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ECo 634: Michael France Nelson

Lab 6: Introduction to Inference

1. rm(list = ls())

sse\_mean = function(X) sd(penguins$body\_mass\_g, na.rm = TRUE) / sqrt(length(penguins$body\_mass\_g))

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

sse\_mean = function(X) sd(mtcars$mpg, na.rm = TRUE) / sqrt(length(mtcars$mpg))

sse\_mean(mtcars$mpg)

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

{

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

x1 = sample(x\_ok, size = n\_1, replace = T)

x2 = sample(x\_ok, size = n\_2, replace = T)

difference\_in\_Mean = mean(x1) - mean(x2)

return(difference\_in\_Mean)

}

1. This function performs a Monte Carlo resampling because the variable “x” is randomly assigned to one of the species since I did not specify; thus, breaking the association and simulating the null hypothesis.
2. Chart, histogram

   Description automatically generated
3. Zero

sum(abs(mean\_differences) > 5.8)

1. It’s impossible to see a difference in mean flipper length that is equal to or greater than 5.8mm.
2. Chart, box and whisker chart

   Description automatically generated
3. Adelie = 3700.662 g

Chinstrap = 3733.088 g

diff\_observed = 32.42598

1. The p-value is 0.5879, so this means that the difference in body mass between the two species are not statistically significant. If the p-value is less than 0.05, we consider that the false positive rate (rejecting a true null hypothesis) is low enough that we can reject the null hypothesis. In this case, the p-value is much greater than 0.05, so we fail to reject the null hypothesis.
2. 608 differences in means greater than diff\_crit
3. Chart, histogram

   Description automatically generated