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Using Models 1

**Q1 (1 pt.): Create a histogram of the salamander reproduction catastrophic rates.**

Chart, histogram

Description automatically generated

**Q2 (1 pt.):** **Conduct a Shapiro-Wilk test of normality of the salamander catastrophic rates. Report the p-value and show the R-code you used to conduct the test.**

shapiro.test(catrate$cat.rate)

p-value = 0.04097

**Q3 (1 pt.):** **What is the null hypothesis for the Shapiro test?**

A Shapiro test null hypothesis is: The data were sampled from a normally distributed population

For this data: The salamander reproduction catastrophe rate was sampled from a normally- distributed population.

**Q4 (1 pt.):** **Based on the Shapiro test results, is there strong evidence that the sample came from a non-normally distributed population?**

Based on the P-value of the Shapiro test, we can reject the null hypothesis and say there is strong evidence that the sample came from a non-normally distributed population.

**Conduct a one-sample t-test of the alternative hypothesis that the catastrophic rate is different from the pond late-filling rate.**

**Q5 (1 pt.): Show the code you used to conduct the t-test.**

t.test(catrate$cat.rate, y = NULL, alternative = "two.sided", mu = 2/7, conf.level = 0.95)

**Q6 (1 pt.): State the null hypothesis of the test, in plain nontechnical English.**

The average of the salamander reproduction catastrophe rate is not different from the chosen average of 0.28

The chosen average is taken from the late pond filling rate instead of using 0.

**Q7 (1 pt.): Is this a one- or two-tailed test?**

This is a two-tailed test because we are trying to determine if the two means are different from one another, not just greater or less than only (as we would in a one-tailed)

**Interpret the results of you one-sample t-test of the alternative hypothesis that the catastrophic rate is different from the pond late-filling rate.**

**Q8 (2 pts.): What is the p-value from your t-test? Interpret the p-value as a *false-positive rate* using nontechnical English that a non-scientist would understand.**

P-value = 0.01193  
This p-value indicates that average catastrophe rate is different from the chosen/expected average.

This means that it is very unlikely that the average catastrophe rate is not different from the chosen average, rather than being likely that they are the same.

Another, easier, example of this explanation in the way I think of a false positive can be described with a pregnancy test. For example, you have a positive test which means that it is very unlikely that you are not pregnant and test positive, but if you did that would be a false positive.

**Q9 (1 pt.): What is the confidence interval for the difference between the null hypothesis and alternative hypothesis means? Did it include zero?**

The confidence interval of the difference between the null and alternative hypothesis is

[0.3526250, 0.7261295]. This confidence interval does not include zero.

**Q10 (2 pts.): Considering the results from your t-test, did you conclude that there was strong evidence to reject the null hypothesis?**

The output of the t-test showed that there is strong evidence to reject the null hypothesis. The p-value of the output was a low value, p-value = 0.01193, which indicates that there is enough evidence to reject the null hypothesis.

**Conduct a one-sample Wilcoxon rank sum test of the alternative hypothesis that the catastrophic rate is different from the pond late-filling rate.**

**Interpret the results of your one-sample Wilcoxon rank sum test of the alternative hypothesis that the catastrophic rate is different from the pond late-filling rate.**

**Q11 (1 pt.): Show the code you used to conduct the test.**

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

**Q12 (1 pt.): Compare the p-value with the p-value you got from the t-test.**

P-value from Wilcoxon test: p-value = 0.006275

P-value from One sample t-test: p-value = 0.01193

The p-values are both different, but they are both low values

**Q13 (2 pts.): Considering the results from your rank sum test, did you conclude that there was strong evidence to reject the null hypothesis?**

Looking at the p-value, which is a low value of 0.006, there is strong evidence to reject the null hypothesis.

**Consider the one sample t-test and Wilcoxon rank sum tests that you preformed on the catastrophic rate data. Explain your reasoning.**

**Q14 (1 pt.): Compare the overall conclusions you could draw from the results of the two tests.**

From the results of the two tests, both had low p-values so we can reject the null hypothesis in both cases. Looking at the results, we can see that the observed mean of the catastrophic rate is different from the observed late-filling rate and seeing as how we are able to reject the null hypothesis that the two means are the same, this tells us that reproductive catastrophe is not solely caused by late filling of the vernal pools.

**Q15 (1 pt.): Considering the numerical and graphical data exploration, which test do you think was more appropriate for these data?**

Looking at both the histogram and the Shapiro test, the results indicate that the sample came from a non-normally distributed population. The sample size is also small, consisting of only 14 ponds. Considering the small sample size and the fact that it is not normally distributed, I think the wilcox ranks sums test may be most appropriate. The wilcox test does not require that the sample mean to come from a population that has a normal distribution.

**Q16 (2 pts.):** Show the R-code you used to conduct tests of normality for the flipper lengths of Chinstrap and Adelie penguins.

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

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

**Q17 (2 pts.):** Interpret the test results. Do you conclude that the flipper lengths are normally distributed for each species? Make sure your answers make reference to the test output.

The null hypothesis for the Shapiro test, which I used to conduct the normality test, is that the data were sampled from a normally distributed population.

The p-value from the normality test of the Adelie penguin flipper length is 0.72. This p-value for the Chinstrap penguin flipper length is 0.81. These are both high p-values so we can’t reject the null hypothesis for both penguin species. So, this concludes that the flipper length from both Adelie and Chinstrap penguins are normally distributed

**Q18 (2 pts.):** Save your figure to a file and include it in your report. Your figure needs to have appropriate dimensions such that the two histograms are not vertically stretched.

Chart, histogram

Description automatically generated

**Q19 (2 pts.):** State the alternative hypothesis of the test, in plain nontechnical English.

Alternative hypothesis: There is a difference in the average flipper length values between Adelie penguins and Chinstrap penguins.

**Q20 (1 pt.):** Include the code you used to conduct the t-test.

t.test(dat\_adelie$flipper\_length\_mm, dat\_chinstrap$flipper\_length\_mm, alternative = "two.sided", mu = 0, conf.level = .95)