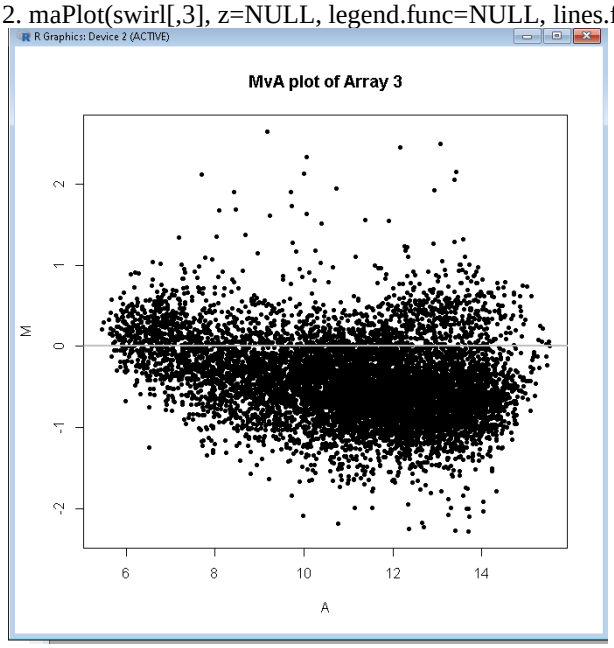
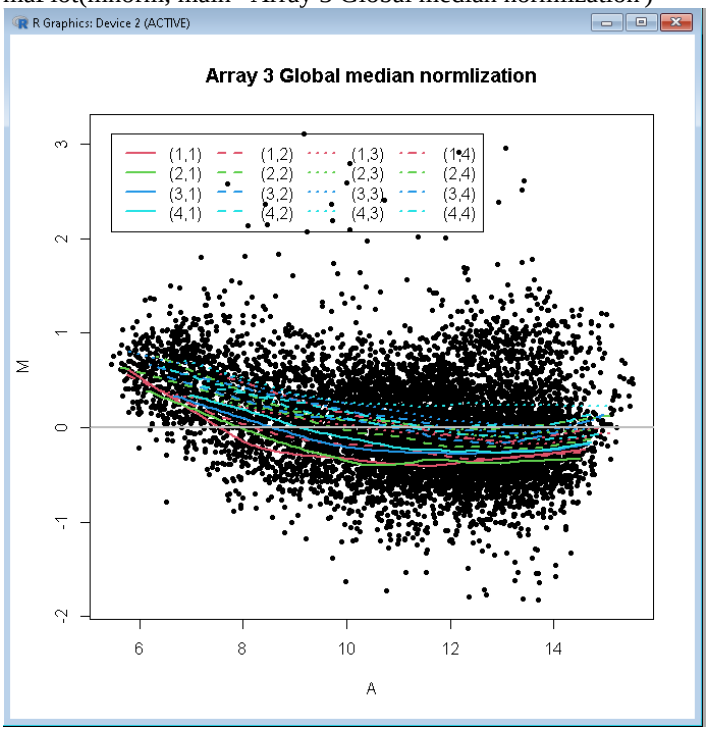
Thomas Muamar

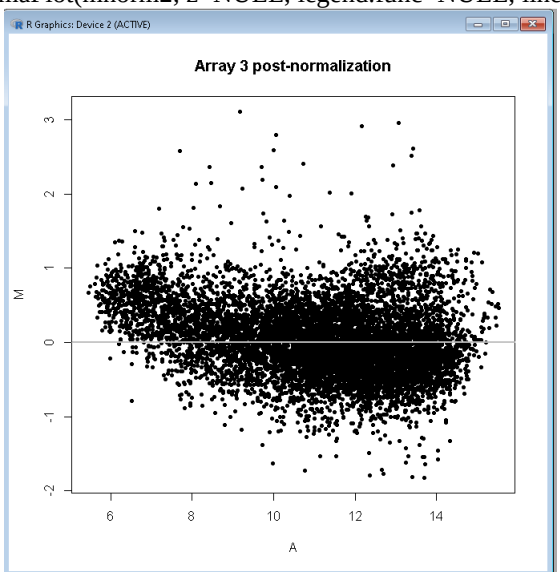
1.library(marray)
Data(swirl)
2. maPlot(swirl[,3], z=NULL, legend.func=NULL, lines.func=NULL, main = "MvA plot of Array 3")



3. mnorm<-maNorm(swirl[,3], norm="median", span=0.45)
maPlot(mnorm, main='Array 3 Global median normlization')

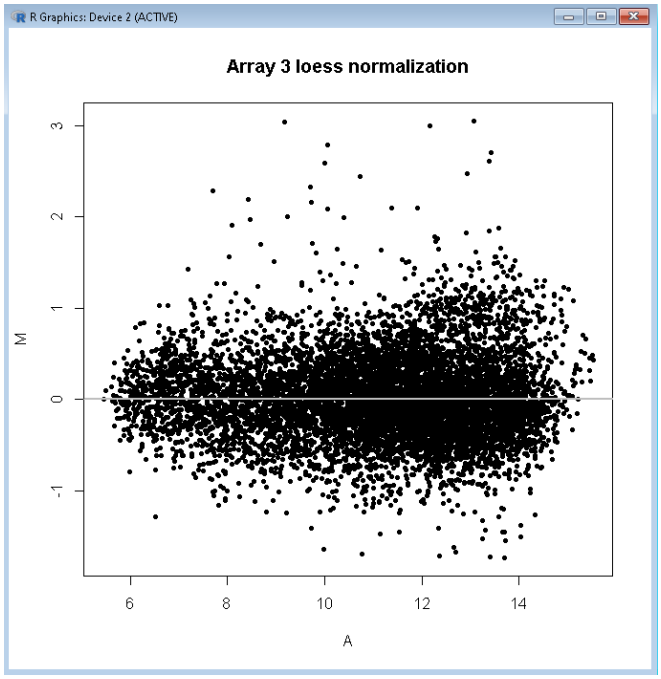


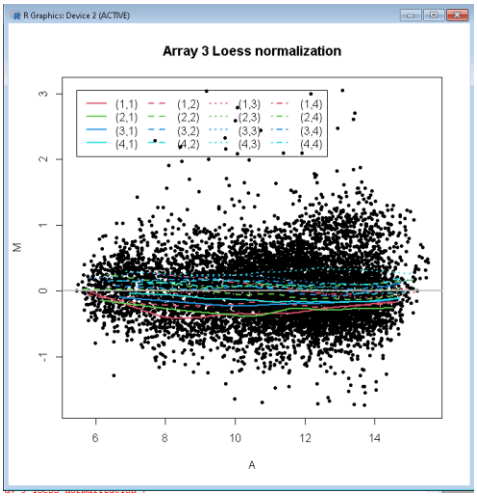
4.
mnorm2<-maNorm(swirl[,3], norm="median", span=0.45)
maPlot(mnorm2, z=NULL, legend.func=NULL, lines.func=NULL, main='Array 3 post-normalization')



5. The normalized data here compared to the non normalized data seems to have shifted the intensity higher than the normal data. As we can see in the graph the normalized data seemed to produce higher values for the plotted points.

6. mnorm3<-maNorm(swirl[,3], norm="loess", span=0.45)
maPlot(mnorm2, z=NULL, legend.func=NULL, lines.func=NULL, main='Array 3 loess normalization')
maPlot(mnorm2, main='Array 3 Loess normalization')





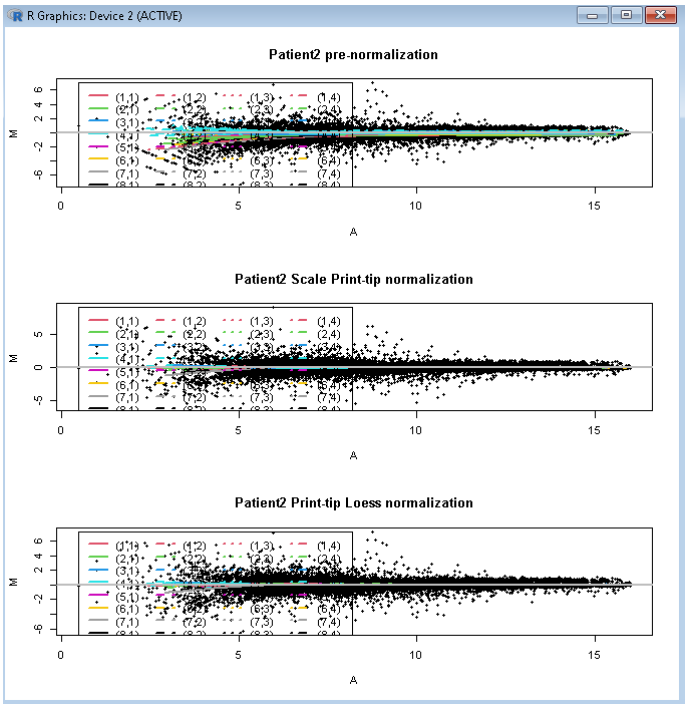
7. for this array the loess normalization appears to be better due to it being more reduced and centralized. It seemed to have removed some of the variation and smoothed out the data a lot more with loess normalization.

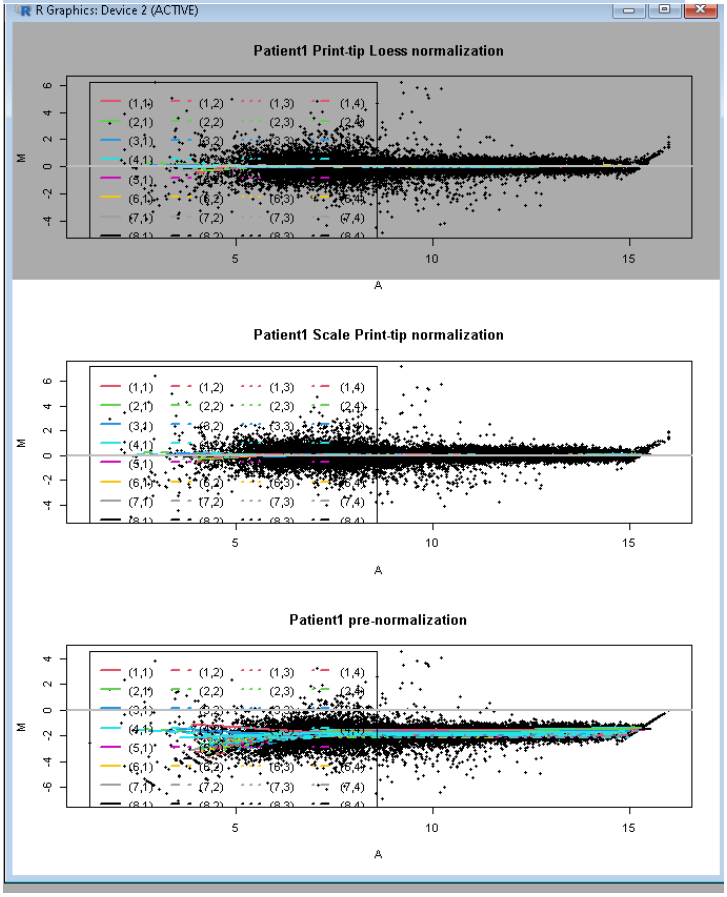
8. a.cdna <- read.GenePix(path=getwd(),name.Gf = "F532 Median",name.Gb ="B532 Median", name.Rf = "F635 Median", name.Rb = "B635 Median",name.W ="Flags")

```
Reading ...   C:/Users/thomas/Documents/patient1.gpr
Reading ...   C:/Users/thomas/Documents/patient2.gpr
```

9.

```
pixnorm1 <- maNorm(a.cdna[,1], norm ="p", span=0.45)
pixnorm1scale <- maNorm(a.cdna[,1], norm ="scalePrintTipMAD", span=0.45)
maPlot(pixnorm1,main='Patient1 Print-tip Loess normalization')
maPlot(pixnorm1scale,main='Patient1 Scale Print-tip normalization')
maPlot(a.cdna[,1],main='Patient1 pre-normalization')
pixnorm2 <- maNorm(a.cdna[,2], norm ="p", span=0.45)
pixnorm2scale <- maNorm(a.cdna[,2], norm ="scalePrintTipMAD", span=0.45)
maPlot(a.cdna[,2],main='Patient2 pre-normalization')
maPlot(pixnorm2scale,main='Patient2 Scale Print-tip normalization')
maPlot(pixnorm2,main='Patient2 Print-tip Loess normalization')
```





10.
Normalized data
pixnorm1 <- maNorm(a.cdna[,1], norm ="p", span=0.45)

pixnorm2 <- maNorm(a.cdna[,2], norm ="p", span=0.45)

data.frame(maGnames(pixnorm1)@maLabels, pixnorm1@maM, pixnorm2@maM)
11. Loaded all libraries
12. > fns <- sort(list.celfiles(path=getwd(),full.names=TRUE))
> data.affy <- ReadAffy(filenames=fns,phenoData=NULL)

13. pmonly <- expresso(data.affy, bgcorrect.method="rma", normalize.method="quantiles", summary.method="medianpolish", pmcorrect.method="pmonly")
mas <- expresso(data.affy, bgcorrect.method="mas", normalize.method="quantiles", summary.method="medianpolish", pmcorrect.method="mas")
pm <- exprs(pmonly)
m <- exprs(mas)

14.

```
> cor(pm)
             normal1.CEL normal2.CEL normal3.CEL
normal1.CEL    1.0000000   0.9766785   0.9758377
normal2.CEL    0.9766785   1.0000000   0.9913585
normal3.CEL    0.9758377   0.9913585   1.0000000
> cor(m)
             normal1.CEL normal2.CEL normal3.CEL
normal1.CEL    1.0000000   0.8959518   0.9003087
normal2.CEL    0.8959518   1.0000000   0.9486851
normal3.CEL    0.9003087   0.9486851   1.0000000
```

The RMA has the better correlation structure amongst the 3 normal healthy subjects. As we see in the tables above from the correlation calculations the pm which is RMA shows that the correlations between the 3 subjects were at a higher value in comparison to the mas.