or global) normalisation method often fails to correct for dye bias as this bias is usually not linear. Although non-linear normalisation procedures have been able to reduce the systematic errors, these methods are based on default parameters and leave it to the user to choose "good" parameters. The optimal adjustment of the normalisation models to the data, however, can be crucial for the efficiency of the normalisation process [1].

The OLIN (*Optimised Local Intensity-dependent Normalisation*) R-package includes two normalisation schemes based on iterative local regression and model selection. Both schemes aim to correct for intensity- and location-dependent dye bias in microarray data. For model selection (parameter optimisation), generalized cross-validation (GCV) is used.

Additionally, several procedures to assess the efficiencies of normalisation are implemented in the package.

A graphical user interface for OLIN has been implemented in the package OLINgui, that is included in the OLINgui package available at the Bioconductor repository.

2   Installation requirements

Following software is required to run the OLIN-package:

- R ($>$ 2.0.0). For installation of R, refer to *http://www.r-project.org*.

- R-packages: methods, stats, locfit. For installation of these add-on packages, refer to *http://cran.r-project.org*.

- Bioconductor packages: Biobase, marray. Refer to *http://www.bioconductor.org* for installation.

If all requirements are fulfilled, the OLIN add-on R-package can be installed. To see how to install add-on R-packages on your computer system, start *R* and type in *help(INSTALL)*. Optionally, you may use the R-function *install.packages()*. Once the OLIN package is installed, you can load the package by

```
>    library(OLIN)
```

3   Inspection for intensity-dependent and spatial artifacts

Microarray data often contains many systematic errors. Such errors have to be identified and removed before further data analysis is conducted. The most basic approach for identification is the visual inspection of MA- and MXY-plots. MA-plots display the logged fold change ($M = log_2(Ch2) - log_2 Ch1$) with respect to the average logged spot intensity ($A = 0.5(log_2(Ch1) + log_2 Ch2)$). MXY-plots display M with respect to the corresponding spot location. More stringent, but also computationally more expensive, are statistical tests presented in section 6.

For illustration, we examine a cDNA microarray experiment comparing gene expression in two colon cancer cell lines (SW480/SW620). The SW480 cell line was derived from a primary tumor, whereas the SW620 cell line was cultured from a lymph node metastasis of the same patient. Sharing the same genetic background, these cell lines serve as a model of cancer progression [3]. The comparison was direct i.e. without using a reference sample. cDNA derived from SW480 cells was labeled by Cy3; cDNA derived from SW620 was labeled by Cy5. The SW480/620 experiment consisted of four technical replicates. The data is stored as object of the class `marrayRaw` (see the documentation for the package `marray`). The average logged spot intensity A and logged fold changes M can be accessed by using the slot accessor methods `maA` and `maM`, respectively.

First we want to load the data and inspect the spatial distribution of foreground and background intensities in both channels. This can be done using the function `fgbg` that plots the spatial distribution of fore- and background spot intensities for both channels (figure 1):

```
>    data(sw)
>    fgbg.visu(sw[,3])
```

The quantity that we are interested in are the (logged) fold-change M. To inspect any existing intensity- or location-dependent bias of M, MA- and MXY-lots can be employed. For MA-lots, the basic `plot` function can be used (figure 2). MXY-lots can be generated by `mxy.plot`(figure 3). Note that the function `mxy.plot` assumes the standard array layout as defined for *marrayRaw/marrayNorm* objects.
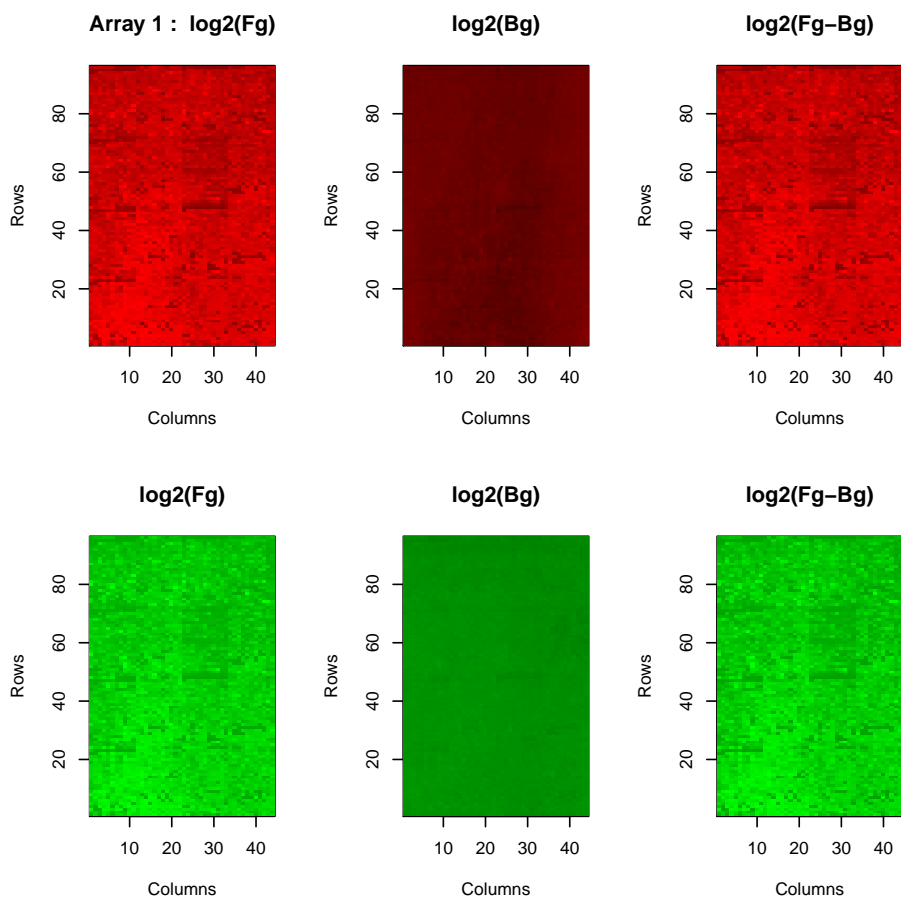
Figure 1: Foreground and background fluorescence intensities for Cy5-channel (top row) and Cy3-channel (bottom) row.
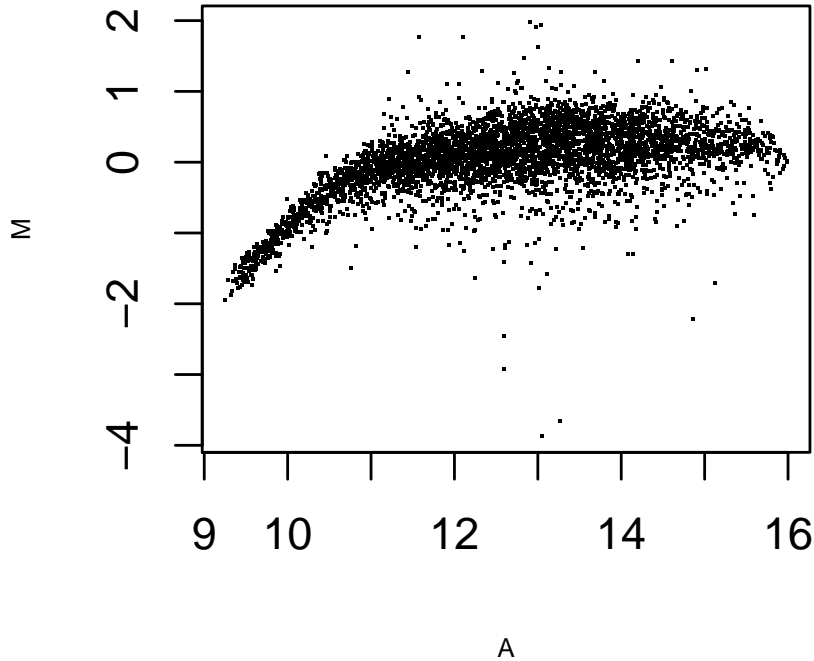
Figure 2: MA-plot of SW480/620 array 3

```
> plot(maA(sw[,3]),maM(sw[,3]),xlab="A",ylab="M")
```

```
> mxy.plot(maM(sw)[,3],Ngc=maNgc(sw),Ngr=maNgr(sw),
+                   Nsc=maNsc(sw),Nsr=maNsr(sw))
```

Additionally the distribution of absolute values of M can be displayed. This visualisation may give an indication whether the span of M is equal across the spatial dimensions of the array (figure 4). To plot $abs(M)$, the function `mxy.abs.plot` can be employed :

```
> data(sw.xy)
> mxy.abs.plot(maM(sw)[,3],Ngc=maNgc(sw),Ngr=maNgr(sw),Nsc=maNsc(sw),Nsr=maNsr(sw))
```

For the two MXY-plots above, the column and row indices were used as proxies for location of the spot. We can use, however, the physical spot location as determined by the scanner for the MXY plots (if the spots' X-and Y-coordinates are available.) Especially, if the gaps between the blocks printed by distinct pins are large, this option may give a better physical representation of the array. Using the function `mxy2.plot`, such plots can be generated (figure 5):
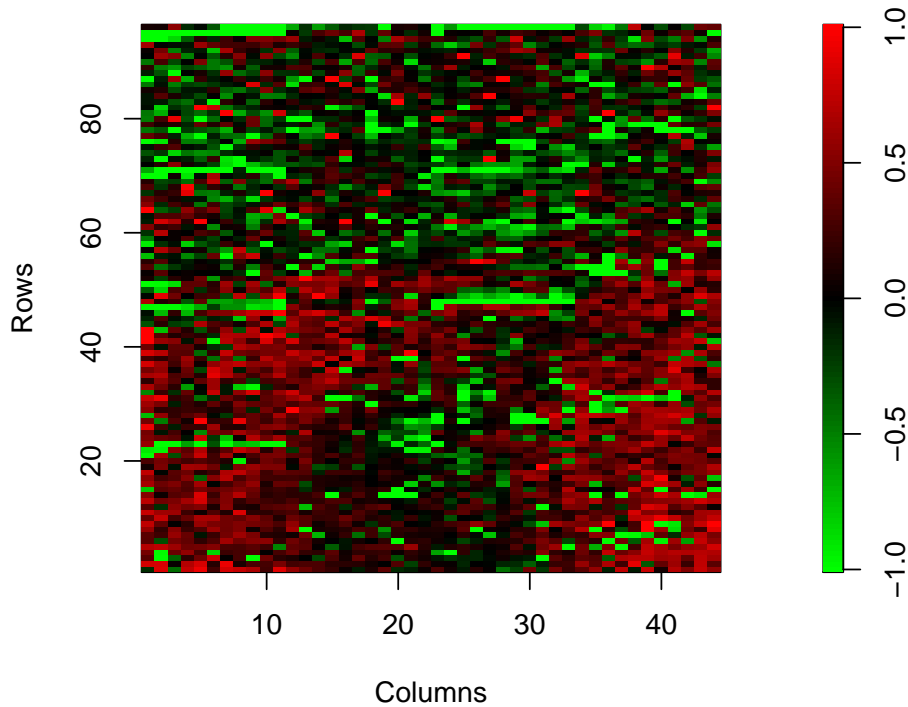
4

Figure 3: MXY-plot of SW480/620 array 3 with columns and rows as proxies for spatial location

```
> data(sw.xy)
> mxy2.plot(maM(sw)[,3],X=sw.xy$X[,3],Y=sw.xy$Y[,3],
+           Ngc=maNgc(sw),Ngr=maNgr(sw),Nsc=maNsc(sw),Nsr=maNsr(sw))
>
```

4   Optimised local intensity-dependent normalisation

Inspection of the MA- and MXY-plots in the previous section indicated a intensity- and location-dependent dye bias. Additionally, the plots show clearly the non-linearity of the biases. To correct for these systematic errors, we apply first a local regression of M with respect to A and spot location X, Y. The residuals of the regression are normalised M. This procedure is motivated by the hybridisation model introduced in reference [1].

The assumption here are: i) Most genes arrayed are not differentially expressed or up-and down-regulation is balanced over the range of A, ii) the spotting procedure did not generate an spatial accumulation of up- or down-regulated genes in localized areas on the array. The validity of both assumptions should be carefully checked for the data to be normalised.

The local regression is performed using LOCFIT algorithm which is based on the same computational ideas as popular lowess method [4, 5] . Required parameters for LOCFIT
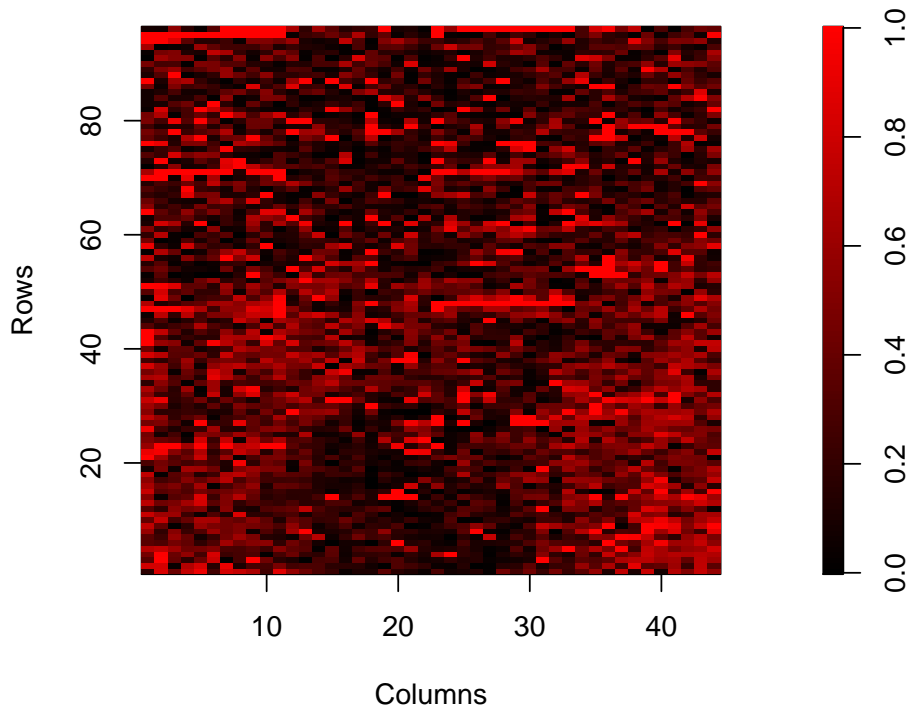
5

Figure 4: MXY-plot of absolute logged fold changes

are the smoothing parameter α and the scale parameter(s) s for multi-dimensional regression. The parameter α specifies the fraction of points that are included in the neighborhood for local fitting and can have a value between 0 and 1. Larger values lead to smoother fits. The setting of scale parameters s is necessary for a local regression with multiple predictor variables. The scale parameters s determine the amount of smoothing in one direction compared to the other directions.

Choosing accurate regression parameters is crucial for the quality of the normalisation. Too large smoothing parameters, for example, lead to a poor fit where local data features are missed and underfitting occurs. If the smoothing parameter is too small, overfitting is produced and the residuals subsequently underestimated. To optimise the parameter setting, two procedures were developed: OLIN and OSLIN. Both methods are based on iterative local regression and parameter selection by GCV. They aim to correct for systematic errors linked with spot intensity and location. A detailed mathematical description can be found in reference [1].

4.1 OLIN

The OLIN (and OSLIN) are implemented in R by the function `olin`:

```
olin(object,X,Y,alpha,iter,OSLIN,scale,weights,genepix,bg.corr,...)
```
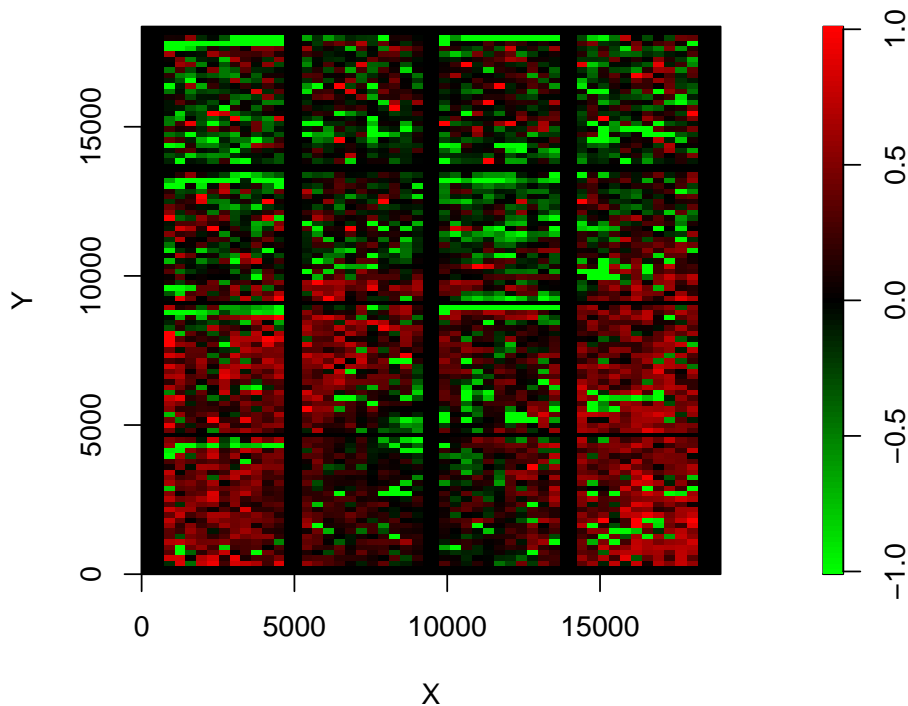
Figure 5: MXY plot of SW480/620 array 1

The input arguments are as follows:

object Object of class *marrayRaw* or *marrayNorm* containing data of the microarray experiment such as spot intensities and array layout for a batch of microarrays. To generate such an object, see the *marryClasses* documentation.

X matrix with x-coordinates of spots. Each column corresponds to one array in the batch. The location is spots detected by scanner is usually found in the output file program of the scanning program. If X=NA, the spotted columns on the array are used as proxies for the location in x-direction (*default*)

Y matrix with y-coordinates of spots. If Y=NA, spotted rows on array are used as proxies for the location in y-direction (*default*).

alpha Vector of α parameters that are tested in the GCV procedure. The α parameter defines the smoothness of fit. The default vector is `seq(0.05,1,0.1)`.

iter Number of iterations in the OLIN or OSLIN procedure. The default value is 3.

OSLIN If OSLIN =TRUE, a subsequent optimised scaling of the range of M across the array is performed. The default value is *FALSE*, i.e. OLIN is performed.

scale Vector of scale parameters s that are tested in a GCV procedure. This allows a different amount of smoothing in Y-direction compared to smoothing in X-direction. The default values of s are `c(0.05,0.1,0.5,1,2,10,20))`.

weights Matrix of prior weights of spots for the regression procedures. Spots can be excluded to be used for the local regression by assigning them to zero. If the weight matrix include negative values, these will be set to zero.

For the weights, the weight matrix stored in the `maW` slot of *marrayRaw* objects can be used (`weights=maW(object)`). Defaults is `NA` resulting in uniform weigths of all spots.

genepix If genepix is set to `TRUE`, spot weights equal zero or larger are set to one for the local regression whereas negative spot with negative weights are not used for the regression. The argument `genepix` should be set to `TRUE`, if `weights=maW(object)` is set and spot quality weights derived by GenePix are stored in `maW(object)`.

bg.corr backcorrection method (for *marrayRaw* objects) : *none* - no background correction, *sub* - simple background subtraction (default), *movingmin* - background intensities are first averaged over 3x3 grids of neighbouring spots and subsequently substracte, *minimum* - zero or negative intensities after background correction are set equal to half the minimum of positive corrected intensities, *edwards*- background correction based on log-linear interpolation, or *normexp*- background correction based on fitting procedure. For further details and references, please refer to to the help page of `backgroundCorrect2` of the *OLIN* package or `backgroundCorrect` of the *limma* package.

... Further arguments passed to the `locfit` function.

For illustration, we apply the OLIN scheme to normalise the third array of the SW480/620 data set. (Note that the function is not restricted to single slide normalisation but normalises all arrays in the given *marray* object.)

```
> norm.olin <- olin(sw[,3],X=sw.xy$X[,3],Y=sw.xy$Y[,3])
```

Inspection of the MA- and MXY-plot indicated that OLIN was able to correct for the intensity- as well as the location-dependent dye bias. The residuals are well balanced around zero in the MA-plot (figure 6). Similarly, spatial bias is no longer apparent (figure 7). Spots with positive and negative log ratio M were evenly distributed across the slide. The statistical tests applied in the next section will confirm these findings.

```
> plot(maA(norm.olin),maM(norm.olin),main="OLIN",pch=".")
> mxy.plot(maM(norm.olin),Ngc=maNgc(norm.olin),Ngr=maNgr(norm.olin),
+                Nsc=maNsc(norm.olin),Nsr=maNsr(norm.olin),main="OLIN")
>
```

OLIN is based on an iterative procedure. In most cases, we found that two or three iterations are already sufficient for normalisation (figure 8).

```
> norm.olin.1 <- olin(sw[,3],X=sw.xy$X[,3],Y=sw.xy$Y[,3],iter=1)
> norm.olin.2 <- olin(norm.olin.1,X=sw.xy$X[,3],Y=sw.xy$Y[,3],iter=1)
> norm.olin.3 <- olin(norm.olin.2,X=sw.xy$X[,3],Y=sw.xy$Y[,3],iter=1)
> M <- cbind(maM(sw)[,3],maM(norm.olin.1),maM(norm.olin.2),maM(norm.olin.3))
> pairs(M,labels= c("raw","1.Iter.","2.Iter.","3.Iter."))
```
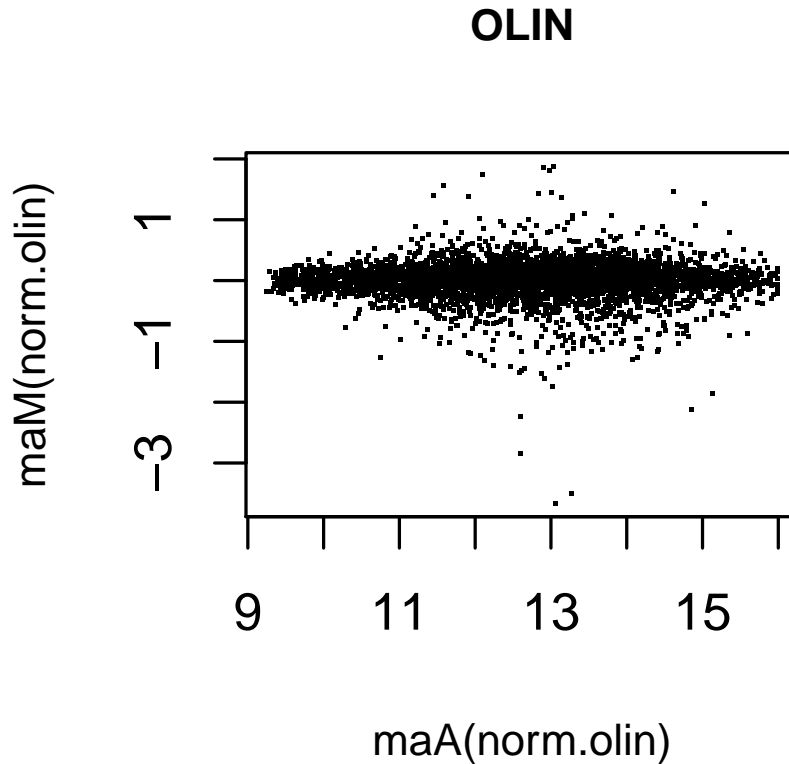
OLIN

Figure 6: MA-plot of array normalized by OLIN

4.2 OSLIN

If we can assume that the variability of log ratios M should be equal across the array, local scaling of M can be performed. As in the previous section, the validity of these assumptions has to be carefully checked for each experiment analyzed. The underlying requirement is again random spotting of arrayed genes. To apply OSLIN:

```
> norm.oslin <- olin(sw[,3],X=sw.xy$X[,3],Y=sw.xy$Y[,3],alpha=c(0.1,1,0.1),OSLIN=TRUE)
```

The local scaling factors are derived by optimized local regression of the absolute log ratio M. The range of regression parameters tested by GCV is [0.1,1] for smoothing parameter. The resulting MA- and MXY-plots for slide 3 are presented in figures 9 and 10.. The variability of log ratios M appears to be even across the array.

```
> plot(maA(norm.oslin),maM(norm.oslin),main="OSLIN",pch=".")
> mxy.plot(maM(norm.oslin),Ngc=maNgc(norm.oslin),Ngr=maNgr(norm.oslin),
+                Nsc=maNsc(norm.oslin),Nsr=maNsr(norm.oslin),main="OSLIN")
>
```
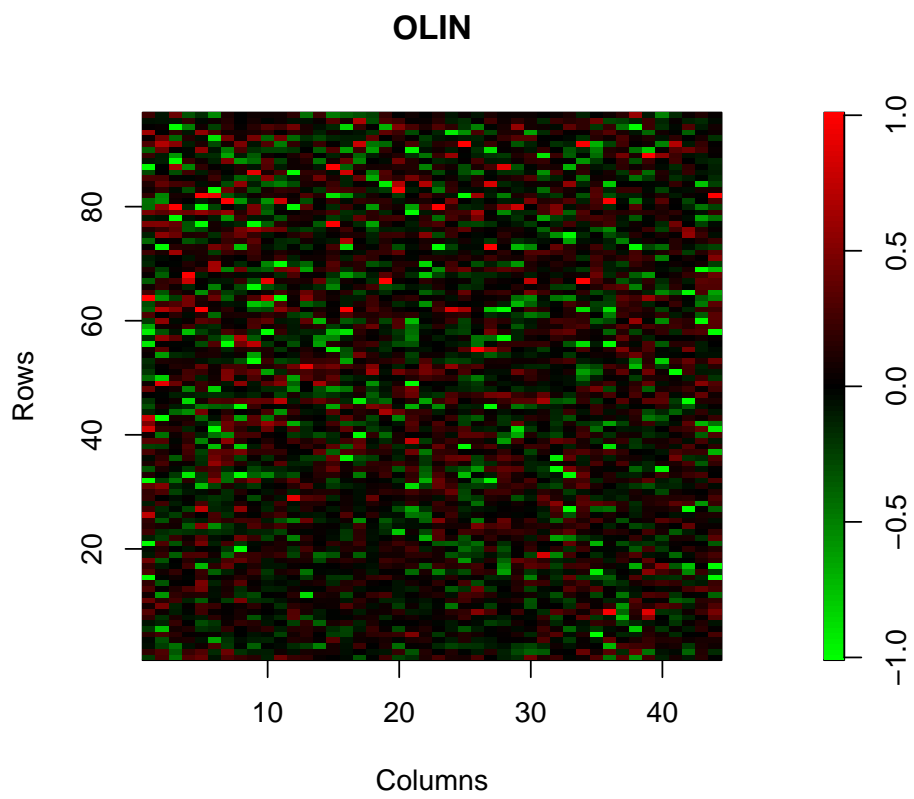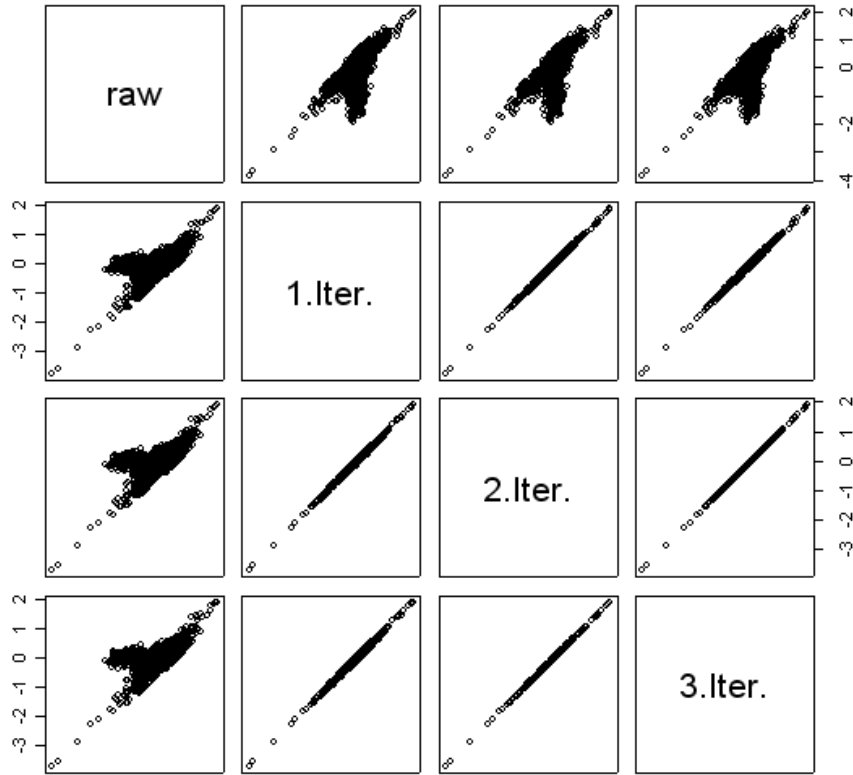
OLIN

Figure 7: MXY-plot of array normalized by OLIN

Figure 8: Convergence of iterative normalisation

The *weights* argument can be used for two purposes. First, it can be to exclude a set of spots (such as control spots) to be used for local regression. Second, it can be used to base the regression on a selected set of genes assumed to be not differentially expressed (*house-keeping genes*). If the normalisation should be based on such a set, weights can be used for local regression. In this case, all weights should be set to zero except for the house-keeping genes for which weights are set to one. In order to achieve a reliable regression, it is important, however, that there is a sufficient number of house-keeping genes that cover the whole expression range and are spotted accross the whole array.

Note that OLIN and OSLIN are sensitive to violations of the assumptions that most genes are not differentially expressed (or up- and down-regulation is balanced) and that genes are randomly spotted across the array. If these assumptions are not valid, local regression can lead to an underestimation of differential expression. In this context, OSLIN is especially sensitive in its performance. However, the sensitivity can be decreased if the minimal smooting parameter `alpha` (default value: 0.05) is set to larger values.

It is also important to note that OLIN/OSLIN is fairly efficient in removing intensity- and spatial-dependent dye bias, so that normalised data will look quite "good" after nor-malisation independently of the true underlying data quality. Normalisation by local re-
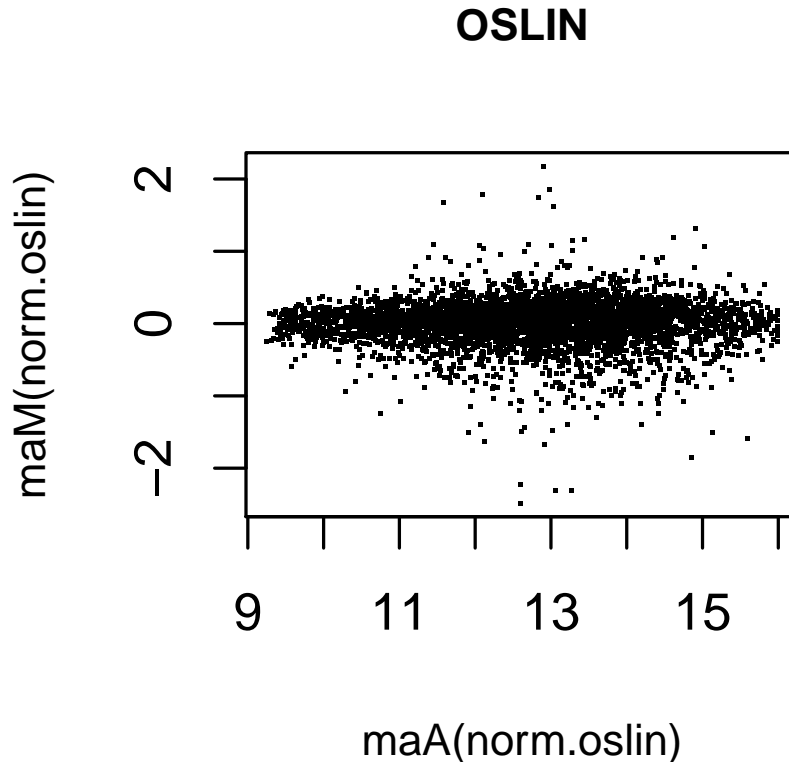
OSLIN

Figure 9: MA-plot of array normalized by OSLIN

gression assumes smoothness of bias. Therefore, localised artifacts such as scratches, edge effects or bubbles should be avoided. Spots of these areas should be flagged (before normalization is applied) to ensure data integrity. To stringently detect artifacts, the OLIN functions `fdr.int`, `fdr.int2`, `fdr.spatial`,`fdr.spatial2`, `p.int`, `p.int2`, `p.spatial` and `p.spatial2` can be used. Flagging of the data spots in regions of intensity- or location-dependent bias can be performed by `sig.mask`. For an example of such an flagging or masking procedure, see the help page of `sig.mask`.

5   Scaling between arrays of a batch

OLIN and OSLIN adjust log ratio M of an array independently of other arrays. A further reduction of variation within experiments may be achieved by additional scaling of M between arrays [7]. This procedure is frequently also termed 'between-array normalisation' in contrast to 'within-array normalisation' as for example performed by O(S)LIN. The log ratios of M will be adjusted in different arrays to achieve a similar overall distribution of M.

However, it assumes that the overall scale of M is the same (or at least similar) in the different arrays to be scaled. This should be carefully checked. Differences in the overall
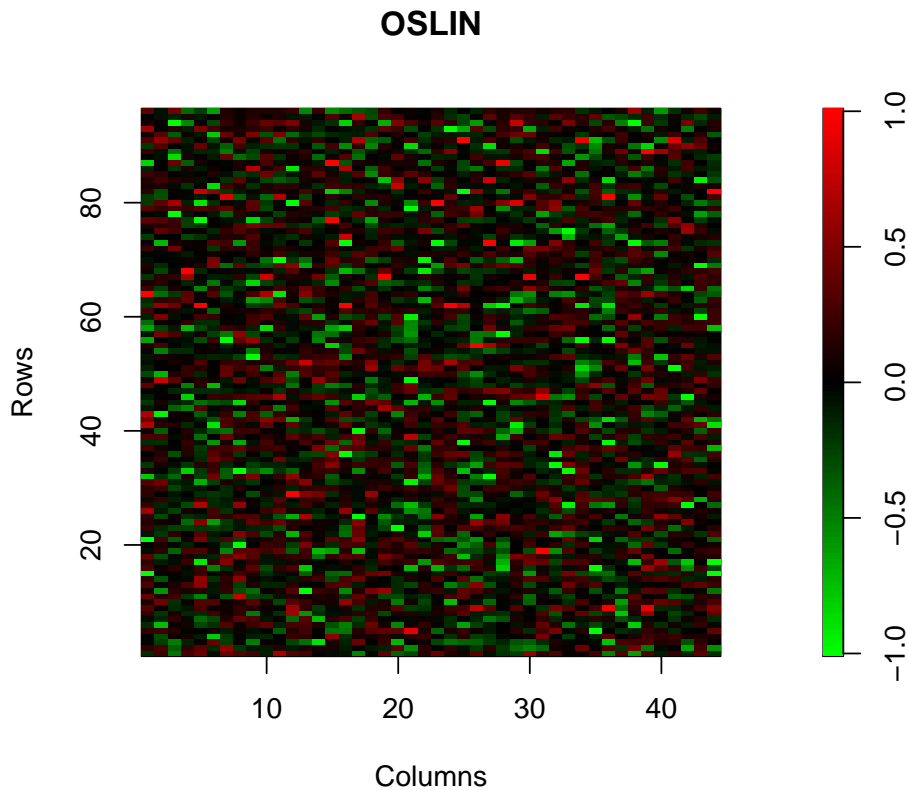
OSLIN

Figure 10: MXY-plot of array normalized by OSLIN

scale of M may indicated e.g. changes in hybridisation conditions or mRNA quality. Caution should also be taken in the interpretation of results for arrays hybridised with biologically divergent samples, if between-array scaling is applied.

Between-array scaling is implemented in the *OLIN* package through function `bas`. Three different scaling procedures are supported:

1. arrays are scaled to have the same variance as calculated by `var`,

2. arrays are scaled to have the same median absolute deviation calculated by `mad`

3. arrays are scaled to have equal values of quantiles.

For illustration, we apply the first scaling procedure to OLIN-adjusted SW480/620 data consisting of four replicate array (figures 11,refdisbas):

```
> data(sw.olin)
> # DISTRIBUTION OF LOGGED RATIOS BEFORE BETWEEN-ARRAY-SCALING
> col <- c("red","blue","green","orange")
> M <- maM(sw.olin)
> plot(density(M[,4]),col=col[4],xlim=c(-2,2))
> for (i in 1:3){
```

13

density.default(x = M[, 4])
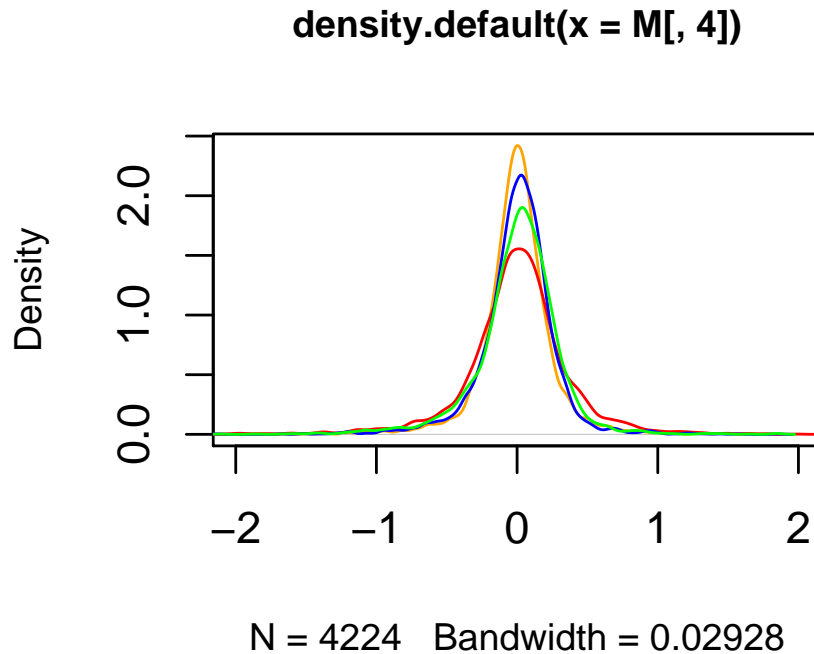

Figure 11: Distribution of M for SW480/620 arrays after OLIN

```
+   lines(density(M[,i]),col=col[i])
+ }
> # BETWEEN-ARRAY SCALING
> sw.olin.s <- bas(sw.olin,mode="var")
> # VISUALISATION
> M <- maM(sw.olin.s)
> plot(density(M[,4]),col=col[4],xlim=c(-2,2))
> for (i in 1:3){
+   lines(density(M[,i]),col=col[i])
+ }
>
>
```

6   Statistical assessment of efficiency of normalisation

An important criterion for the quality of normalisation is its efficiency in removing systematic errors. Although visual inspection might readily reveal prominent artifacts in the microarray data (as shown in section 3), it does not allow for their stringent detection. To overcome this limitation, several methods for statistical detection of systematic errors were implemented in the OLIN package. They might be especially valuable for the comparison of the efficiency

density.default(x = M[, 4])
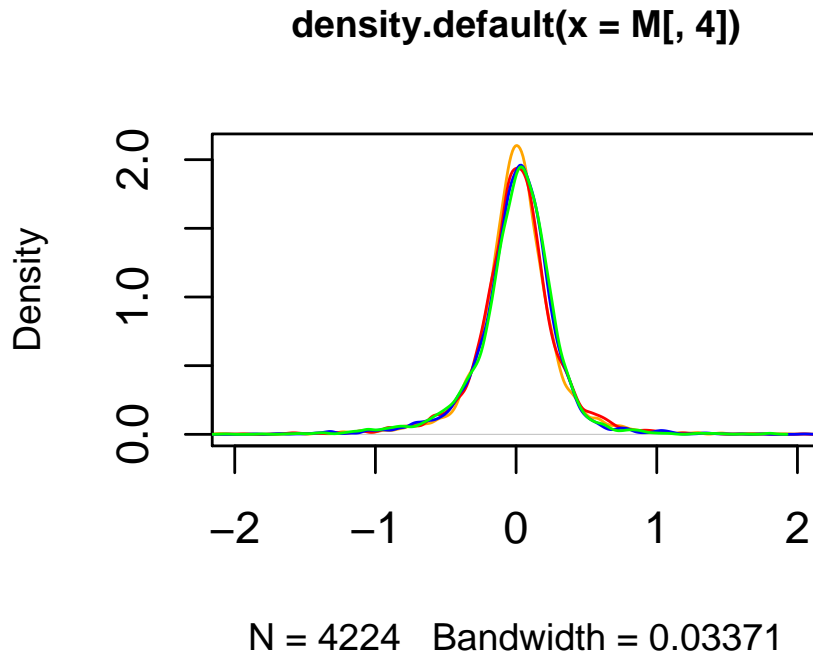

N = 4224   Bandwidth = 0.03371

Figure 12: Distribution of M for SW480/620 arrays after OLIN and between-array scaling

of different normalisation methods. They also might be helpful for newcomers in the field of microarray data analysis, since they can assist the detection of artifacts and may help to improve the experimental procedures.

A simple method to detect intensity- or location-dependent bias is to calculate the correlation between the log ratio M of a spot and the average M in the spot's neighbourhood [6]. A neighourhood on the intensity scale can be defined by a symmetrical window of size $(2*delta + 1)$ around the spot. A correlation of zero can be expected assuming the log ratios are uncorrelated. In contrast, a large positive correlation indicates intensity-dependent bias.

```
>  A <- maA(sw[,3])
>  M <- maM(sw[,3])
> # Averaging
>  Mav <- ma.vector(A,M,av="median",delta=50)
> # Correlation
>  cor(Mav,M,use="pairwise.complete.obs")

          [,1]
[1,] 0.6416701
```

Similarly, the location-dependent bias can be assessed:

```
> # From Vector to Matrix
>  MM <-  v2m(maM(sw)[,3],Ngc=maNgc(sw),Ngr=maNgr(sw),Nsc=maNsc(sw),Nsr=maNsr(sw),visu=FAL
```

```
> # Averaging of matrix M
>  MMav <- ma.matrix(MM,av="median",delta= 2,edgeNA=FALSE)
> # Backconversion to vector
>  Mav <- m2v(MMav,Ngc=maNgc(sw),Ngr=maNgr(sw),Nsc=maNsc(sw),Nsr=maNsr(sw),visu=FALSE)
> # Correlation
>  cor(Mav,M,use="pairwise.complete.obs")

          [,1]
[1,] 0.4377952
```

Although correlation analysis can be readily applied, it cannot deliver localization of experimental bias in the data. To detect areas of bias in the microarray data, alternative methods can be applied.

The OLIN package contains two four models. The first model (`anovaint`) can be used to assess intensity-dependent bias. For this task, the A-scale is divided into N intervals containing equal number of spots. The null hypothesis tested is the equality of the means of M for the different intervals. The input argument `index` indicates which array stored in object sw should be examined. The function `anovaint` is a wrapper around the core function `lm`. The output of `anovaint` equals `summery(lm)`.

```
>  print(anovaint(sw,index=3,N=10))

Call:
lm(formula = Mo ~ intensityint - 1)

Residuals:
    Min      1Q  Median      3Q     Max
-4.0615 -0.1897  0.0190  0.2388  1.7778

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
intensityint1  -0.86456    0.01856 -46.578  < 2e-16 ***
intensityint2  -0.11228    0.01856  -6.049 1.58e-09 ***
intensityint3   0.01868    0.01856   1.006 0.314355
intensityint4   0.06458    0.01856   3.479 0.000508 ***
intensityint5   0.16762    0.01856   9.030  < 2e-16 ***
intensityint6   0.19606    0.01856  10.563  < 2e-16 ***
intensityint7   0.25546    0.01856  13.763  < 2e-16 ***
intensityint8   0.21835    0.01856  11.763  < 2e-16 ***
intensityint9   0.24910    0.01856  13.420  < 2e-16 ***
intensityint10  0.21253    0.01869  11.369  < 2e-16 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 0.3818 on 4214 degrees of freedom
Multiple R-squared: 0.4198,        Adjusted R-squared:  0.4185
F-statistic: 304.9 on 10 and 4214 DF,  p-value: < 2.2e-16
```

```
> data(sw.olin)
> print(anovaint(sw.olin,index=3,N=10))

Call:
lm(formula = Mo ~ intensityint - 1)

Residuals:
    Min      1Q  Median      3Q     Max
-3.5997 -0.1259  0.0250  0.1640  1.8671

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
intensityint1  -0.0049581  0.0153753  -0.322    0.747
intensityint2   0.0085228  0.0153753   0.554    0.579
intensityint3   0.0100288  0.0153753   0.652    0.514
intensityint4   0.0092998  0.0153753   0.605    0.545
intensityint5  -0.0006992  0.0153753  -0.045    0.964
intensityint6  -0.0047550  0.0153753  -0.309    0.757
intensityint7  -0.0156696  0.0153753  -1.019    0.308
intensityint8  -0.0051047  0.0153753  -0.332    0.740
intensityint9   0.0030058  0.0153753   0.195    0.845
intensityint10  0.0005948  0.0154856   0.038    0.969


Residual standard error: 0.3162 on 4214 degrees of freedom
Multiple R-squared:  0.0005903,       Adjusted R-squared:  -0.001781
F-statistic: 0.2489 on 10 and 4214 DF,  p-value: 0.991
```

Similarly, the location-dependent bias can be examined by an ANOVA model implemented as anovaspatial. The array is divided into (xN x yN) rectangular blocks. The null hypothesis tested is the equality of the means of M for the different blocks. The function anovaspatial is a wrapper around functipn lm. The output is the summary of lm (which is suppressed in following examples). Additionally, anovaspatial allows for visualisation of the results (see figure 13 and 14.) The figures display the log10-transformed p-values as derived in the block-wise t-tests. Note that the differences in scales.

```
> anovaspatial(sw,index=3,xN=8,yN=8,visu=TRUE)

> anovaspatial(sw.olin,index=3,xN=8,yN=8,visu=TRUE)
```

Additionally, simple one-factorial ANOVA models were implemented to test microarray data for pin- and plate-dependent bias. Testing for pin bias by anovapin is similar to testing for spatial bias by anovaspatial. The factors in anovapin are the pin indices. The null hypothesis is the equality of the means of M for the different pins. In the same manner, it can be tested if there is a significant variation of M due to the use of distinct microtiter plate for spotting. An ANOVA model for this task is implemented in function anovaplate.In this case, the null hypothesis is the equality of the means of M for the different plates.
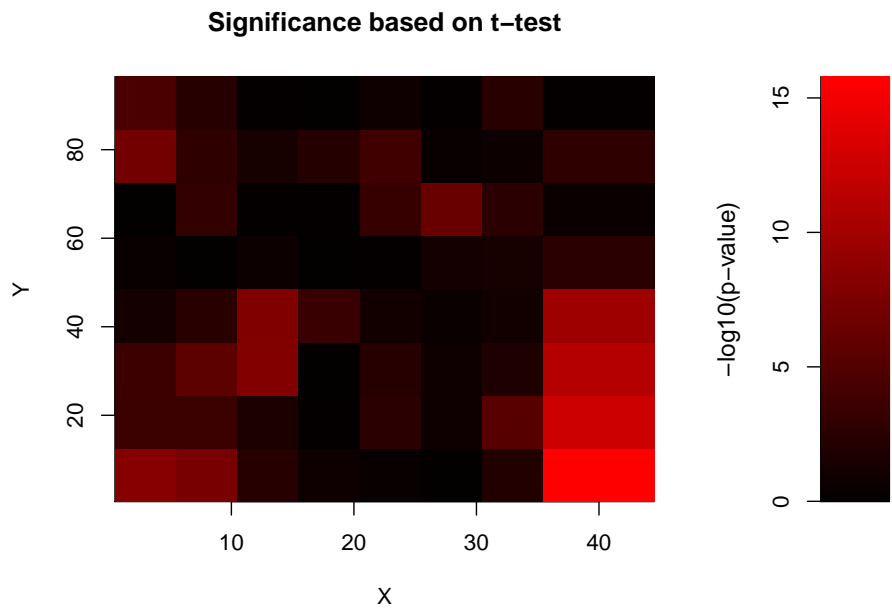
```
> print(anovapin(sw.olin,index=3))
```

Significance based on t–test

Figure 13: ANOVA for raw data

```
Call:
lm(formula = M ~ pin - 1)

Residuals:
    Min      1Q  Median      3Q     Max
-3.6096 -0.1244  0.0253  0.1640  1.8608

Coefficients:
        Estimate Std. Error t value Pr(>|t|)
pin1   0.0057223  0.0194744   0.294    0.769
pin2   0.0009404  0.0194744   0.048    0.961
pin3  -0.0011836  0.0194744  -0.061    0.952
pin4  -0.0002191  0.0194744  -0.011    0.991
pin5  -0.0077155  0.0194744  -0.396    0.692
pin6  -0.0051030  0.0194744  -0.262    0.793
pin7  -0.0077761  0.0194744  -0.399    0.690
pin8   0.0144356  0.0194744   0.741    0.459
pin9   0.0005014  0.0194744   0.026    0.979
pin10  0.0015559  0.0194744   0.080    0.936
pin11  0.0184692  0.0194744   0.948    0.343
pin12 -0.0047442  0.0194744  -0.244    0.808
pin13  0.0051594  0.0194744   0.265    0.791
pin14 -0.0087071  0.0194744  -0.447    0.655
pin15  0.0068432  0.0194744   0.351    0.725
pin16 -0.0177670  0.0194744  -0.912    0.362
```
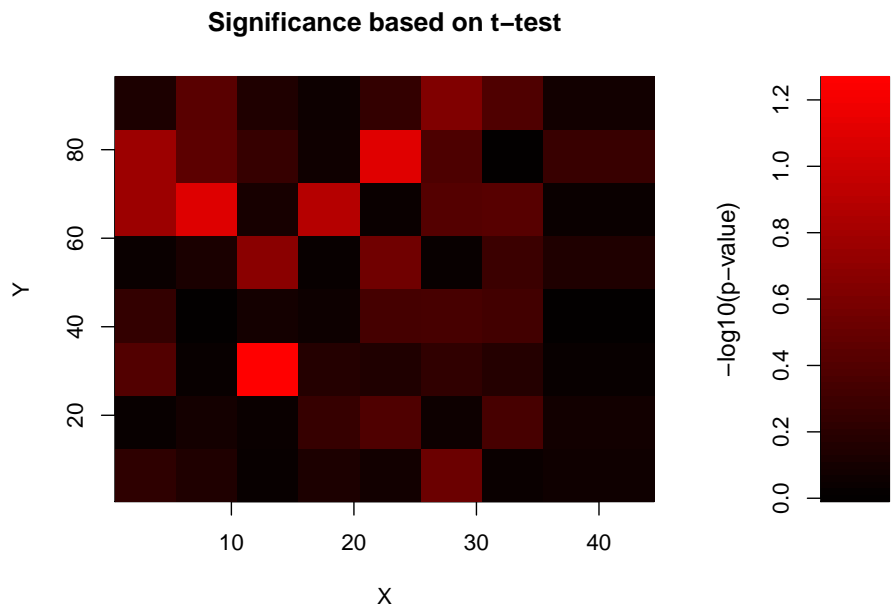
Significance based on t–test

Figure 14: ANOVA for normalised data

```
Residual standard error: 0.3164 on 4208 degrees of freedom
Multiple R-squared:  0.0007643,      Adjusted R-squared:  -0.003035
F-statistic: 0.2012 on 16 and 4208 DF,  p-value: 0.9997


> print(anovaplate(sw.olin,index=3))

Call:
lm(formula = M ~ plate - 1)

Residuals:
    Min      1Q  Median      3Q     Max
-3.5987 -0.1278  0.0261  0.1658  1.8466

Coefficients:
         Estimate Std. Error t value Pr(>|t|)
plate1 -0.0226044  0.0161246  -1.402    0.161
plate2  0.0287166  0.0161246   1.781    0.075 .
plate3 -0.0057500  0.0161246  -0.357    0.721
plate4  0.0018882  0.0161246   0.117    0.907
plate5 -0.0125836  0.0161246  -0.780    0.435
plate6 -0.0015375  0.0161246  -0.095    0.924
plate7  0.0003773  0.0161246   0.023    0.981
plate8 -0.0128983  0.0161246  -0.800    0.424
plate9  0.0157338  0.0161246   0.976    0.329
```

```
plate10 -0.0134014  0.0161246  -0.831    0.406
plate11  0.0223422  0.0161246   1.386    0.166
---
Signif. codes:   0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

Residual standard error: 0.316 on 4213 degrees of freedom
Multiple R-squared:  0.002391,       Adjusted R-squared:   -0.0002133
F-statistic: 0.9181 on 11 and 4213 DF,  p-value: 0.5216
```

ANOVA methods assume normality of the analysed data. This, however, may not be the general case for microarray data. To relax this restriction, permutation tests can be applied. Permutation (or randomization) tests have the advantage that a particular data distribution is not assumed. They rely solely on the observed data examples and can be applied with a variety of test statistics. A major restriction, however, is that permutation tests are computationally very intensive. Generally, such tests are not used in interactive mode but are performed in batch-mode.

Four permutation tests procedures were implemented in the OLIN package. The functions `fdr.int` and `p.int` assess intensity-dependent bias. The functions `fdr.spatial` and `p.spatial` assess location-dependent bias. The basic procedure is similar for all four functions. First, a (intensity or location) neighbourhood of spots is defined similarly to the procedure we used for the correlation analysis . Next, a test statistic is constructed by calculating the *median* or *mean* of M the spot's neighbourhood of chosen size. An empirical distribution of the test statistic $\bar{M}$ is then produced based on random permutations of the data. Comparing $\bar{M}$ of the original data with the empirical distribution, the significance of observing $\bar{M}$ is derived. (Note that a rather low number of random permutations was chosen to avoid time-consuming calculations here. Generally, however, a larger number should be chosen.)

The functions `fdr.int`, `p.int`, `fdr.spatial` and `p.spatial` perform two one-sided random permutation tests. The result can be visualised by the plotting functions `sigint.plot` and `sigxy.plot`. The significance of a spot neighbourhood with large positive deviations of $\bar{M}$ is displayed in red along the A-scale or across the spatial dimensions of the array. Correspondingly, the significance of spot neighbourhood with large negative deviations of $\bar{M}$ are displayed in green.

```
> FDR <- fdr.int(maA(sw)[,3],maM(sw)[,3],delta=50,N=10,av="median")
> sigint.plot(maA(sw)[,3],maM(sw)[,3],FDR$FDRp,FDR$FDRn,c(-5,-5))


> data(sw.olin)
> FDR <- fdr.int(maA(sw.olin)[,3],maM(sw.olin)[,3],delta=50,N=10,av="median")
> sigint.plot(maA(sw.olin)[,3],maM(sw.olin)[,3],FDR$FDRp,FDR$FDRn,c(-5,-5))
```

For slide 3, an significant intensity-dependent bias towards channel 2 (Cy3) was detected for low spot intensities, whereas high-intensity spots are biased towards channel 2 (figure 15). After OLIN normalisation, no significant intensity-dependent bias is apparent (figure 16). A similar result can be found for the removal of location-dependent bias by OLIN (figure 17 and 18).
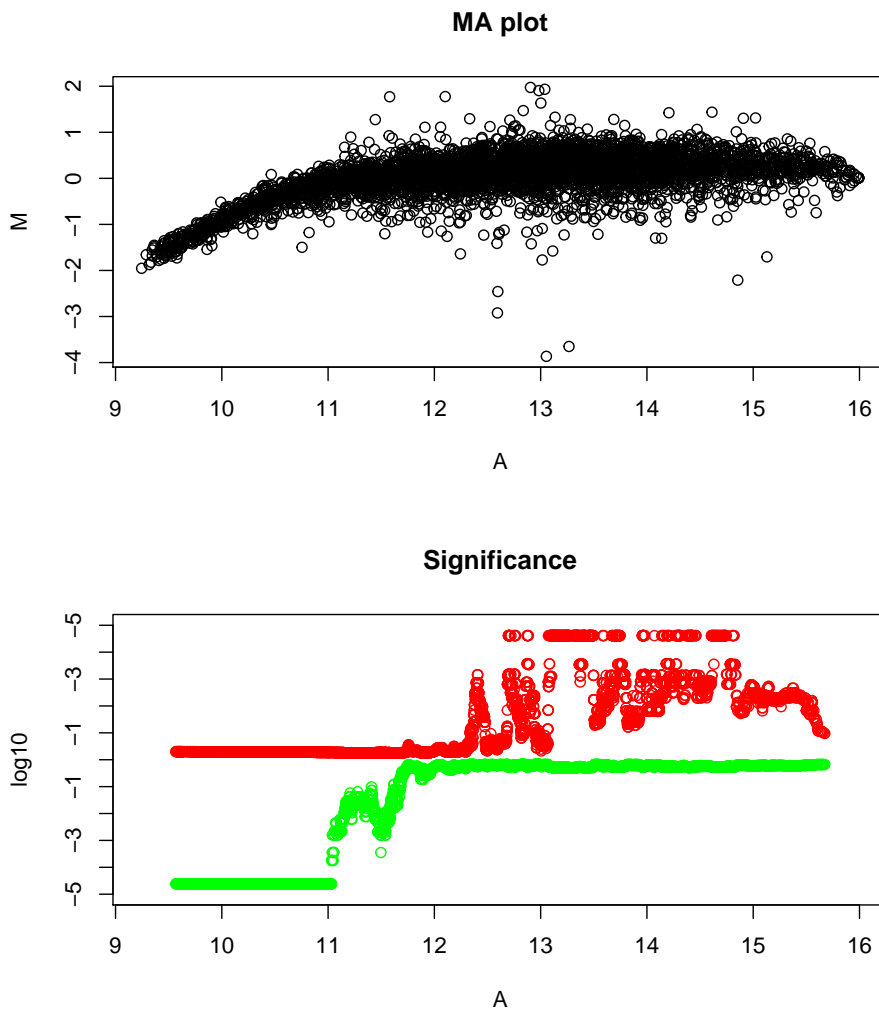
Figure 15: MA-plot and FDRs of intensity-dependent bias for raw data

```
> M <- v2m(maM(sw)[,3],Ngc=maNgc(sw),Ngr=maNgr(sw),
+               Nsc=maNsc(sw),Nsr=maNsr(sw),main="MXY plot of SW-array 1")
> FDR <- fdr.spatial(M,delta=2,N=10,av="median",edgeNA=TRUE)
> sigxy.plot(FDR$FDRp,FDR$FDRn,color.lim=c(-5,5),main="FDR")


> M<- v2m(maM(sw.olin)[,3],Ngc=maNgc(sw.olin),Ngr=maNgr(sw.olin),
+               Nsc=maNsc(sw.olin),Nsr=maNsr(sw.olin),main="MXY plot of SW-array 1")
> FDR <- fdr.spatial(M,delta=2,N=10,av="median",edgeNA=TRUE)
> sigxy.plot(FDR$FDRp,FDR$FDRn,color.lim=c(-5,5),main="FDR")
```

Fold changes should be treated with care if the corresponding spots have significantly biased neighborhoods even after normalisation.

The functions `fdr.int` and `fdr.spatial` assess the significance of dye bias using the false discovery rate whereas the related functions `p.int` and `p.spatial` produce (adjusted)
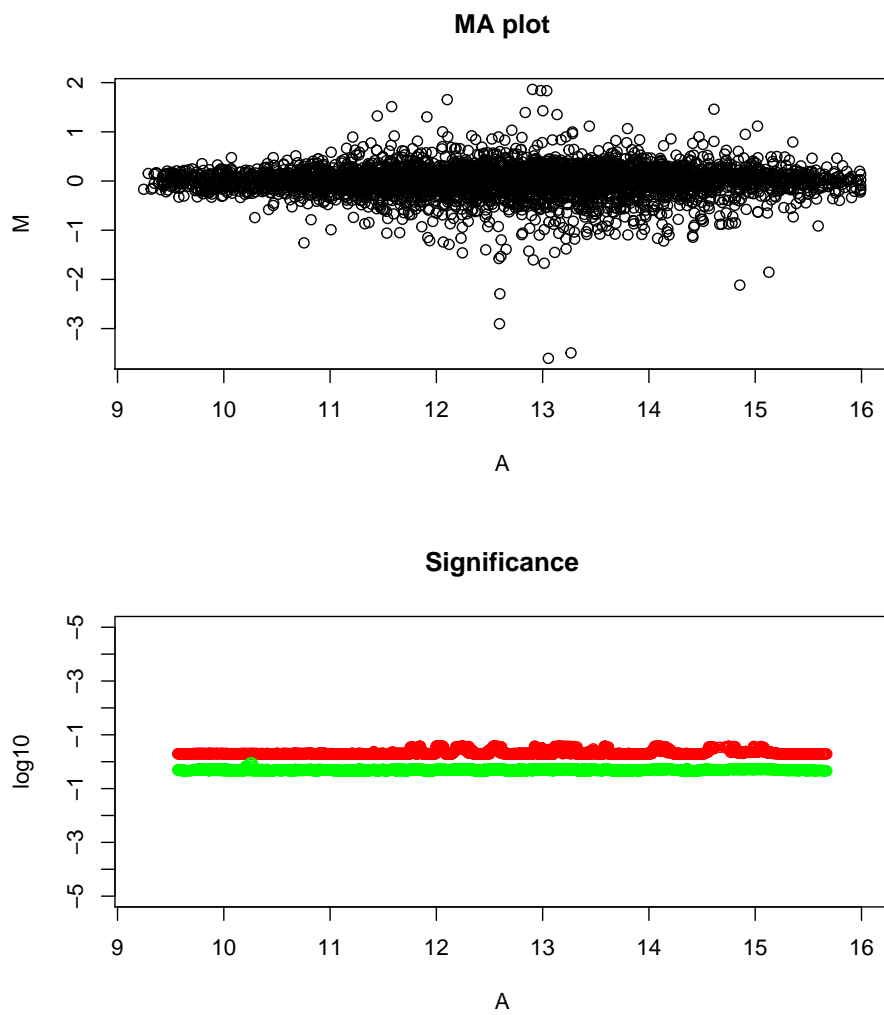
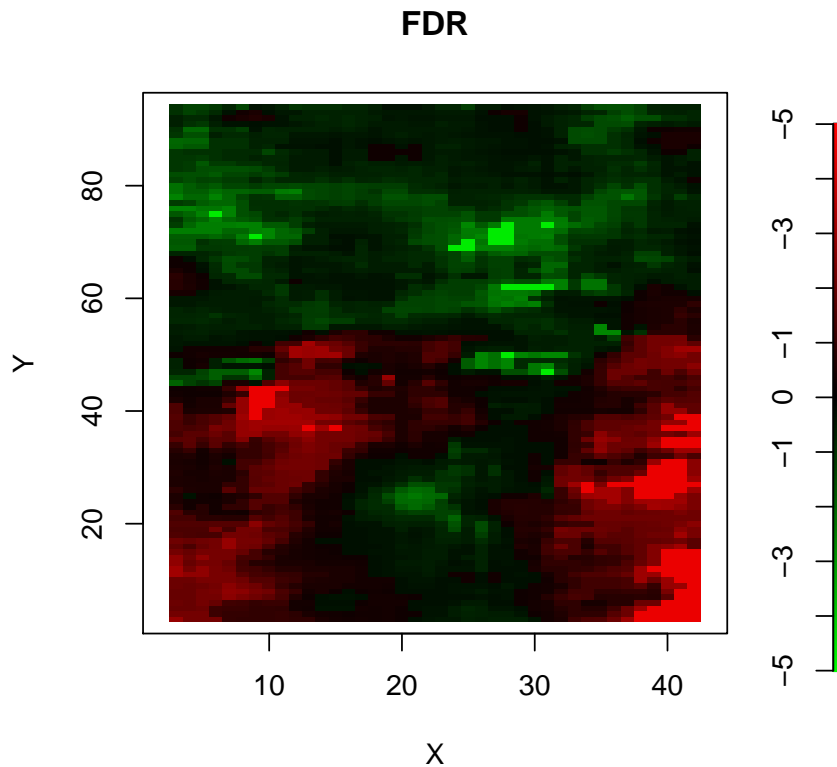Figure 16: MA-plot and FDRs of intensity-dependent bias for data normalised by OLIN

Figure 17: FDR of location-dependent bias for raw data

p-values. Another difference between the functions is the procedure to generate random permutation. The function `fdr.int` and `fdr.spatial` are based on re-sampling without replacement, whereas `p.int` and `p.spatial` are based on re-sampling with replacement. A more detailed description of the permutation tests can be found in the *help*-pages of these functions.

Finally, a second set of functions (`fdr.int2, p.int2, fdr.spatial2, p.spatial2, sigint.plot2,sigxy.plot2` has been introduced for the present version of the OLIN package. Their functionality is the same as for the first set (i.e. `fdr.int, p.int,...`). However, the input arguments and output objects of the functions may differ (see the relevant *help*). Both sets will be merged based on S4-style functions in future versions.

References

[1] M.Futschik and T. Crompton (2004) Model selection and efficiency testing for normalisation of cDNA microarray data, *Genome Biology*, 5:R60

[2] M.E. Futschik and T. Crompton (2005) OLIN: optimized normalization, visualization and quality testing of two-channel microarray data, Bioinformatics, 21(8):1724-6
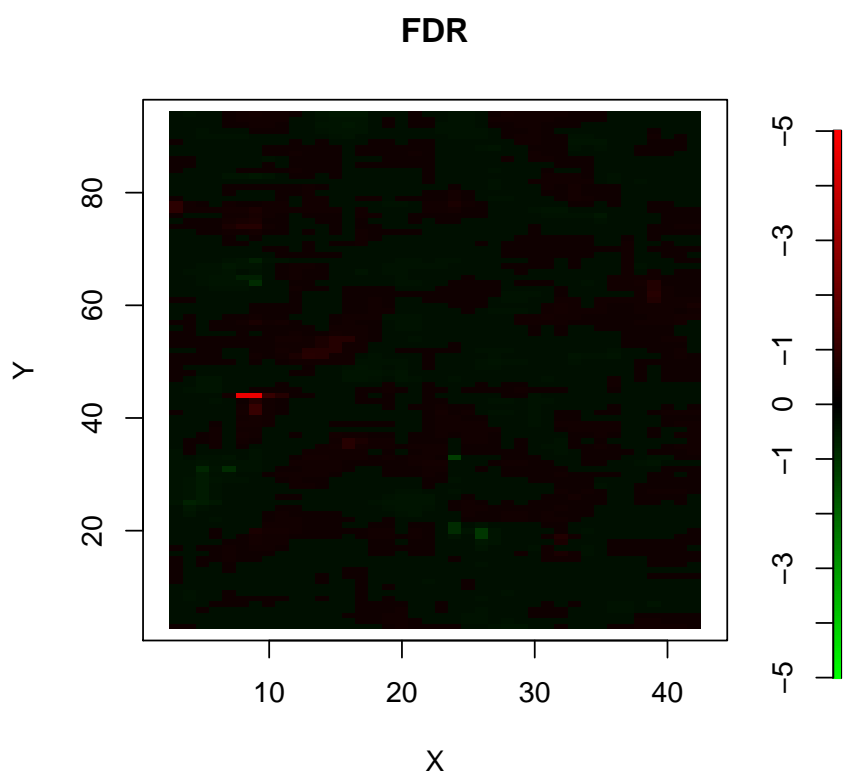
Figure 18: FDR of location-dependent bias for data normalised by OLIN

[3] M. Futschik, A.Jeffs, S.Pattison, N.Kasabov, M.Sullivan, A.Merrie and A.Reeve (2002) Gene expression profiling of metastatic and non-metastatic colorectal cancer cell-lines, *Genome Letters*, 1(1) , 26-34

[4] C. Loader (1999) Local regression and likelihood, Springer, New York

[5] WS Cleveland (1979) Robust locally weighted regression and smoothing scatterplots, *J Am Stat Ass*, 74, 829-836

[6] J. Schuchhardt, D. Beule, A. Malik, E. Wolski, H. Eickhoff, H. Lehrach and H.Herzel (2000) Normalization strategies for cDNA microarrays. *Nucleic Acid Research* 28:e47

[7] Y. H. Yang, S. Dudoit, P. Luu, D. M. Lin, V. Peng, J. Ngai, and T. P. Speed (2002). Normalization for cDNA microarray data: a robust composite method addressing single and multiple slide systematic variation. *Nucleic Acids Research*, Vol. 30, No. 4.