

Homework 2

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1. Read the provided text file into R, making sure to account for headers. This is a truncated cDNA array expression file that has only the Cy5 and Cy3 foreground and background values for 5 separate arrays. The numbers in the suffix of the names are time points (though not necessary for our purposes). (2.5 pts)

```
file <- 'five.txt'
data <- read.table(file, header = T)
```

2. Load the sma library and the MouseArray data file (with data()). (2.5 pts)

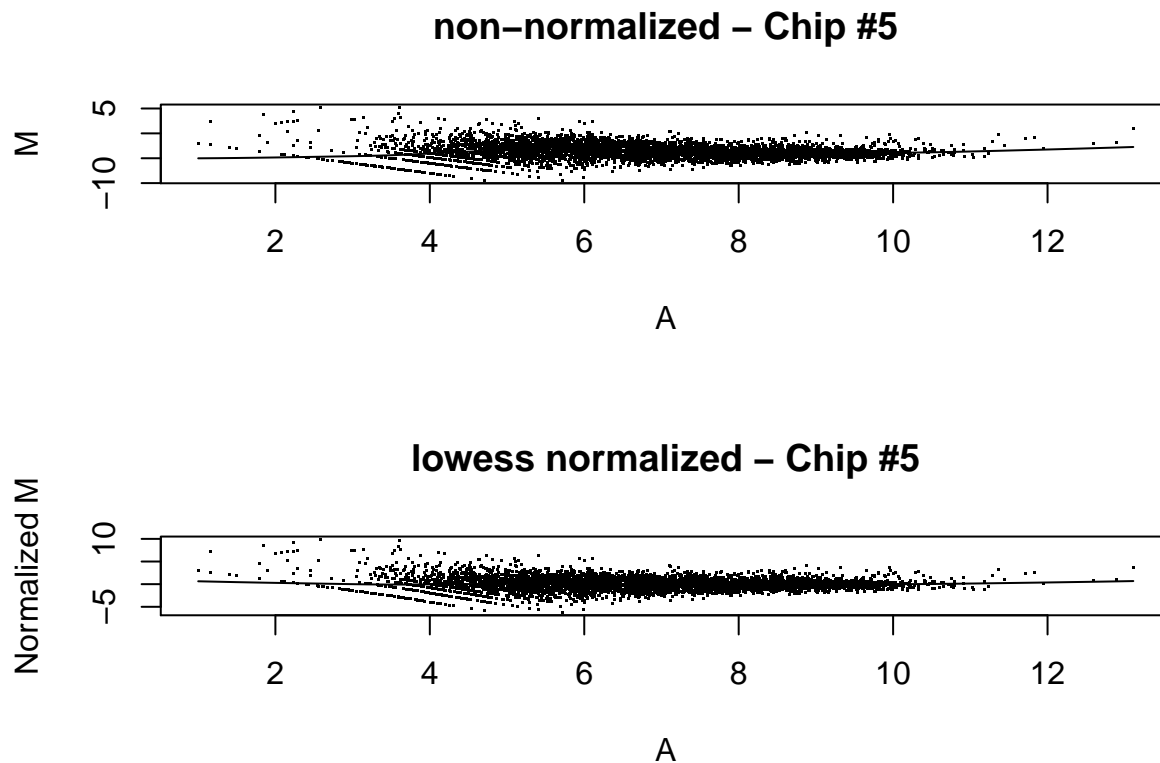
```
library(sma)
data(MouseArray)
```

3. Using list commands, turn the five_arrays matrix file into the list object that is similar to the mouse.data example. See hints below. (10 pts)

```
five.data <- list('R' = data[,c(1:5)],
                  'G' = data[, c(6:10)],
                  'Rb' = data[,c(11:15)],
                  'Gb' = data[, c(16:20)]
                  )
```

4. Now create a plot of both un-normalized and lowess normalized data for chip #5 (image.id argument) using the `plot.mva` function. Make sure to use a `par` command to put both plots on the same page. Title both plots. For the layout argument in `plot.mva()`, use the `mouse.setup` file. (15 pts)

```
par(mfrow=c(2,1))
plot.mva(five.data, layout = mouse.setup, plot.type = 'r',
         norm = "n", extra.type = "pci", image.id = 5, main = "non-normalized - Chip #5")
plot.mva(five.data, layout = mouse.setup, plot.type = 'n',
         norm = "l", extra.type = "pci", image.id = 5, main = "lowess normalized - Chip #5")
```



5. How do the 2 plots differ? What has lowess normalization done to the distribution of expression values? (5 pts)

A normalização fez com que os valores de expressão ficassem mais uniformemente distribuídos em torno do eixo traçado na linha zero. Enquanto os dados não normalizados tem uma janela maior de variação, alterando a linha desenhada que gira perto do -5.