UsingModels1.R

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```
catrate =
read.csv("/Users/stonehuang/Documents/environmental_data/data/catrate.csv")
head(catrate)

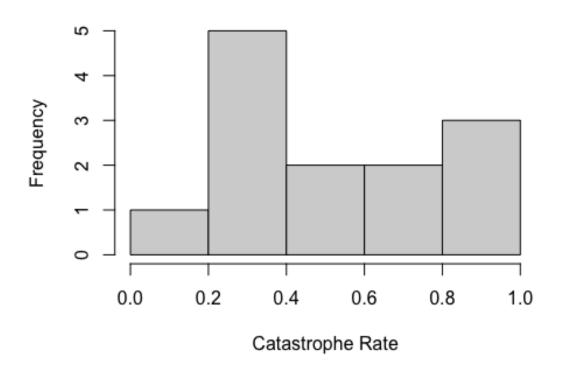
## pond success years cat.rate
## 1 2 5 7 0.2857143
## 2 3 5 7 0.2857143
## 3 4 6 7 0.1428571
## 4 5 4 7 0.4285714
## 5 6 0 7 1.00000000
## 6 7 1 4 0.7500000

summary(catrate)

## pond success years cat.rate
## Min. : 2 Min. :0.000 Min. :1.000 Min. :0.1429
## 1st Qu.: 5 1st Qu.:1.000 1st Qu.:3.000 1st Qu.:0.2857
## Median : 8 Median :2.000 Median :4.000 Median :0.4286
## Mean : 8 Mean :2.538 Mean :4.692 Mean :0.5394
## 3rd Qu.:11 3rd Qu.:5.000 3rd Qu.:7.000 3rd Qu.:0.7500
## Max. :14 Max. :6.000 Max. :7.000 Max. :1.0000

#Q1.
hist(catrate$cat.rate, xlab = "Catastrophe Rate", main = "Histogram of Catastrophe Rates")
```

Histogram of Catastrophe Rates



```
#Q2. p-value = 0.04097
shapiro.test(catrate$cat.rate)

##

## Shapiro-Wilk normality test

##

## data: catrate$cat.rate

## W = 0.86202, p-value = 0.04097

#Q3. The null hypothesis for the Shapiro-Wilk test is that the data were
sampled from a normally-distributed population.

#Q4. There is strong evidence that the sample came from a non-normally-
distributed population.

#Q5.

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

##

## One Sample t-test

##

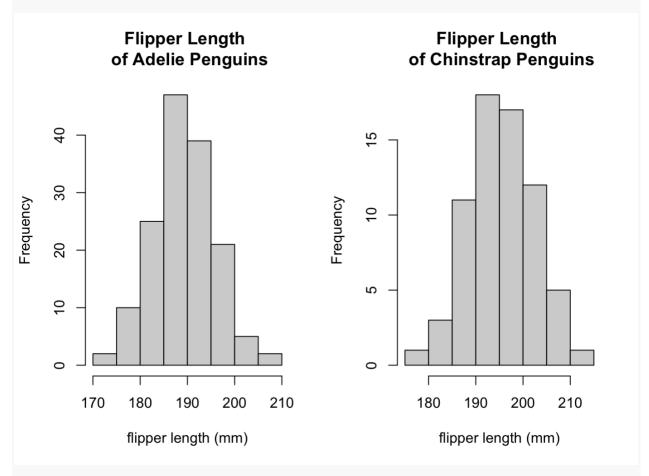
## data: catrate$cat.rate

## data: catrate$cat.rate
```

```
#Q6. The catastrophic rate is equal to the pond late-filling rate.
#07. This is a two-tailed test.
#Q8. p-value = 0.01193. Even if the p-value is very small and we think there
is no pattern, there is still a small chance that a pattern exists.
#Q9. 0.3526250 0.7261295, it does not include 0
#Q10. I conclude that there is strong evidence to reject the null hypothesis
because the p-value is lower than 0.05.
#Q11.
wilcox.test(catrate$cat.rate, mu = 2 / 7, exact=FALSE)
#Q12. The p-value is 0.006275, lower than the p-value from the t-test.
#Q13. I conclude that there is strong evidence to reject the null hypothesis
because the p-value is lower than 0.05.
#Q14. The overall conclusions I could draw from the results of the two tests
are the same.
#Q15. The Wilcoxon Rank Sum Test is more appropriate because the data are not
normally-distributed.
#016.
require(palmerpenguins)
## Loading required package: palmerpenguins
penguin_dat = droplevels(subset(penguins, species != "Gentoo"))
dat adelie = subset(penguin dat, species == "Adelie")
shapiro.test(dat_adelie$flipper_length_mm)
dat Chinstrap = subset(penguin dat, species == "Chinstrap")
shapiro.test(dat Chinstrap$flipper length mm)
```

#Q17. I conclude that the flipper lengths are normally-distributed for both species because the p-values (0.72 for Adelie, 0.8106 for Chinstrap) are higher than 0.05. We fail to reject the null hypothesis. #018.

```
par(mfrow = c(1, 2))
hist(dat_adelie$flipper_length_mm, xlab = "flipper length (mm)", main =
"Flipper Length \n of Adelie Penguins")
hist(dat_Chinstrap$flipper_length_mm, xlab = "flipper length (mm)", main =
"Flipper Length \n of Chinstrap Penguins")
```



#Q19. Adelie and Chinstrap penguins have different flipper lengths. (two-tailed test) #Q20.

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

```
##
## Welch Two Sample t-test
##
## data: flipper_length_mm by species
## t = -5.7804, df = 119.68, p-value = 6.049e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -7.880530 -3.859244
```

```
## sample estimates:
## mean in group Adelie mean in group Chinstrap
## 189.9536 195.8235
```