Lab 3: Introduction to Bioconductor marray Packages

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In this lab, we demonstrate the main functions in the marray suite of packages for diagnostic plots and normalization of two-color spotted microarray data. Efforts are underway to interact (read and write) with MAGE-ML documents. A brief description of the four main marray packages is given next.

marrayClasses. This package contains class definitions and associated methods for pre- and post-normalization intensity data for batches of arrays. Methods are provided for the creation and modification of microarray objects, basic computations, printing, subsetting, and class conversions.

marrayInput. This package provides functionality for reading microarray data into R, such as intensity data from image processing output files (e.g., .spot and .gpr files for the Spot and GenePix packages, respectively) and textual information on probes and targets (e.g., from .gal files and god lists). tcltk widgets are supplied to facilitate and automate data input and the creation of microarray-specific R objects for storing these data.

marrayPlots. This package provides functions for diagnostic plots of microarray spot statistics, such as boxplots, scatterplots, and spatial color images. Examination of diagnostic plots of intensity data is important in order to identify printing, hybridization, and scanning artifacts that can lead to biased inferences concerning gene expression.

marrayNorm. This package implements robust adaptive location and scale normalization procedures, which correct for different types of dye biases (e.g., intensity, spatial, plate biases) and allow the use of control sequences spotted onto the array and possibly spiked into the mRNA samples. Normalization is needed to ensure that observed differences in intensities are indeed due to differential expression and not experimental artifacts; fluorescence intensities should therefore be normalized before any analysis that involves comparisons among gene expression measures within or between arrays.

To load the packages

```
> library(marrayNorm)
```

```
Loading required package: marrayClasses
Creating a new generic function for "print" in package
marrayClasses
Creating a new generic function for "rbind" in package
marrayClasses
Creating a new generic function for "cbind" in package
marrayClasses
Loading required package: stepfun
Loading required package: marrayInput
Loading required package: marrayPlots
```

For a more detailed introduction, consult the package vignettes which can be listed by the command `openVignette()`. A demo for `marrayPlots` can also be accessed by `demo(marrayPlots)`. We will work with the sample dataset `swirl`; for a description of `swirl`, type `?  swirl`. To load this dataset

```
> data(swirl)
```

1 Basic classes and methods: `marrayClasses` package

One of the main classes in `marrayClasses` is the `marrayLayout` class; it is used to keep track of important layout parameters, such as the total number of spotted probe sequences on the array, the dimensions of the spot and grid matrices, the plate origin of the probes, information on spotted control sequences. For details on this class consult the help file, `?  marrayLayout`. Two other important classes are `marrayRaw` and `marrayNorm`, which represent, respectively, pre-normalization and post-normalization intensity data for a batch of spotted microarrays. Methods for manipulating instances of these classes are also described in the help files.

The object `swirl` is an instance of the class `marrayRaw`. Try the following commands to obtain information on this object

```
> class(swirl)
```

```
[1] "marrayRaw"
```

```
> slotNames(swirl)
```

```
[1] "maRf"      "maGf"      "maRb"      "maGb"      "maW"       "maLayout"
[7] "maGnames"  "maTargets" "maNotes"
```

```
> swirl

Pre-normalization intensity data:         Object of class marrayRaw.

Number of arrays:         4 arrays.

A) Layout of spots on the array:
Array layout:         Object of class marrayLayout.

Total number of spots:                        8448
Dimensions of grid matrix:                4 rows by 4 cols
Dimensions of spot matrices:                22 rows by 24 cols

Currently working with a subset of 8448 spots.

Control spots:
There are   2 types of controls :
Control       N
    768    7680


Notes on layout:
No Input File

B) Samples hybridized to the array:
Object of class marrayInfo.

  maLabels # of slide        Names experiment Cy3 experiment Cy5      date
1       81         81 swirl.1.spot          swirl      wild type 2001/9/20
2       82         82 swirl.2.spot      wild type          swirl 2001/9/20
3       93         93 swirl.3.spot          swirl      wild type 2001/11/8
4       94         94 swirl.4.spot      wild type          swirl 2001/11/8
  comments
1       NA
2       NA
3       NA
4       NA

Number of labels:  4
Dimensions of maInfo matrix:  4  rows by  6  columns

Notes:
C:/GNU/R/rw1041/library/marrayInput/data/SwirlSample.txt
```

```
C) Summary statistics for log-ratio distribution:
              Min. 1st Qu. Median  Mean 3rd Qu. Max.
swirl.1.spot -2.73   -0.79  -0.58 -0.48   -0.29 4.42
swirl.2.spot -2.72   -0.15   0.03  0.03    0.21 2.35
swirl.3.spot -2.29   -0.75  -0.46 -0.42   -0.12 2.65
swirl.4.spot -3.21   -0.46  -0.26 -0.27   -0.06 2.90

D) Notes on intensity data:
```

To access individual slots

```
> maLayout(swirl)
```

```
Array layout:         Object of class marrayLayout.

Total number of spots:                        8448
Dimensions of grid matrix:                4 rows by 4 cols
Dimensions of spot matrices:                22 rows by 24 cols

Currently working with a subset of 8448 spots.

Control spots:
There are   2 types of controls :
Control       N
    768    7680



Notes on layout:
No Input File
```

```
> maGnames(swirl)
```

```
Object of class marrayInfo.

   maLabels    "ID" "Name"
1     geno1 control  geno1
2     geno2 control  geno2
3     geno3 control  geno3
4     3XSSC control  3XSSC
5     3XSSC control  3XSSC
6      EST1 control   EST1
7     geno1 control  geno1
```

```
8     geno2 control  geno2
9     geno3 control  geno3
10    3XSSC control  3XSSC
...

Number of labels:  8448
Dimensions of maInfo matrix:  8448  rows by  2  columns

Notes:
C:/GNU/R/rw1041/library/marrayInput/data/fish.gal
```

As with other microarray objects in Bioconductor packages, you can use subsetting commands for marrayRaw objects. For data on the first 100 genes in the second array in the swirl batch

```
> sw <- swirl[1:100, 2]
> class(sw)

[1] "marrayRaw"

> sw

Pre-normalization intensity data:         Object of class marrayRaw.

Number of arrays:         1 arrays.

A) Layout of spots on the array:
Array layout:         Object of class marrayLayout.

Total number of spots:                        8448
Dimensions of grid matrix:                4 rows by 4 cols
Dimensions of spot matrices:                22 rows by 24 cols

Currently working with a subset of 100 spots.

Control spots:
There are   2 types of controls :
Control       N
     48      52


Notes on layout:
No Input File
```

```
B) Samples hybridized to the array:
Object of class marrayInfo.

  maLabels # of slide        Names experiment Cy3 experiment Cy5      date
2       82         82 swirl.2.spot      wild type          swirl 2001/9/20
  comments
2       NA

Number of labels:  1
Dimensions of maInfo matrix:  1  rows by  6  columns

Notes:
C:/GNU/R/rw1041/library/marrayInput/data/SwirlSample.txt

C) Summary statistics for log-ratio distribution:
              Min. 1st Qu. Median  Mean 3rd Qu. Max.
swirl.2.spot -1.08   -0.26  -0.12 -0.12       0 1.72

D) Notes on intensity data:
```

You can access red and green foreground and background intensities, and log ratios as follows

```
> Gb <- maGb(swirl)
> dim(Gb)
```

```
[1] 8448    4
```

```
> Gb[1:5, ]
```

```
     [,1] [,2] [,3] [,4]
[1,]  182  175   86   97
[2,]  171  183   86   85
[3,]  153  183   86   85
[4,]  153  142   71   87
[5,]  153  142   71   87
```

```
> Rf <- maRf(swirl)
> dim(Rf)
```

```
[1] 8448    4
```

```
> Rf[1:5, ]
```

```
     swirl.1.spot swirl.2.spot swirl.3.spot swirl.4.spot
[1,]    19538.470    16138.720    2895.1600   14054.5400
[2,]    23619.820    17247.670    2976.6230   20112.2600
[3,]    21579.950    17317.150    2735.6190   12945.8500
[4,]     8905.143     6794.381     318.9524     524.0476
[5,]     8676.095     6043.542     780.6667     304.6190
```

```
> M <- maM(swirl)
> dim(M)
```

```
[1] 8448    4
```

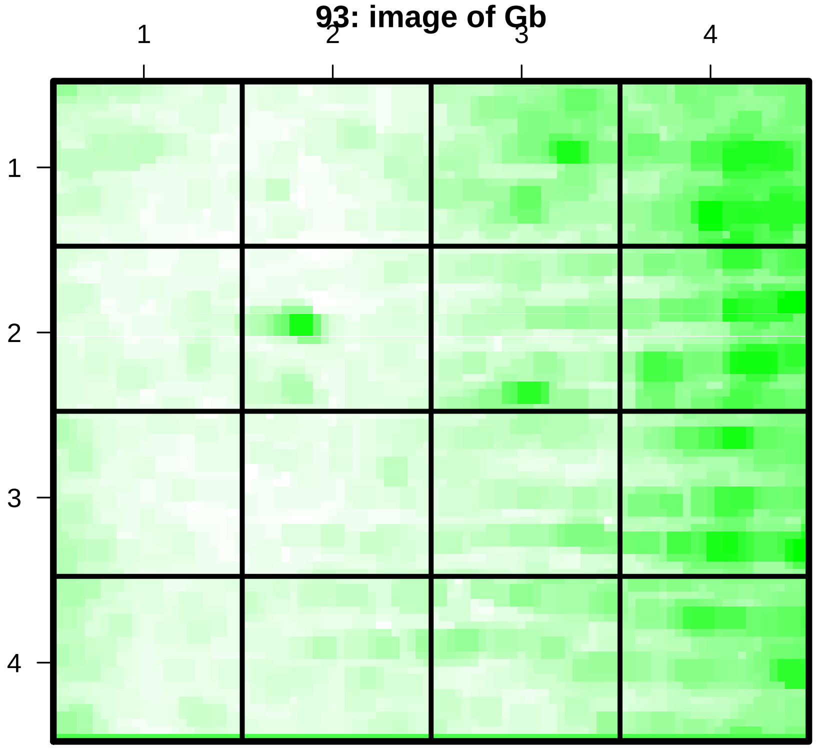
2 Reading in data: marrayInput package

This package provides functionality for reading microarray data into R, such as intensity data from image processing output files (e.g., .spot and .gpr files for the Spot and GenePix packages, respectively) and textual information on probes and targets (e.g., from .gal files and god lists). tcltk widgets are supplied to facilitate and automate data input and the creation of microarray-specific R objects for storing these data.
See for example ? read.marrayRaw or ? widget.marrayRaw.

3 Diagnostic plots: marrayPlots package

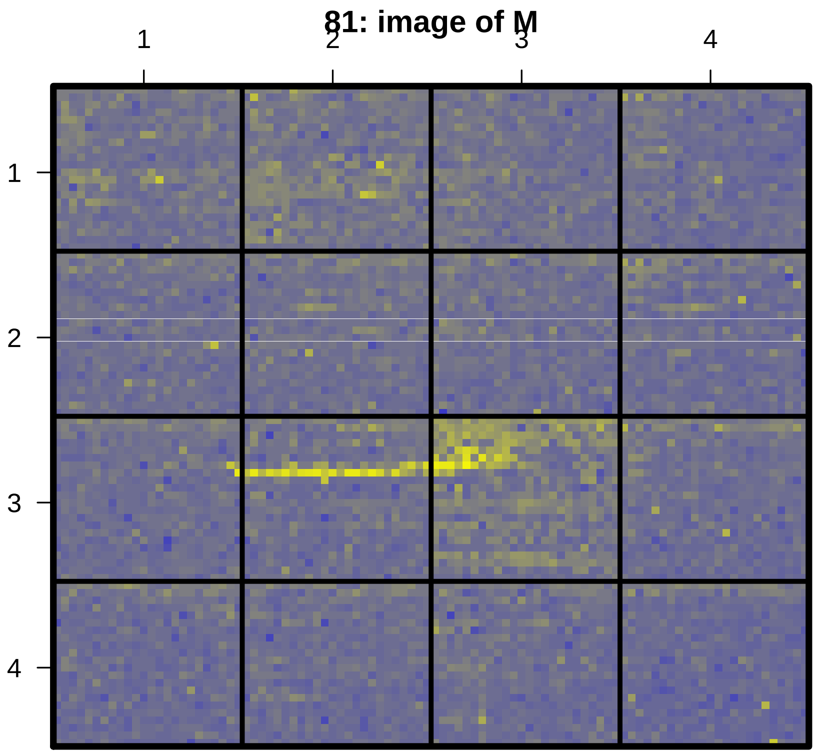
The marrayPlots package provides functions for diagnostic plots of microarray spot statistics, such as boxplots, scatterplots, and spatial color images. To produce a spatial image of background intensities for the Cy3 channel in the third array

```
> tmp <- maImage(swirl[, 3], x = "maGb", bar = FALSE)
```



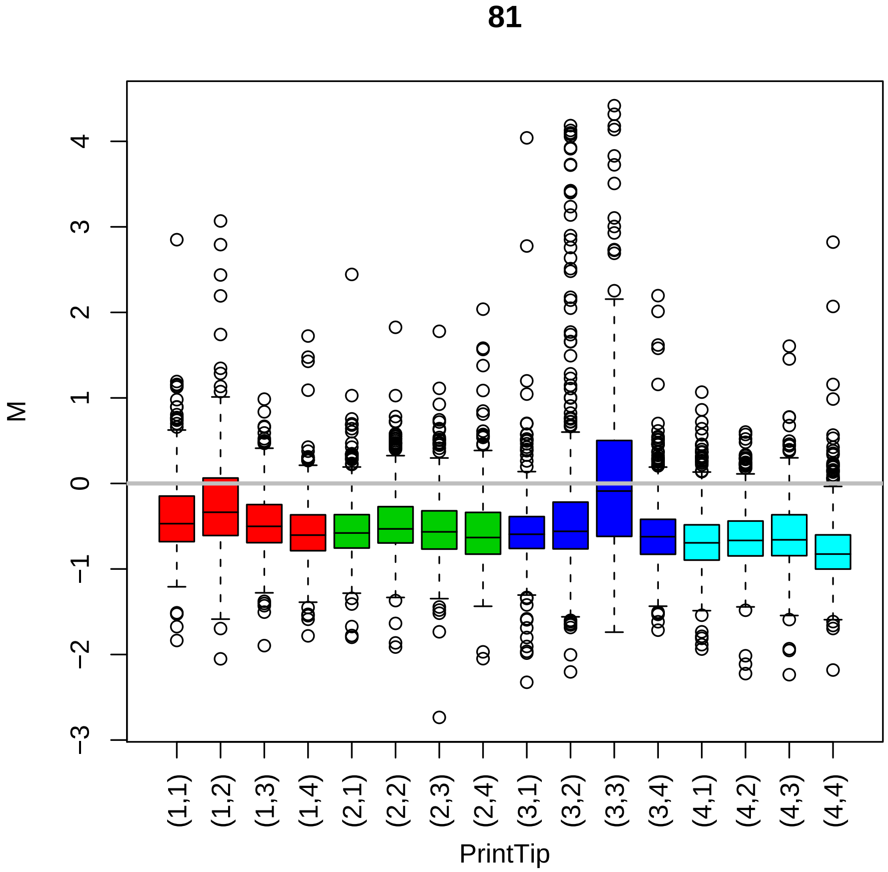
To produce a spatial image of log ratios for the first array in the batch

```
> tmp <- maImage(swirl[, 1], col = maPalette(low = "blue", high = "yellow"),
+     bar = FALSE)
```



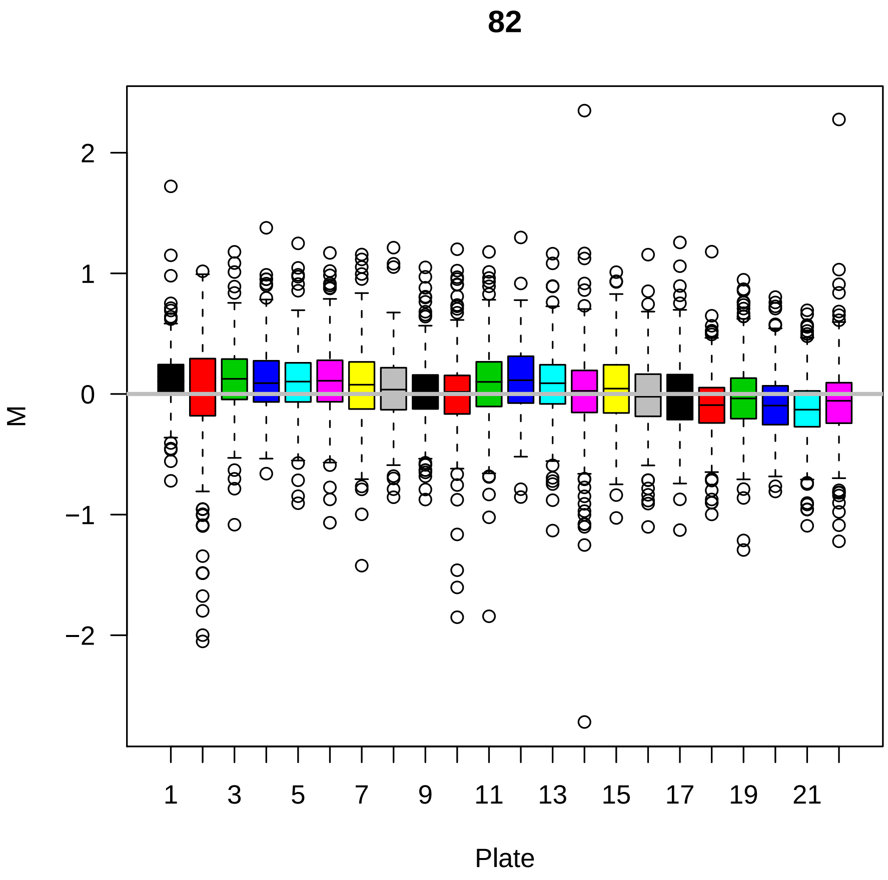
To produce boxplots of log ratios by sector for the first array in the batch

```
> maBoxplot(swirl[, 1])
```



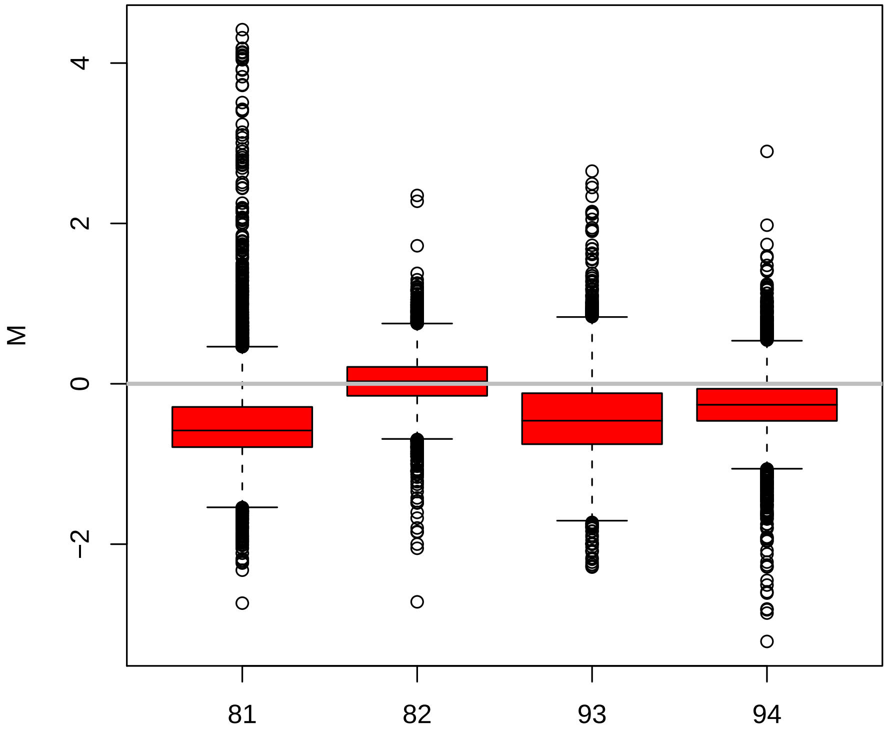
To produce boxplots of log ratios by plate for the second array in the batch

```
> maPlate(swirl) <- maCompPlate(swirl, n = 384)
> maBoxplot(swirl[, 2], x = "maPlate", names = NULL)
```



For boxplots of log ratios for all four arrays

```
> maBoxplot(swirl)
```



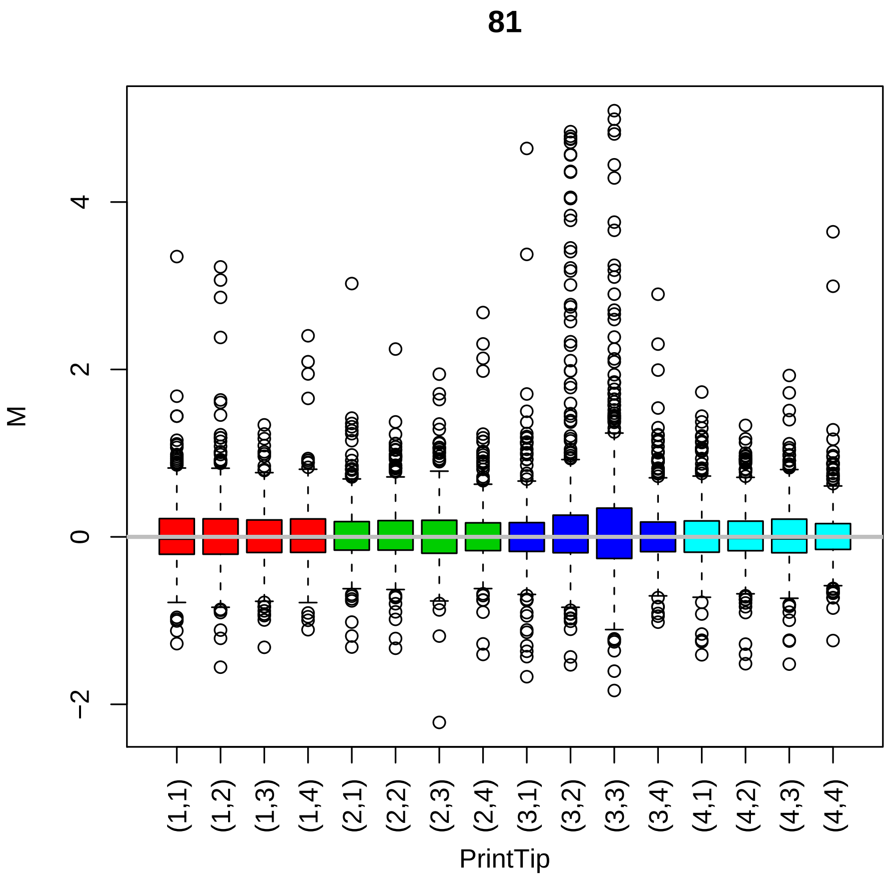
4 Normalization: `marrayNorm` package

The `marrayNorm` package implements robust adaptive location and scale normalization procedures, which correct for different types of dye biases (e.g., intensity, spatial, plate biases). The main location and scale normalization function is `maNormMain`. Simpler wrapper functions are provided in `maNorm` and `maNormScale`. The functions operate on objects of class `marrayRaw` (or possibly `marrayNorm`, if normalization is performed in several steps) and return objects of class `marrayNorm`. For within-print-tip-group loess location normalization of the batch `swirl`

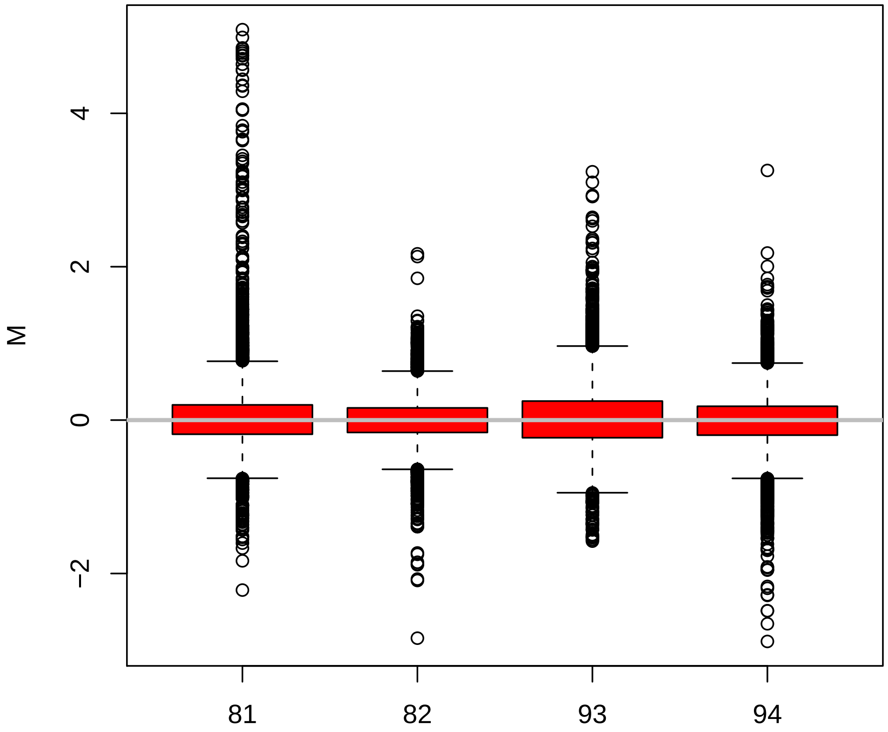
```
> swirl.norm <- maNormMain(swirl)
```

For boxplots of post-normalization log ratios

```
> maBoxplot(swirl.norm[, 1])
```



```
> maBoxplot(swirl.norm)
```



5 Miscellaneous tools: marrayTools package

The marrayTools package provides additional functions for handling two-color spotted microarray data, including a number of user-friendly wrapper functions for performing standard analyses.

The spotTools and gpTools functions in the development version of marrayTools start from Spot (.spot and .gal) and GenePix (.gpr and .gal) image analysis output files, respectively, and automatically read in these data into R, perform standard normalization (within print-tip-group loess), and create a directory with a standard set of diagnostic plots (jpeg format), excel files of quality measures, and tab delimited files of normalized log ratios M and average log intensities A. In addition, an object of class marrayRaw or marrayNorm is returned. The package also includes functions for computing various gene statistics and for generating HTML pages for gene lists (htmlPage).

```
> datadir <- system.file("data", package="marrayInput")
> normdata <- spotTools(path=datadir, quality=FALSE)
```