# MATH 588

HW1

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# 1(a)

**Null Hypothesis:** Mean weights are same in group 0 and 1.
**Alternative Hypothesis:** Mean weights are not same in group 0 and 1.

```
library(readr)
fullBumpus <- read_table2("E:/NMT MS/Spring 22/MATH 588/Home_Work/Spring-2022---MATH-588-01-Advanced-Da


ttst1 = t.test(Weight~Survive,var.equal=TRUE,data = fullBumpus)
ttst1
```

```
##
##  Two Sample t-test
##
## data:  Weight by Survive
## t = 2.6093, df = 134, p-value = 0.0101
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.1569291 1.1399459
## sample estimates:
## mean in group 0 mean in group 1
##        25.86094        25.21250
```

**Comments:** According to the p-value [considering variance are same in both group] (0.0101) it can be said that there is statistically significant difference between two group (0 and 1) in terms of weights, at level of significance is 0.05.

```
ttst2 = t.test(Weight~Survive,var.equal=FALSE,data = fullBumpus)
ttst2
```

```
##
##  Welch Two Sample t-test
##
## data:  Weight by Survive
## t = 2.5703, df = 117.95, p-value = 0.01141
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.1488463 1.1480287
## sample estimates:
## mean in group 0 mean in group 1
##        25.86094        25.21250
```

**Comments:** According to the p-value [considering variance are not equal in both group] (0.01141) it can be said that there is statistically significant difference between two group (0 and 1) in terms of weights, at level of significance is 0.05.

So, in both case (variance same or different), the null hypothesis is rejected.

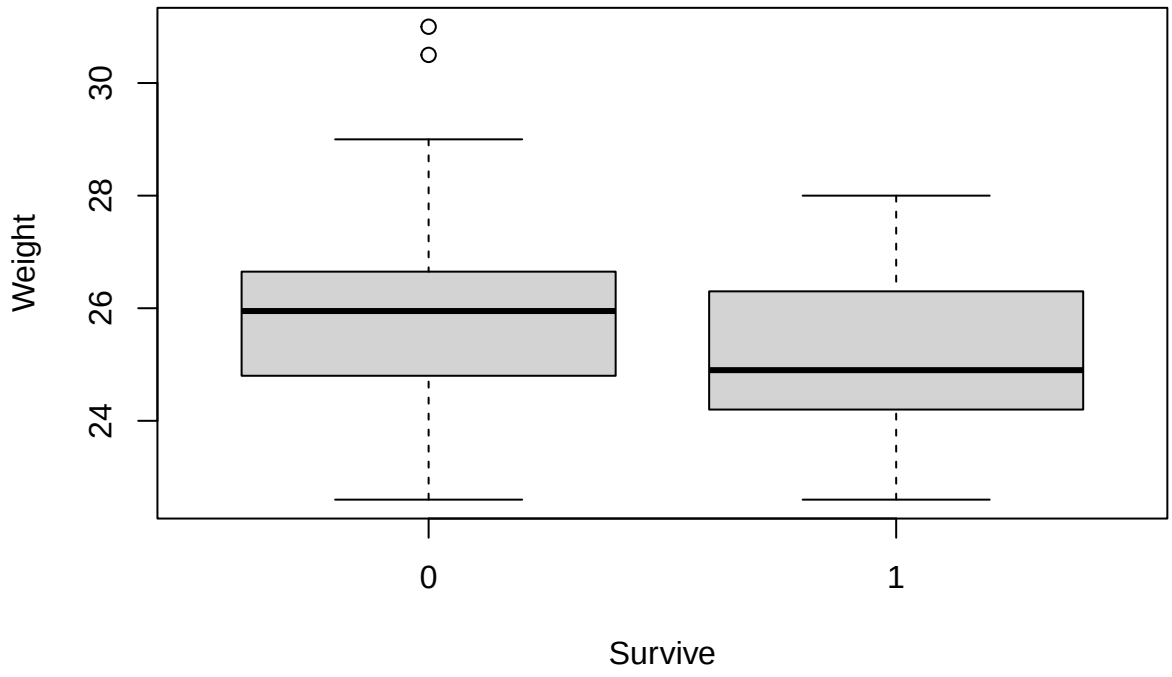
## 1(b)

After observing the normal qqplot of the residual we can interpret that the data does not follow normal distribution. Because the lower tail and upper part in the plot not goes close to the straight line. We should take some sort of transformation before carry out the t-test. The data distribution seems right skewed, so log-transformation could leads the data to normal shape and we know normality is the key assumption for t-test.

```
res = resid(lm(Weight~Survive, data = fullBumpus))
qqnorm(res)
qqline(res)
```

## 1(c)

```
boxplot(Weight~Survive,data=fullBumpus)
```




```
# Showing IQR
aggregate(Weight~Survive,fullBumpus,IQR)
```

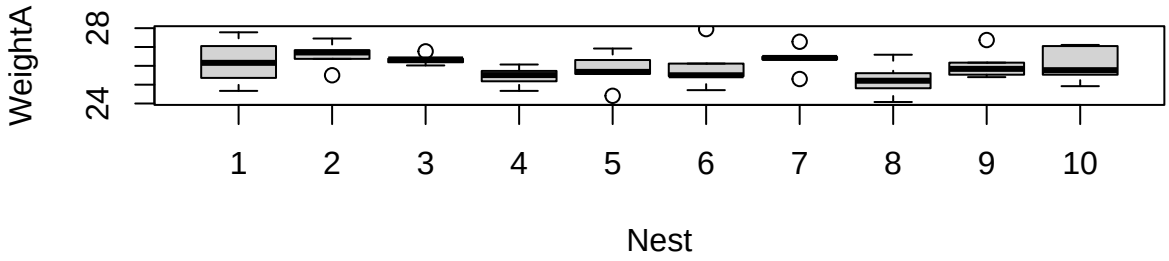
```
##   Survive Weight
## 1       0  1.775
## 2       1  2.100
```

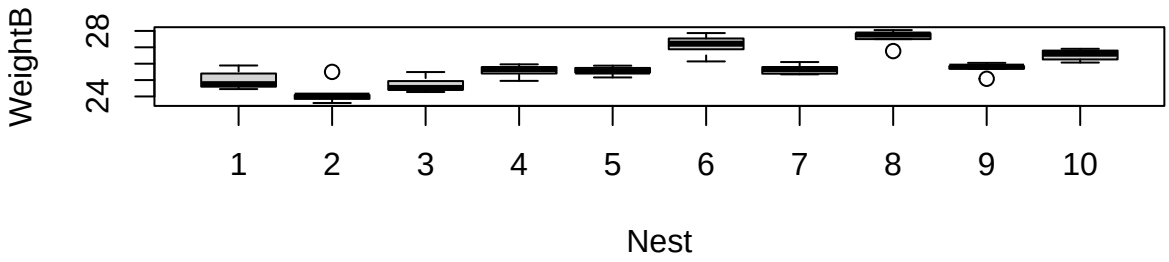
As we know if the IQRs is between 0.5 and 2.0, there is no cause for concern about unequal variances. But in our case we observed that the IQR is greater than 2 for the surviving sparrow (1). So, the variability seems different between this two groups for the weight.

## 1(d)

```
HW1FakeCor <- read_table2("E:/NMT MS/Spring 22/MATH 588/Home_Work/Spring-2022---MATH-588-01-Advanced-Da


{par(mfrow=c(2,1))
boxplot(WeightA~Nest,data=HW1FakeCor)
boxplot(WeightB~Nest,data=HW1FakeCor)}
```




From the boxplot we have seen that Nest 4 and 9 have close mean values and similar types of weight distribution. So, birds in nest 4 and 9 are similar in weights and have correlated errors.

## 2(a)

```
fullBumpus <- read_table2("E:/NMT MS/Spring 22/MATH 588/Home_Work/Spring-2022---MATH-588-01-Advanced-Da


mdl <- lm(Alar~Female+Weight,data = fullBumpus)
summary(mdl)
```

```
##
## Call:
```

```
## lm(formula = Alar ~ Female + Weight, data = fullBumpus)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.2387  -2.6125   0.2613   2.8729  11.0747
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 202.1958     6.1318  32.975  < 2e-16 ***
## Female       -4.8027     0.7271  -6.605 8.71e-10 ***
## Weight        1.7553     0.2372   7.401 1.37e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.942 on 133 degrees of freedom
## Multiple R-squared:  0.4961, Adjusted R-squared:  0.4885
## F-statistic: 65.47 on 2 and 133 DF,  p-value: < 2.2e-16
```

## 2(b)

```
b0M = coef(mdl)[1]
b0M
```

```
## (Intercept)
##    202.1958
```

```
b0F = coef(mdl)[1] + coef(mdl)[2]
b0F
```

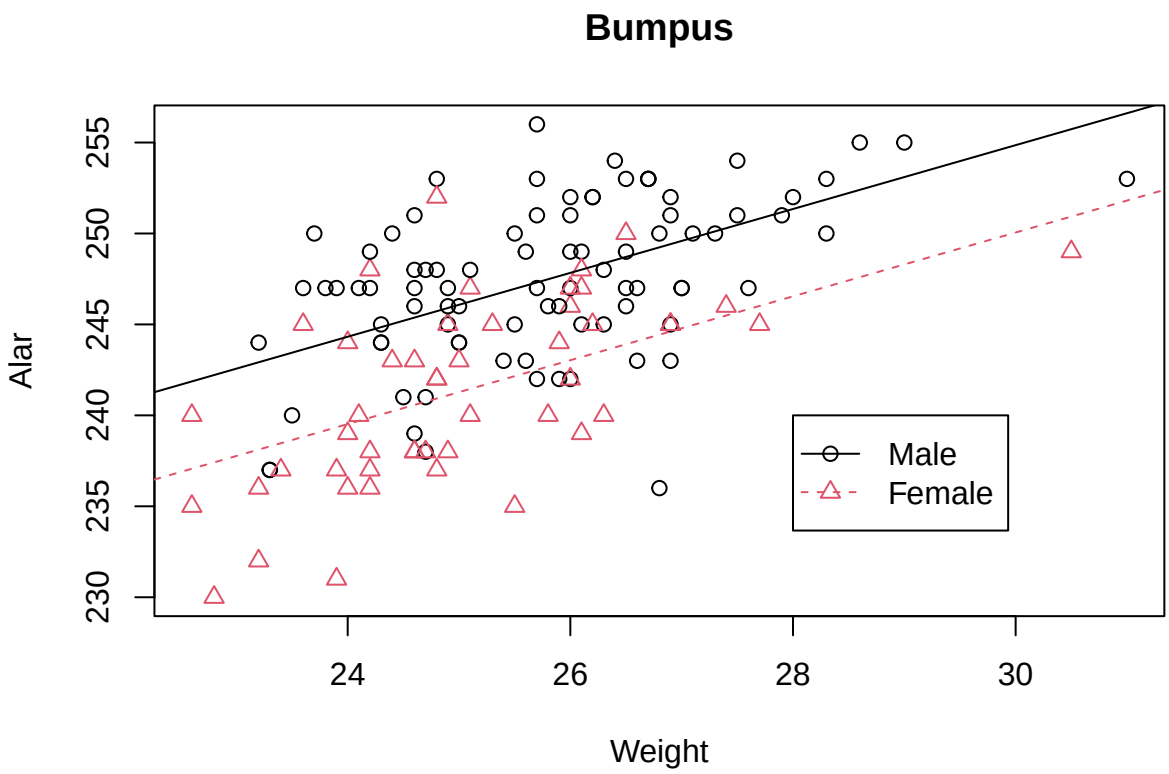
```
## (Intercept)
##    197.3931
```

```
b1 = coef(mdl)[3]
b1
```

```
##  Weight
## 1.75533
```

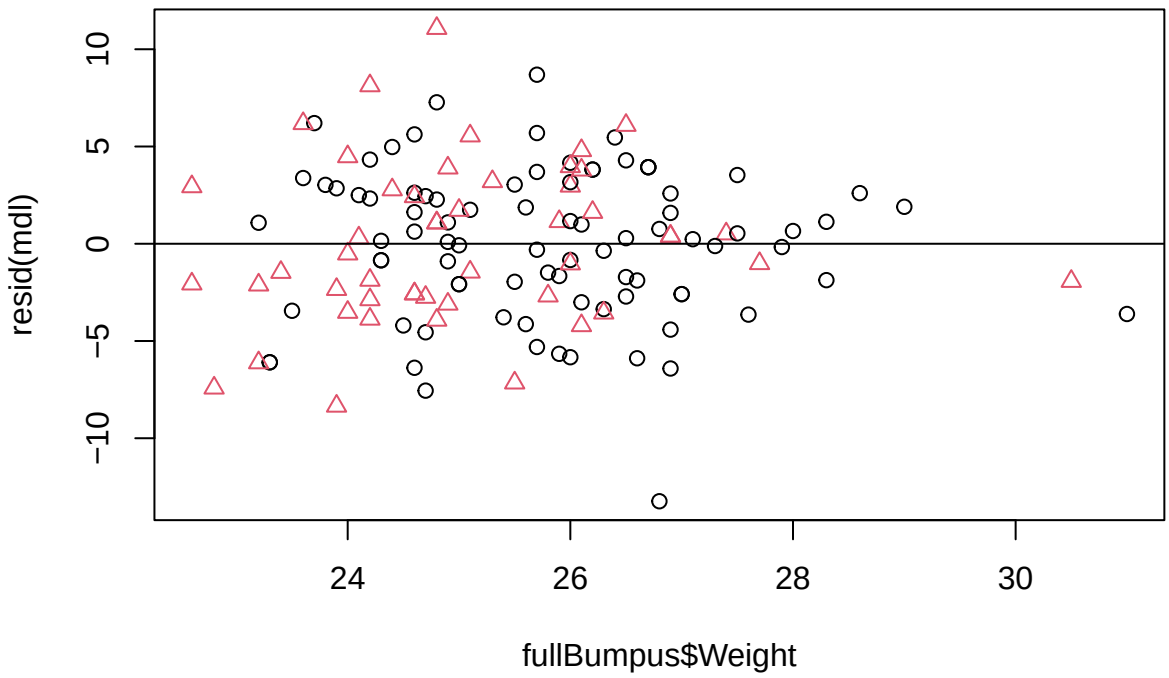
## 2(c)

```
fullBumpus$Female <- as.factor(fullBumpus$Female)
#with(fullBumpus, table(Female, as.numeric(Female)))
{plot(Alar~Weight, pch=as.numeric(Female),col=as.numeric(Female), main="Bumpus",data=fullBumpus)
abline(b0M, b1, col=1, lty=1)
abline(b0F, b1, col=2, lty=2)
legend(28, 240, c("Male", "Female"), col=1:2, lty=1:2, pch=1:2)}
```




Without the interaction between Female and weights, the fitted lines are parallel. Let's explore residual vs X plot

```
{plot(resid(mdl)~fullBumpus$Weight, col=as.numeric(fullBumpus$Female),
pch=as.numeric(fullBumpus$Female))
abline(h=0)}
```

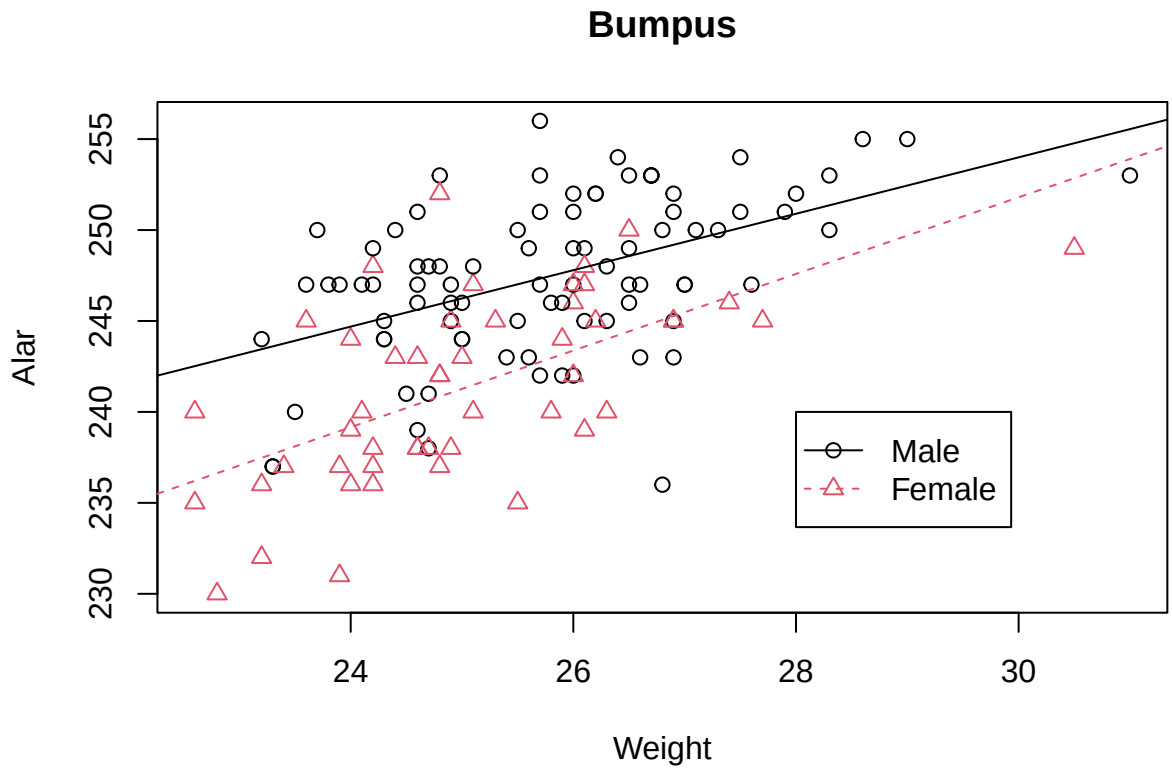



## 2(d)

```
mdlI = lm(Alar~Female*Weight, data=fullBumpus)
summary(mdlI)
```

```
##
## Call:
## lm(formula = Alar ~ Female * Weight, data = fullBumpus)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.0332  -2.5531   0.0527   2.8415  11.1550
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    207.4608     7.6956  26.958  < 2e-16 ***
## Female1        -18.8586    12.4580  -1.514    0.132
## Weight           1.5512     0.2979   5.207 7.18e-07 ***
## Female1:Weight   0.5554     0.4914   1.130    0.260
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.938 on 132 degrees of freedom
## Multiple R-squared:  0.5009, Adjusted R-squared:  0.4896
## F-statistic: 44.16 on 3 and 132 DF,  p-value: < 2.2e-16
```

```
b0M = coef(mdlI)[1]
b0F = coef(mdlI)[1] + coef(mdlI)[2]
b1M = coef(mdlI)[3]
b1F = coef(mdlI)[3] + coef(mdlI)[4]
{with(fullBumpus, plot(Alar~Weight, pch=as.numeric(Female),
col=as.numeric(Female), main="Bumpus"))
abline(b0M, b1M, col=1, lty=1)
abline(b0F, b1F, col=2, lty=2)
legend(28, 240, c("Male", "Female"), col=1:2, lty=1:2, pch=1:2)}
```




## 2(e)

```
anova(mdl,mdlI)
```

```
## Analysis of Variance Table
##
## Model 1: Alar ~ Female + Weight
## Model 2: Alar ~ Female * Weight
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    133 2067.1
## 2    132 2047.3  1     19.81 1.2773 0.2605
```

The p-value for the F-statistic is greater than 0.05. So, at 5% level of significance we conclude that the non-parallel slops are not significant or the interaction term is insignificant. So, we don't have good evidance of non-aparallel slopes.

## 2(f)

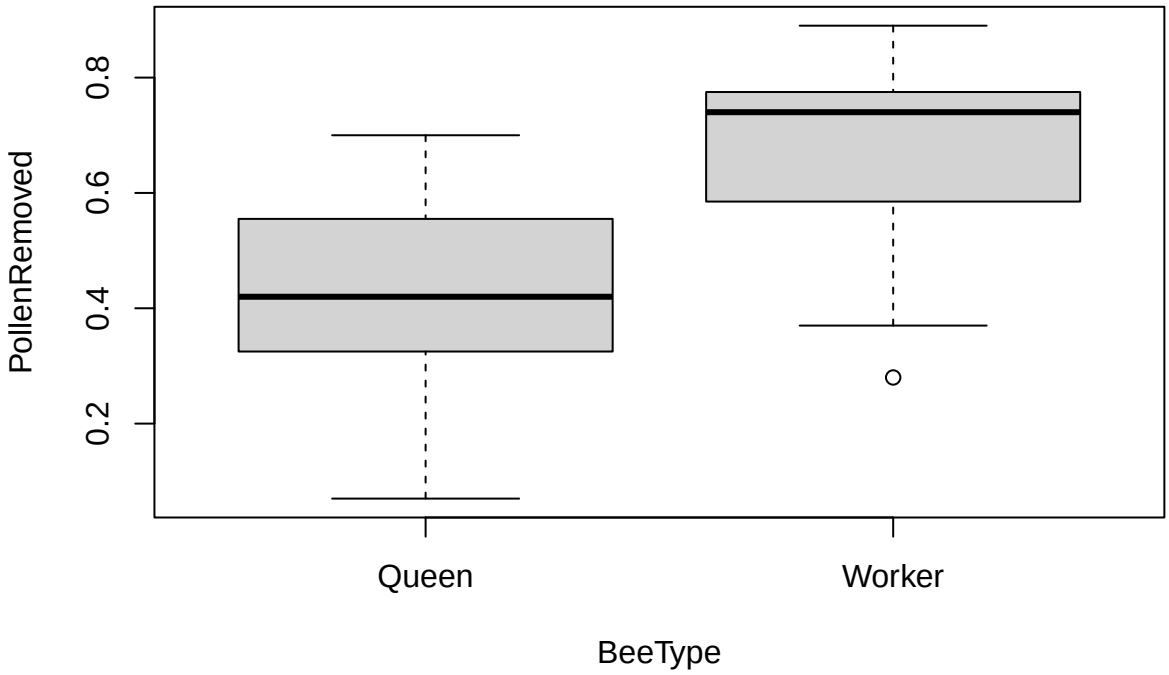
```
confint(mdlI)
```

```
##                       2.5 %     97.5 %
## (Intercept)     192.2381377 222.683434
## Female1         -43.5018377   5.784645
## Weight            0.9619145   2.140502
## Female1:Weight   -0.4166585   1.527374
```

The 95% CI for the difference of slopes (female-male)=[−0.4166585 ,1.527374] because interaction term representing difference between male and feamale.

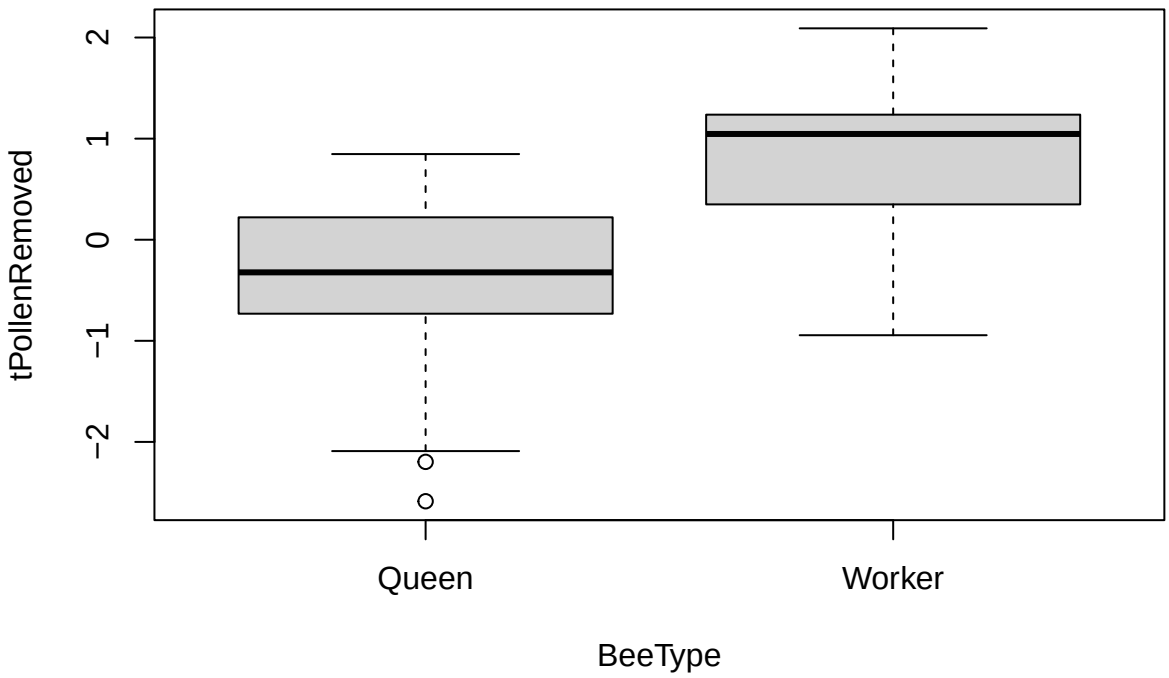
## 3(a) (1)

```
#install.packages("Sleuth3")
library(Sleuth3)
boxplot(PollenRemoved~BeeType,data=ex0327)
```




## 3(a) (2)

```
ex0327$tPollenRemoved <- log(ex0327$PollenRemoved/(1-ex0327$PollenRemoved))
boxplot(tPollenRemoved~BeeType,data=ex0327)
```




## 3(a) (3)

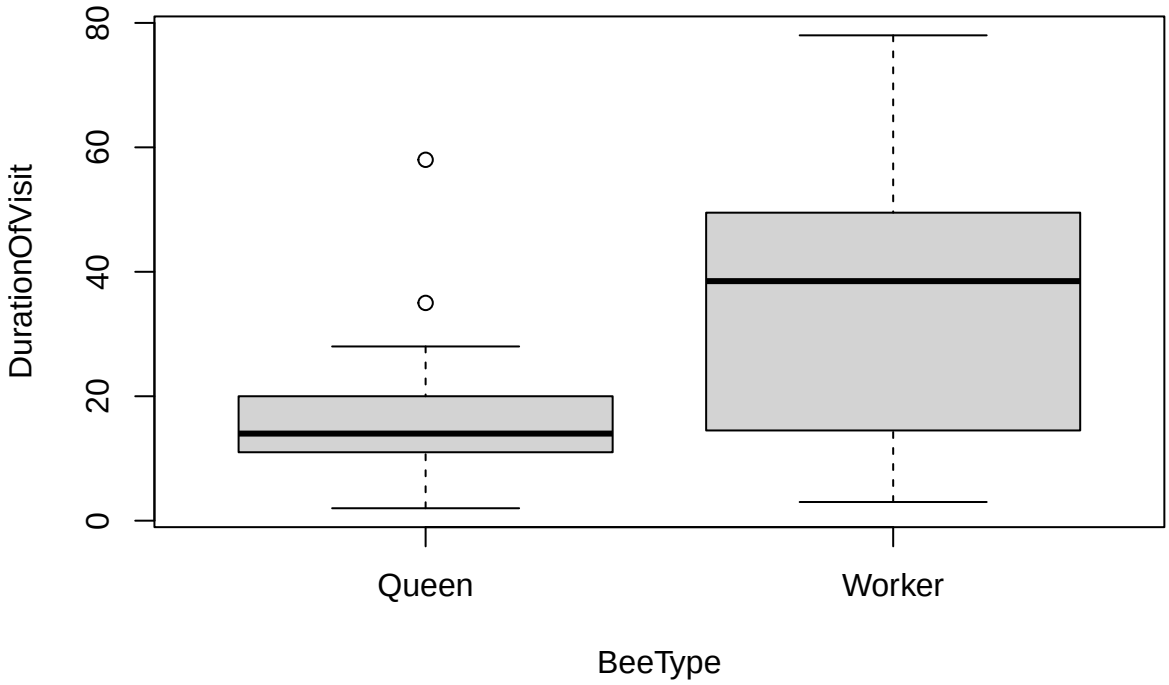
```
t.test(tPollenRemoved~BeeType,var.equal=TRUE,data = ex0327)
```

```
##
##  Two Sample t-test
##
## data:  tPollenRemoved by BeeType
## t = -3.8493, df = 45, p-value = 0.0003715
## alternative hypothesis: true difference in means between group Queen and group Worker is not equal t
## 95 percent confidence interval:
##  -1.7490870 -0.5474536
## sample estimates:
##  mean in group Queen mean in group Worker
##           -0.3812734            0.7669968
```

The calculated p-value is less than 0.05. So, at 5% level of significance we can conclude that there is significant difference between Bee types in terms of Pollen removal proportion.

## 3 (b) (1)

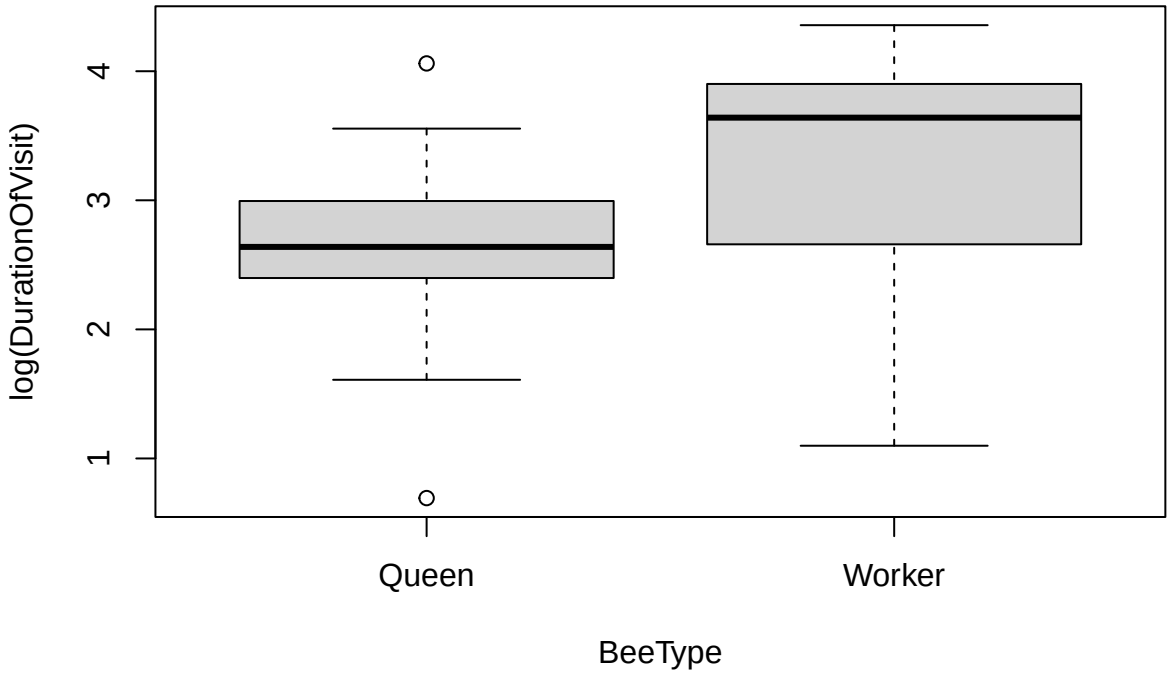
```
boxplot(DurationOfVisit~BeeType,data=ex0327)
```




From the side by side box plot of original Duration variable we observed that there is outlier present for Queen bees.

## 3 (b) (2)

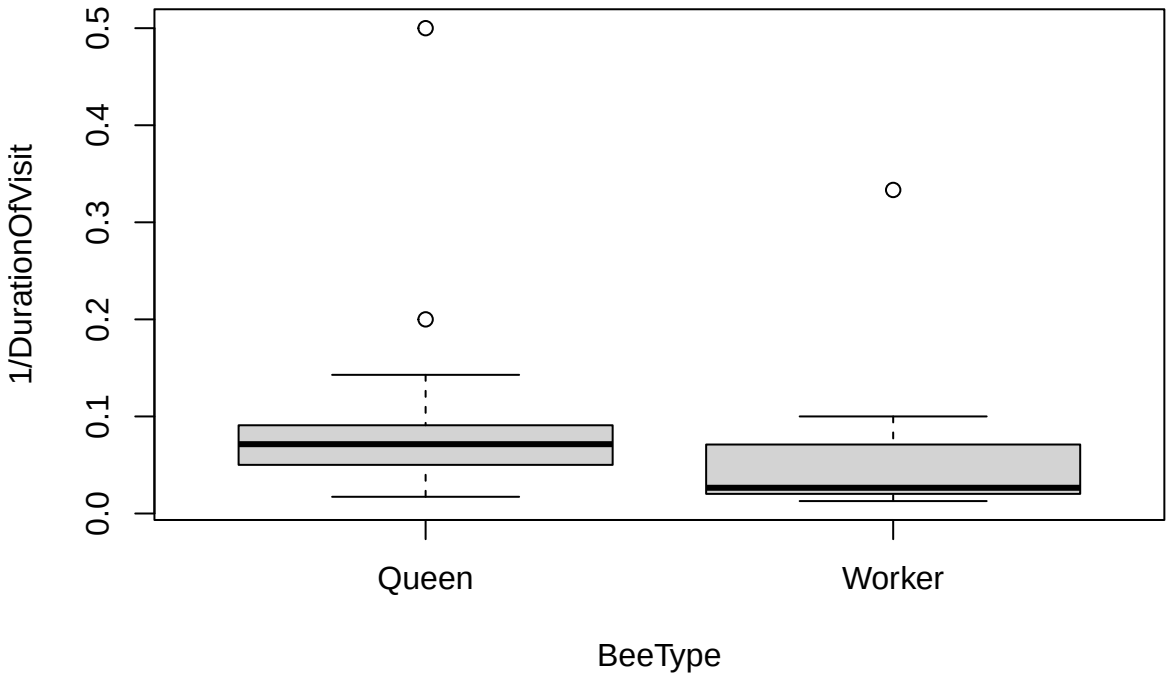
```
boxplot(log(DurationOfVisit)~BeeType,data=ex0327)
```




Again we observed outliers for queen bees for log transformed duration but the distribution looks symmetric for this transformation.

## 3 (b) (3)

```
boxplot(1/DurationOfVisit~BeeType,data=ex0327)
```




Outlier present for both type of bee types when we consider reciprocal of the variable.

## 3 (b) (4)

Among these three transformation, log transformation looks appropriate for t-tools or performing t-test because median are nearer to the center than other transformation.

## 3 (b) (5)

```
t.test(log(DurationOfVisit)~BeeType,var.equal=TRUE,data = ex0327)
```

```
##
##  Two Sample t-test
##
## data:  log(DurationOfVisit) by BeeType
## t = -2.8074, df = 45, p-value = 0.007357
## alternative hypothesis: true difference in means between group Queen and group Worker is not equal t
## 95 percent confidence interval:
##  -1.118323 -0.184007
## sample estimates:
##  mean in group Queen mean in group Worker
```

```
##             2.625945             3.277111
```

The 95% confidence interval is $(-1.118, -0.184)$.

## 3 (b) (6)

What are relative advantages of the three scales as far as interpretation goes?

In applying different parametric statistical tests like t-test, we need the normality assumption to fulfill. Different scales helps to check whether the transformed data presenting the required shape or distribution to carry out the tests as far as interpretation goes.

## 3 (b) (7)

Based on your experience with this problem, comment on the difficulty in assessing equality of population standard deviations from small samples.

```
aggregate(PollenRemoved ~ BeeType, data = ex0327, length)
```

```
##   BeeType PollenRemoved
## 1   Queen            35
## 2  Worker            12
```

```
aggregate(PollenRemoved ~ BeeType, data = ex0327, sd)
```

```
##   BeeType PollenRemoved
## 1   Queen     0.1819678
## 2  Worker     0.1830280
```

```
aggregate(tPollenRemoved ~ BeeType, data = ex0327, sd)
```

```
##   BeeType tPollenRemoved
## 1   Queen      0.9051312
## 2  Worker      0.8489944
```

```
aggregate(DurationOfVisit ~ BeeType, data = ex0327, sd)
```

```
##   BeeType DurationOfVisit
## 1   Queen        10.01318
## 2  Worker        23.22942
```

```
aggregate(log(DurationOfVisit)~ BeeType, data = ex0327, sd)
```

```
##   BeeType log(DurationOfVisit)
## 1   Queen            0.5883546
## 2  Worker            0.9469616
```

From the analysis I observed that the population standard deviation is fluctuating too much as we are changing the scale of measurement in this data set. The reason might be the small sample in groups.