

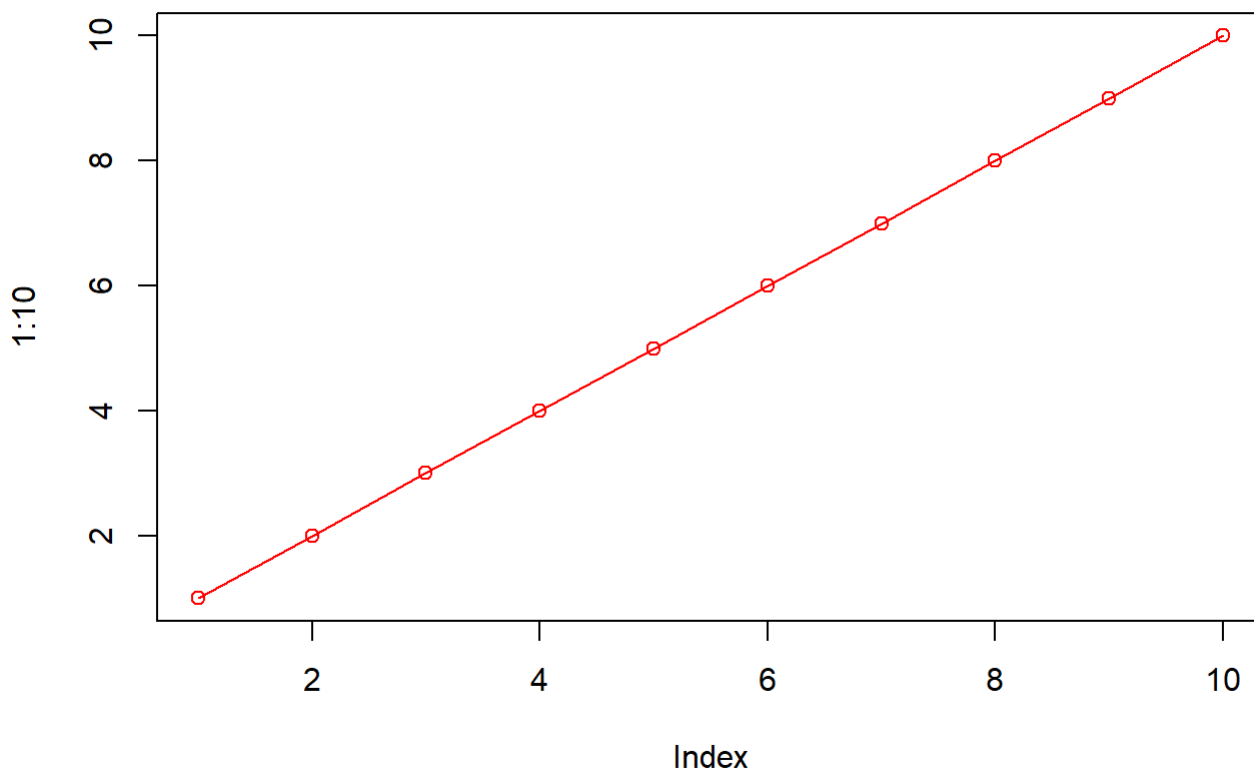
# class05\_script.R

sarra

2020-01-21

```
#Class 5
# Data Visualization and graphs in R

plot(1:10, col="red", typ="o")
```

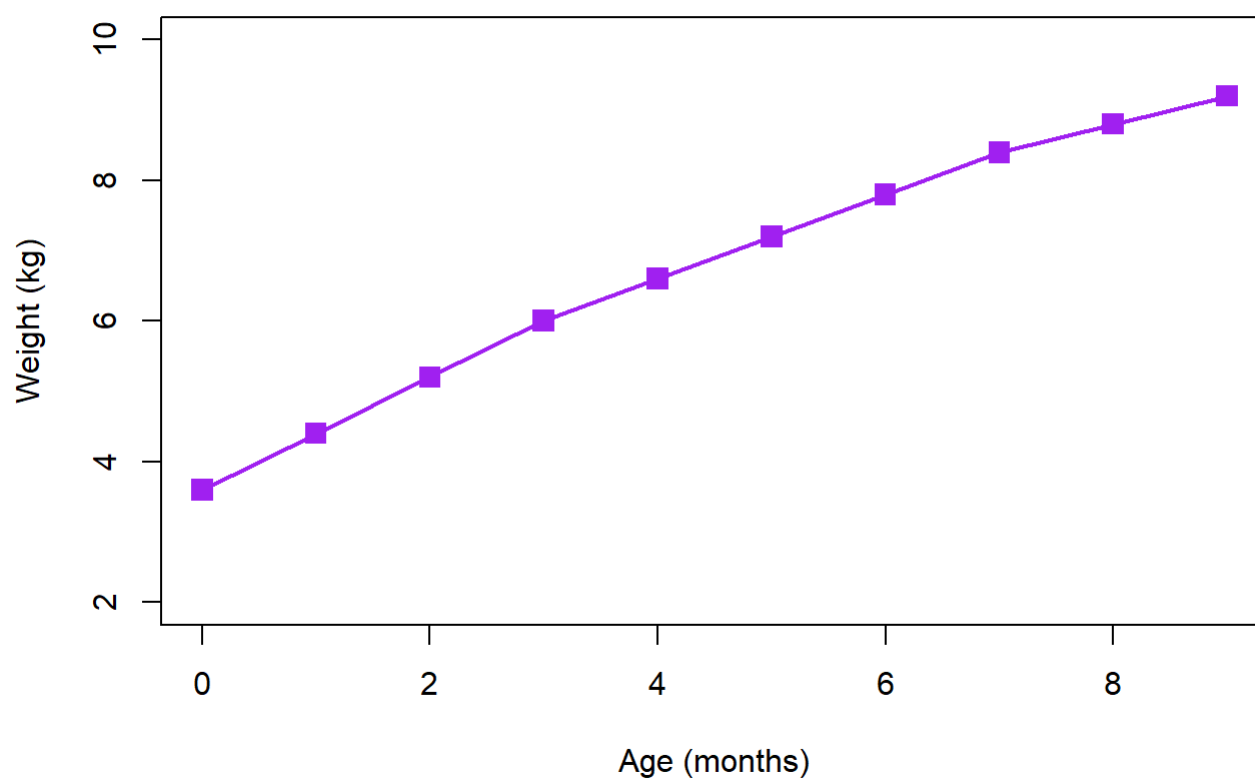


```
#Need to send script to R consol for it to actually execute code
#Can copy/paste or do control+enter (cursor must be on line you want to execute)
#Can also press "Run" button to run line or "Source" to run everything

#Need to import/read input data file first
baby <- read.table("bimm143_05_rstats/weight_chart.txt")
#Have to "argue" with it to make headers in header space rather than as 2 data points
baby <- read.table("bimm143_05_rstats/weight_chart.txt", header = TRUE)

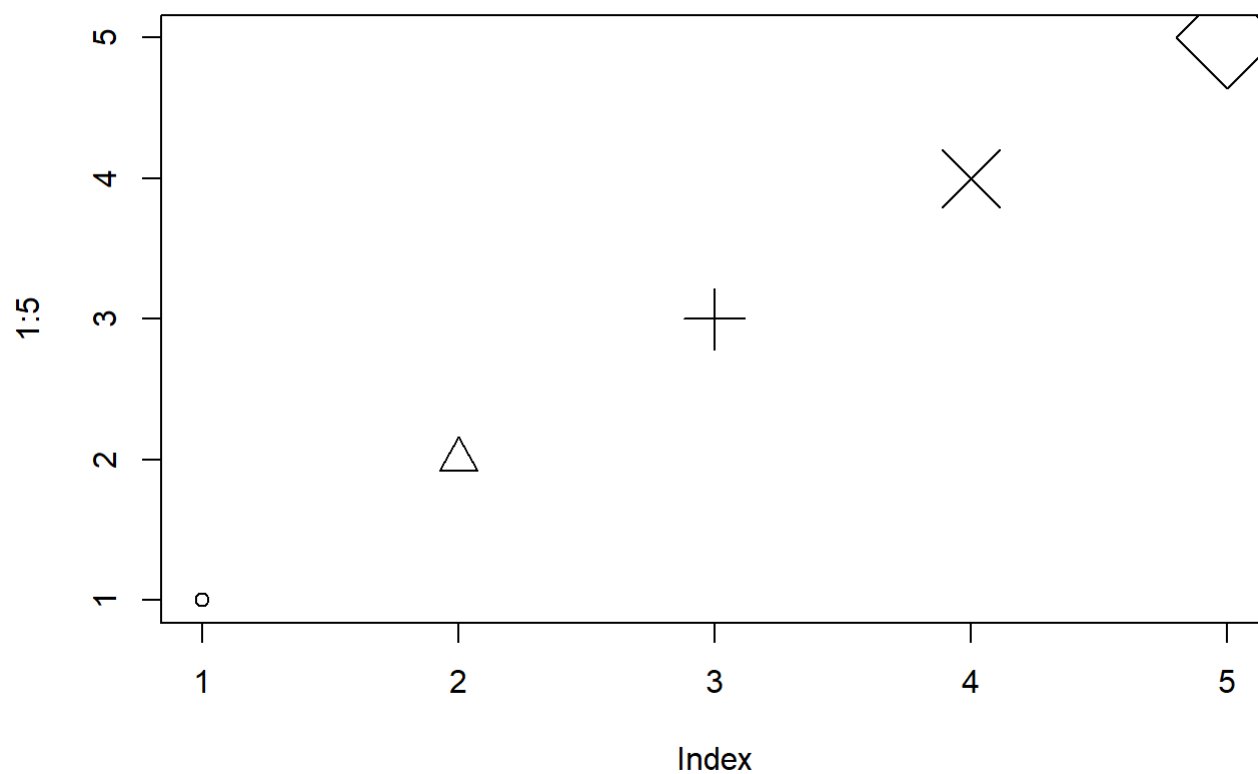
#A basic plot of age vs. weight
plot(baby$Age, baby$Weight, col="purple", type = "o", pch = 15, cex = 1.5, lwd = 2,
      ylim = c(2,10), xlab = "Age (months)", ylab = "Weight (kg)", main = "Suitable Title" )
```

## Suitable Title



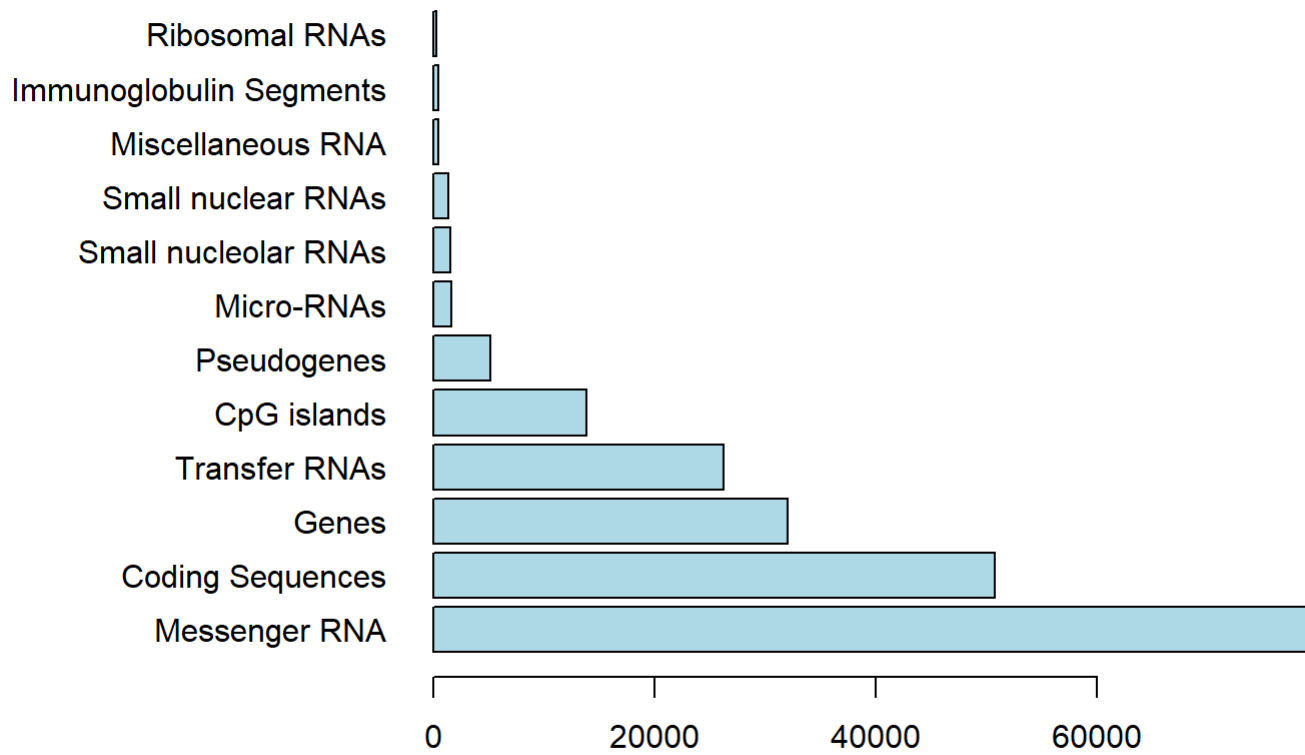
```
#$ or [] accesses that column of the table  
#MAKE SURE TO PUT ALL ARGUMENTS IN QUOTATION MARKS
```

```
#An example of 'pch' plot character and 'cex' size  
plot(1:5, cex = 1:5, pch = 1:5)
```

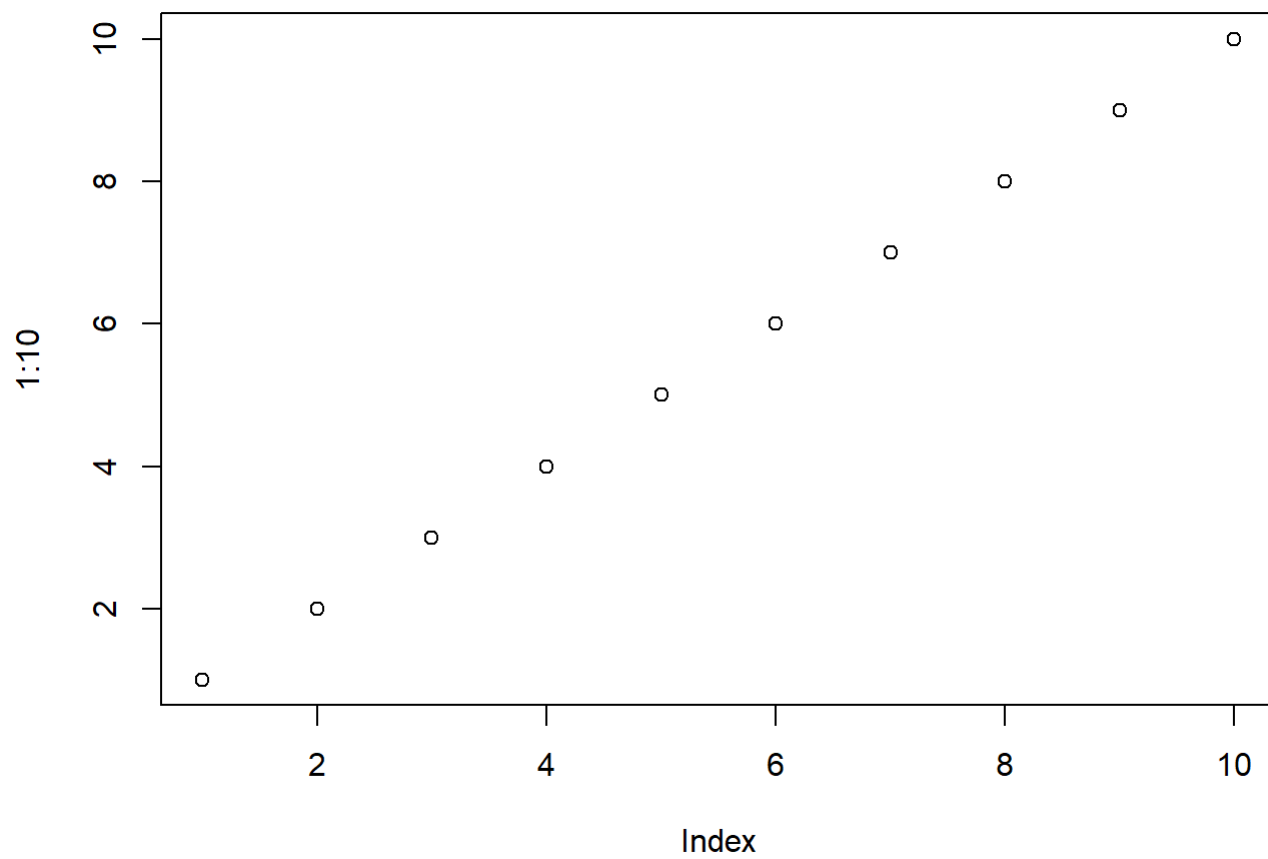


```
#Bar plot with mouse genome features
# mouse <- read.table("bimm143_05_rstats/bimm143_05_rstats/feature_counts.txt")
#Doesn't work because "Line three did not have 3 elements" because line 3 has a tab, not space
mouse <- read.table("bimm143_05_rstats/feature_counts.txt", header = TRUE, sep = "\t")
barplot(mouse$Count, horiz = TRUE, col = "lightblue",
        names.arg = mouse$Feature, las = 1)

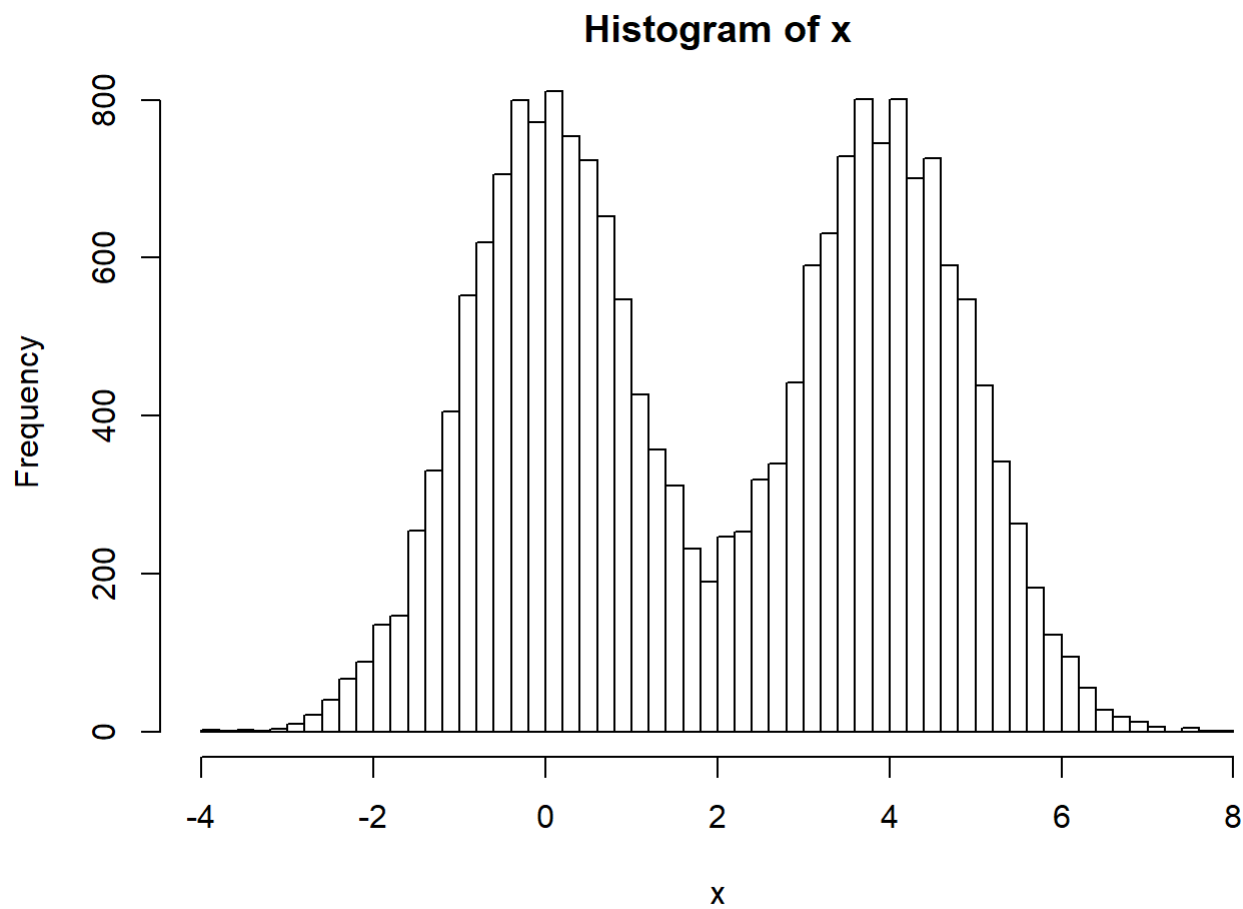
par(mar=c(5,11,2,1))
barplot(mouse$Count, horiz = TRUE, col = "lightblue",
        names.arg = mouse$Feature, las = 1)
```



```
par(mar=c(5,4,2,2))  
plot(1:10)
```



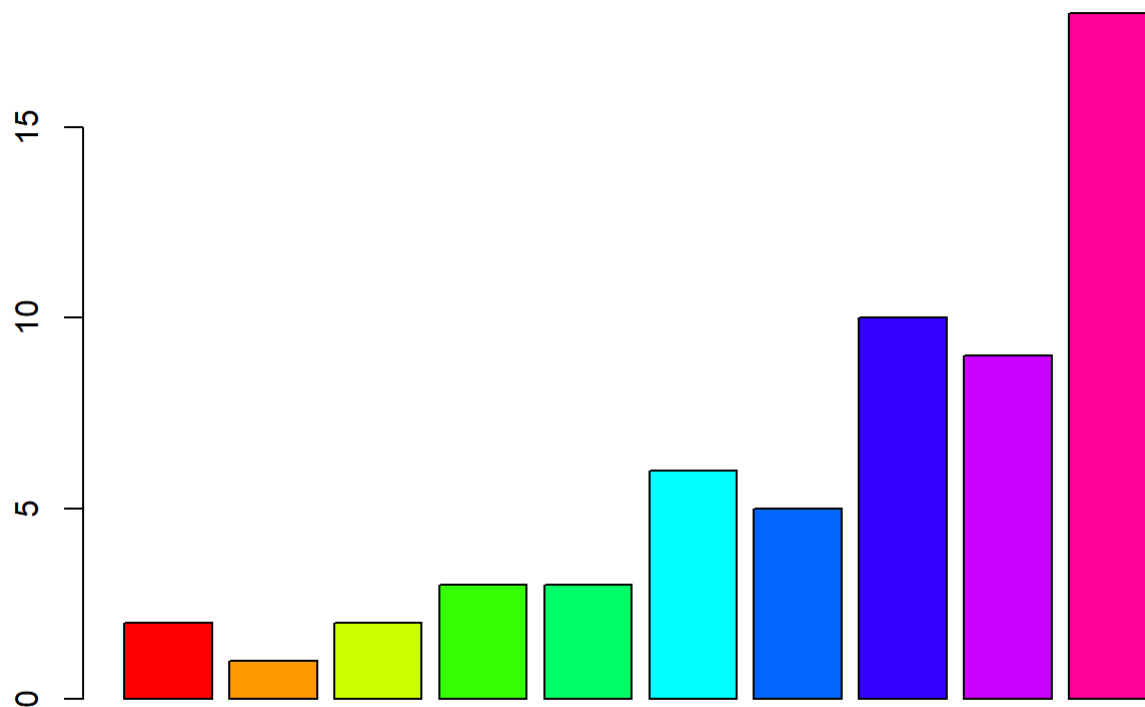
```
#Histogram  
x <- c(rnorm(10000),rnorm(10000)+4)  
hist(x, breaks=50)
```



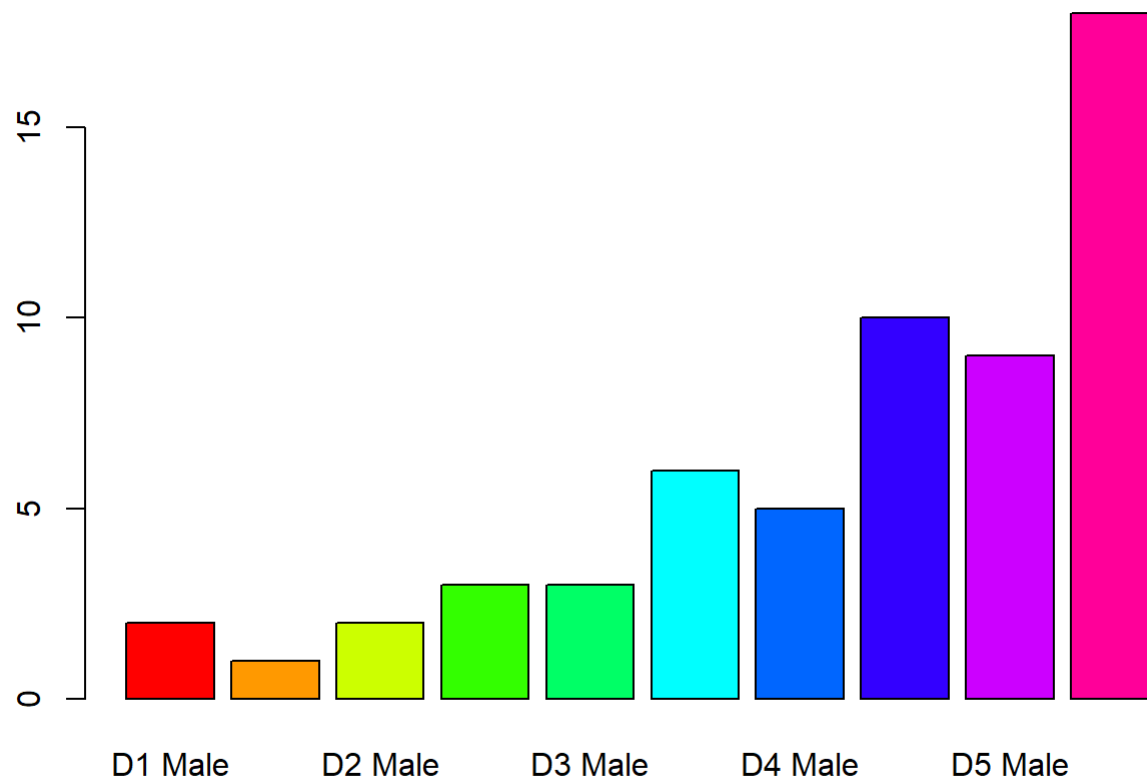
```
#Color vectors  
gender <- read.table("bimm143_05_rstats/male_female_counts.txt", header = TRUE, sep="\t")  
nrow(gender)
```

```
## [1] 10
```

```
barplot(gender$Count, col = rainbow(10))
```



```
#Prof's way  
mf <- read.delim("bimm143_05_rstats/male_female_counts.txt")  
barplot(mf$Count, names.arg = mf$Sample, col=rainbow(10))
```



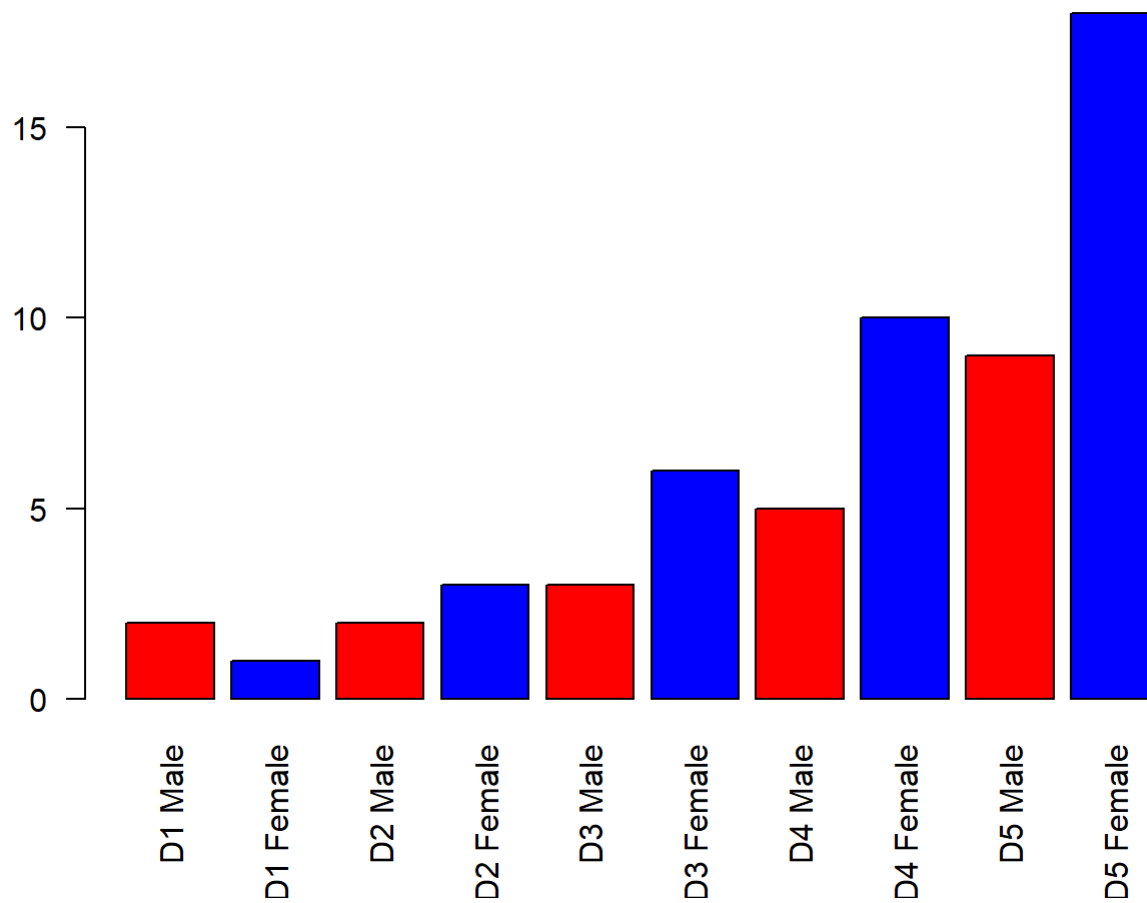
```
nrow(mf)
```

```
## [1] 10
```

```
#same plot, different colors
```

```
barplot(mf$Count, names.arg = mf$Sample, col=c("red", "blue"), las = 2)
```





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

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