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Prof. Nelson

Lab 6

25 Oct 2021

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1.

rm(list = ls())

require(palmerpenguins)

sse\_mean = function(x)

{

n= length(x) - sum(as.numeric(is.na(x)))

return(sd(x, na.rm = TRUE)/ sqrt(n))

}

sse\_mean(penguins$body\_mass\_g)

sse\_mean(mtcars$mpg)

2.

two\_group\_resample = function(x, n\_1, n\_2)

{

d\_1 = sample(x, n\_1, replace = TRUE)

d\_2 = sample(x, n\_2, replace = TRUE)

diff\_in\_means = mean(d\_1, na.rm = TRUE) - mean(d\_2, na.rm = TRUE)

return(diff\_in\_means)}

3. It must be Monte Carlo sampling because when I run the line the output changes every time and it changes more than what can be expected.

4.

Chart, histogram

Description automatically generated

5. Yes, ten of the samples

n = 2000

mean\_differences = c()

for (i in 1:n)

{

mean\_differences = c(

mean\_differences,

two\_group\_resample(dat\_penguins$flipper\_length\_mm, 68, 152)

)

}

hist(mean\_differences, main = "N= 2000", xlab = "Mean Differences", col = "yellow")

t\_test = t.test(flipper\_shuffled ~ dat\_pen$species)

sum(abs(mean\_differences) >= diff\_observed)

6. You would have to run the stimulation over ten million times to see a flipper length greater than 5.8mm.

7.

Chart, box and whisker chart

Description automatically generated

8.

Species bill\_depth\_mm means

Adelie 18.34636

Chinstrap 18.42059

Difference in Means

0.0742

9. The p-value from the t-test for the difference in mean bill depth was not significant. The p-value surpassed our 0.05 cutoff with a value of 0.6623, which means we cannot reject the null hypothesis that there is no difference between the means of bill depth between Adelie and Chinstrap species.

10. There are 1,941 difference in means that are greater than diff\_crit.

11.

Chart, histogram

Description automatically generated