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ECO – 602 Environmental Data Analysis

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Partners: NA

**Modeling 1**

**Q1:**Chart, histogram

Description automatically generated

**Q2:** Shapiro-Wilk normality test

data: catrate$cat.rate

W = 0.86202, p-value = 0.04097

shapiro.test(catrate$cat.rate)

**Q3:** The Null hypothesis for the Shapiro-Wilk test is that the data was sampled from a normally distributed population.

**Q4:** There is strong evidence that the sample came from a normally distributed population because of the low p-value.

**Q5:** t.test(catrate$cat.rate, catrate$pond)

**Q6:** The null hypothesis is that there is no difference between the catastrophic rate and the pond late filling rate.

**Q7:** This is a two-tailed t-test because we are looking at the difference between two things.

**Q8:** The p-value is 1. This means that is there is most likely a difference between the catastrophic rate and the pond fill rate.

**Q9:** alternative = -9.389766 Inf

Null = -Inf -5.53148

They do not include zero.

**Q10:** There is not strong evidence to reject the null hypothesis from the t.test because the 95% confidence interval for the null hypothesis is -Inf.

**Q11:** wilcox.test(catrate$cat.rate, catrate$pond mu = 2 / 7)

**Q12:** wilcox: p-value = 1.601e-05 t.test: p-value = 1.579e-05

The p-values from the wilcox test and the t.test are extremely close.

**Q13:** There is strong evidence to reject the null hypothesis because the p-value is so small.

**Q14:** The t.test gives you more information than the wilcox. From the t.test I can see that the p-value is extremely small the CI are in the negative and do not contain zero between them, and I can see that the mean flipper length between the two species is ~2.5 mm in length all showing evidence that there is a significant difference. For the wilcox test I can only see the p-value.

**Q15:** The t.test is better because it gives you more information to build evidence off of.

**Q16:** shapiro.test(dat\_adelie$flipper\_length\_mm)

shapiro.test(dat\_chinstrap$flipper\_length\_mm)

**Q17:** Because the p-values are so high for each penguin species I would say that they did not come from a normally distributed population.

Chinstrap: p-value = 0.8106 Adelie: p-value = 0.72

**Q18:** Chart, histogram

Description automatically generated

**Q19:** The alternative hypothesis is that there is a difference between average flipper length of the adelie penguins and the average flipper length of the chinstrap penguins.

**Q20:** t.test(dat\_adelie$flipper\_length\_mm, dat\_chinstrap$flipper\_length\_mm)