Class05_R.R

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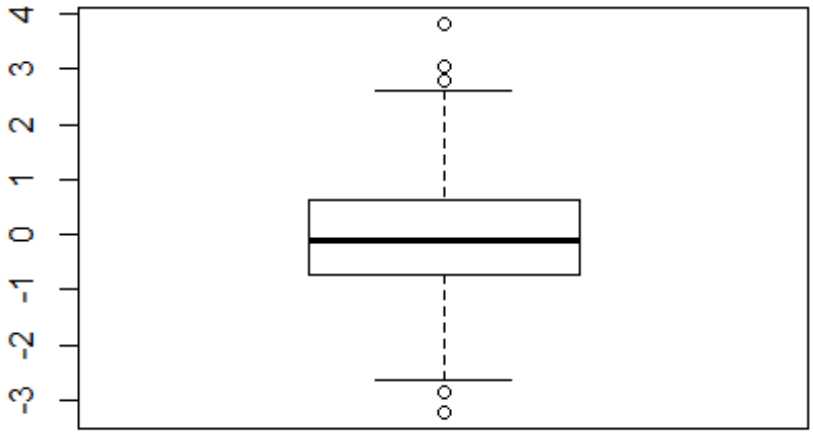
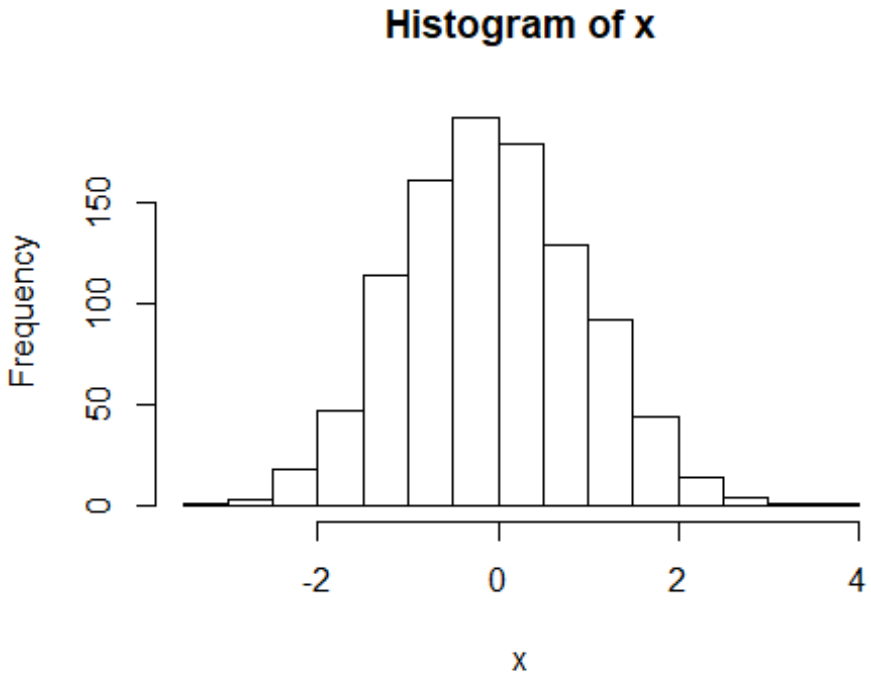
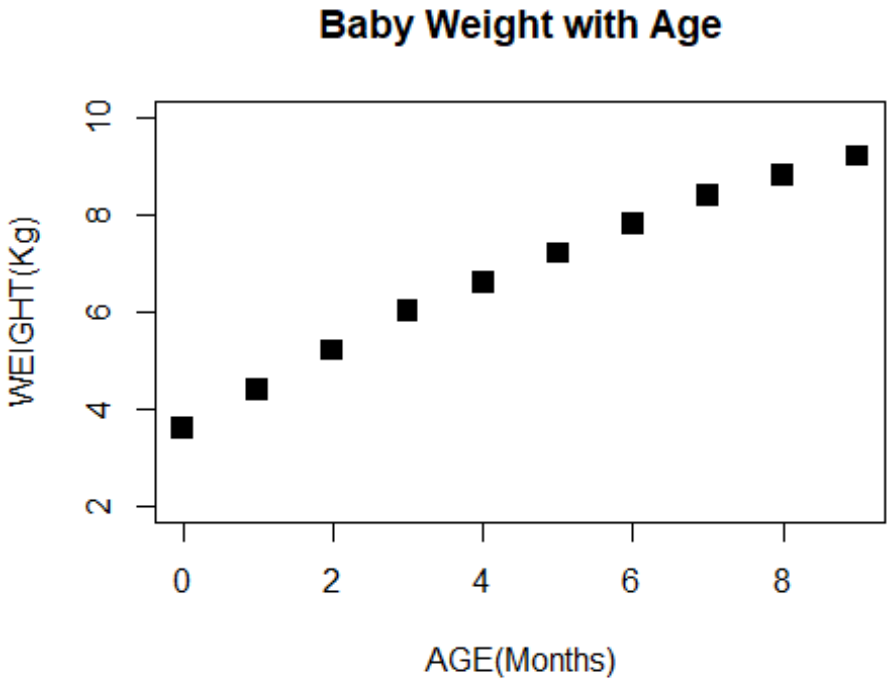
```
# Class 05 R grapgic intro

# my first boxplot
x <- rnorm(1000,0)
boxplot(x)
```



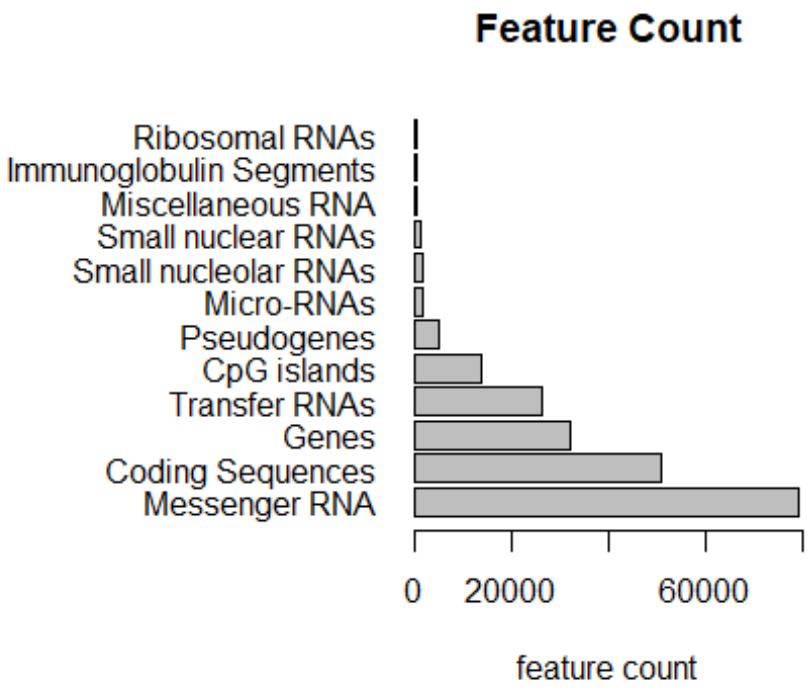

```
summary(x)

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

hist(x)
```



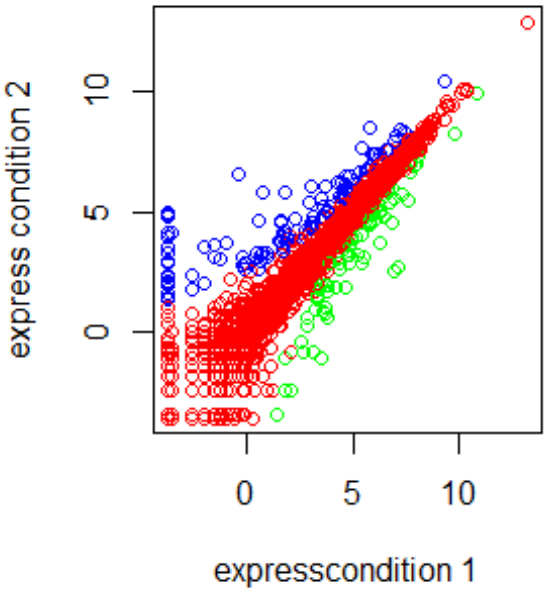

```
weight <- read.table("bimm143_05_rstats/weight_chart.txt", header=TRUE)
plot(weight, pch=15, cex=1.5, lwd=2, ylim=c(2,10), xlab="AGE(Months)",
     ylab="WEIGHT(Kg)", main="Baby Weight with Age")
```



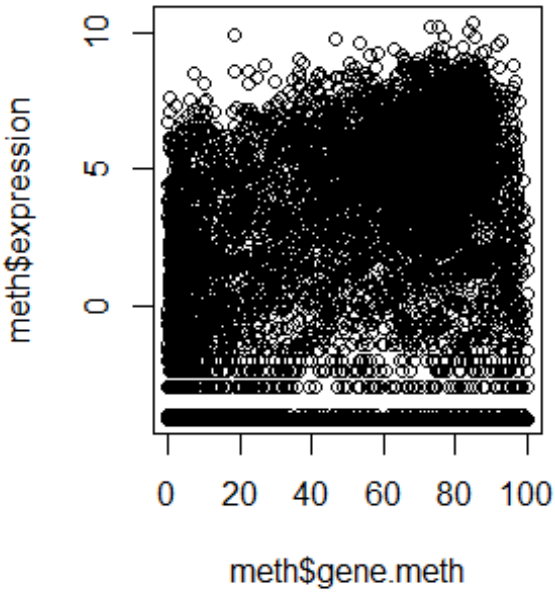
```
feature <- read.table("bimm143_05_rstats/feature_counts.txt", header = TRUE,
sep = "\t")

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))
```



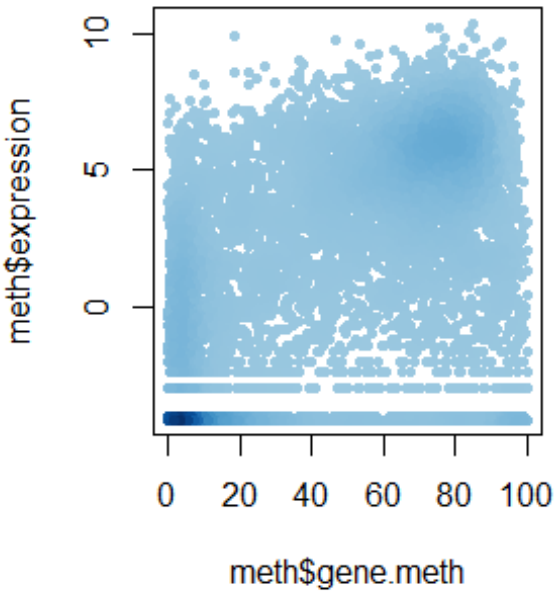

```
phenotype <- read.table("bimm143_05_rstats/up_down_expression.txt", header=
TRUE)
table(phenotype$State)

##
##       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")
```



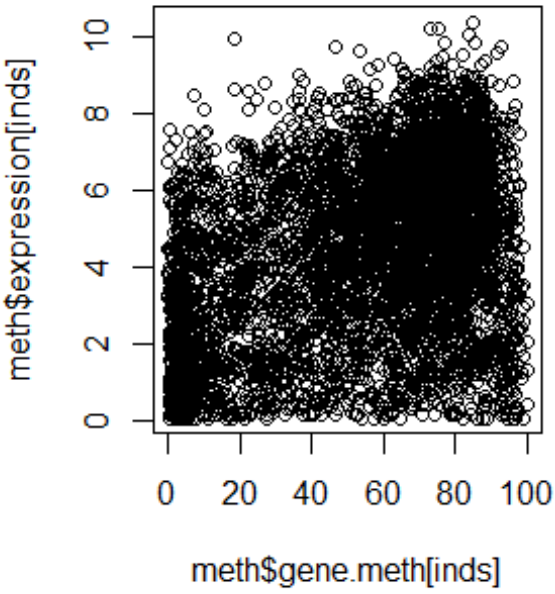

```
# Lets plot expresion vs gene regulation
meth <- read.delim("bimm143_05_rstats/expression_methylation.txt")
plot(meth$gene.meth, meth$expression)
```



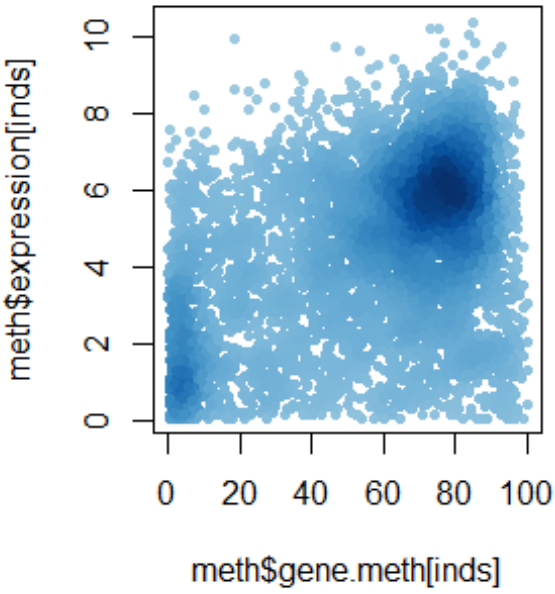
```r
dcols <- densCols(meth$gene.meth, meth$expression)

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



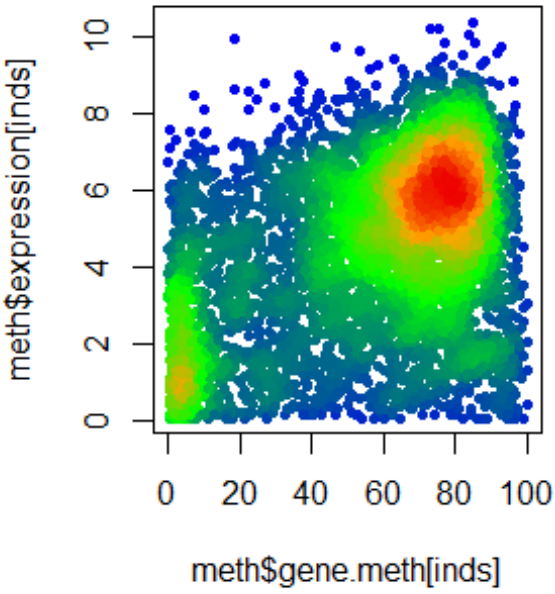

```r
# Find the indices of genes with above 0 expresion
inds <- meth$expression > 0

# 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)
```


meth$expression[inds]
0
2
4
6
8
10
0
20
40
60
80
100
meth$gene.meth[inds]