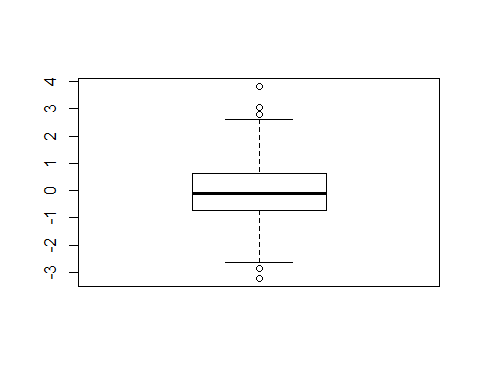
Class05\_R.R

Zhuohang\_Wu

Thu Jan 24 09:32:32 2019

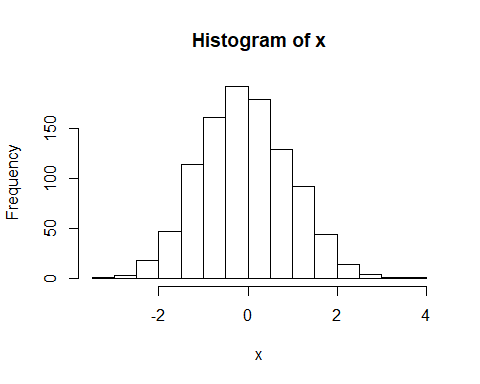
# Class 05 R grapgic intro  
  
# my first boxplot  
x <- rnorm(1000,0)  
boxplot(x)



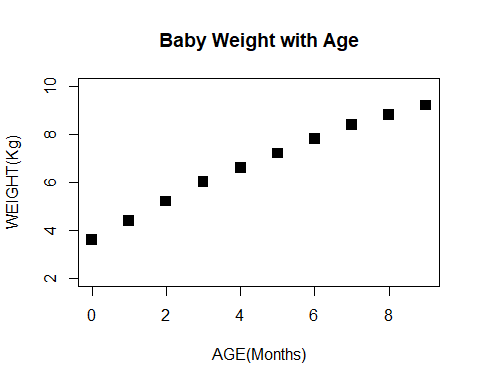
summary(x)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## -3.21338 -0.73939 -0.08479 -0.05734 0.63727 3.82046

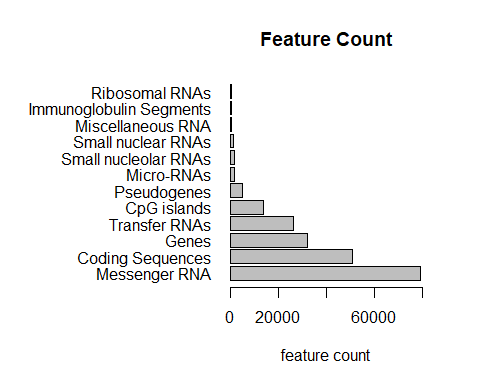
hist(x)



weight <- read.table("bimm143\_05\_rstats/weight\_chart.txt", header=TRUE)  
plot(weight, pch=15, cex=1.5, lwd=2, ylim=c(2,10), xlab="AGE(Months)",   
 ylab="WEIGHT(Kg)", main="Baby Weight with Age")



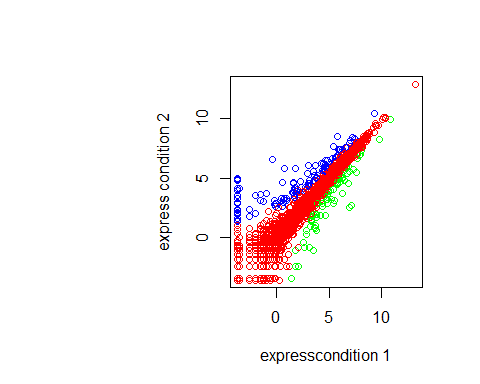
feature <- read.table("bimm143\_05\_rstats/feature\_counts.txt", header = TRUE, sep = "\t")  
  
par(mar=c(5,12,4,3))  
barplot(feature$Count, horiz=TRUE, xlab="feature count", names.arg = feature$Feature,   
 main= "Feature Count", las=1, xlim = c(0,80000))



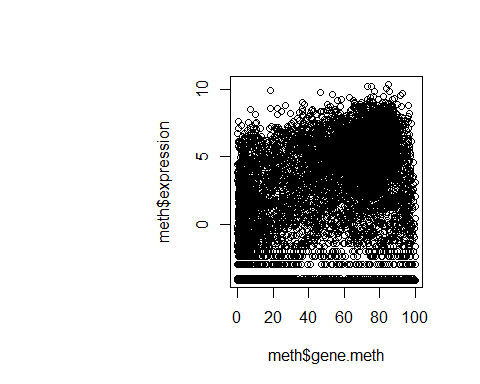
phenotype <- read.table("bimm143\_05\_rstats/up\_down\_expression.txt", header= TRUE)  
table(phenotype$State)

##   
## down unchanging up   
## 72 4997 127

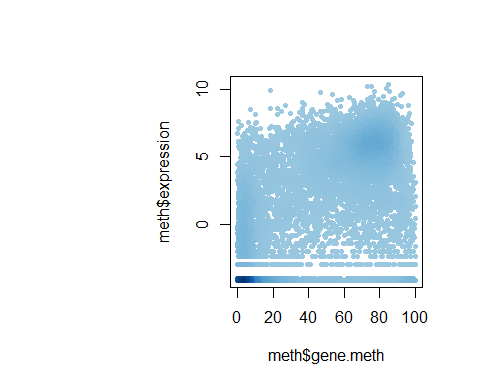
palette(c("green", "red", "blue"))  
plot(phenotype$Condition1, phenotype$Condition2, col=phenotype$State,   
 xlab="expresscondition 1", ylab="express condition 2")



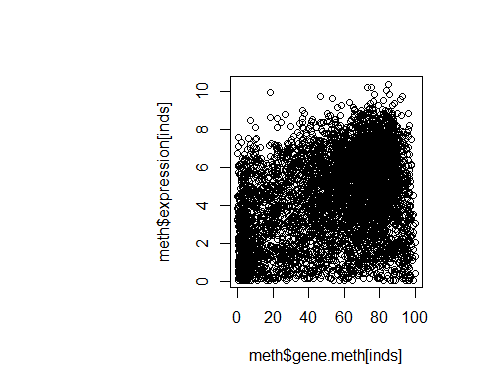
# Lets plot expresion vs gene regulation  
meth <- read.delim("bimm143\_05\_rstats/expression\_methylation.txt")  
plot(meth$gene.meth, meth$expression)



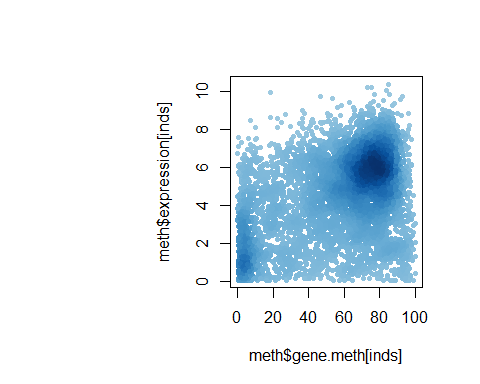
dcols <- densCols(meth$gene.meth, meth$expression)  
  
# Plot changing the plot character ('pch') to a solid circle  
plot(meth$gene.meth, meth$expression, col = dcols, pch = 20)



# Find the indices of genes with above 0 expresion  
inds <- meth$expression > 0  
  
# Plot just these genes  
plot(meth$gene.meth[inds], meth$expression[inds])



## Make a desnisty color vector for these genes and plot  
dcols <- densCols(meth$gene.meth[inds], meth$expression[inds])  
  
plot(meth$gene.meth[inds], meth$expression[inds], col = dcols, pch = 20)



dcols.custom <- densCols(meth$gene.meth[inds], meth$expression[inds],  
 colramp = colorRampPalette(c("blue2",  
 "green",  
 "orange",  
 "red2")) )  
  
plot(meth$gene.meth[inds], meth$expression[inds],   
 col = dcols.custom, pch = 20)

