

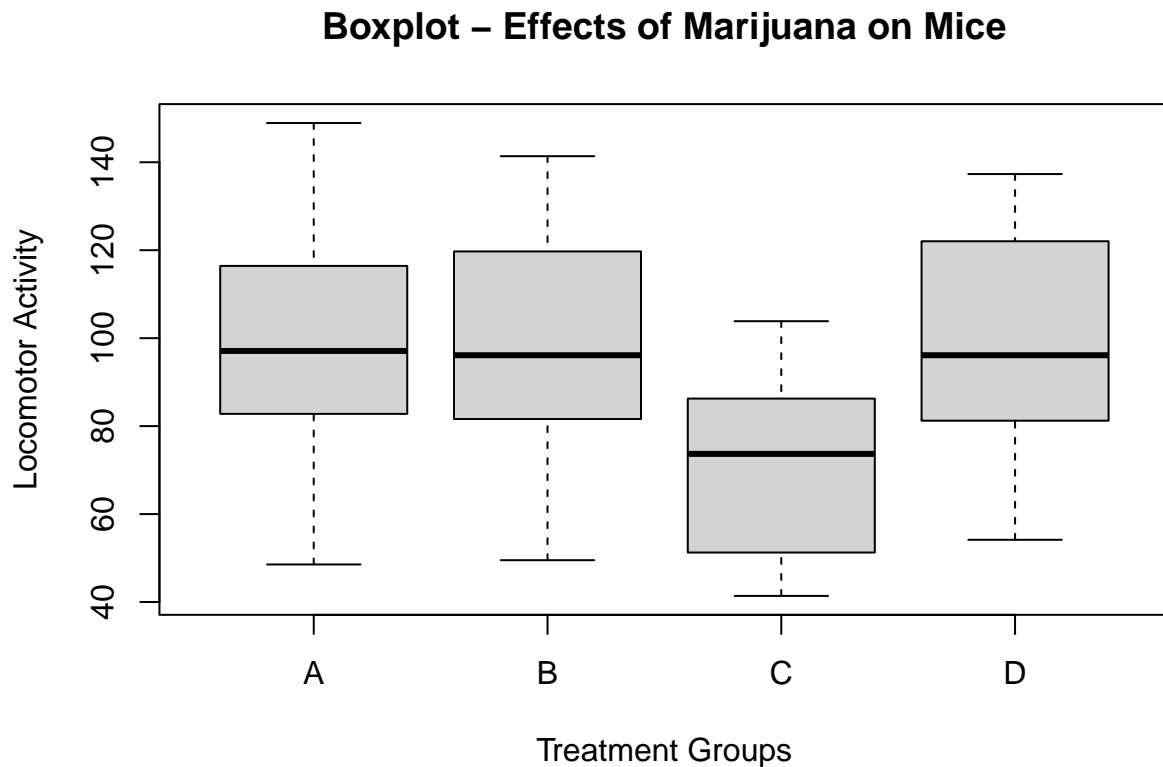
STAT6180 Statistical Analysis

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Question 1 (a).

```
library(readxl)
mice_pot <- read_excel("C:/Users/harsh/Desktop/mice_pot.xlsx")
data <- data.frame(A = mice_pot$`Group 0.3`, B = mice_pot$`Group 1`, C = mice_pot$`Group 3`, D = mice_pot$`Group 4`)
boxplot(data, main = "Boxplot - Effects of Marijuana on Mice", xlab = "Treatment Groups", ylab = "Locomotor Activity")
```



The boxes seem to be equally sized, implying that the locomotor activity appears to have the same variability, although there are differences in the median activity levels.

Question 1 (b).

$H_0 = \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4$ $H_1 \neq 0$ For Atleast One $\alpha_i, i = 1, 2, 3, 4$ Where α_i = level of activity as measured by the total distance

```
summary <- read.table('mice_pottxt.txt', header = TRUE)
summary.aov = aov(percent_of_act ~ group, data = summary)
summary(summary.aov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## group         3   6329   2109.7    3.126 0.0357 *
## Residuals    42  28344    674.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Question 1 (c).

$H_0 : \mu_3 \text{ doses as a whole} = \mu_{3\text{mg/Kg}}$ $H_1 : \mu_3 \text{ doses as a whole} \neq \mu_{3\text{mg/Kg}}$ Test Statistic Value = 3.1222 Degree of Freedom = 44 P-Value = 0.003169

```
library(readxl)
JointAnalysis <- read_excel("C:/Users/harsh/Desktop/JointAnalysis.xlsx")
t.test(JointAnalysis$`Group Joint`, JointAnalysis$`Group 3`, var.equal = TRUE)
```

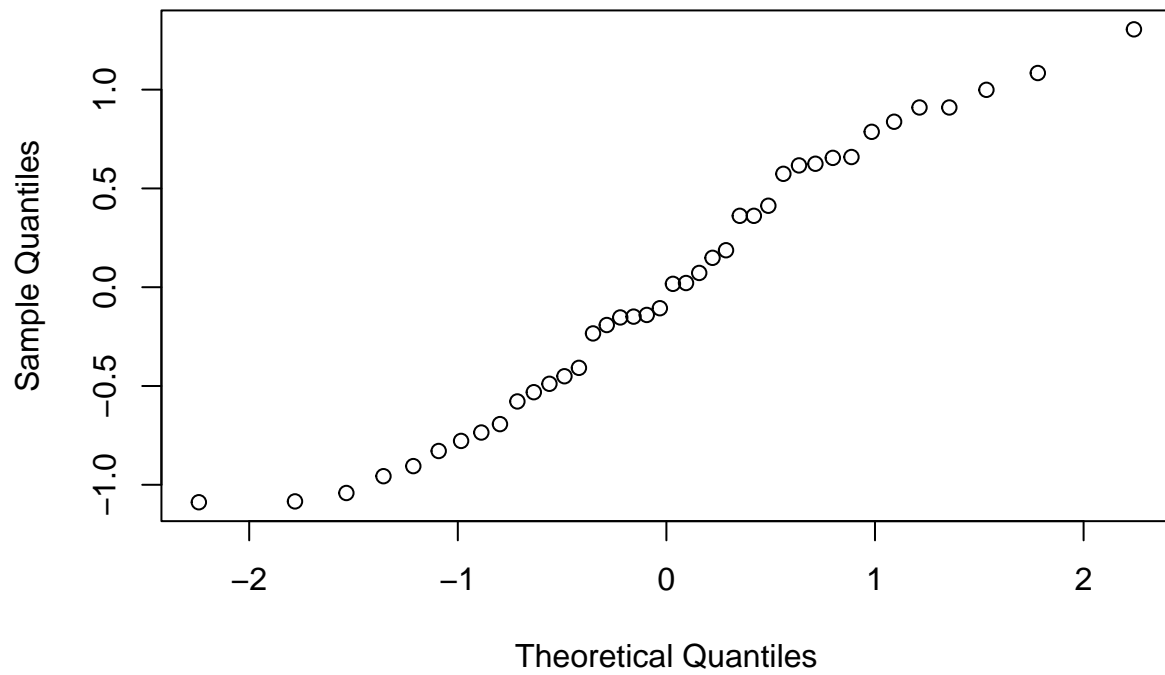
```
##
## Two Sample t-test
##
## data: JointAnalysis$`Group Joint` and JointAnalysis$`Group 3`
## t = 3.1222, df = 44, p-value = 0.003169
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  10.04934 46.64441
## sample estimates:
## mean of x mean of y
##  99.01474 70.66787
```

Question 2 (a).

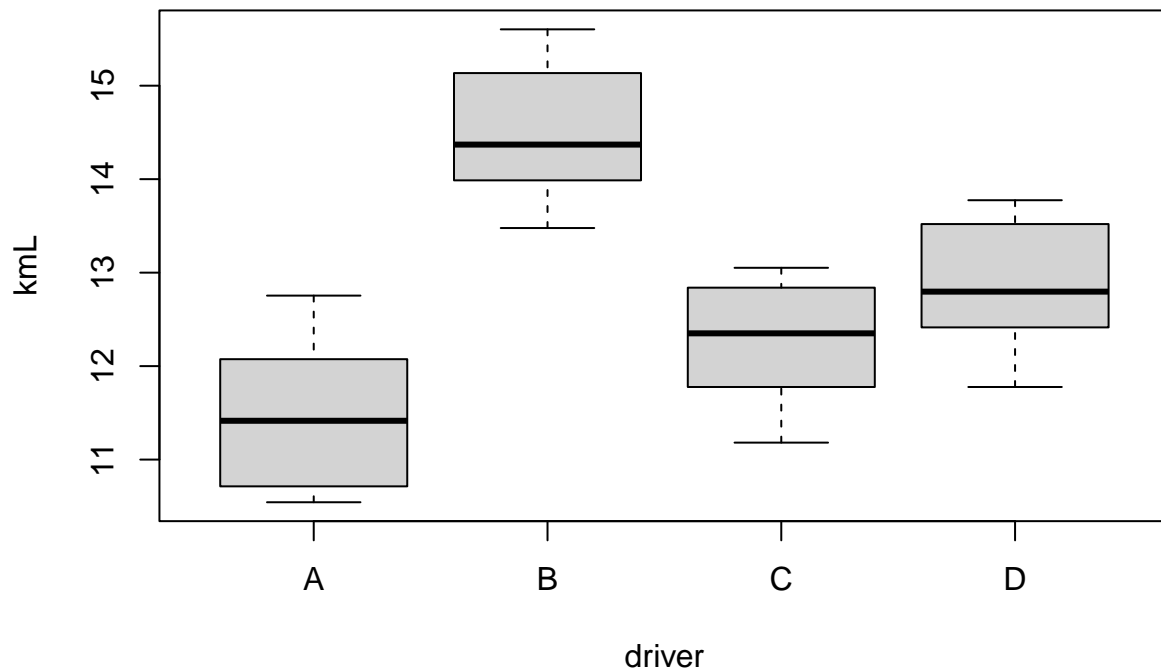
This design is a balanced study as the number of replicates for each treatment is the same

```
kml <- read.table('kml.dat', header = TRUE)
kml.aov = aov(kmL ~ driver, data = kml)
qqnorm(kml.aov$residuals)
```

Normal Q-Q Plot



```
boxplot(kmL ~ driver, data = km1)
```



Question 2 (b). - See Above As Well

The Normal Q-Q plot of the residuals seems to show a strong linear trend meaning the residuals are closely normally distributed.

Question 2 (c).

```
summary(kml.aov)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## driver      3  50.66   16.887    33.41 1.67e-10 ***
## Residuals   36   18.20    0.505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$ H_1 : Not all means equal μ_i is effect of driver for production variation The assumptions seem to be satisfied.

Question 2 (d).

Conclude since P-Value < significance level (0.05) therefore we have evidence to reject null in favour of alternative. Hence evidence suggests that the mean kmL is different for at least one driver.