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Lab06

*Worked with Jessica Bonin

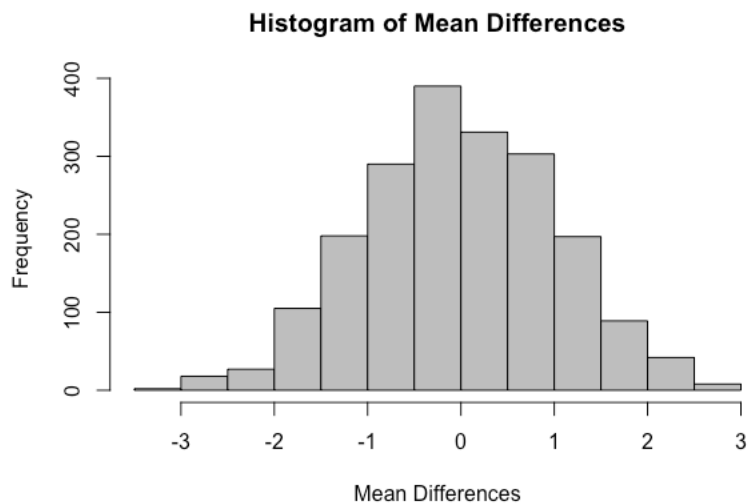
1.

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

```
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. It is using the bootstrap method because the function is preserving the associations between the data (body mass and species) and is not breaking the association as it would in the Monte Carlo method while it is being resampled. This is to simulate an alternative hypothesis.
- 4.

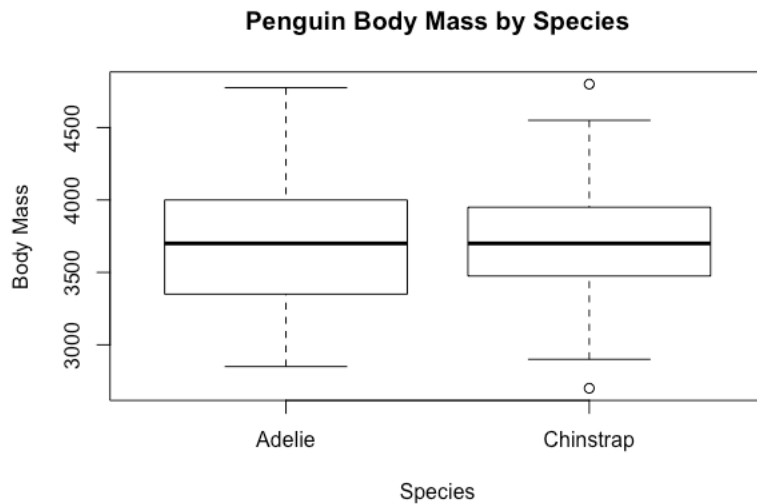


5. None of the differences in the sampled means were greater than the observed value of 5.8

```
sum(abs(mean_differences) >= diff_observed)
```

6. It would have to be run 10 million or more times to get a result greater than 5.8mm

7.



8. Group means:

1 Adelie 3700.662

2 Chinstrap 3733.088

Difference in means:

32.42598

9. The p-value is 0.5879. This means that you could expect to see a difference in body masses in about 1 in 58 experiments. Essentially there is no true difference in body mass between the species.

10. 605

11.

Histogram of Mean Differences
Body Mass

