

Jahiya Clark
Prof. Nelson
Lab 6
25 Oct 2021

Lab 6

1.

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

```
require(palmerpenguins)
```

```
sse_mean = function(x)
{
  n=length(x) - sum(as.numeric(is.na(x)))
  return(sd(x, na.rm = TRUE)/ sqrt(n))
}
```

```
sse_mean(penguins$body_mass_g)
sse_mean(mtcars$mpg)
```

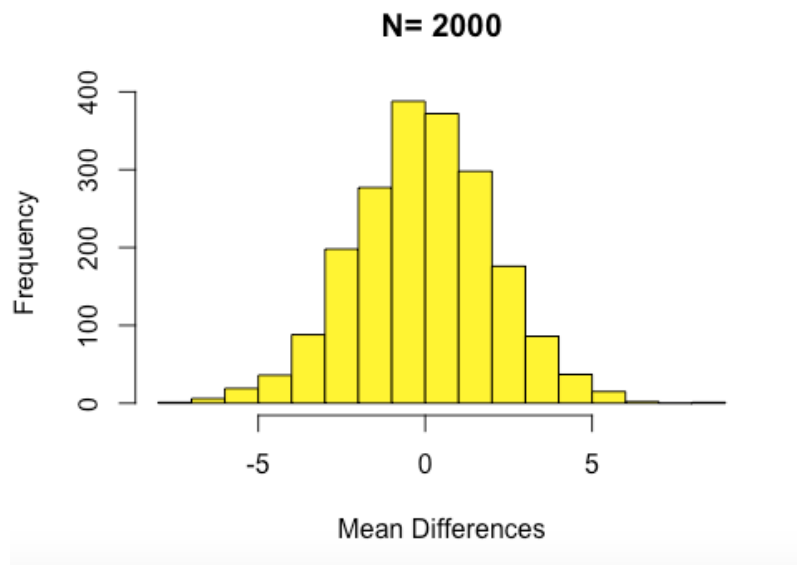
2.

```
two_group_resample = function(x, n_1, n_2)
{
  d_1 = sample(x, n_1, replace = TRUE)
  d_2 = sample(x, n_2, replace = TRUE)
  diff_in_means = mean(d_1, na.rm = TRUE) - mean(d_2, na.rm = TRUE)

  return(diff_in_means)}
```

3. It must be Monte Carlo sampling because when I run the line the output changes every time and it changes more than what can be expected.

4.



5. Yes, ten of the samples

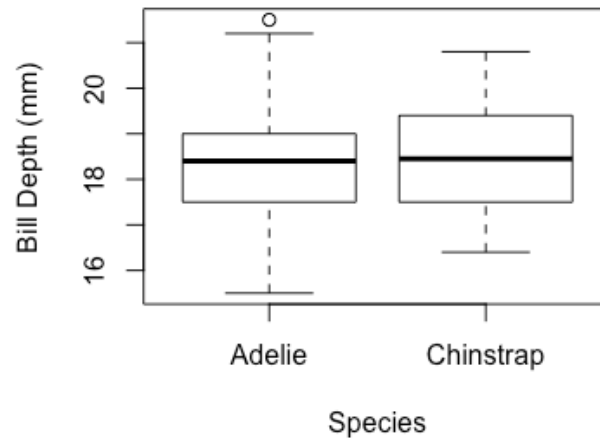
```
n = 2000
mean_differences = c()
for (i in 1:n)
{
  mean_differences = c(
    mean_differences,
    two_group_resample(dat_penguins$flipper_length_mm, 68, 152)
  )
}
hist(mean_differences, main = "N= 2000", xlab = "Mean Differences", col = "yellow")

t_test = t.test(flipper_shuffled ~ dat_pen$species)

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

6. You would have to run the stimulation over ten million times to see a flipper length greater than 5.8mm.

7.



8.

Species	bill_depth_mm	means
---------	---------------	-------

Adelie	18.34636
--------	----------

Chinstrap	18.42059
-----------	----------

Difference in Means

0.0742

9. The p-value from the t-test for the difference in mean bill depth was not significant. The p-value surpassed our 0.05 cutoff with a value of 0.6623, which means we cannot reject the null hypothesis that there is no difference between the means of bill depth between Adelie and Chinstrap species.

10. There are 1,941 difference in means that are greater than diff_crit.

11.

