

Analysis of Environmental Data – Lab 6

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Q1:

```
rm(list = ls())
sse_mean = function(x)
{
  sse = sd(x, na.rm = TRUE)/sqrt(length(x) - sum(is.na(x)))
  return(sse)
}
```

```
sum(is.na(penguins$body_mass_g) #example
```

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

Q2:

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

  x1 = sample(x_ok, n_1, replace = TRUE)
  x2 = sample(x_ok, n_2, replace = TRUE)

  difference_in_means =
    mean(x1, na.rm = TRUE) - mean(x2, na.rm = TRUE)
  return(difference_in_means)
}
```

```
set.seed(54321)
two_group_resample_diff(dat_pen$flipper_length_mm, 68, 152)
```

Q3:

It is Monte Carlo because it's shuffling and randomly selecting from one of the two species. We don't specify from which species we want the value.

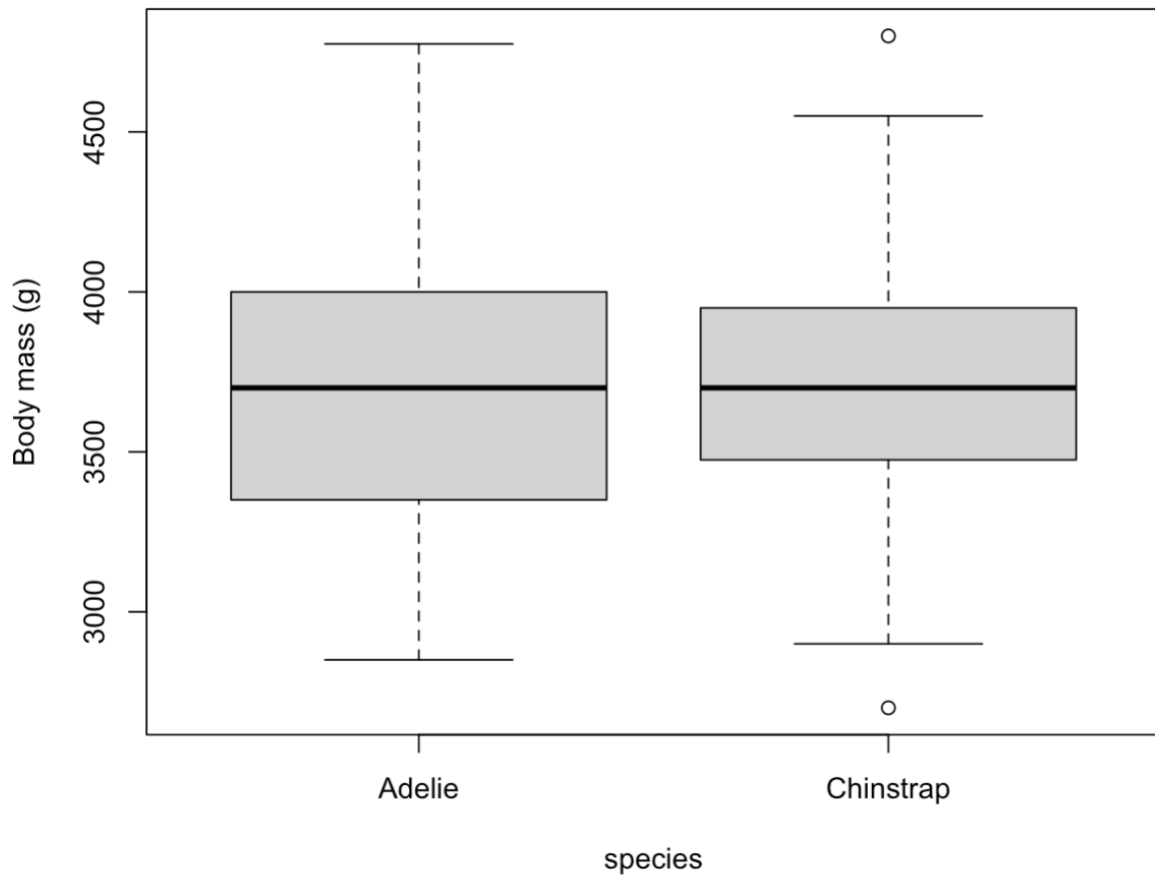
Q4+5

```
sum(abs(mean_differences) > 5.8)
result: 0
```

Q6:

You would never observe a mean greater than 5.8 because there is no flipper length greater than 5.8 in both ways (+/-).

Q7:



8Q:

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

Q9:

p-value = 0.5879

There is no significant difference in the body mass between the two species. If the result would be less than 0.05 there would be a significant difference.

Q10:

```
sum(abs(mean_differences)> diff_crit)
result: 628
```

Q11:

