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Lab 6 Report

1. rm(list=ls())

sse\_mean= function(x)

{sse= sd(x, na.rm=TRUE)/(sqrt(length(x[! is.na (x)])))

return(sse)

}

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

sse\_mean(mtcars$mpg)

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

{ dat\_1=sample(x, n\_1, replace=TRUE)

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

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

return(difference\_in\_means)

}

1. The function performs bootstrap resampling. There is nothing within the function that breaks the data’s associations, nor does the function generate new data.
2. Chart, histogram

   Description automatically generated
3. 0 of my differences of means were greater than 5.8

sum(abs(mean\_differences) >5.8)

1. You would have to run 10 million or more simulations to possibly see a difference.
2. Chart, box and whisker chart

   Description automatically generated
3. Adelie= 38.79139, Chinstrap=48.83382, diff\_crit= 10.04243
4. If I ran an experiment to collect random bill lengths of Adelie and Gentoo penguins from a pool of normally expected (no crazy long or short bills) bill lengths I would expect to see that the difference between the average for each species would be 10.04mm or more from less than 1 in 1000 experiments.
5. There were no differences in means that were greater than the diff\_crit.
6. Chart, histogram

   Description automatically generated