Key - Linear Models Two-Way ANOVA — Biometry

Question 3.3

a. On the original scale the variances are unequal (Levene's $p = 0.0201$), the residuals are not normal (Anderson-Darling $p = 0.0017$) nor symmetric (Figure 1), and there is one possible outlier (individual 44; $p = 0.0002$). The trial-and-error method suggested an inverse cube-root transformation for the number of active crayfish (response variable). This transformation provided equal variances (Levene's $p = 0.8116$) and residuals that are not normal (Anderson-Darling $p = 0.0017$) but, even though they were right-skewed, it is not "long-tailed" (Figure 2). There are no outliers according to the outlier test ($p = 0.0778$; Figure 2). Thus, the assumptions have been largely met on the inverse cube-root scale with no individuals removed.

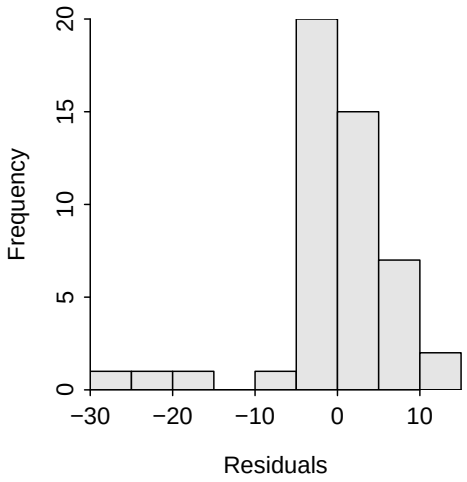

Figure 1. Histograms of residuals from the two-way ANOVA of activity level by feeding regime and temperature.

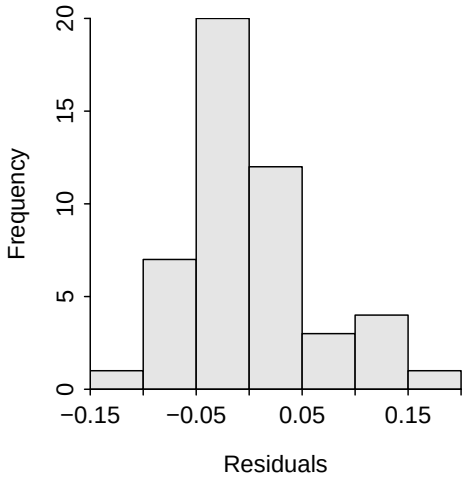

Figure 2. Histograms of residuals from the two-way ANOVA of the inverse square root of activity level by feeding regime and temperature.

b. There is a significant interaction effect ($p = 0.0225$; Table 1). The main effects cannot be interpreted.

Table 1. 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 1.15668 1.15668 243.2105 < 2.2e-16
time       2 0.19293 0.09646  20.2829 6.846e-07
feed:time  2 0.03955 0.01978   4.1583   0.02251
Residuals 42 0.19975 0.00476
Total     47 1.58890
```

c. 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 crayfish in the UNFED treatment are significantly *more* active at 1700 and 1900 than at 1200, with no significant difference between 1700 and 1900 (Table 2).

Table 2. 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   -0.219161658 0.03981569  -5.5044047 2.994161e-05
Fed.17 - Fed.12 = 0     -0.087153396 0.03448140  -2.5275483 1.368465e-01
Unfed.17 - Fed.12 = 0   -0.409487846 0.03448140 -11.8756166 2.220446e-16
Fed.19 - Fed.12 = 0     -0.078829372 0.03981569  -1.9798571 3.663783e-01
Unfed.19 - Fed.12 = 0   -0.456866531 0.03981569 -11.4745358 5.884182e-15
Fed.17 - Unfed.12 = 0    0.132008261 0.03448140   3.8283908 5.110242e-03
Unfed.17 - Unfed.12 = 0 -0.190326189 0.03448140  -5.5196775 2.596090e-05
Fed.19 - Unfed.12 = 0    0.140332286 0.03981569   3.5245476 1.224987e-02
Unfed.19 - Unfed.12 = 0 -0.237704873 0.03981569  -5.9701311 1.536097e-05
Unfed.17 - Fed.17 = 0   -0.322334450 0.02815394 -11.4489987 2.109424e-15
Fed.19 - Fed.17 = 0      0.008324024 0.03448140   0.2414062 9.998762e-01
Unfed.19 - Fed.17 = 0   -0.369713134 0.03448140 -10.7221044 3.053113e-14
Fed.19 - Unfed.17 = 0    0.330658475 0.03448140   9.5894745 1.561107e-11
Unfed.19 - Unfed.17 = 0 -0.047378684 0.03448140  -1.3740361 7.383362e-01
Unfed.19 - Fed.19 = 0   -0.378037159 0.03981569  -9.4946787 2.718048e-12
```

d. The summary plot of these results is shown in (Figure 3).

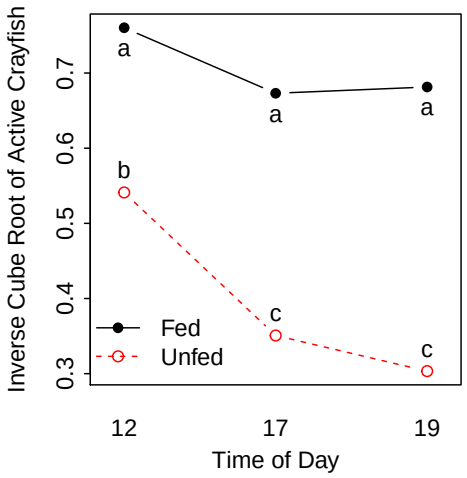

Figure 3. Interaction plot for the two-way ANOVA of the inverse square root of activity level by feeding regime and temperature. Treatment means with different letters are significantly different.

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)
> lm1 <- lm(active~feed*time,data=cray)
> leveneTest(lm1)
> adTest(lm1$residuals)
> hist(lm1$residuals,main="")
> outlierTest(lm1)
> transChooser(lm1)
> cray$t.active <- cray$active^(-1/3)
> lm2 <- lm(t.active~feed*time,data=cray)
> residPlot(lm2,main="")
> leveneTest(lm2)
> adTest(lm2$residuals)
> hist(lm2$residuals,main="")
> outlierTest(lm2)
> anova(lm2)
> cray$group <- interaction(cray$feed*cray$time)
> lm3 <- lm(t.active~group,data=cray)
> mc3 <- glht(lm3,mcp(group="Tukey"))
> fitPlot(lm2,change.order=TRUE,interval=FALSE,xlab="Time of Day"
 ,ylab="Inverse Cube Root of Active Crayfish",main="",legend="bottomleft")
> addSigLetters(lm2,change.order=TRUE,lets=c("a","b","a","c","a","c"),pos=c(1,3,1,3,1,3))
```

Notes from the Professor

- Note that the data were analyzed with an inverse transformation. This means that "small" values on the transformed scale are actually "large" values on the original scale. Thus, small means on the transformed scale actually represent more active crayfish on the original scale.