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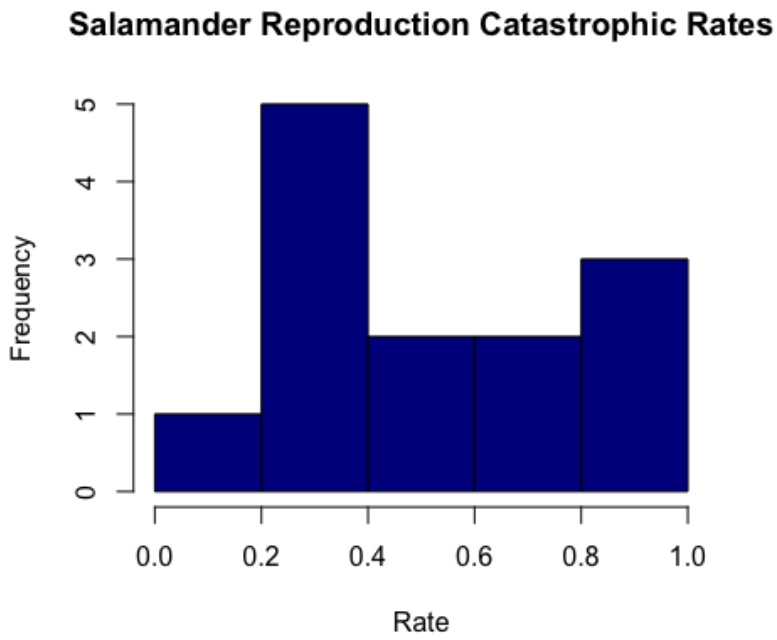
Analysis of Environmental Data
Using Models 1 Lecture Assignment
November 4, 2021
Worked with Juliana Berube and Julia Vineyard

Q1: Create a histogram of the salamander reproduction catastrophic rates.
Make sure you include an appropriate title and label for the x-axis.




Q2: 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)
```
**0.04097**

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

**The data were sampled from a normally distributed population.**

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

**Yes, because the p-value is less than 0.05, there data are significant enough to reject the null. This means the data were sampled from a non-normally distributed population.**

Q5: Show the code you used to conduct the t-test.

```
t.test(catrate$cat.rate, mu = 0.28)
```

Q6: State the null hypothesis of the test, in plain nontechnical English.

**The true mean is equal to 0.28.**

Q7: Is this a one- or two-tailed test?

**Two-tailed**

Q8: 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.

**0.01054**. **This means that we would see a difference in mean catastrophic rate of .28 only about 1% of the time.**

Q9: What is the confidence interval for the difference between the null hypothesis and alternative hypothesis means? Did it include zero?

**0.3526250 0.7261295. It does not include 0.**

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

**Yes, we do reject the null. The p-value 0.01054 < 0.05, this makes the test significant. We can conclude that the true mean is different than 0.28.**

Q11: Show the code you used to conduct the test.

```
wilcox.test(catrate$cat.rate, mu = 2 / 7, exact = FALSE, alternative = "greater")
```

Q12: Compare the p-value with the p-value you got from the t-test.

**Wilcoxon: 0.003137, t-test: 0.005271. Both are less than 0.05 suggesting a significant relationship.**

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

**Yes, we do reject the null. The p-value of 0.003137 < 0.05, this makes the test significant. We can conclude that the true mean is greater than 0.28.**

Q14: Compare the overall conclusions you could draw from the results of the two tests.

**Both lead to the conclusion to reject the null and accept that the true mean is greater than 0.28.**

Q15: Considering the numerical and graphical data exploration, which test do you think was more appropriate for these data?

**The Wilcoxon test is more appropriate because it is a non-parametric test and our data is not normally distributed.**

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

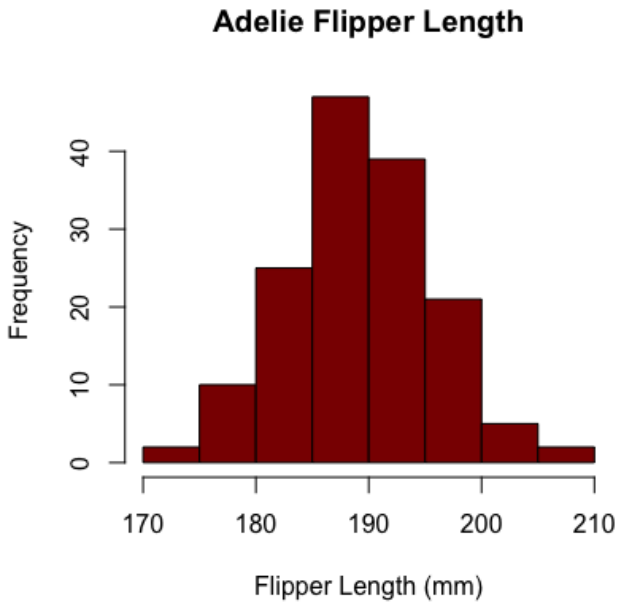
```
dat_adelie = subset(penguin_dat, species == "Adelie")
dat_chinstrap = subset(penguin_dat, species == "Chinstrap")
shapiro.test(dat_adelie$flipper_length_mm)
shapiro.test(dat_chinstrap$flipper_length_mm)
```

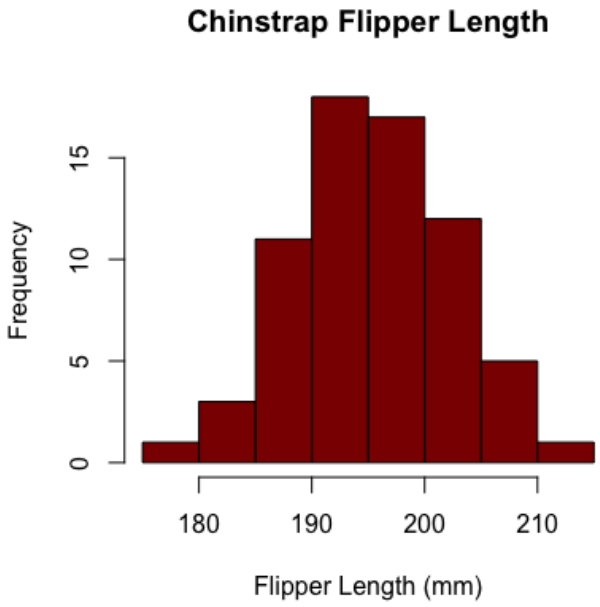
Q17: Interpret the test results. Do you conclude that the flipper lengths are normally distributed for each species?

shapiro.test(dat_adelie$flipper_length_mm): P-value = **0.72**
shapiro.test(dat_chinstrap$flipper_length_mm): P-value= **0.8106**

**Both p-values are much greater than 0.05. This would conclude to accepting the null hypothesis, meaning the data were sampled from normally distributed population.**

Q18: 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.




Q19: State the alternative hypothesis of the test, in plain nontechnical English. Consider whether you used a one- or two- tailed test.

> **The true difference in means of flipper length for Adelie penguins and Chinstrap penguins is not equal to 0. In other words, there is a difference between the mean flipper length for Adelie penguins and flipper length for Chinstrap penguins.**

Q20: Include the code you used to conduct the t-test.

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