- 3.4 – **[10 pts]**

    1. On the original scale the variances are unequal (Levene's p=0.0201), the residuals are not normal (Anderson-Darling p=0.0009) nor symmetric **(Figure B.5)**, and there is one possible outlier (individual 44; p=0.0002). The trial-and-error method suggested an inverse fourth-root transformation for the number of active crayfish (response variable). This transformation provided equal variances (Levene's p=0.8076) and residuals that were not normal (Anderson-Darling p=0.0009) but were largely symmetric **(Figure B.7)**. There is still one possible outlier (individual 28) according to the outlier test (p=0.0002) but it did not appear large on the residual plot **(Figure B.6)** nor the histogram of residuals **(Figure B.7)**. Thus, the assumptions have been largely met on the inverse fourth-root scale with no individuals removed.
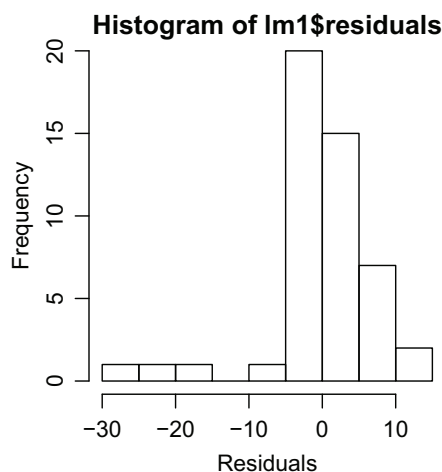

Figure B.5: Histograms of residuals from the two-way ANOVA of activity level by feeding regime and temperature.
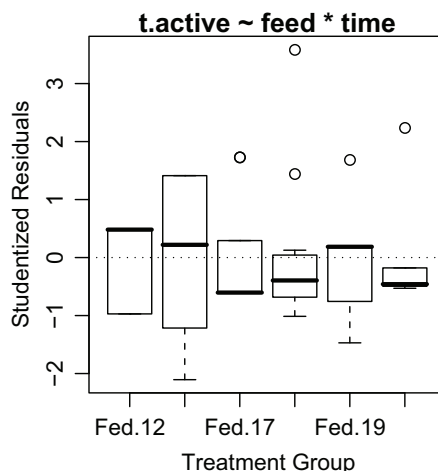

Figure B.6: Residual plot from the two-way ANOVA of the inverse square root of activity level by feeding regime and temperature.

    2. There is a significant interaction effect (p=0.0091; **Table B.13**). The main effects cannot be
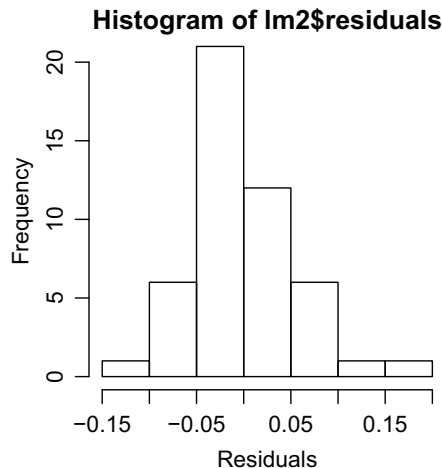
Histogram of lm2$residuals

Figure B.7: Histograms of residuals from the two-way ANOVA of the inverse square root of activity level by feeding regime and temperature.

interpreted.

Table B.13: Analysis of variance table for inverse square-root transformed crayfish activity level by feeding regime and temperature.

```
          Df  Sum Sq Mean Sq  F value      Pr(>F)
feed       1 0.91202 0.91202 245.9386   < 2.2e-16
time       2 0.15504 0.07752  20.9050   5.001e-07
feed:time  2 0.03905 0.01953   5.2657    0.009109
Residuals 42 0.15575 0.00371
Total     47 1.26187
```

3. Tukey's HSD method applied to the interaction term suggests that there is no significant difference among the three FED treatments, all UNFED treatments have significantly more active crayfish then the FED treatments, and that crayfish in the UNFED treatment are significantly more active at 1700 and 1900 than at 1200 (**Table B.14**).

4. The summary plot of these results is shown in (**Figure B.8**).

R Commands

```
> active <- c(3, 2, 3, 2, 2, 2, 7, 14, 4, 4, 10, 5, 4, 2, 4, 3, 2, 4,
+    4, 3, 4, 3, 4, 4, 24, 33, 41, 6, 22, 28, 12, 35, 31, 30, 24, 39,
+    3, 3, 4, 2, 5, 3, 49, 13, 40, 48, 47, 47)
> feed <- c(rep("Fed", 6), rep("Unfed", 6), rep("Fed", 12), rep("Unfed",
+    12), rep("Fed", 6), rep("Unfed", 6))
> feed <- factor(feed)
> time <- c(rep(12, 12), rep(17, 24), rep(19, 12))
> time <- factor(time)
> cray <- data.frame(active, feed, time)
> attach(cray)
> lm1 <- lm(active ~ feed * time)
> levene.test(lm1)
> ad.test(lm1$residuals)
```

Table B.14: Tukey's multiple comparison results for the interaction term in the two-way ANOVA of inverse square-root transformed crayfish activity level by feeding regime and temperature.

```
                              Estimate Std. Error     t value       p value
Unfed.12 - Fed.12 = 0       -0.184366755 0.03515831  -5.2439024 6.229517e-05
Fed.17 - Fed.12 = 0         -0.071288892 0.03044799  -2.3413332 1.978746e-01
Unfed.17 - Fed.12 = 0       -0.359619387 0.03044799 -11.8109397 1.809664e-14
Fed.19 - Fed.12 = 0         -0.064501079 0.03515831  -1.8345898 4.509730e-01
Unfed.19 - Fed.12 = 0       -0.406208909 0.03515831 -11.5537091 3.663736e-15
Fed.17 - Unfed.12 = 0        0.113077863 0.03044799   3.7138037 7.246339e-03
Unfed.17 - Unfed.12 = 0     -0.175252631 0.03044799  -5.7558027 1.202741e-05
Fed.19 - Unfed.12 = 0        0.119865676 0.03515831   3.4093126 1.658757e-02
Unfed.19 - Unfed.12 = 0     -0.221842153 0.03515831  -6.3098068 2.378253e-06
Unfed.17 - Fed.17 = 0       -0.288330494 0.02486068 -11.5978520 1.543210e-14
Fed.19 - Fed.17 = 0          0.006787813 0.03044799   0.2229314 9.999164e-01
Unfed.19 - Fed.17 = 0       -0.334920016 0.03044799 -10.9997410 2.453593e-14
Fed.19 - Unfed.17 = 0        0.295118308 0.03044799   9.6925379 1.651790e-12
Unfed.19 - Unfed.17 = 0     -0.046589522 0.03044799  -1.5301345 6.430631e-01
Unfed.19 - Fed.19 = 0       -0.341707830 0.03515831  -9.7191194 2.472134e-12
```
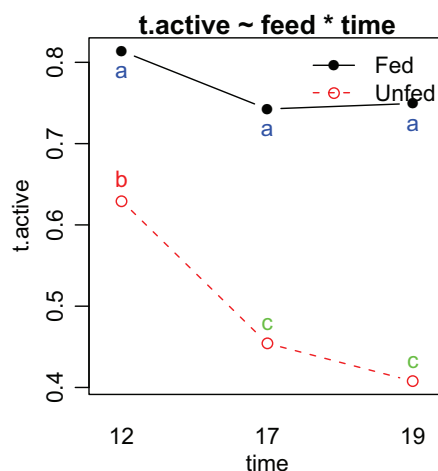

Figure B.8: Interaction plot for the two-way ANOVA of the inverse square root of activity level by feeding regime and temperature. Treatment means with different letters were significantly different.

```
> hist(lm1$residuals)
> outlier.test(lm1)
> trans.chooser(lm1)
> detach(cray)
> cray$t.active <- cray$active^(-0.25)
> attach(cray)
> lm2 <- lm(t.active ~ feed * time)
> residual.plot(lm2)
> levene.test(lm2)
> ad.test(lm2$residuals)
> hist(lm2$residuals)
> outlier.test(lm2)
```

```
> anova(lm2)
> detach(cray)
> cray$group <- interaction(cray$feed * cray$time)
> attach(cray)
> lm3 <- lm(t.active ~ group)
> mc3 <- glht(lm3, mcp(group = "Tukey"))
> fit.plot(lm2, change.order = TRUE)
> add.sig.letters(lm2, change.order = TRUE, lets = c("a", "b", "a", "c",
+     "a", "c"), pos = c(1, 3, 1, 3, 1, 3), col = c("blue", "red", "blue",
+     "green", "blue", "green"))
```