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October 19, 2022

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)
```

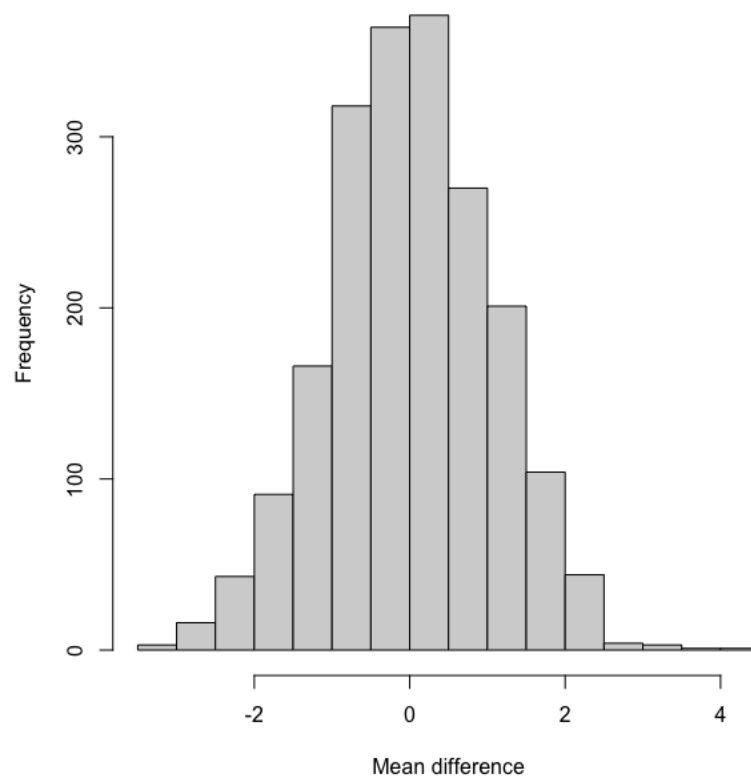
2. `two_group_resample_diff = function(x, n_1, n_2)`

```
{  
  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)  
}
```

3. 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.

4.

Histogram of Mean Difference in Penguin Flipper Length

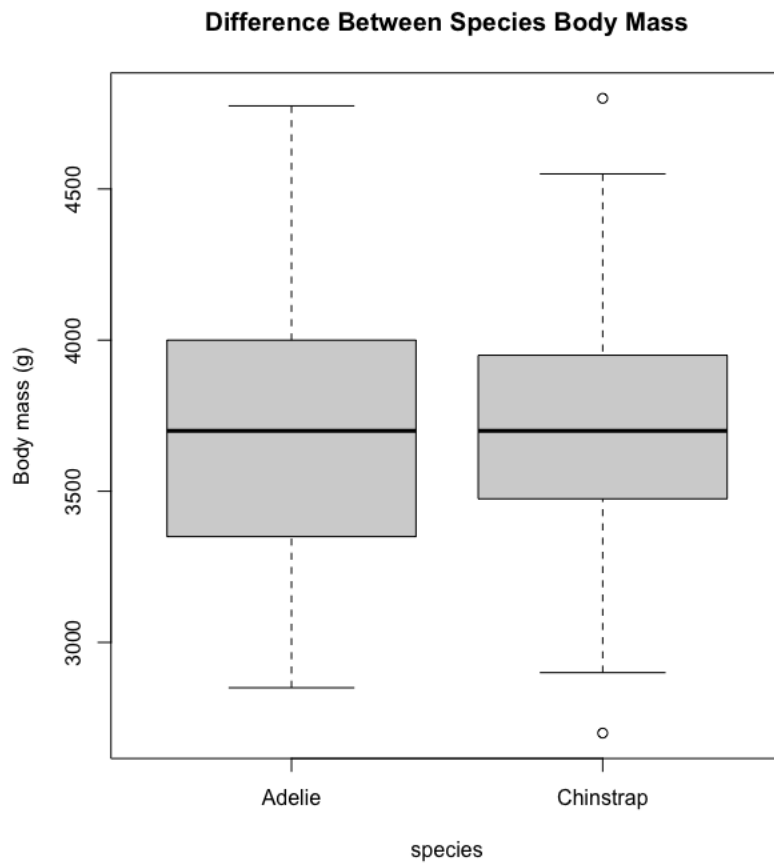


5. Zero

`sum(abs(mean_differences) > 5.8)`

6. It's impossible to see a difference in mean flipper length that is equal to or greater than 5.8mm.

7.



8. Adelie = 3700.662 g

Chinstrap = 3733.088 g

diff_observed = 32.42598

9. 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.

10. 608 differences in means greater than diff_crit

11.

