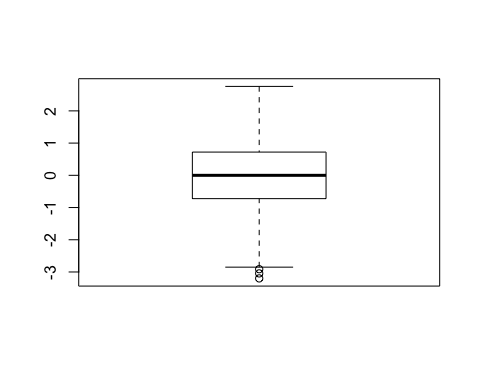
Class 05 R Graphics Intro

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Jan 22nd, 2019

# Class 05 R Graphics Intro

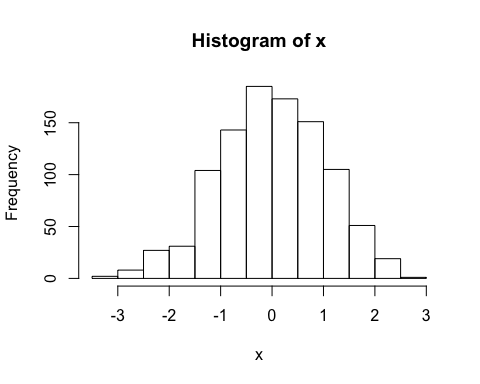
# my first boxplot   
x <- rnorm(1000,0)  
boxplot(x)



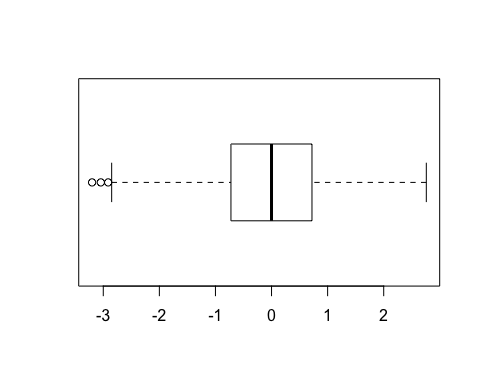
summary(x)

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## -3.199365 -0.723720 -0.000420 -0.006078 0.720524 2.759563

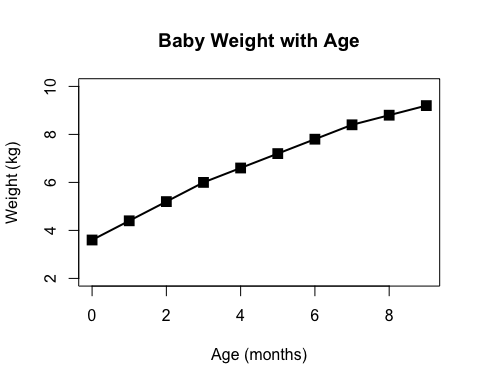
hist(x)



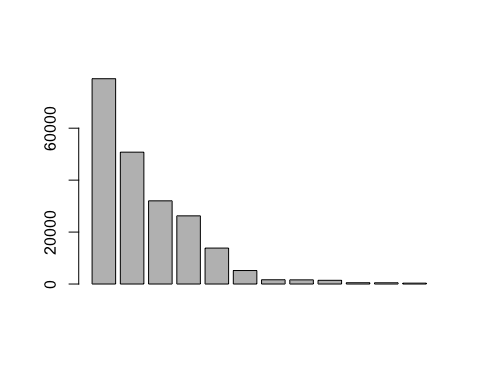
boxplot(x, horizontal = TRUE)



# Hands On Session  
  
#import weight chart into R  
#read.table("weight\_chart.txt", header = TRUE)  
#read.table("weight\_chart.txt", header = FALSE)  
weight <- read.table("bimm143\_05\_rstats/weight\_chart.txt", header = TRUE)  
#graph weight chart with changes  
#plot(weight)  
plot(weight, typ = "o", pch = 15, cex = 1.5, lwd = 2, ylim = c(2,10), xlab = "Age (months)", ylab = "Weight (kg)", main = "Baby Weight with Age")



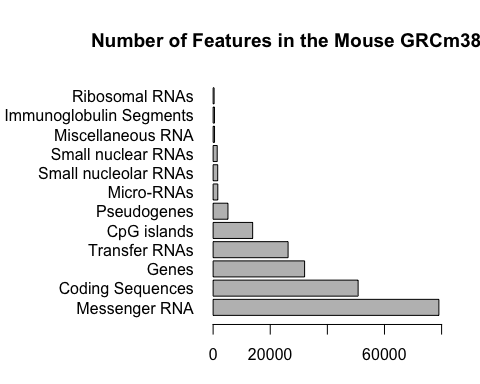
#import feature counts  
#read.table("feature\_counts.txt", header = TRUE, sep = "\t")  
feature\_counts <- read.table("bimm143\_05\_rstats/feature\_counts.txt", header = TRUE, sep = "\t")  
#plot feature counts  
barplot(height = feature\_counts[,2])  
barplot(feature\_counts$Count)



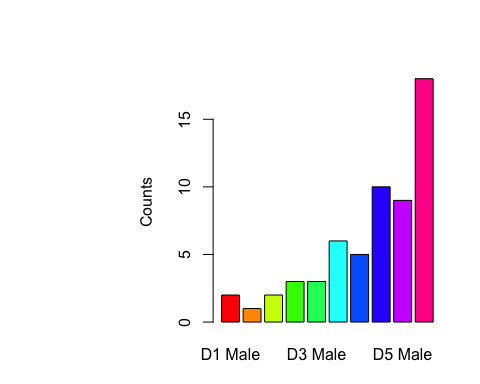
barplot(feature\_counts$Count, horiz = TRUE, names.arg = feature\_counts$Feature, main = "Number of Features in the Mouse GRCm38 Genome", las = 1, xlim = c(0,80000))  
#change margins so we can see the labels   
par()$mar

## [1] 5.1 4.1 4.1 2.1

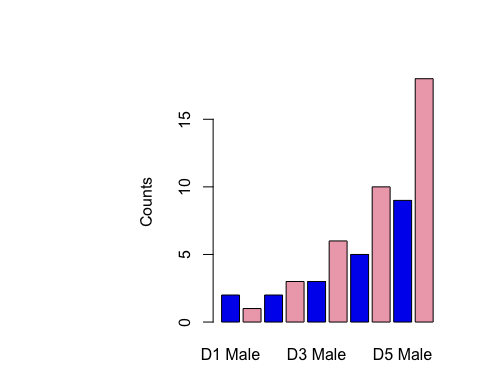
par(mar = c(3.1, 11.1, 4.1, 2))  
barplot(feature\_counts$Count, horiz = TRUE, names.arg = feature\_counts$Feature, main = "Number of Features in the Mouse GRCm38 Genome", las = 1, xlim = c(0,80000))



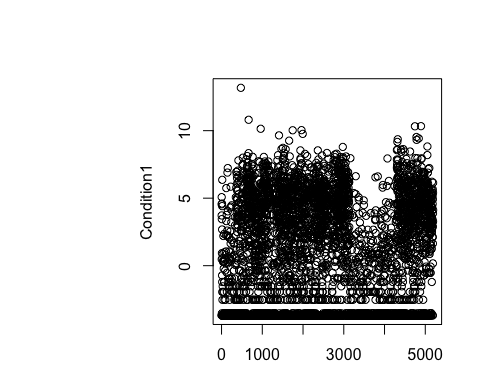
#import male female counts  
#read.table("male\_female\_counts.txt", header = TRUE, sep = "\t")  
male\_female\_counts <- read.table("bimm143\_05\_rstats/male\_female\_counts.txt", header = TRUE, sep = "\t")  
#plot male female counts  
barplot(male\_female\_counts$Count, names.arg = male\_female\_counts$Sample, ylab = "Counts", col = rainbow(10))  
barplot(male\_female\_counts$Count, names.arg = male\_female\_counts$Sample, ylab = "Counts", col = rainbow(nrow(male\_female\_counts)))



#plot with color by gender  
barplot(male\_female\_counts$Count, names.arg = male\_female\_counts$Sample, ylab = "Counts", col = c("blue2", "pink2"))



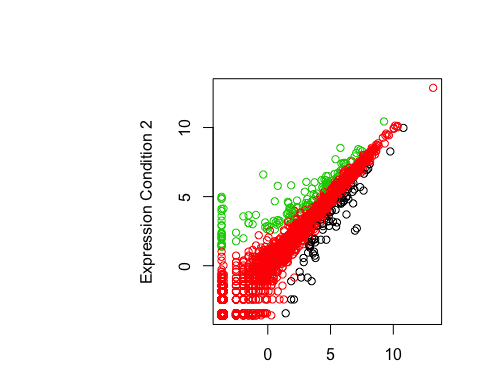
#import up down expression  
#read.table("up\_down\_expression.txt", header = TRUE, sep = "\t")  
up\_down\_expression <- read.table("bimm143\_05\_rstats/up\_down\_expression.txt", header = TRUE, sep = "\t")  
#plot up down expression  
plot.default(up\_down\_expression)



## determine how many genes are up, down, or unchanging  
table(up\_down\_expression$State)

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

## plot w color by up, down, unchanging   
plot.default(up\_down\_expression$Condition1, up\_down\_expression$Condition2, ylab = "Expression Condition 2", xlab = "Expression Condition 1", col = up\_down\_expression$State)



palette()

## [1] "black" "red" "green3" "blue" "cyan" "magenta" "yellow"   
## [8] "gray"

levels(up\_down\_expression$State)

## [1] "down" "unchanging" "up"

palette(c("blue", "gray", "red"))  
plot.default(up\_down\_expression$Condition1, up\_down\_expression$Condition2, ylab = "Expression Condition 2", xlab = "Expression Condition 1", col = up\_down\_expression$State)

