Perform two-way Anova

Aniket Roy and Kruitk Shah

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Example

Moth dataset are stored in csv file and then reading csv file to get data from csv file.

```
data1 <- read.csv('moth.csv')
data1
```

```
##      X28     Top Scent
## 1    19     Top Scent
## 2    32     Top Scent
## 3    15     Top Scent
## 4    13     Top Scent
## 5    35     Top Sugar
## 6    22     Top Sugar
## 7    33     Top Sugar
## 8    21     Top Sugar
## 9    17     Top Sugar
## 10   31 Middle Scent
## 11   21 Middle Scent
## 12   14 Middle Scent
## 13   18 Middle Scent
## 14   24 Middle Scent
## 15   25 Middle Sugar
## 16   12 Middle Sugar
## 17   19 Middle Sugar
## 18   21 Middle Sugar
## 19   27 Middle Sugar
## 20   21 Middle Scent
## 21   34 Middle Scent
## 22   32 Middle Scent
## 23   11 Middle Scent
## 24   10 Bottom Scent
## 25   39 Bottom Sugar
## 26   37 Bottom Sugar
## 27   30 Bottom Sugar
## 28   22 Bottom Sugar
## 29   28 Bottom Sugar
```

```
data2<-data.frame("Moth"=data1[,1],"Position"=data1[,2],"lure"=data1[,3])
data2
```

```
##    Moth Position  lure
## 1    19      Top Scent
## 2    32      Top Scent
## 3    15      Top Scent
## 4    13      Top Scent
## 5    35      Top Sugar
## 6    22      Top Sugar
## 7    33      Top Sugar
## 8    21      Top Sugar
## 9    17      Top Sugar
## 10   31   Middle Scent
## 11   21   Middle Scent
## 12   14   Middle Scent
## 13   18   Middle Scent
## 14   24   Middle Scent
## 15   25   Middle Sugar
## 16   12   Middle Sugar
## 17   19   Middle Sugar
## 18   21   Middle Sugar
## 19   27   Middle Sugar
## 20   21   Middle Scent
## 21   34   Middle Scent
## 22   32   Middle Scent
## 23   11   Middle Scent
## 24   10   Bottom Scent
## 25   39   Bottom Sugar
## 26   37   Bottom Sugar
## 27   30   Bottom Sugar
## 28   22   Bottom Sugar
## 29   28   Bottom Sugar
```

The hypothesis testing problem is:

H0:There is no Significance difference between means of all

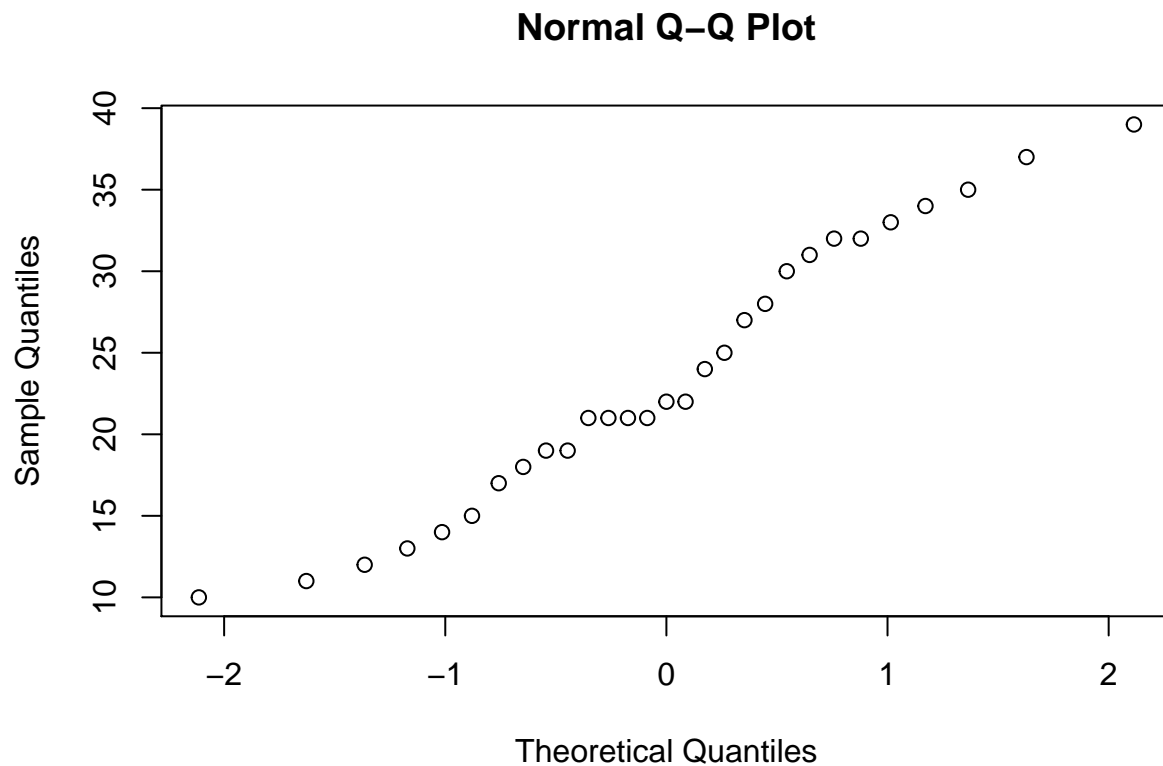**H1:There is a significant difference among means of all.**

To check the normality of a data we have to do the shapiro test

```
res <- shapiro.test(data2$Moth)
res
```

```
##
##  Shapiro-Wilk normality test
##
## data:  data2$Moth
## W = 0.96219, p-value = 0.3717
```

Testing Normality Graphically

```
qqnorm(data2$Moth)
```

Normal Q–Q Plot

Bartlett's test is used to test if k samples have equal variances. Equal variances across samples is called homogeneity of variances.

```
bartlett.test(Moth~Position,data=data2)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Moth by Position
## Bartlett's K-squared = 1.1313, df = 2, p-value = 0.568
```

```
bartlett.test(Moth~lure,data=data2)
```

```
##
##  Bartlett test of homogeneity of variances
##
## data:  Moth by lure
## Bartlett's K-squared = 0.059131, df = 1, p-value = 0.8079
```

Here in moth by position p-vlaue is 0.568 which is greater than 0.05 so we accept NULL Hypothesis. And in moth by lure p-value is 0.8079 which is greater than 0.05 so we accept NULL Hypothesis.

```
twoway <- aov(Moth~Position+lure,data=data2)
summary(twoway)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Position    2  132.1   66.06   0.974  0.391
## lure        1   91.5   91.50   1.349  0.256
## Residuals  25 1695.5   67.82
```

```
twoway
```

```
## Call:
##    aov(formula = Moth ~ Position + lure, data = data2)
##
## Terms:
##                  Position      lure Residuals
## Sum of Squares   132.1248   91.5042 1695.5435
## Deg. of Freedom         2         1        25
##
## Residual standard error: 8.235395
## Estimated effects may be unbalanced
```

```
TK <- TukeyHSD(twoway,"Position")
TK
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Moth ~ Position + lure, data = data2)
##
## $Position
##                     diff        lwr      upr     p adj
## Middle-Bottom -5.5238095 -15.533115 4.485495 0.3690257
## Top-Bottom    -4.6666667 -15.477952 6.144618 0.5378869
## Top-Middle     0.8571429  -7.906955 9.621241 0.9678568
```

```
plot(TK)
```

95% family−wise confidence level

Differences in mean levels of Position