R Code

```
# cDNA array plots
#library(marrayInput)
#library(marrayNorm)
#library(marrayPlots)
#library(sma)
library(affydata)
library(marray)

# signal vs. noise plot for a single cDNA array
data(MouseArray)                                    # get mouse array data
plot.svb(mouse.data, "red",image.id=1,col='red',main='Singal vs. Noise for Cy5 channel on array #1')

# Examples use swirl dataset
data(swirl)

# look at image file from swirl data
maImage(swirl)

# look at boxplot from swirl data by print-tip
maBoxplot(swirl[,3])

# one form of an MvA plot
library(sma)

# mouse array
data(MouseArray)
plot.mva(mouse.data, mouse.setup, norm="l", 2, extra.type="pci",plot.type="n")

# Pre-normalization MvA-plot for the Swirl 93 array, with the lowess fits for
# individual print-tip-groups.
# - Default arguments
maPlot(swirl[,1],main='Print-tip Loess pre-normalization')

# Post-normalization using print-tip loess
mnorm<-maNorm(swirl[,1], norm="p", span=0.45)
maPlot(mnorm,main='Print-tip Loess post-normalization')
```

R Code

```
# import eisen data
dat <- read.table("eisen.txt",header=T)
dimnames(dat)[[1]] <- as.character(dat[,1])
dat <- dat[,-1]
dat <- as.data.frame(dat)

# scatter plot
cars.lm <- lm(dist~speed,data=cars)
plot(cars$speed,cars$dist,xlab="speed",ylab="dist",main="regression(cars)")
abline(as.numeric(cars.lm$coefficients[1]),as.numeric(cars.lm$coefficients[2]),col='red',lwd=2)

# lowess smoothing plot
data(cars)
plot(cars, main = "lowess(cars)")
lines(lowess(cars), col = 2,lwd=2)
lines(lowess(cars, f=.2), col = 3,lwd=2)
legend(5, 120, c(paste("f = ", c("2/3", ".2"))), lty = 1, col = 2:3)

# load affy library
library(affy)
library(affydata)

 # get data
data(Dilution)

# plot data both before and after loess normalization using PM data
x <- pm(Dilution)
mva.pairs(x)
x <- normalize.loess(x,subset=1:nrow(x))
mva.pairs(x)
```

R Code

```
# affy normalization parameters for expresso function
> bgcorrect.methods
[1] "mas"  "none" "rma"  "rma2"

> normalize.AffyBatch.methods
[1] "constant" "contrasts" "invariantset" "loess"
[5] "qspline" "quantiles" "quantiles.robust"

> pmcorrect.methods
[1] "mas" "pmonly" "subtractmm"

> express.summary.stat.methods
[1] "avgdiff" "liwong" "mas" "medianpolish" "playerout"


eset <- expresso(Dilution,bgcorrect.method="rma",
            normalize.method="quantiles",
            pmcorrect.method="pmonly",
            summary.method="medianpolish")

# look at data frame of RMA values
attributes(eset)$exprs

# first scatter plot of R vs. G and un-normalized MvA plot with Mouse cDNA data
> plot(log(mouse.data$G),log(mouse.data$R),xlab='Cy3',ylab='Cy5',main='logR vs. logG')
> plot.mva(mouse.data, mouse.setup, norm="n", 2, extra.type="p",plot.type="r",main="MvA plot of R/G")
```