- 2.4 – **[10 pts]**
  1. The `anova()` results of the one-way ANOVA are shown in **Table B.5**.

Table B.5: Analysis of variance table for the egg length by bird species.

```
          Df Sum Sq Mean Sq F value Pr(>F)
species    2  0.410   0.205  0.1992 0.8202
Residuals 41 42.182   1.029
Total     43 42.592
```

     - MS_{Within} is the variability in egg length around the mean egg length of each bird species group or the variability left unexplained by using a separate mean for each group.
     - $MS_{species}$ is MS_{Among} and is the variability in egg length that is explained by using separate means that was not explained when only one mean was used to represent all three groups.
     - df_{Within} is one less than the number of groups (bird species) in the analysis.
     - $MS_{species}$ is MS_{Among} is the total number of eggs minus the total number of groups in the analysis.
     - The F test statistic is the ration of the variability explained by using separate means to the variability not explained by using a single mean to represent all three groups.
  2. The `summary` results of the one-way ANOVA are shown in **Table B.6**.

Table B.6: Coefficients from the one-way ANOVA fit of egg length by bird species.

```
               Estimate Std. Error t value Pr(>|t|)
(Intercept)    23.09000    0.26189  88.165   <2e-16
speciesSparrow  0.03143    0.37693   0.083    0.934
speciesWagtail -0.18667    0.37037  -0.504    0.617
---
Residual standard error: 1.014 on 41 degrees of freedom
Multiple R-squared: 0.009624,        Adjusted R-squared: -0.03869
F-statistic: 0.1992 on 2 and 41 DF,  p-value: 0.8202
```

     - The "Intercept" estimate is the sample mean egg length in the pipet (reference group) nests.
     - The "speciesSparrow" estimate is the difference in the sample mean egg length in the sparrow and pipet nests. In this case the mean egg length in the sparrow nests is 0.0314 mm longer then the mean egg length in the pipet nests.
     - The "speciesWagtail" estimate is the difference in the sample mean egg length in the wagtail and pipet nests. In this case the mean egg length in the wagtial nests is 0.1867 mm shorter then the mean egg length in the pipet nests.
     - The "intercept" p-value is used to determine if the mean egg length in the pipet (reference group) nests differs from zero. The very small p-value in this case suggests that it is different from zero.
     - The "speciesSparrow"p-values is used to determine if the difference in the mean egg length in the sparrow and pipet nests is different from zero. In this case, the very large p-value suggests that this difference in not different than zero suggesting that there is no difference in the mean egg length between the sparrow and pipet nests.
     - The "speciesWagtail"p-values is used to determine if the difference in the mean egg length in the wagtail and pipet nests is different from zero. In this case, the very large p-value suggests that this difference in not different than zero suggesting that there is no difference in the mean egg length between the wagtail and pipet nests.

Table B.7: Coefficients confidence intervals from the one-way ANOVA fit of egg length by bird species.

```
                   2.5 %     97.5 %
(Intercept)    22.5610944 23.6189056
speciesSparrow -0.7297967  0.7926538
speciesWagtail -0.9346522  0.5613189
```

3. The `confint()` results of the one-way ANOVA are shown in **Table B.7**.
   - One is 95% confident that the mean egg length in the pipet nests is between 22.56 and 23.62 mm.
   - One is 95% confident that the mean egg length in the sparrow nests is between 0.73 mm shorter and 0.79 mm longer then the mean egg length in the pipet nests.
   - One is 95% confident that the mean egg length in the wagtail nests is between 0.93 mm shorter and 0.56 mm longer then the mean egg length in the pipet nests.
4. No, the overall p-value (p=0.8202) is greater than 0.05. There is no difference in mean cuckoo length among the three species of host birds.
5. Not needed because no difference was identified.

R commands

```
> cuc <- read.table("cuckoos.txt", head = TRUE)
> attach(cuc)
> lm1 <- lm(length ~ species)
> anova(lm1)
> summary(lm1)
> confint(lm1)
```