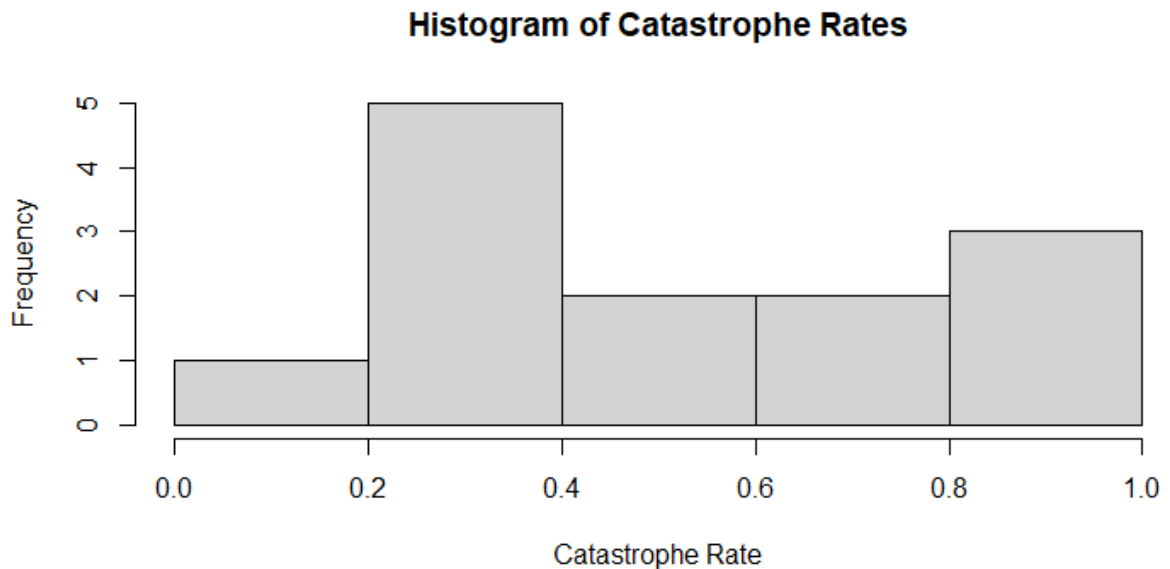


Keegan Moynahan

Using Models 1

1)



2) p-value = 0.04097

`shapiro.test(catrate$cat.rate)`

3) The null hypothesis is the data was sampled from a normally distributed population.

4) The lower p-value (0.041) indicates that there is good evidence against the null hypothesis, so the data would not have come from a normally distributed population.

5)

`t.test(catrate$cat.rate, mu = 2/7)`

6) The null hypothesis is that the mean of the late pond filling is not different than the mean of the catastrophe rate.

7) This is a default t-test, so it is a two-tailed test

8) The p-value is 0.01193, interpreting this p-value as a false positive rate can be understood by knowing it is an error and is not giving you the correct information. For example, if this value was in favor of a statement when it should have been against a statement, this would be a false positive.

9) The 95 % CI is 0.3526250 0.7261295, 0 is not included in the interval

10) Yes, I would conclude that there is strong evidence to reject the null hypothesis. I would do this because the low p-value of 0.01193 indicates that the mean of the late pond filling and catastrophe rate are not the same.

11)

```
wilcox.test(catrate$cat.rate, mu = 2 / 7)
```

12) The p-value of this test is 0.006275, this p-value is even lower than the t-test p-value showing that the means are greatly different.

13) I would again conclude that there is strong evidence to reject the null hypothesis, there is even more evidence with this test versus the t-test because the p-value (0.006275) is even smaller than the p-value of the t-test.

14) Both tests in my opinion run the same type of test. The t-test had a greater p-value than the Wilcoxon test. I would say both tests helped me draw the same conclusion, but the Wilcoxon test provided a stronger p-value to reject the null hypothesis.

15) I think the Wilcoxon test was the most appropriate for this set of data because the data was from a non-normal distribution and was a small set of data compared to other data sets. The Wilcoxon test is made for this type of data. It can also be seen in the results from the lower and stronger p-value.

16)

```
dat_adelie = subset(penguin_dat, species == "Adelie")
```

```
shapiro.test(dat_adelie$flipper_length_mm)
```

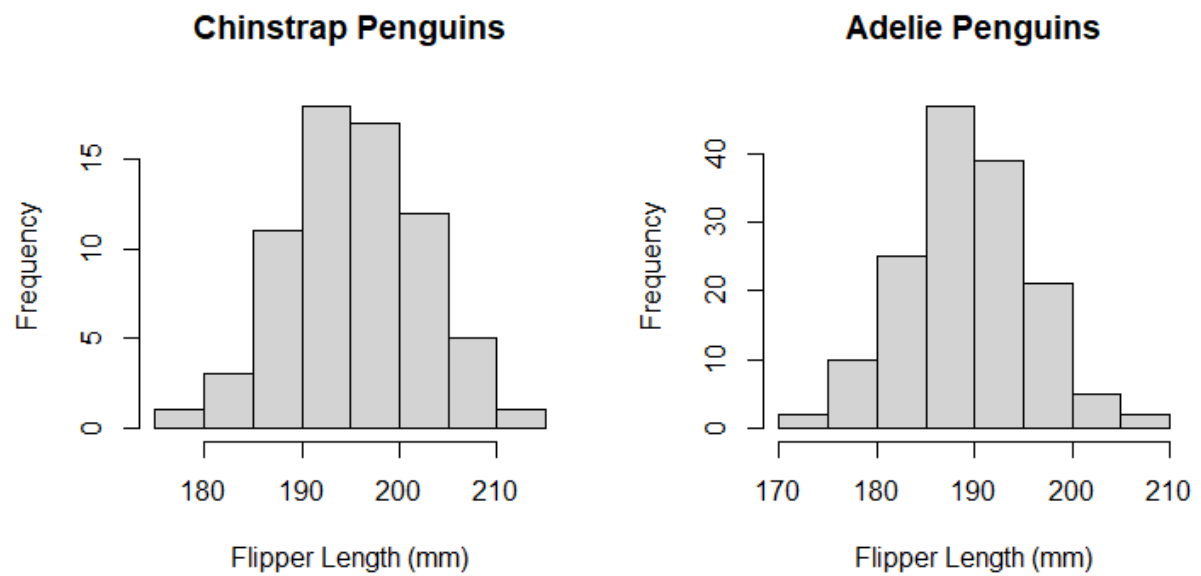
```
dat_chin = subset(penguin_dat, species == "Chinstrap")
```

```
shapiro.test(dat_chin$flipper_length_mm)
```

17) The Chinstrap Penguin: p-value = 0.8106, Adelie Penguins: p-value = 0.72

These p-values are both relatively high p-values so I would say there is good evidence that the flipper lengths are normally distributed for each species.

18)



19) The alternative hypothesis is that there is a difference between the meaning of flipper lengths of chinstrap and Adelie penguins. This can also be seen in the very small p-value of 6.049e-08. This was again a two tailed test.

20) `t.test(flipper_length_mm ~ species, data = dat_pen)`