

• 2.6 – [8 pts]

1. The individuals are still independent, the variances are approximately equal (Levene's ($p=0.2601$)), the residuals are not approximately normal (Anderson-Darling $p=0.0257$) but are largely symmetric (**Figure B.3**), and there are no significant outliers (outlier test $p=0.1765$). Thus, the assumptions have been largely met when the 20th individual is removed.

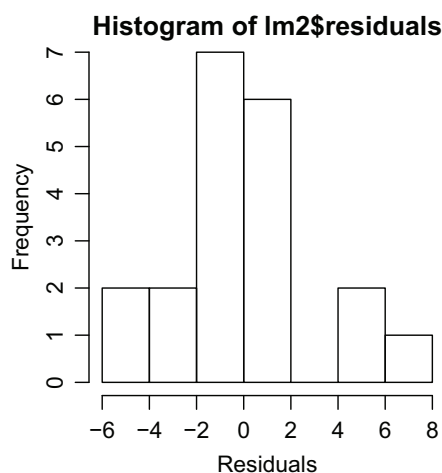


Figure B.3: Histograms of residuals from the one-way ANOVA of UTH levels by syndrome type with the 20th individual removed.

2. The means are significantly different among the three groups ($p=0.0017$; **Table B.8**).

Table B.8: Analysis of variance table for the UTH values by syndrome type with the 20th individual removed.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cause	2	181.12	90.56	9.4911	0.001706
Residuals	17	162.21	9.54		
Total	19	343.33			

3. It appears that the adenoma group is significantly different from both the bilateral hyperplasia ($p=0.0119$; **Table B.9**) and carcinoma ($p=0.0019$; **Table B.9**) groups and that the bilateral hyperplasia and carcinoma groups are NOT statistically different ($p=0.2498$; **Table B.9**).

Table B.9: Tukey's multiple comparison results for the UTH values by syndrome type with the 20th individual removed.

	Estimate	Std. Error	t value	p value
BiHyper - Adenoma = 0	5.213333	1.595136	3.268268	0.011864495
Carcinoma - Adenoma = 0	8.233333	1.993920	4.129218	0.001888107
Carcinoma - BiHyper = 0	3.020000	1.827458	1.652568	0.249797568

4. The mean of the bilateral hyperplasia group is between 1.13 and 9.3 units greater than the mean for the adenoma group (**Table B.10**). The mean for the carcinoma group is between 3.13 and 13.34 units greater than the mean for the adenoma group (**Table B.10**). The means for the bilateral hyperplasia and carcinoma groups are not statistically different.

R commands

Table B.10: Tukey's confidence interval results for the difference in mean UTH values by syndrome type with the 20th individual removed.

	Estimate	lwr	upr
BiHyper - Adenoma	5.213333	1.131292	9.295374
Carcinoma - Adenoma	8.233333	3.130782	13.335885
Carcinoma - BiHyper	3.020000	-1.656566	7.696566

```
> detach(d)
> d2 <- d[-20, ]
> attach(d2)
> lm2 <- lm(uth.m20 ~ cause.m20)
> levene.test(lm2)
> residual.plot(lm2)
> ad.test(lm2$residuals)
> hist(lm2$residuals, xlab = "Residuals")
> outlier.test(lm2)
> anova(lm2)
> glht(lm2, mcp(cause = "Tukey"))
> fit.plot(lm2, xlab = "Cause", ylab = "Urine Tetrahydrocortisone Level")
> add.sig.letters(lm2, c("a", "b", "b"), pos = c(2, 2, 2), col = c("red",
+      "blue", "blue"))
```