

Keegan Moynahan *** Worked on with Steph ***

Lab 6

1)

```
rm(list = ls())  
require(palmerpenguins)  
sse_mean <- function(x){  
  values <- !is.na(x)  
  y <- x[values]  
  sd(y)/sqrt(length(y))  
}  
sse_mean(penguins$bill_depth_mm)  
sse_mean(mtcars$mpg)
```

2)

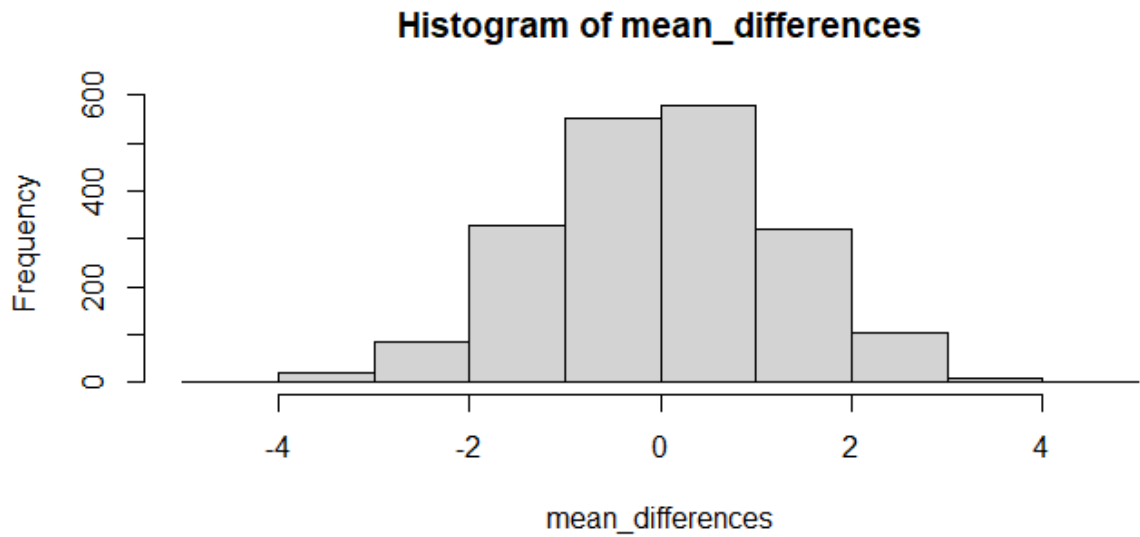
```
two_group_resample_diff = function(x, n_1, n_2)
```

```
{  
  values <- !is.na(x)  
  y <- x[values]  
  z <- sample(y, n_1, replace = TRUE)  
  v <- sample(y, n_1, replace = TRUE)  
  diff_in_means =  
    mean(z) - mean(v)  
  
  return(diff_in_means)  
}
```

```
two_group_resample_diff(penguins$bill_depth_mm, 100, 300)
```

3) This function performs Monte Carlo resampling, and it stimulates a NULL hypothesis.

4)

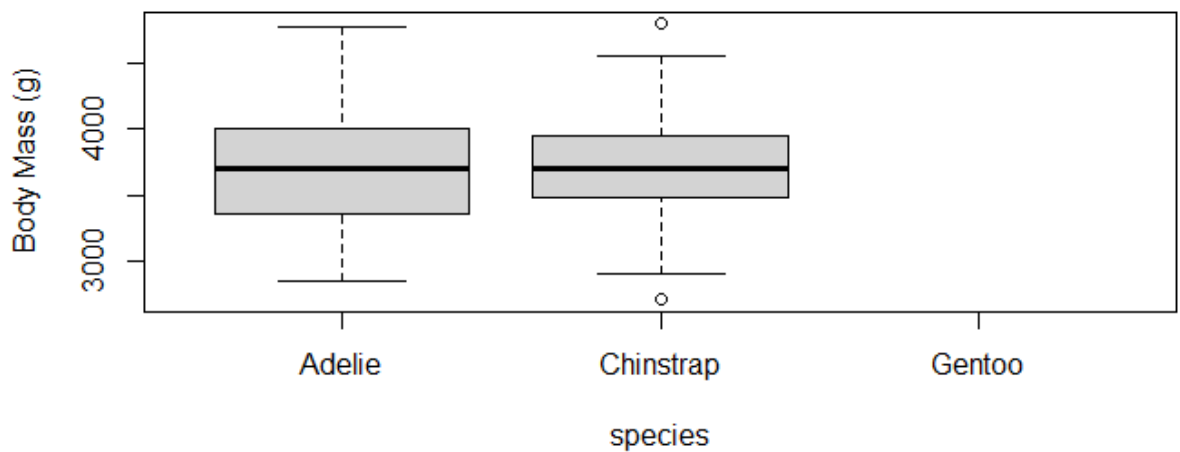


5) 0 mean differences had a magnitude of 5.8 or greater.

```
flipleng_mean<-sum(abs(mean_differences)>=5.8)
```

6) I would expect to observe a difference in mean flipper length of 5.8mm or greater in 1 of 10 million experiments

7)



```
> agg_means
  species body_mass_g
1  Adelie    3700.662
2 Chinstrap    3733.088
> diff_crit
[1] 32.42598
```

8)

- 9) The p-value of 0.5879 or 58.7% is saying that 58.7% of the differences in means will be greater or equal to the mean.

```
welch Two Sample t-test

data: dat_pen$body_mass_g by dat_pen$species
t = -0.54309, df = 152.45, p-value = 0.5879
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -150.38481  85.53284
sample estimates:
 mean in group Adelle mean in group Chinstrap
      3700.662           3733.088
```

- 10) 663 or 66.3% of differences were greater than "diff_crit"

11)

