• 2.7 - [10 pts]

1. The individuals appear to be independent because the tanks were placed randomly and two treatments were not placed on a single tile. There is weak evidence for a non-constant variance (Levene's p=0.0790) and the residuals do not appear to be normally distributed (Anderson-Darling p=0.0101; **Figure B.4**). There is evidence for a significant outlier (outlier test p=0.0001). The assumptions do not appear to be met on the original scale.

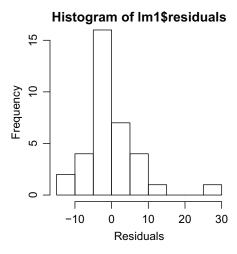


Figure B.4: Histograms of residuals from the one-way ANOVA of grazing level by treatment.

- 2. A log transformation for the response variable was selected through a trial-and-error method. With this transformation the variances are approximately equal (Levene's p=0.5112) and the residuals are approximately normal (Anderson-Darling p=0.9172) on this scale. In addition, there are no significant outliers on this scale (outlier test p>1).
- 3. The one-way ANOVA results indicate strong evidence for a difference in mean natural log of algal biovolumes among the five treatments (p=0.0017; **Table B.11**).

Table B.11: Analysis of variance table for log-transformed crayfish grazing by treatment.

```
Df Sum Sq Mean Sq F value Pr(>F)
group 4 7.2149 1.8037 9.1656 5.818e-05
Residuals 30 5.9038 0.1968
Total 34 13.1187
```

4. Dunnett's results show that all grazers, except for *Orconectes rusticus* (p=0.0500), significantly reduced the algal biovolume relative to the control treatment (p \leq 0.0034). It should be noted that *Orconectes rusticus* is just barely insignificant using an $\alpha = 0.05$.

Table B.12: Dunnett's multiple comparison results for the log-transformed crayfish levels by treatment.

5. Orconectes virilis 0.63 and 1.86 more algal biovolume than the control group on average on the natural log scale. The ratio of mean algal biovolume for Orconectes virilis relative to the control treatment is between 0.16 and 0.53. Thus, the Orconectes virilis appears to have removed between 0.47 and 0.84% of the algal biovolume.

R commands

```
> data <- c(16.7, 59.2, 30.2, 20.2, 17.6, 24.3, 38.5, 10, 10.9, 10.2,
     14.7, 16.5, 8.8, 9.4, 26.3, 6.5, 14.6, 16.8, 22.4, 11.8, 12.4, 3.3,
      8.5, 5.1, 6.4, 13.3, 8.1, 16.4, 8.6, 15, 5.5, 4.3, 10.7, 6.2, 11.8)
> group <- rep(c("Control", "Op", "Or", "Ov", "Am"), each = 7)
> group <- factor(group, levels = c("Control", "Op", "Or", "Ov", "Am"))</pre>
> d <- data.frame(data, group)</pre>
> attach(d)
> lm1 <- lm(data ~ group)</pre>
> levene.test(lm1)
> residual.plot(lm1)
> ad.test(lm1$residuals)
> hist(lm1$residuals)
> trans.chooser(lm1)
> detach(d)
> d$logdata <- log(data)</pre>
> attach(d)
> lm2 <- lm(log.data ~ group)</pre>
> levene.test(1m2)
> residual.plot(1m2)
> ad.test(lm2$residuals)
> hist(lm2$residuals)
> outlier.test(lm2)
> anova(lm2)
> mc2 <- glht(lm2, mcp(group = "Dunnett"))</pre>
> confint(mc2)
```