

Julia Vineyard

Worked with: Juliana Berube

## Lab 6 Report

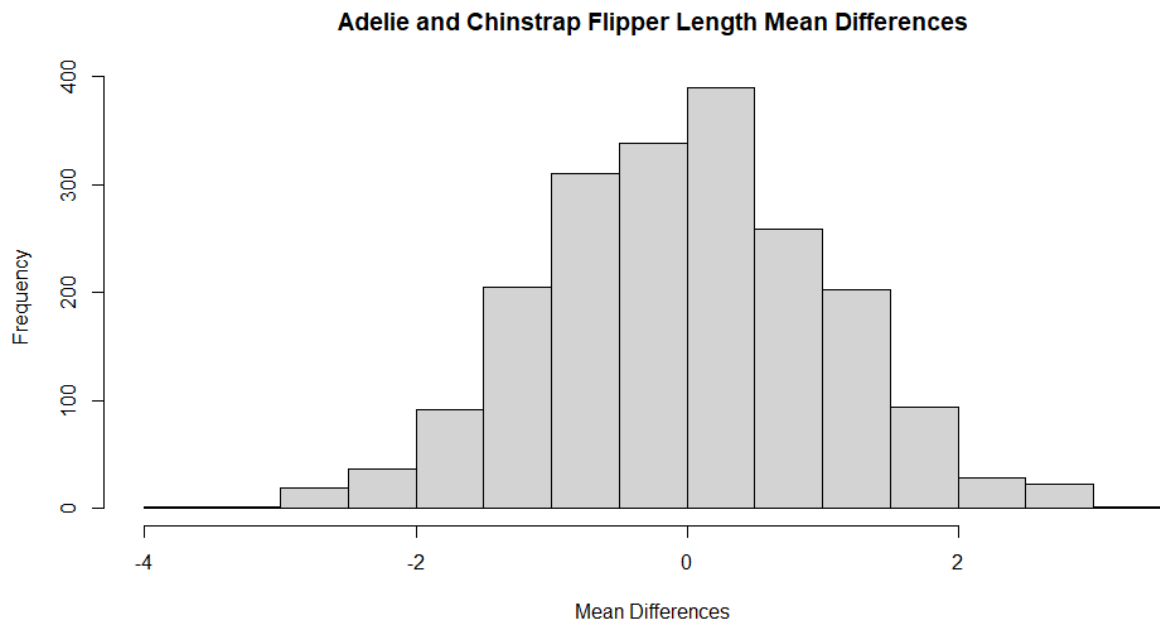
1. `rm(list=ls())`

```
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)
```

2. `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)`

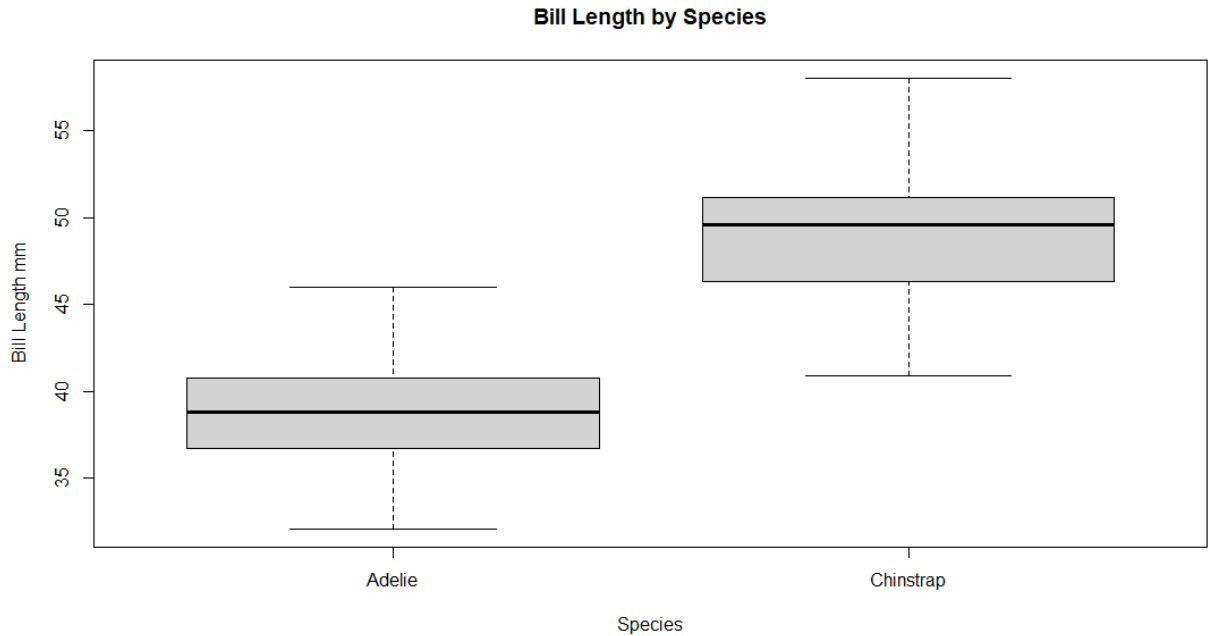
```
difference_in_means=mean(dat_1, na.rm=TRUE) - mean(dat_2, na.rm=TRUE)
return(difference_in_means)
}
```

3. The function performs bootstrap resampling. There is nothing within the function that breaks the data's associations, nor does the function generate new data.

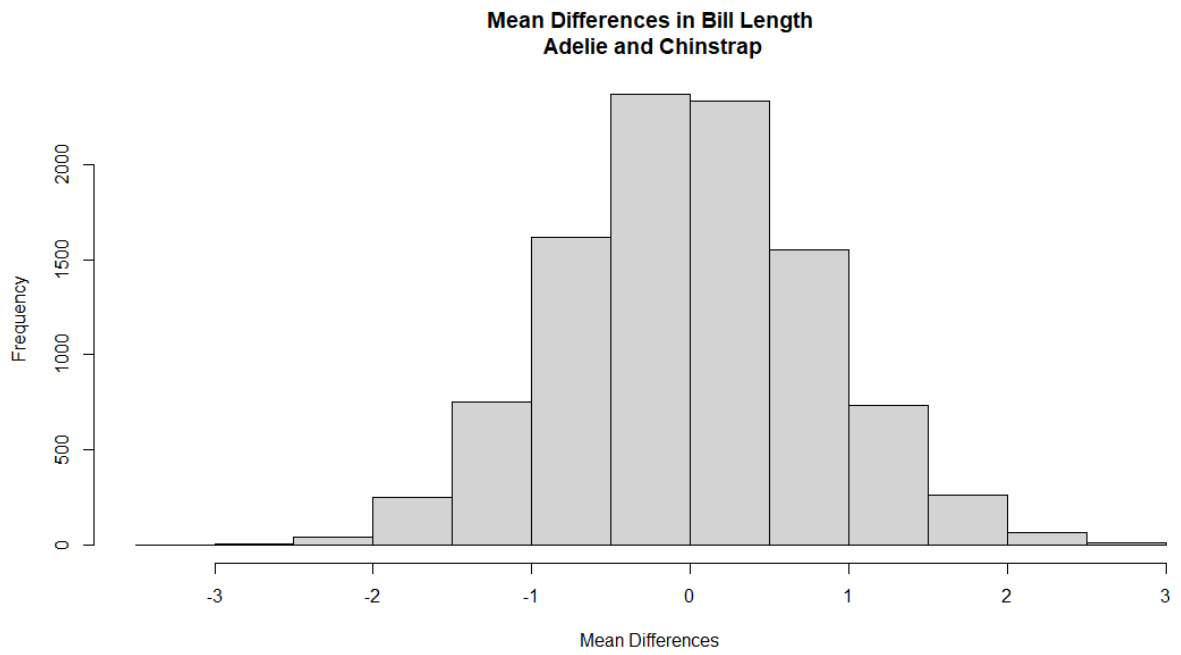


- 4.

5. 0 of my differences of means were greater than 5.8  
`sum(abs(mean_differences) > 5.8)`
6. You would have to run 10 million or more simulations to possibly see a difference.



- 7.
8. Adelie= 38.79139, Chinstrap=48.83382, diff\_crit= 10.04243
9. 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.
10. There were no differences in means that were greater than the diff\_crit.



11.