Class Final Project

```r
#load necessary packages
library(readxl)
library(tidyverse)

## ─ Attaching packages ──────────────────────────────────────────
tidyverse 1.2.1 ─

##    ggplot2 3.0.0        purrr   0.2.5
##    tibble  1.4.2        dplyr   0.7.6
##    tidyr   0.8.1        stringr 1.3.1
##    readr   1.1.1        forcats 0.3.0

## ─ Conflicts ──────────────────────────────────────────────
tidyverse_conflicts() ─
##    dplyr::filter() masks stats::filter()
##    dplyr::lag()    masks stats::lag()

library (dplyr)
library(ggplot2)

#import data
BarnesMazedata <- read_excel("~/Cronin1/Rproject_MC_121518.xlsx")

#checking data
#library(tidyverse)
#library (dplyr)
anyNA(BarnesMazedata)

## [1] TRUE

names(BarnesMazedata)

##  [1] "Animal ID"
##  [2] "X__1"
##  [3] "Sex"
##  [4] "Day 1 Latency to Escape (s)"
##  [5] "Day 2  Latency to Escape  (s)"
##  [6] "Day 3 Latency to Escape  (s)"
##  [7] "Day 4 Latency to Escape  (s)"
##  [8] "Distance"
##  [9] "Target : entries"
## [10] "Target : latency to first entry (s)"
## [11] "Time in Correct Zone  (s)"
## [12] "Total Errors"

#fixing column name
names(BarnesMazedata)[2]<-"Genotype"
names(BarnesMazedata)
```

```
##  [1] "Animal ID"
##  [2] "Genotype"
##  [3] "Sex"
##  [4] "Day 1 Latency to Escape (s)"
##  [5] "Day 2  Latency to Escape  (s)"
##  [6] "Day 3 Latency to Escape  (s)"
##  [7] "Day 4 Latency to Escape  (s)"
##  [8] "Distance"
##  [9] "Target : entries"
## [10] "Target : latency to first entry (s)"
## [11] "Time in Correct Zone  (s)"
## [12] "Total Errors"
```

```r
table(BarnesMazedata$Genotype)
```

```
##
## KO/KO WT/KO WT/WT
##     13     14     12
```

```r
#mutate data - create variable
BarnesMazedata$PercentCorrect<-((BarnesMazedata$`Time in Correct Zone
(s)`/90)*100)

anyNA(BarnesMazedata$PercentCorrect)
```
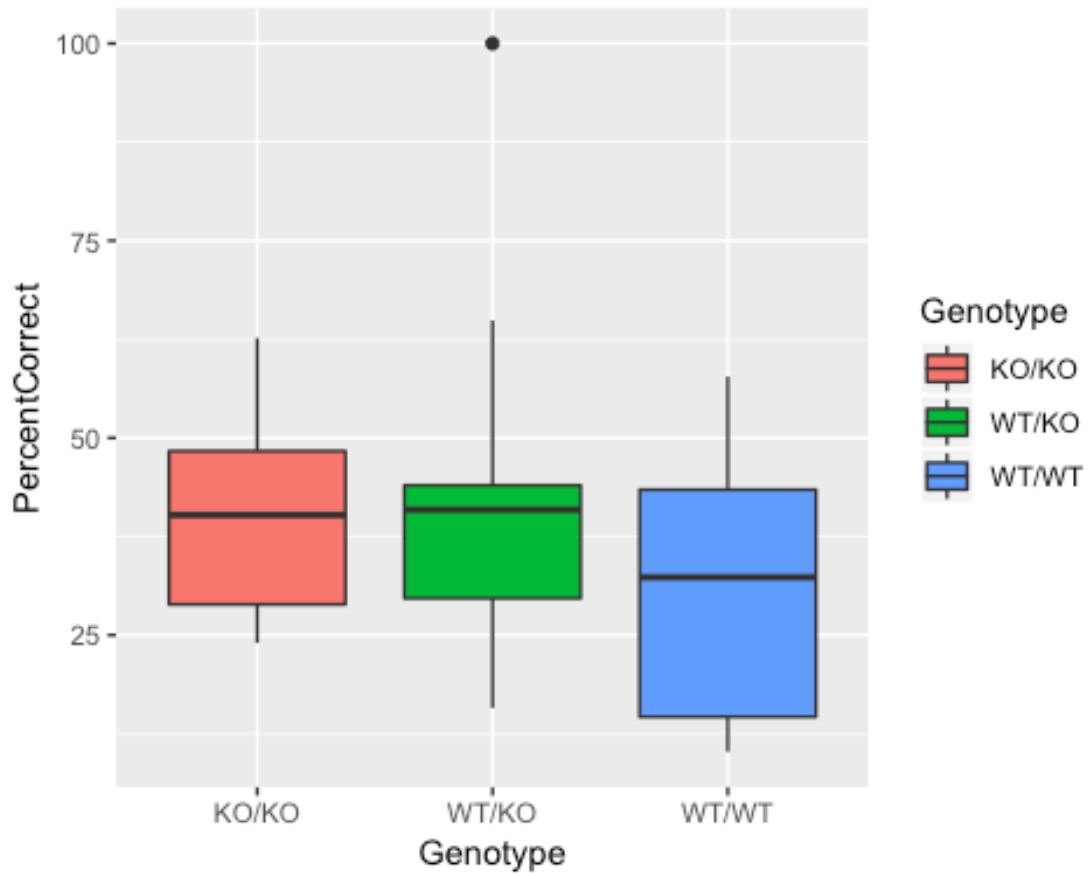
```
## [1] FALSE
```

```r
summary(BarnesMazedata$PercentCorrect)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   10.22   27.56   39.22   37.93   45.11  100.00
```

```r
#visualize data

ggplot(BarnesMazedata,aes(x=Genotype,y=PercentCorrect,fill=Genotype))+geom_boxplot()
```

```
#statisticaltest: One-Way ANOVA
anova<-aov(PercentCorrect~Genotype,data=BarnesMazedata)
summary(anova)

##            Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2    723   361.6   1.271  0.293
## Residuals  36  10247   284.6
```