

Question 1:

```
rm(list = ls())

sse_mean= function(x)
{
  n = sum(!is.na(x))

  SSE= (sd(x, na.rm = TRUE)) / sqrt(n)

  return(SSE)
}

require(palmerpenguins, mtcars)

sse_mean(penguins$body_mass_g)

sse_mean(mtcars$mpg)
```

Question 2

```
two_group_resample_diff = function(x, n_1, n_2)
{
  x = x[!is.na(x)]

  resamp_1 = sample(x, n_1, replace = TRUE)

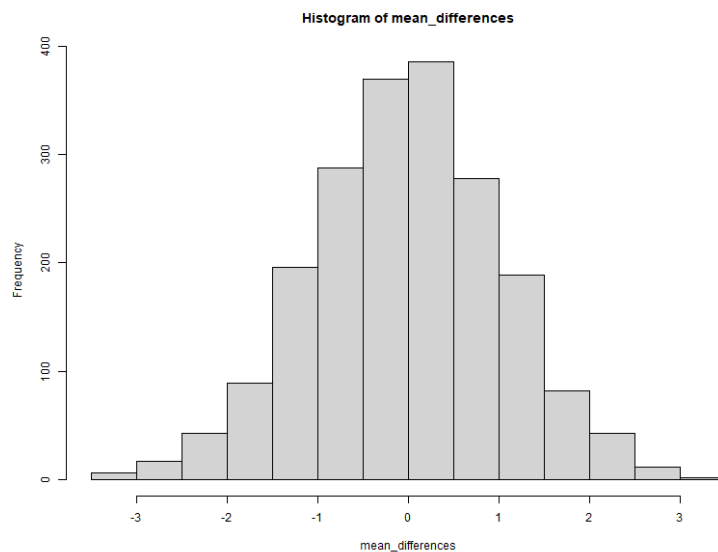
  resamp_2 = sample(x, n_2, replace = TRUE)

  difference_in_means =
  mean(resamp_1, na.rm = TRUE) -
  mean(resamp_2, na.rm = TRUE)

  return(difference_in_means)
}
```

Question 3

The function performs a Monte Carlo because it does not specify by species, all values are resampled completely (no association).

Question 4 histogram to the right

Question 5

I got that there were zero means of my resampled differences that had a magnitude greater than 5.8.

```
sum(abs(mean_differences) >= 5.8)
```

Question 6

I think you would have to do an infinite number of simulations before you see a difference in mean flipper length equal to or greater than 5.8mm because the extremely low p value means that the data did not occur by chance and there is a suggested direct correlation.

Question 7 Box and whiskers →

Question 8

species	Body Mass (g)
Adelie	3700.662
Chinstrap	3733.088

Difference in Means

32.42598

Question 9

The p-value from the t-test is 0.5879.
This p-value suggests that there is not a strong case that there is a difference in body mass by species. There is a 0.5 or 50% probability that the difference occurred by chance or is not guaranteed to happen every time.

Question 10

```
sum(abs(mean_differences) >= diff_observed) = 616
```

Question 11 Histogram to the right

