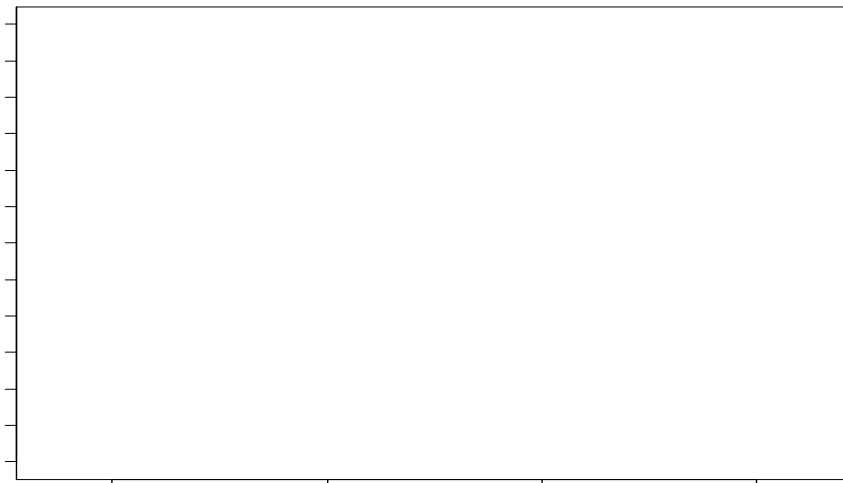


Polich *et al.* (2013) examined the effects of tail-clipping on survivorship and growth of larval California Tiger Salamanders (*Ambystoma californiense*). In one part of their study, randomly selected larval salamanders were designated for one of four treatment groups which were defined by how much of the salamander's tail was clipped: "Control", "Small", "Medium", and "Large" were 0.0-, 2.5-, 5.0-, and 10.0-mm tail clips, respectively. The larvae were then released into experimental simulated vernal pools where they were fed *ad libitum* for two weeks. At the end of two weeks, the total length (snout to the end of the tail; mm) was measured and recorded. Their goal for this particular portion of the study was to compare *all pairs* of tail-clips to determine if the amount of tail-clip had a significant impact on the resultant total length. These data were entered into R and analyzed as provided at the end of the quiz handout. Answer the questions below **with the fullest amount of detail that you can provide – be specific and refer to results where appropriate** (you may want to label figures and tables on the output).

- a. **[8 pts]** FULLY assess ALL assumptions appropriate to this analysis, **on the original scale only**.

Answers to b-d should refer to either the original or transformed results. Questions b-d will refer to "total length" but this may be interpreted as "transformed total length" if you choose to use the transformed scale. Either way, you should be very precise with your language.

- b. **[3 pts]** What specific conclusion about salamander "total length" and tail-clip treatment can be made from the results in the ANOVA table?
- c. **[3 pts]** What is the difference in **sample** mean "total length" between the "Control" and "Medium" tail-clip treatments? Be sure to explicitly state which treatment had a longer "total length."
- d. **[3 pts]** Interpret the first (when read from the top) confidence interval in the appropriate multiple comparison results that corresponds to a significant difference. Be sure to explicitly state which treatment had a longer total length. Back-transform to the original scale if appropriate.
- e. **[6 pts]** On the schematic below, manually construct a means plot (i.e., a `fitPlot()` but without confidence intervals) from the provided results. Include letters by each mean that show which treatments were statistically different. Make sure to fully label the axes.



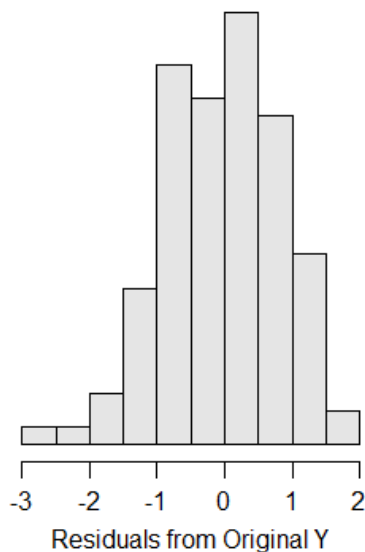
- f. **[2 pts]** Briefly summarize the findings of this portion of the author's study (i.e., what is the "take-home message" from these results).

Results for Salamander Questions

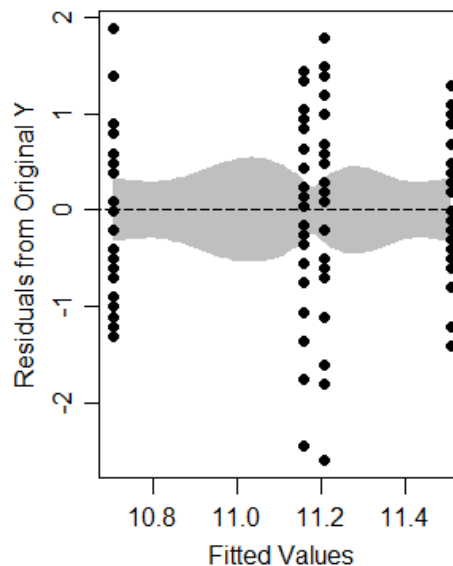
```
> library(NCStats)
> library(multcomp)
> d <- read.csv("salamanders.csv")
> d$Treatment <- factor(d$Treatment, levels=c("Control", "Small", "Medium", "Large"))

> lm1 <- lm(TL~Treatment, data=d)
> transChooser(lm1)
```

Anderson-Darling p-value= 0.6193
Outlier test p-value= 0.2732



Levene's test p-value= 0.2119



```
> anova(lm1)
Response: TL
      Df Sum Sq Mean Sq F value    Pr(>F)
Treatment   3   9.348   3.1161   3.953 0.01017
Residuals 109  85.924   0.7883
```

```
> summary(lm1)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    11.5071     0.1678  68.581  < 2e-16
TreatmentSmall  -0.3500     0.2373  -1.475 0.143100
TreatmentMedium -0.3000     0.2373  -1.264 0.208829
TreatmentLarge  -0.8002     0.2352  -3.402 0.000937

Residual standard error: 0.8879 on 109 degrees of freedom
Multiple R-squared:  0.09812,    Adjusted R-squared:  0.0733 
F-statistic: 3.953 on 3 and 109 DF,  p-value: 0.01017
```

```
> mcl1a <- glht(lm1, mcp(Treatment="Dunnett"))
> summary(mcl1a)
              Estimate Std. Error t value Pr(>|t|)
Small - Control == 0  -0.3500     0.2373  -1.475  0.32318
Medium - Control == 0  -0.3000     0.2373  -1.264  0.44633
Large - Control == 0   -0.8002     0.2352  -3.402  0.00275
```

```
> confint(mcl1a)
```

	Estimate	lwr	upr
Small - Control == 0	-0.3500	-0.9150	0.2150
Medium - Control == 0	-0.3000	-0.8650	0.2650
Large - Control == 0	-0.8002	-1.3603	-0.2402

```
> mcl1b <- glht(lm1, mcp(Treatment="Tukey"))
```

```
> summary(mcl1b)
```

	Estimate	Std. Error	t value	Pr(> t)
Small - Control == 0	-0.3500	0.2373	-1.475	0.45606
Medium - Control == 0	-0.3000	0.2373	-1.264	0.58753
Large - Control == 0	-0.8003	0.2352	-3.402	0.00505
Medium - Small == 0	0.0500	0.2373	0.211	0.99667
Large - Small == 0	-0.4502	0.2352	-1.914	0.22826
Large - Medium == 0	-0.5002	0.2352	-2.127	0.15115

```
> confint(mcl1b)
```

	Estimate	lwr	upr
Small - Control == 0	-0.3500	-0.9687	0.2687
Medium - Control == 0	-0.3000	-0.9187	0.3187
Large - Control == 0	-0.8002	-1.4136	-0.1869
Medium - Small == 0	0.0500	-0.5687	0.6687
Large - Small == 0	-0.4502	-1.0636	0.1631
Large - Medium == 0	-0.5002	-1.1136	0.1131

```
> #####
```

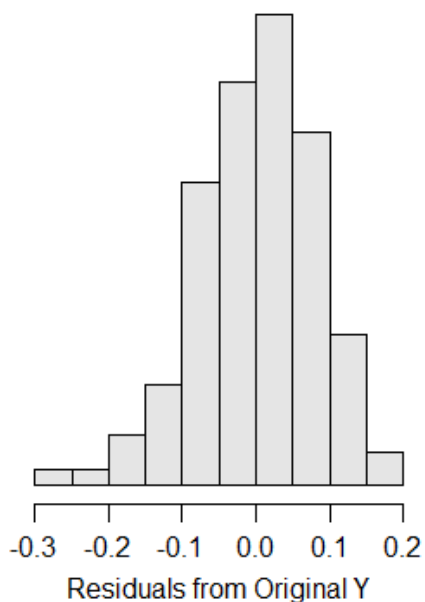
```
> d$logTL <- log(d$TL)
```

```
> lm2 <- lm(logTL~Treatment, data=d)
```

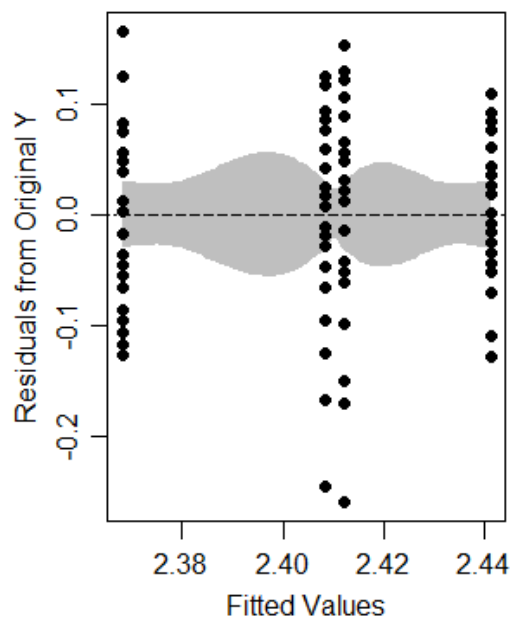
```
> transChooser(lm2)
```

Anderson-Darling p-value= 0.2941

Outlier test p-value= 0.1031



Levene's test p-value= 0.2043



```

> anova(lm2)
      Response: logTL
            Df Sum Sq   Mean Sq F value   Pr(>F)
Treatment    3 0.0773 0.0257661   3.8867 0.01106
Residuals  109 0.7226 0.0066294

> summary(lm2)

            Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.44122    0.01539  158.653 < 2e-16
TreatmentSmall -0.03279    0.02176   -1.507 0.134694
TreatmentMedium -0.02916    0.02176   -1.340 0.182996
TreatmentLarge -0.07306    0.02157   -3.387 0.000985

Residual standard error: 0.08142 on 109 degrees of freedom
Multiple R-squared: 0.09663,    Adjusted R-squared: 0.07177
F-statistic: 3.887 on 3 and 109 DF,  p-value: 0.01106

> mc2a <- glht(lm2,mcp(Treatment="Dunnett"))
> summary(mc2a)

            Estimate Std. Error t value Pr(>|t|)
Small - Control == 0 -0.03279    0.02176   -1.507 0.30645
Medium - Control == 0 -0.02916    0.02176   -1.340 0.39954
Large - Control == 0 -0.07306    0.02157   -3.387 0.00285

> confint(mc2a)

            Estimate lwr      upr
Small - Control == 0 -0.03279 -0.08461  0.01902
Medium - Control == 0 -0.02916 -0.08098  0.02266
Large - Control == 0 -0.07306 -0.12443 -0.02169

> mc2b <- glht(lm2,mcp(Treatment="Tukey"))
> summary(mc2b)

            Estimate Std. Error t value Pr(>|t|)
Small - Control == 0 -0.032794    0.021761   -1.507 0.4368
Medium - Control == 0 -0.029162    0.021761   -1.340 0.5396
Large - Control == 0 -0.073056    0.021572   -3.387 0.0051
Medium - Small == 0    0.003632    0.021761    0.167 0.9983
Large - Small == 0    -0.040262    0.021572   -1.866 0.2487
Large - Medium == 0   -0.043894    0.021572   -2.035 0.1818

> confint(mc2b)

            Estimate lwr      upr
Small - Control == 0 -0.032794 -0.089568  0.023980
Medium - Control == 0 -0.029162 -0.085935  0.027612
Large - Control == 0 -0.073056 -0.129338 -0.016774
Medium - Small == 0    0.003632 -0.053141  0.060406
Large - Small == 0    -0.040262 -0.096544  0.016020
Large - Medium == 0   -0.043894 -0.100176  0.012388

```