Lab 6 Jackie Stephens

**Question 1:**

rm(list = ls())

sse\_mean= function(x)

{

n = sum(!is.na(x))

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

return(SSE)

}

require(palmerpenguins, mtcars)

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

sse\_mean(mtcars$mpg)

**Question 2**

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

{

x = x[!is.na(x)]

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

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

difference\_in\_means = mean(resamp\_1, na.rm = TRUE) - mean(resamp\_2, na.rm = TRUE)

return(difference\_in\_means)

**Chart, histogram

Description automatically generated**}

**Question 3**

The function performs a Monte Carlo because it does not specify by species, all values are resampled completely (no association).

**Question 4 histogram to the right**

**Question 5**

I got that there were zero means of my resampled differences that had a magnitude greater than 5.8.

sum(abs(mean\_differences) >= 5.8)

**Question 6**

I think you would have to do an infinite number of simulations before you see a difference in mean flipper length equal to or greater than 5.8mm because the extremely low p value means that the data did not occur by chance and there is a suggested direct correlation.

Chart, box and whisker chart

Description automatically generated**Question 7 Box and whiskers 🡪**

**Question 8**

species Body Mass (g)

Adelie 3700.662

Chinstrap 3733.088

Difference in Means

32.42598

**Question 9**

Chart, histogram

Description automatically generatedThe p-value from the t-test is 0.5879. This p-value suggests that there is not a strong case that there is a difference in body mass by species. There is a 0.5 or 50% probability that the difference occurred by chance or is not guaranteed to happen every time.

**Question 10**

sum(abs(mean\_differences) >= diff\_observed) = 616

**Question 11 Histogram to the right**