Lab 3: Introduction to Bioconductor \texttt{marray} Packages

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In this lab, we demonstrate the main functions in the \texttt{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 \texttt{marray} packages is given next.

\texttt{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.

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

\texttt{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.

\texttt{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.

<table>
<thead>
<tr>
<th>maLabels</th>
<th># of slide</th>
<th>Names</th>
<th>experiment</th>
<th>Cy3</th>
<th>experiment</th>
<th>Cy5</th>
<th>date</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>81</td>
<td>81 swirl.1.spot</td>
<td>swirl</td>
<td>wild type</td>
<td>2001/9/20</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>82</td>
<td>82 swirl.2.spot</td>
<td>wild type</td>
<td>swirl</td>
<td>2001/9/20</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>93</td>
<td>93 swirl.3.spot</td>
<td>swirl</td>
<td>wild type</td>
<td>2001/11/8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>94</td>
<td>94 swirl.4.spot</td>
<td>wild type</td>
<td>swirl</td>
<td>2001/11/8</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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:

<table>
<thead>
<tr>
<th></th>
<th>Min.</th>
<th>1st Qu.</th>
<th>Median</th>
<th>Mean</th>
<th>3rd Qu.</th>
<th>Max.</th>
</tr>
</thead>
<tbody>
<tr>
<td>swirl.1.spot</td>
<td>-2.73</td>
<td>-0.79</td>
<td>-0.58</td>
<td>-0.48</td>
<td>-0.29</td>
<td>4.42</td>
</tr>
<tr>
<td>swirl.2.spot</td>
<td>-2.72</td>
<td>-0.15</td>
<td>0.03</td>
<td>0.03</td>
<td>0.21</td>
<td>2.35</td>
</tr>
<tr>
<td>swirl.3.spot</td>
<td>-2.29</td>
<td>-0.75</td>
<td>-0.46</td>
<td>-0.42</td>
<td>-0.12</td>
<td>2.65</td>
</tr>
<tr>
<td>swirl.4.spot</td>
<td>-3.21</td>
<td>-0.46</td>
<td>-0.26</td>
<td>-0.27</td>
<td>-0.06</td>
<td>2.90</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th></th>
<th>ID</th>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>geno1</td>
<td>control geno1</td>
</tr>
<tr>
<td>2</td>
<td>geno2</td>
<td>control geno2</td>
</tr>
<tr>
<td>3</td>
<td>geno3</td>
<td>control geno3</td>
</tr>
<tr>
<td>4</td>
<td>3XSSC</td>
<td>control 3XSSC</td>
</tr>
<tr>
<td>5</td>
<td>3XSSC</td>
<td>control 3XSSC</td>
</tr>
<tr>
<td>6</td>
<td>EST1</td>
<td>control EST1</td>
</tr>
<tr>
<td>7</td>
<td>geno1</td>
<td>control geno1</td>
</tr>
</tbody>
</table>
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:

```r
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.

<table>
<thead>
<tr>
<th>maLabels</th>
<th># of slide</th>
<th>Names</th>
<th>experiment</th>
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<tr>
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<td>82</td>
<td>swirl.2.spot</td>
<td>wild type</td>
<td>swirl</td>
<td>2001/9/20</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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:

<table>
<thead>
<tr>
<th>Min.</th>
<th>1st Qu.</th>
<th>Median</th>
<th>Mean</th>
<th>3rd Qu.</th>
<th>Max.</th>
</tr>
</thead>
<tbody>
<tr>
<td>-1.08</td>
<td>-0.26</td>
<td>-0.12</td>
<td>-0.12</td>
<td>0</td>
<td>1.72</td>
</tr>
</tbody>
</table>

D) Notes on intensity data:

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

```r
> Gb <- maGb(swirl)
> dim(Gb)
[1] 8448 4
> Gb[1:5, ,]
[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
```

```r
> Rf <- maRf(swirl)
> dim(Rf)
[1] 8448 4
> Rf[1:5,]
```
```r
> 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

```r
> tmp <- maImage(swirl[, 3], x = "maGb", bar = FALSE)
```
To produce a spatial image of log ratios for the first array in the batch

```r
> 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

```r
> 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])

12
> 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)