

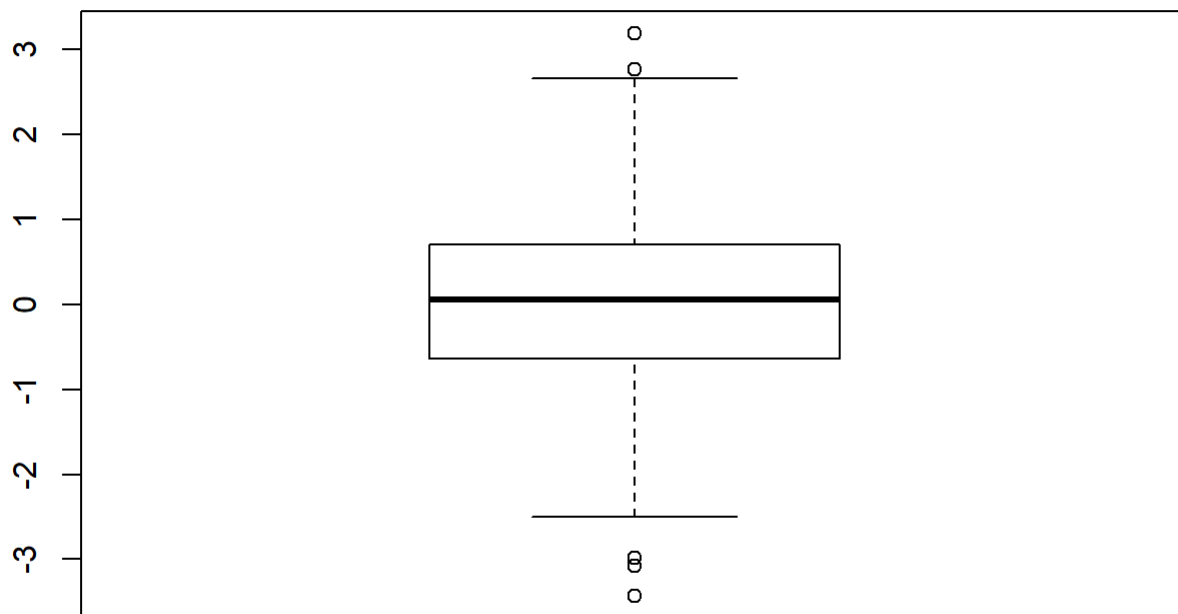
Lecture05.R

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Tue Jan 22 12:11:52 2019

```
# Lecture 5 R Graphics Intro
```

```
x <- rnorm(1000,0)
boxplot(x)
```

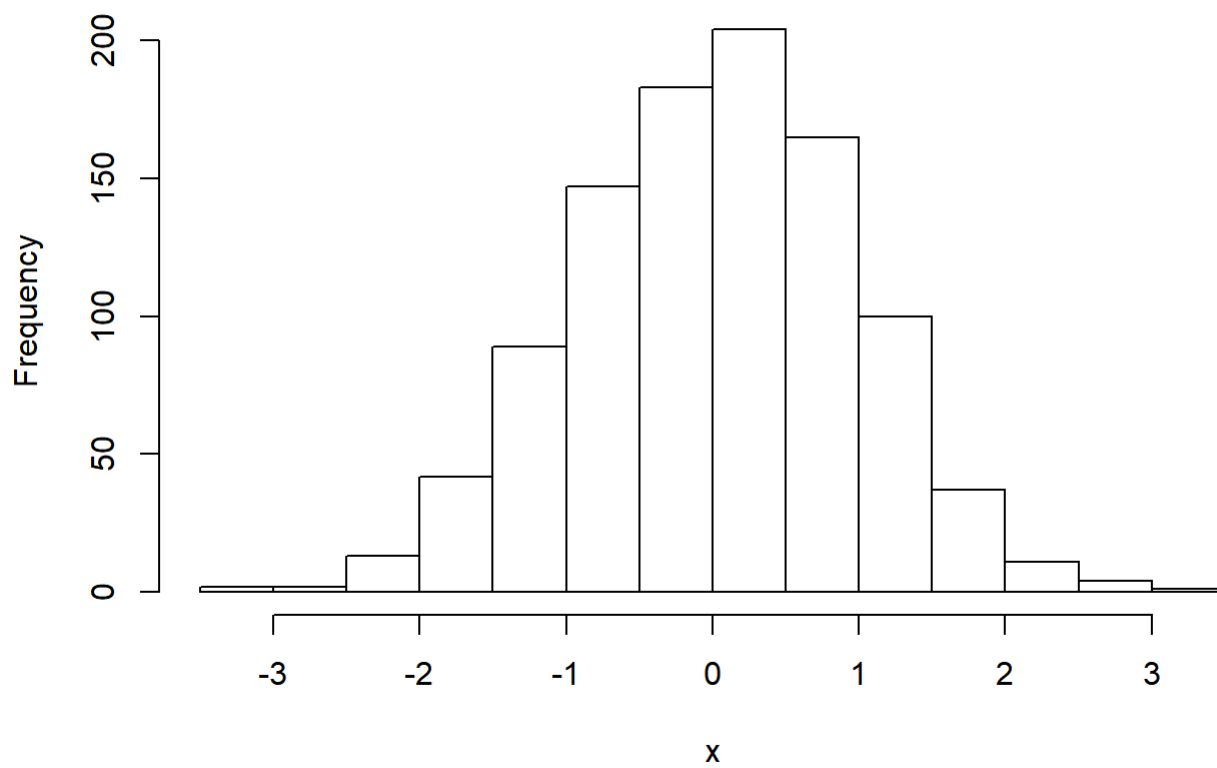


```
summary(x)
```

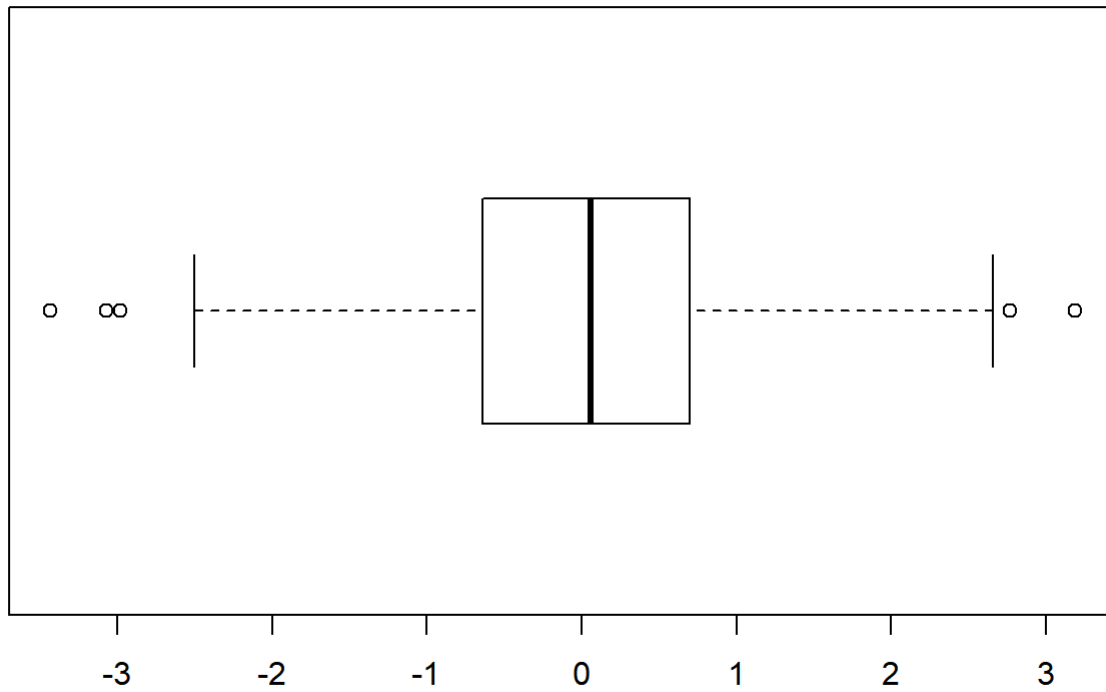
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -3.43278 -0.63861  0.06186  0.02008  0.70032  3.18699
```

```
hist(x)
```

Histogram of x

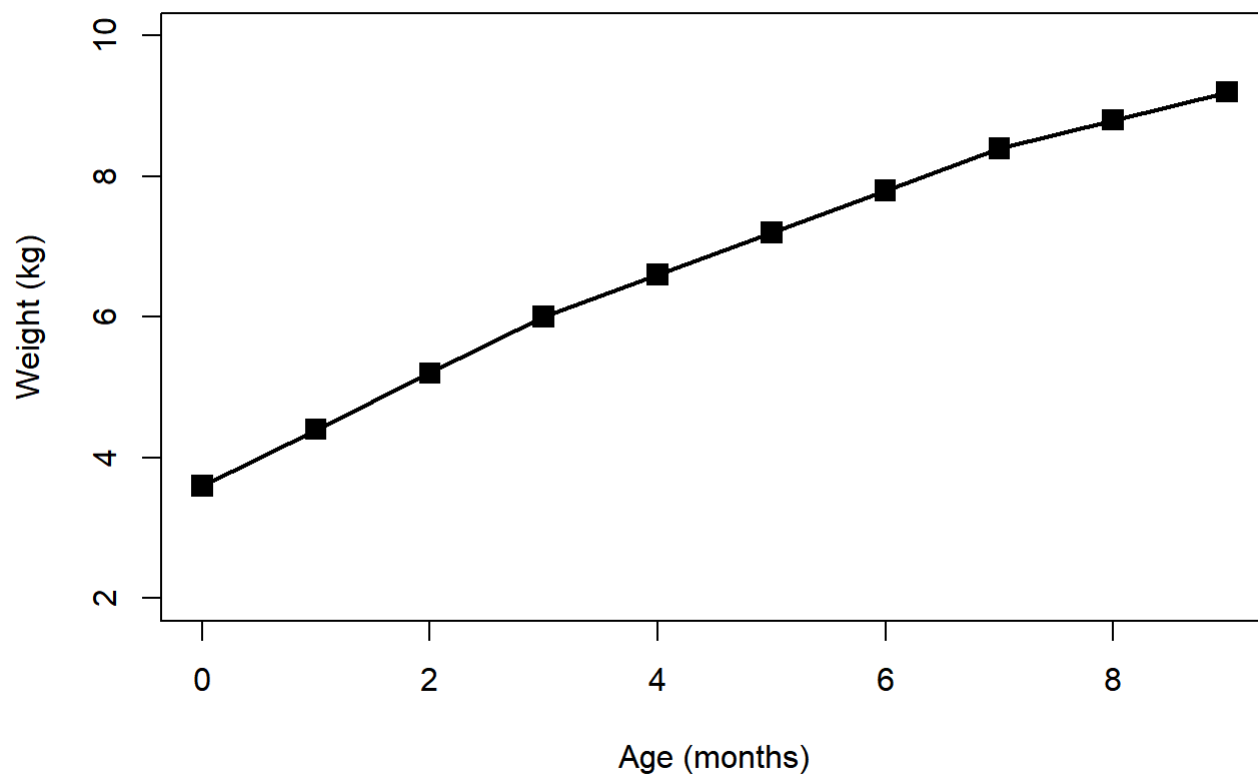


```
boxplot(x, horizontal = TRUE)
```

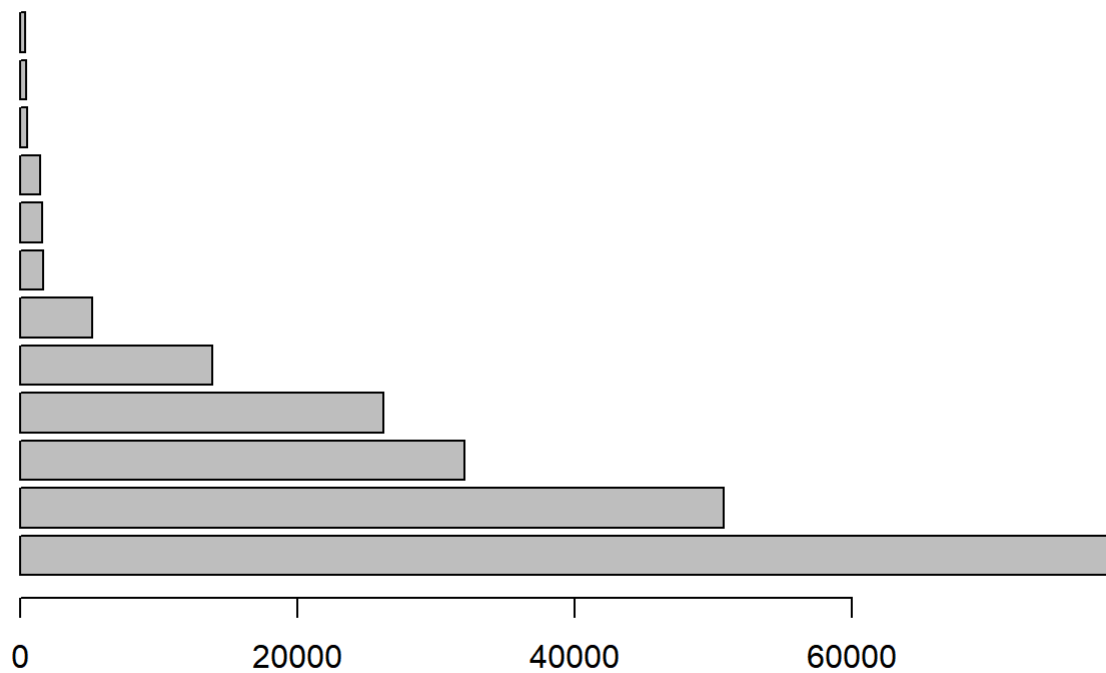


```
# Hands on Section 2
weight <- read.table("bimm143_05_rstats/weight_chart.txt", header=TRUE)
plot(weight$Age, weight$Weight, typ="o",
      pch=15, cex=1.5, lwd=2, ylim=c(2,10),
      xlab="Age (months)", ylab="Weight (kg)",
      main="Baby weight with age")
```

Baby weight with age

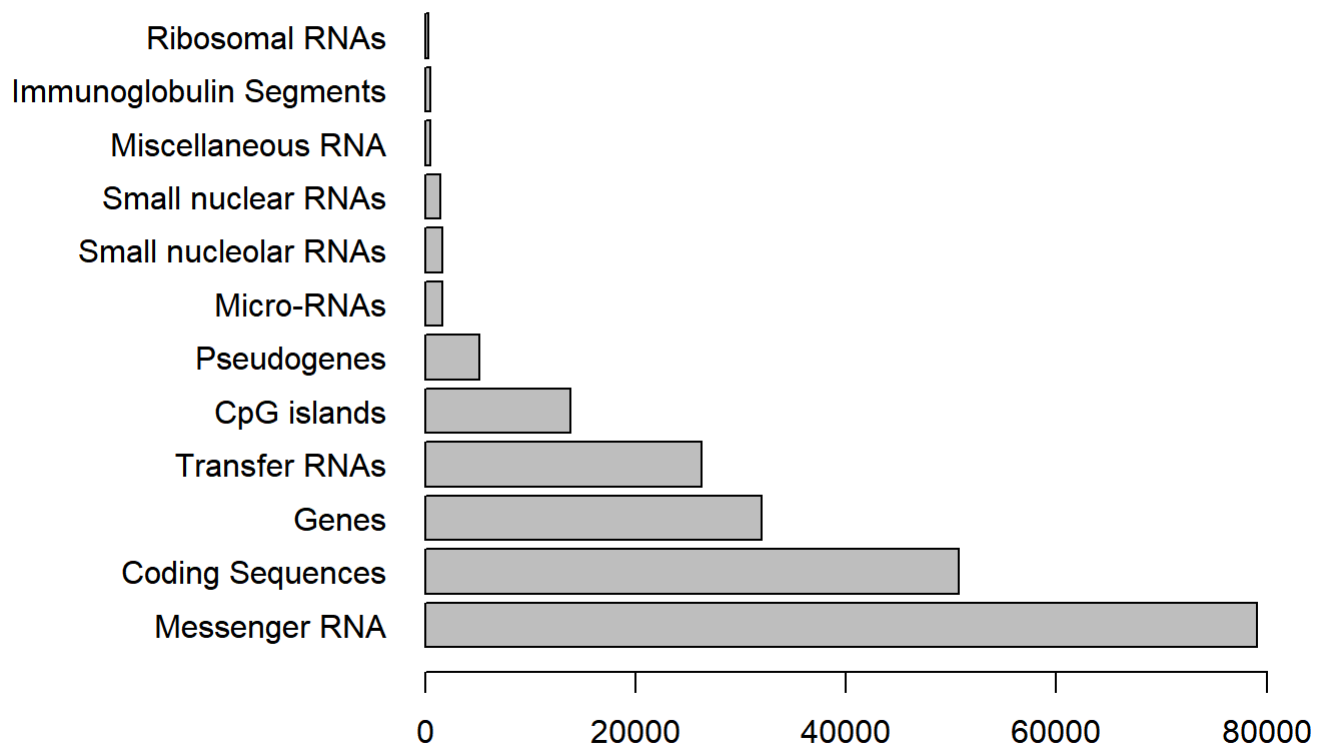


```
mouse <- read.table("bimm143_05_rstats/feature_counts.txt", sep="\t", header=TRUE)
barplot(mouse$Count, horiz = TRUE)
```



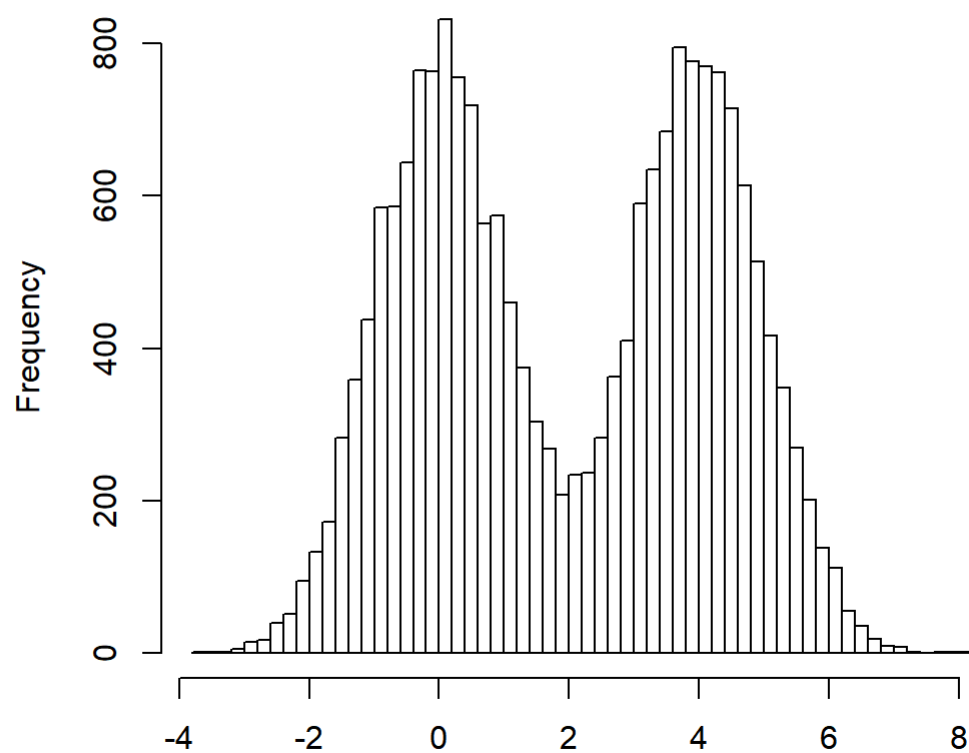
```
par(mar=c(3.1, 11.1, 4.1, 2))
barplot(mouse$Count, names.arg=mouse$Feature,
        horiz=TRUE, ylab="",
        main="Number of features in the mouse GRCm38 genome",
        las=1, xlim=c(0,80000))
```

Number of features in the mouse GRCm38 genome

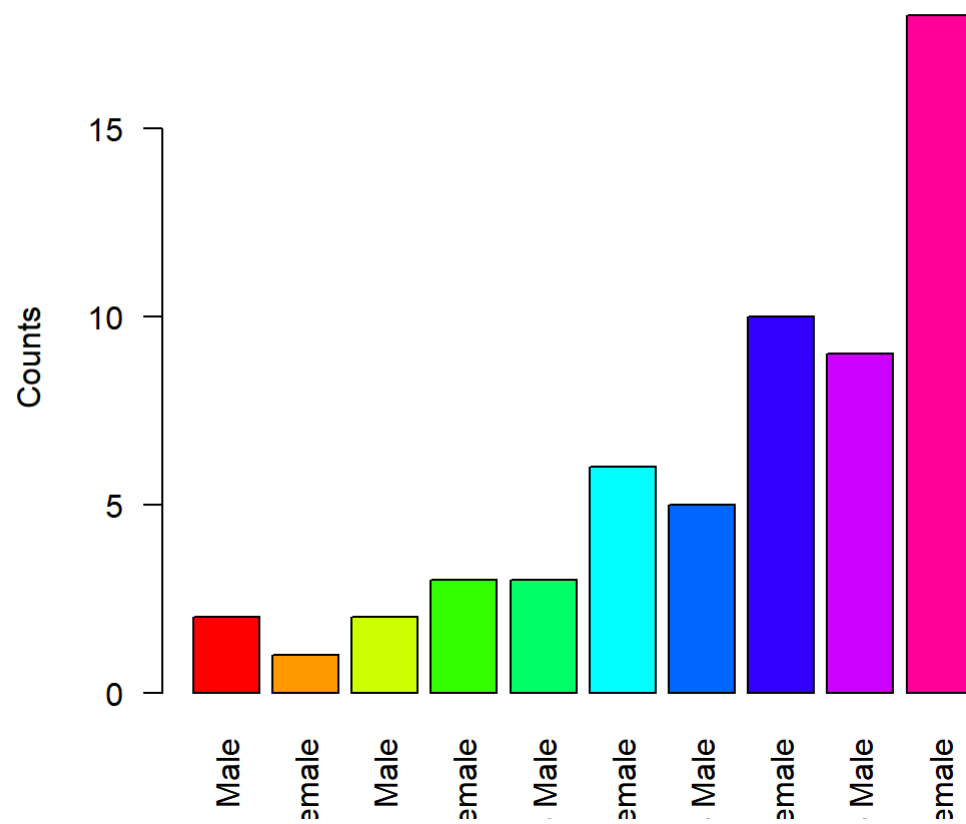


```
x <- c(rnorm(10000),rnorm(10000)+4)
hist(x, breaks=80)
```

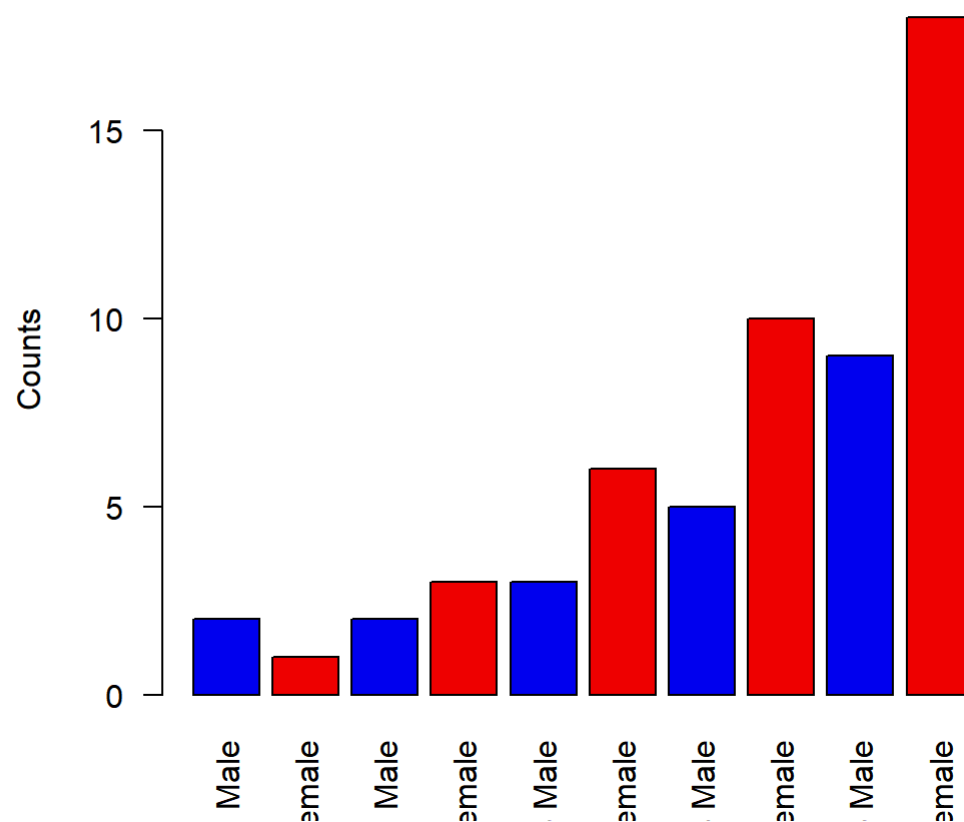
Histogram of x



```
mf <- read.delim("bimm143_05_rstats/male_female_counts.txt")
barplot(mf$Count, names.arg=mf$Sample, col=rainbow(nrow(mf)),
        las=2, ylab="Counts")
```



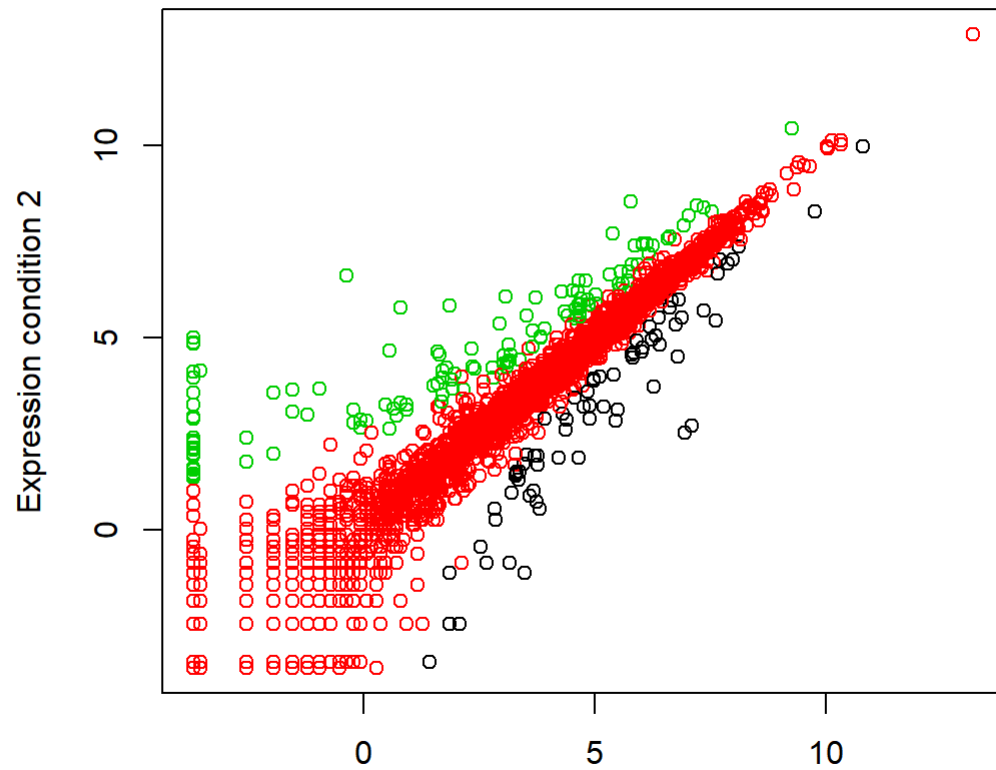
```
barplot(mf$Count, names.arg=mf$Sample, col=c("blue2","red2"),  
        las=2, ylab="Counts")
```

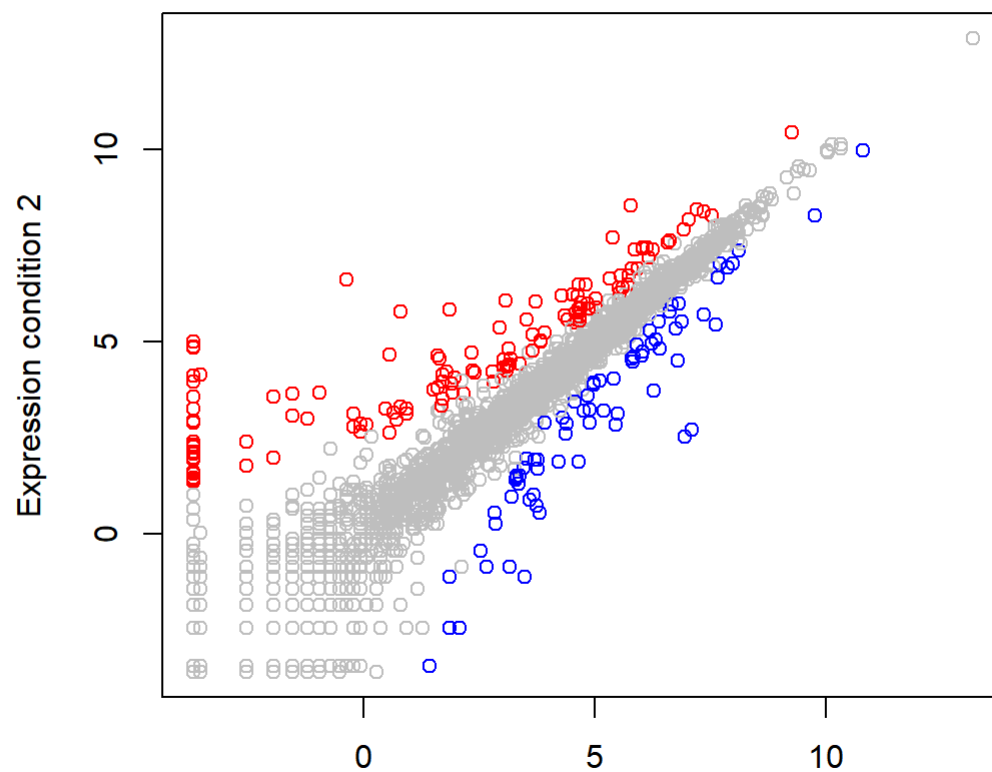
```
genes <- read.delim("bimm143_05_rstats/up_down_expression.txt")
table(genes$State)
```

```
##
##      down  unchanged      up
##      72      4997      127
```

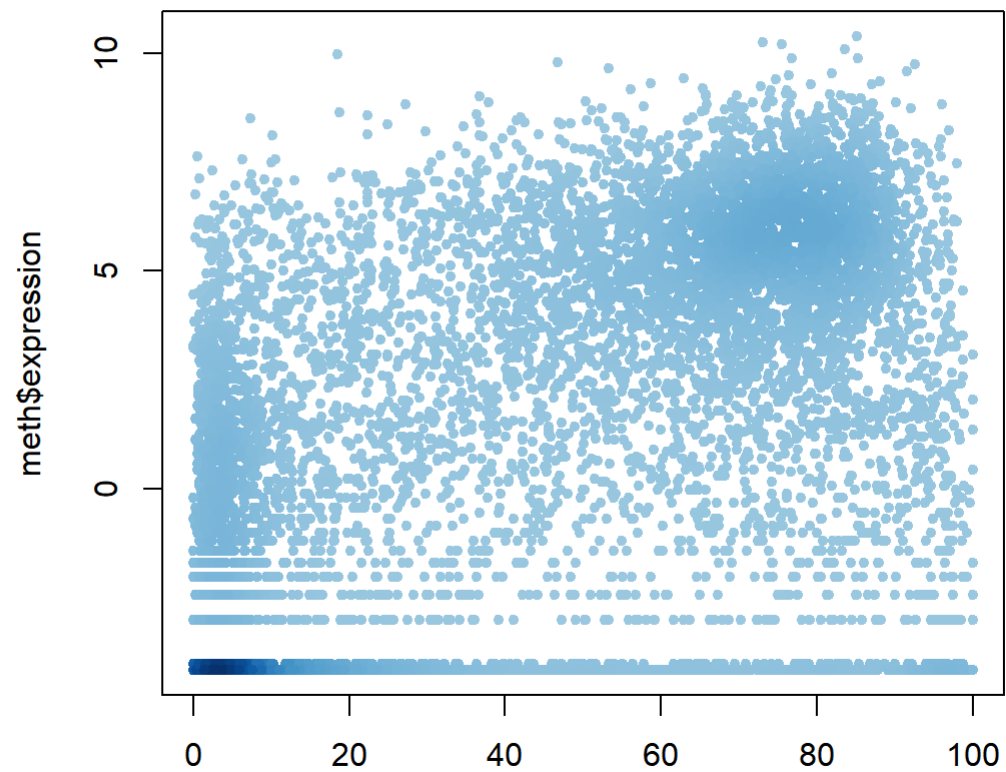
```
plot(genes$Condition1, genes$Condition2, col=genes$State,
      xlab = "Expression condition 1", ylab = "Expression condition 2")
```



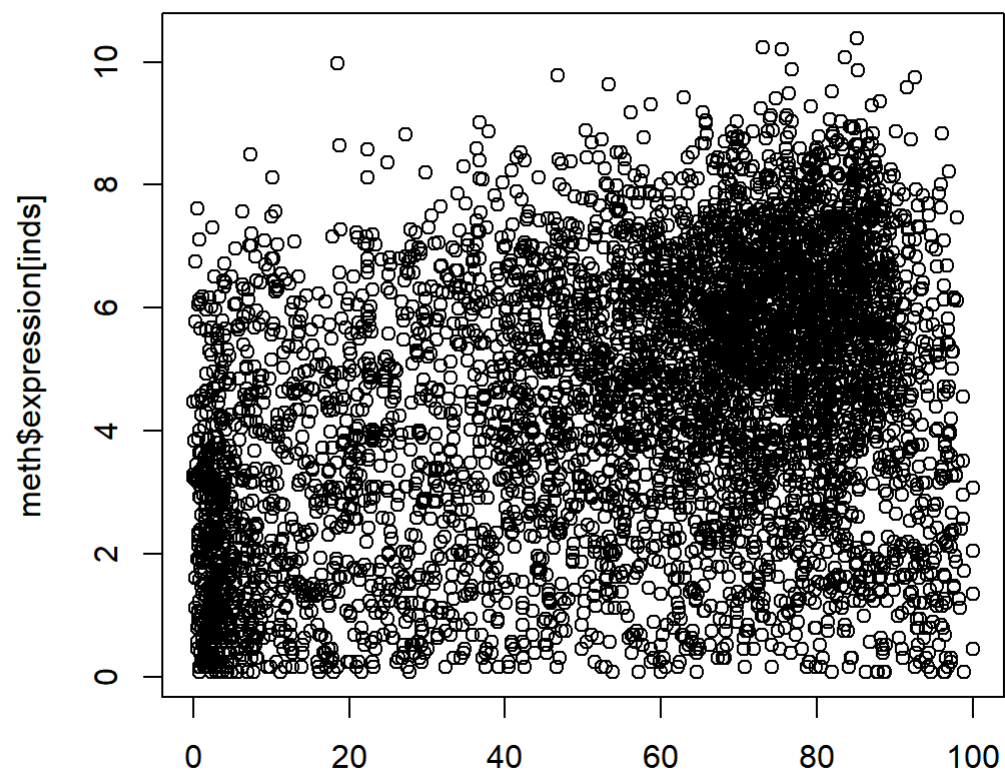
```
palette(c("blue","gray","red"))  
plot(genes$Condition1, genes$Condition2, col=genes$State, xlab="Expression condition 1", ylab="E  
xpression condition 2")
```



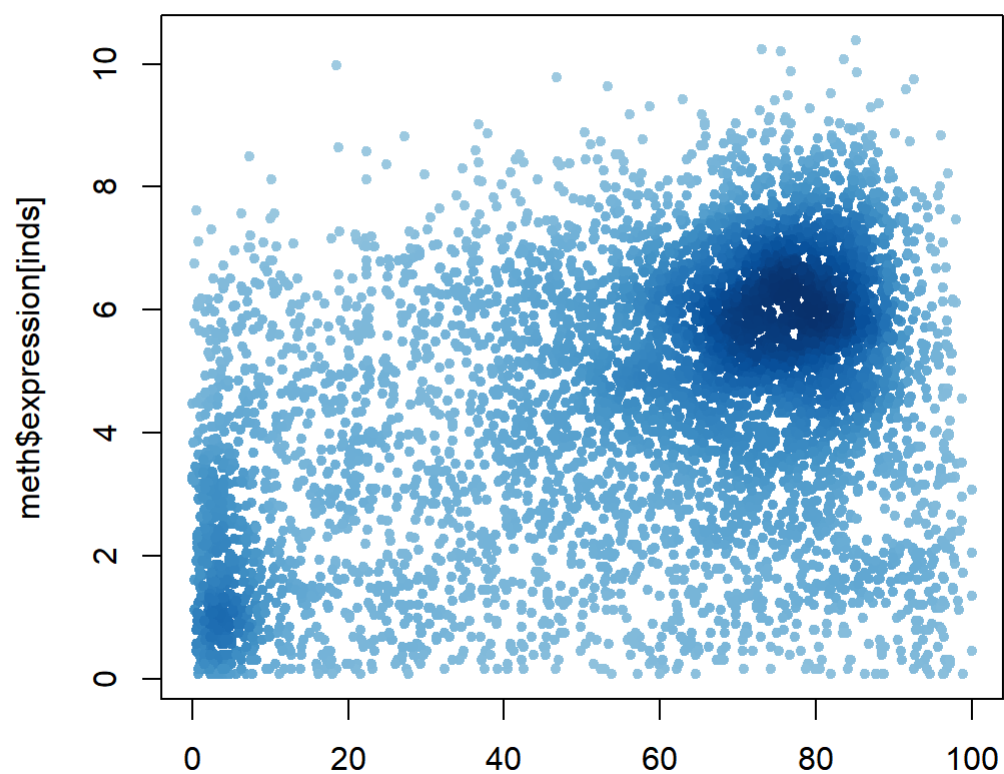
```
# Let's plot expression vs gene regulation
meth <- read.delim("bimm143_05_rstats/expression_methylation.txt")
dcols <- densCols(meth$gene.meth, meth$expression)
plot(meth$gene.meth, meth$expression, col=dcols, pch=20)
```



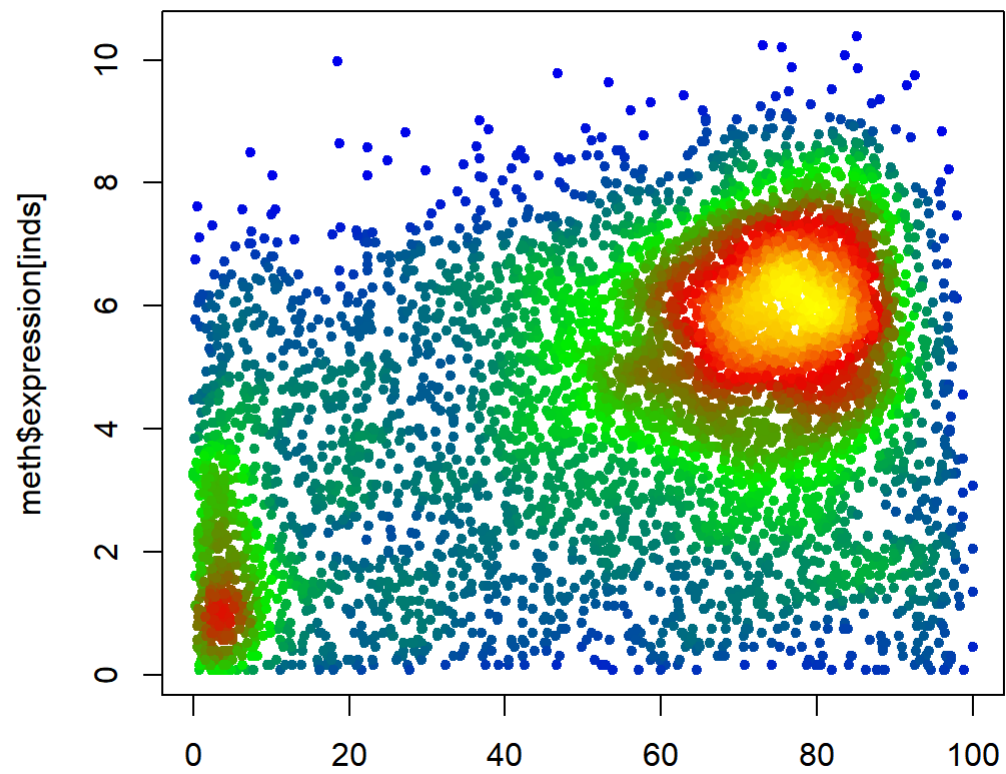
```
# Find the indices of genes with above 0 expression  
inds <- meth$expression > 0  
  
# Plot just these genes  
plot(meth$gene.meth[inds], meth$expression[inds])
```



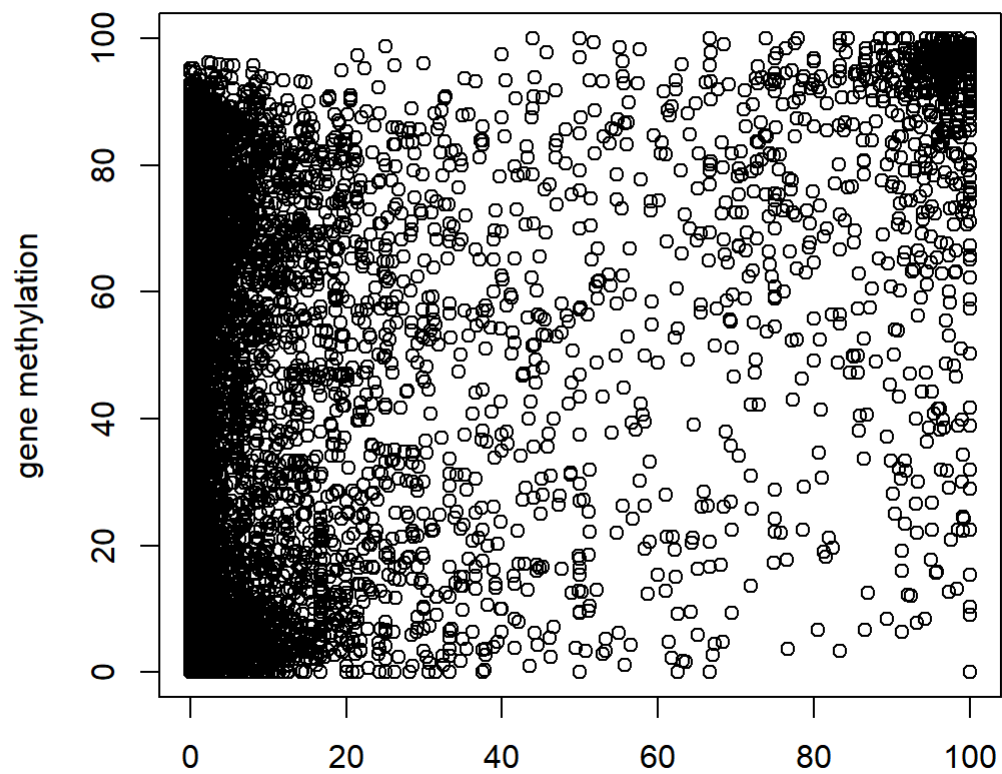
```
## Make a desnisty color vector for these genes and plot  
dcols <- densCols(meth$gene.meth[inds], meth$expression[inds])  
  
plot(meth$gene.meth[inds], meth$expression[inds], col = dcols, pch = 20)
```



```
dcols.custom <- densCols(meth$gene.meth[inds], meth$expression[inds],  
                          colramp = colorRampPalette(c("blue2",  
                                                        "green2",  
                                                        "red2",  
                                                        "yellow")) )  
  
plot(meth$gene.meth[inds], meth$expression[inds],  
     col = dcols.custom, pch = 20)
```



```
plot(meth$promoter.meth, meth$gene.meth, ylab="gene methylation", xlab="promoter methylation")
```



```
# source the provided function so we can use it
source("bimm143_05_rstats/color_to_value_map.r")

mycols=map.colors(meth$expression,
                  c(max(meth$expression), min(meth$expression)),
                  colorRampPalette(c("blue","red"))(100))

plot(meth$promoter.meth, meth$gene.meth,
     ylab="Gene Methylation",
     xlab="Promoter Methylation",
     col=mycols)
```