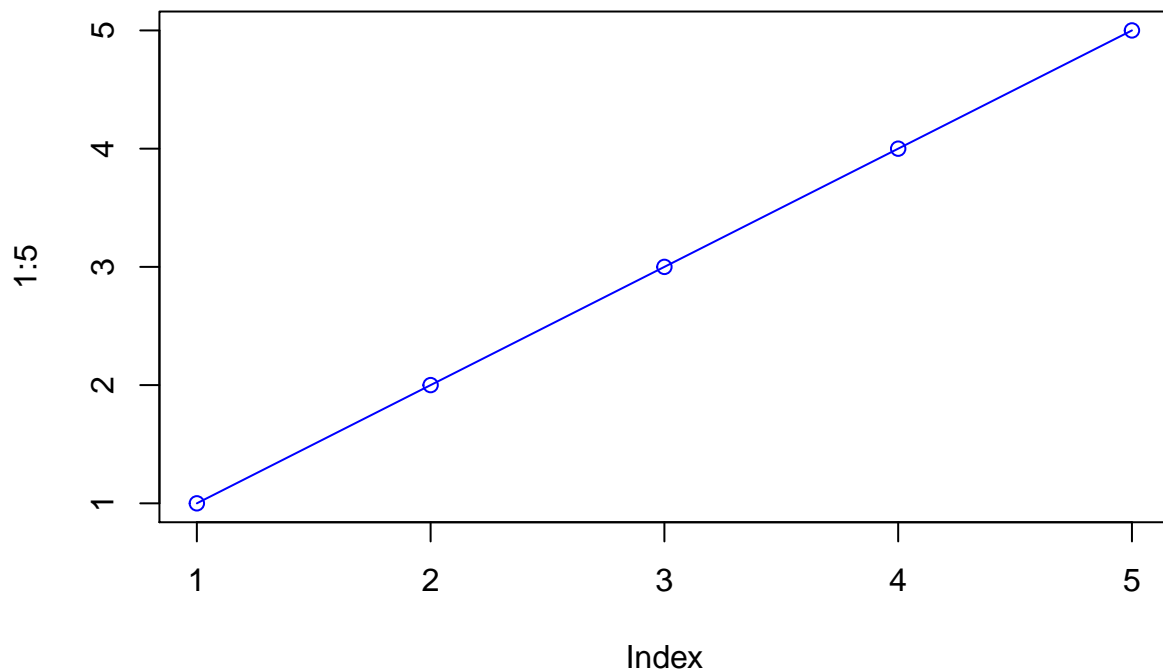


# Class 5: Data visualization and graphics in R

Tiffany Luong

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```
#Class 5  
#Data visualization and graphics in R  
  
#GRAPH 1: practice plot  
plot(1:5, col="blue", typ="o")
```

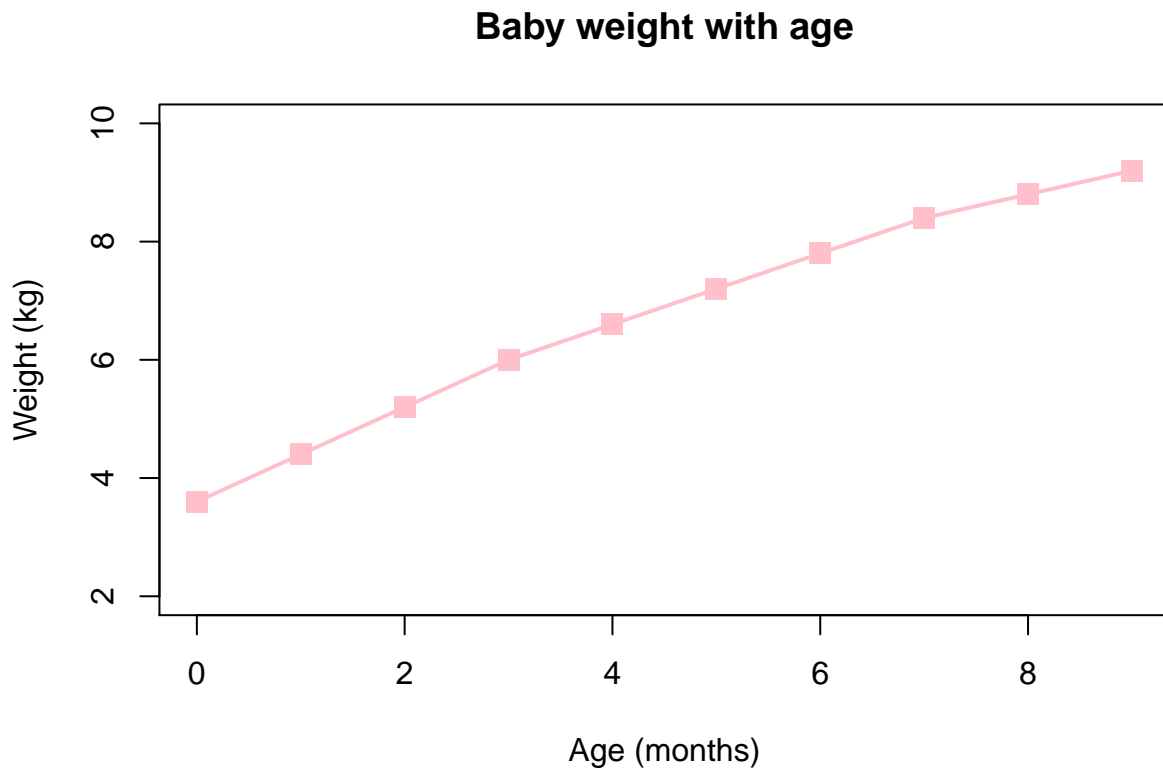


```
#following the lecture exercise  
#set WD to lecture_5  
setwd("C:/Users/hitif/Desktop/R_Shiny_Things/lecture_5")  
  
#read table for weight_chart  
weight <- read.table("bimm143_05_rstats/weight_chart.txt", header = TRUE)  
  
#GRAPH 2: HOW TO MAKE A LINE PLOT  
#change the scatterplot produced to a line plot
```

```

#pch = point type
#cex = point size
#lwd = line density
#ylim = limit the y-axis
#xlab = x-axis label
#ylab = y-axis label
#main = title
#col = pink
plot(weight$Age, weight$Weight, typ="o", pch=15, cex=1.5, lwd=2, ylim=c(2,10), xlab = "Age (months)", y

```

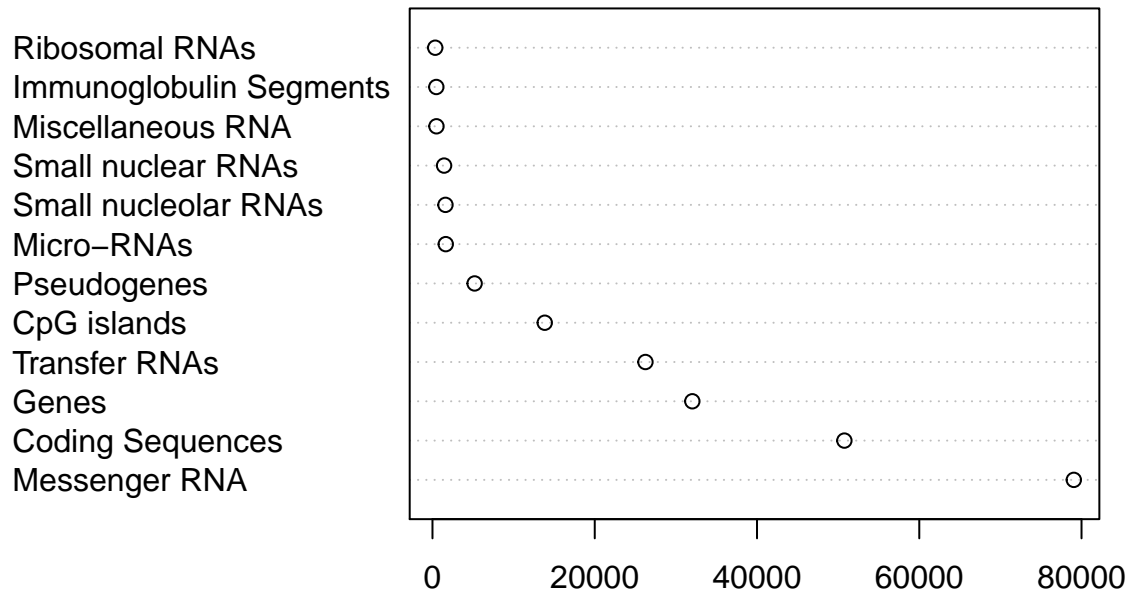


```

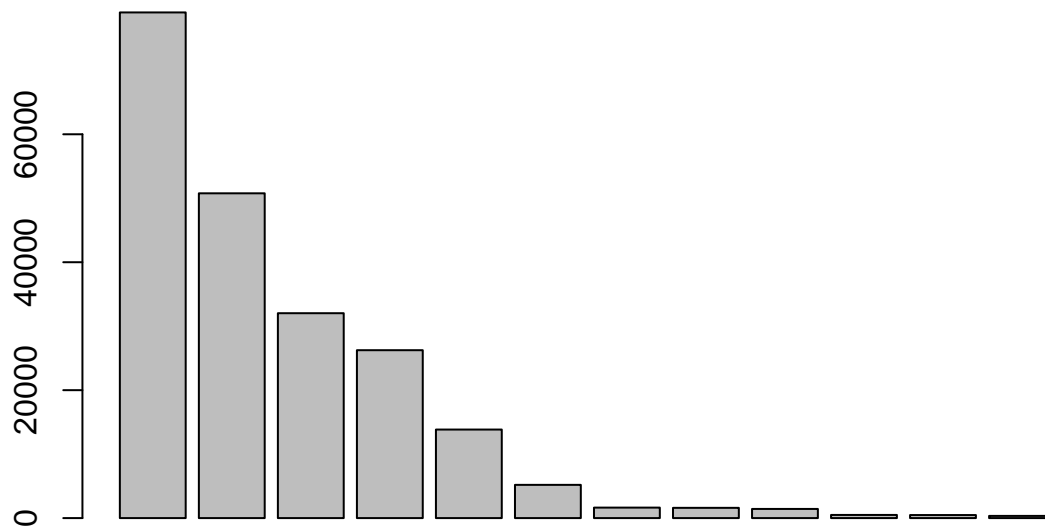
#sep="\t" SEPARATE BY TAB!!!! to include the row names
mouse <- read.table("bimm143_05_rstats/feature_counts.txt", header = TRUE, sep="\t")

#GRAPH 3: DotChart(X, labels)
dotchart(mouse$Count, labels = mouse$Feature)

```



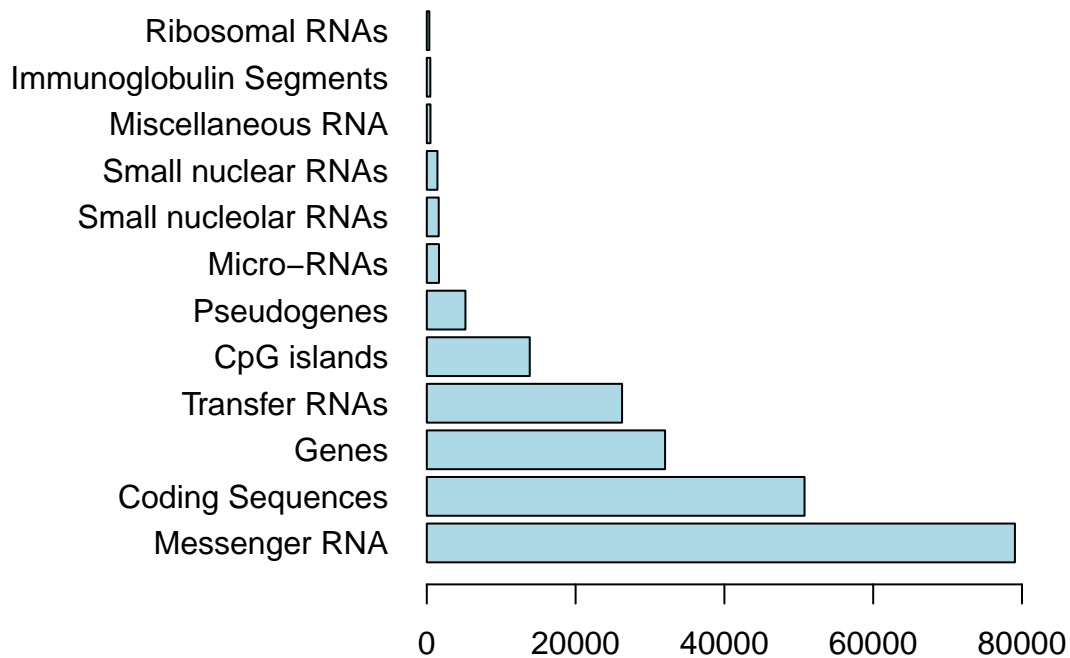
```
#GRAPH 4: barplot basic
barplot(mouse$Count)
```



```
#make changes
#PAR (bottom, left, top, right)
par(mar=c(4, 12, 3, 5))

#GRAPH 5: BARPLOT pretty
barplot(mouse$Count, horiz= TRUE, names.arg = mouse$Feature, main = "# of features in the mouse GRCh38 ,
```

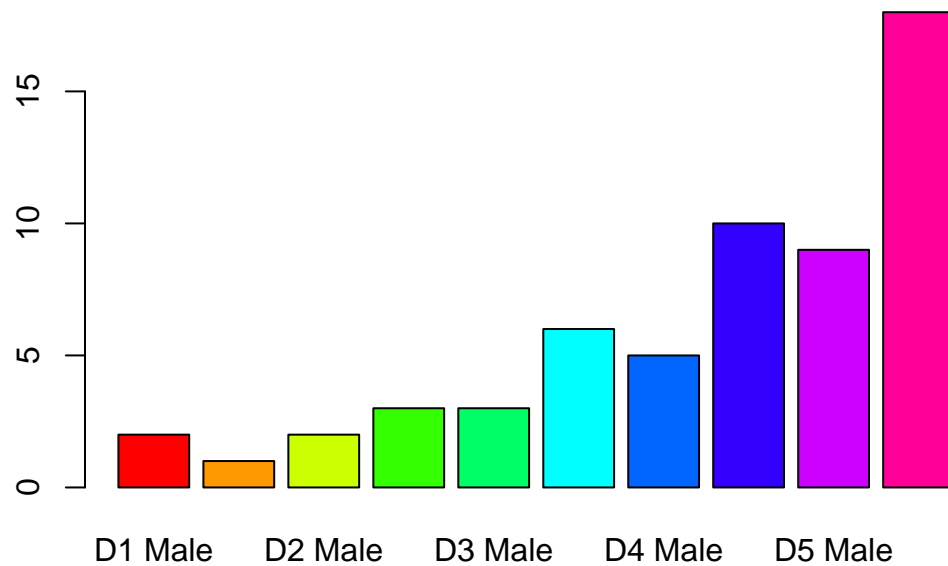
## # of features in the mouse GRCm38 genome



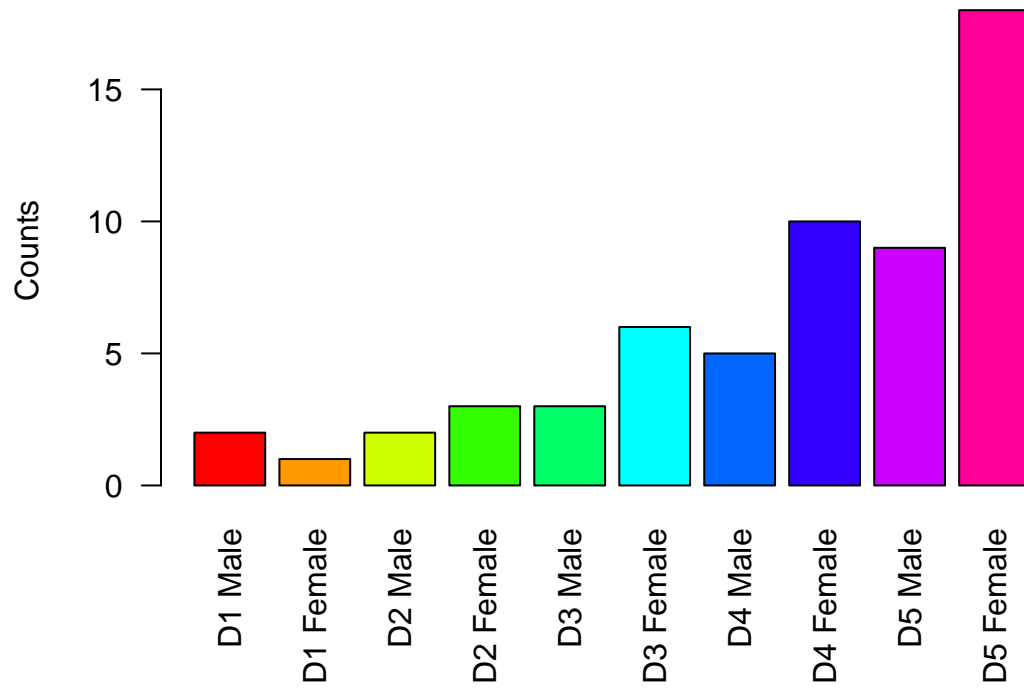
```
#Providing Color Vectors!
mfcoun<- read.delim("bimm143_05_rstats/male_female_counts.txt")

#change the margins!
par(mar=c(7,5,3,4))

#GRAPH 6: hard code the number of rainbows
barplot(mfcoun$Count, names.arg = mfcoun$Sample, col=rainbow(10))
```



```
#GRAPH 7: code the number of rainbows by 'nrows'  
barplot(mfcount$Count, names.arg = mfcount$Sample, col=rainbow(nrow(mfcount)), las=2, ylab = "Counts")
```



```
#GRAPH 8: code by every other color (list them)
barplot(mfcount$Count, names.arg = mfcount$Sample, col=c("pink", "blue"), las=2, ylab = "Counts")
```

