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Eco 634 – Lab 6

Q1. Show the R code you used to define your sse_mean() function. Include the following line before your function definition:

rm(list = ls())

sse_mean = function(x)

{

  sse = sd(x,na.rm=TRUE)/sqrt(length(x)-sum(is.na(x)))

  return(sse)

}

sse_mean(penguins$body_mass_g)

sse_mean(mtcars$mpg)

Q2. Include the code you used to define your two_group_resample() function into the text input:

two_group_resample = 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)

}

Q3. Does your function perform Monte Carlo or bootstrap resampling, i.e. does it simulate a null or an alternative hypothesis?

It simulates a null hypothesis. Therefore, the function uses Monte Carlo resampling. We re-shuffle the flipper length with no regard for species labels. The Monte Carlo resampling breaks the association between flipper length and species of penguin. Monte Carlo is a great way to simulate what would happen if the null hypothesis were true, and therefore you can compare it to the original data. In this

case, Monte Carlo resampling results in a null distribution in which there appears to be no difference in flipper length between the two penguin species.

Q4. Create histogram of the resampled differences of means (flipper length)

Histogram of Resampled Differences of Means
Flipper Length (mm) between Adelie and Chinstrap penguins
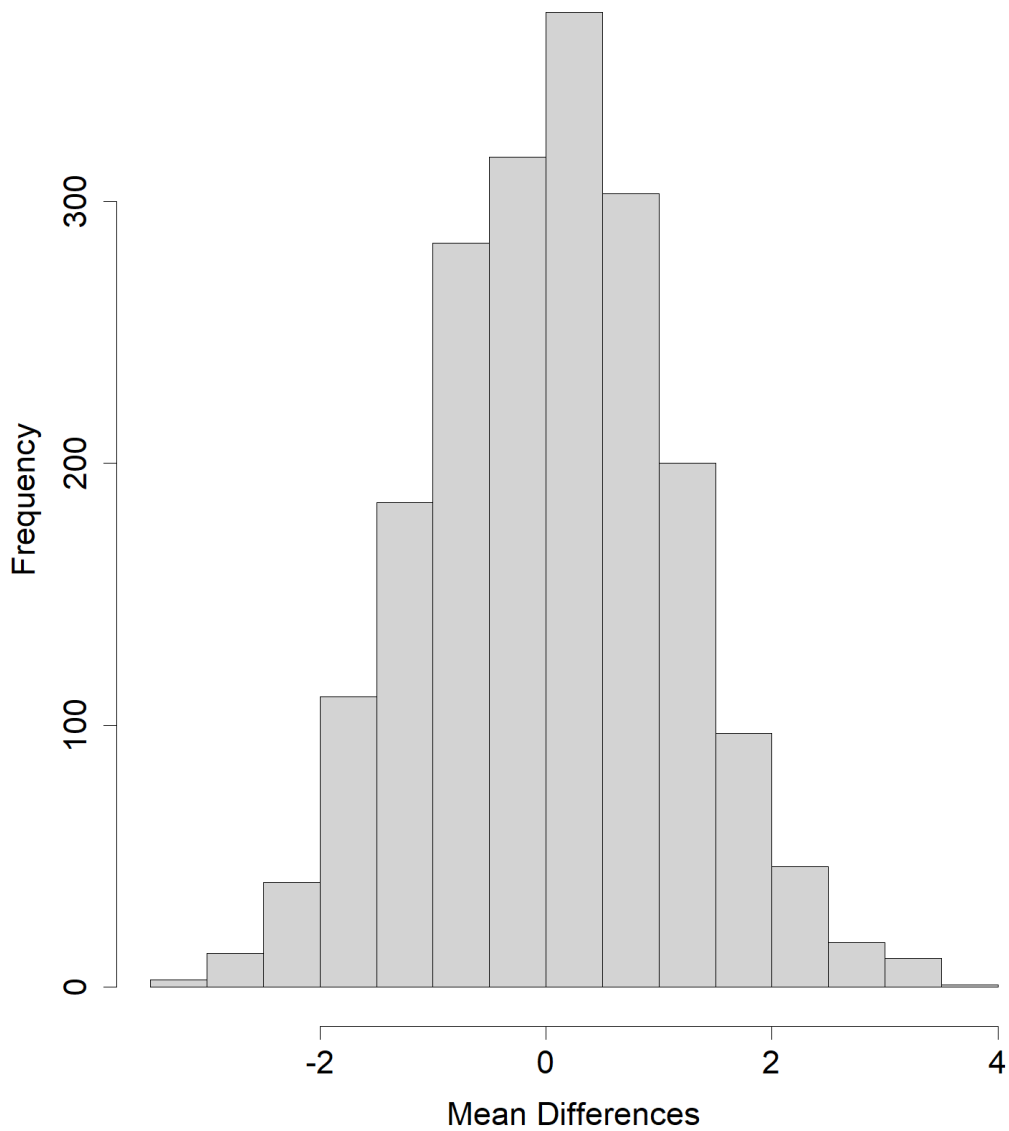
Q5. How many of your resampled differences of means were greater than 5.8?

Assume that we are doing a 2-sided test: we don't care which species has longer flippers, we only want to know if they are different. Include the R code you used to check the number of differences greater than 5.8:

#code to check differences in means greater than 5.8

sum(abs(mean_differences) >= 5.8)

There are NO resampled differences of means that were greater than the observed difference of means, 5.8. The code I used to check this uses the sum of the absolute value of the mean differences. We use absolute value since it's a two-sided test and we don't necessarily care which species has longer flippers, just that there is a difference in that one species has longer flippers. If we just run abs(mean_differences) >= 5.8 then we would get a large output of a list of TRUE and FALSE. In this case, all scenarios were false. We use sum to add up all of the potential difference in means values that were greater than 5.8. IN this case the sum is 0, in that we have no difference in mean values higher than 5.8


Q6. Given a p value of less than 1 per 10 million, how many simulations do you think you would have to do to see a difference in mean flipper length equal to or greater than 5.8 mm?

I believe it would take at least 10 million resampling simulations to see a difference in mean flipper length greater than or equal to 5.8.   In other words:

If I repeatedly sampled flipper lengths for Adelie and Gentoo penguins randomly from a normally distributed population of measurements, I would expect to observe a difference in mean flipper length of 5.8mm or greater in less than 1 in 10 million experiments.

This is due to the extremely small p-value demonstrating the very small chance there is in replicating the 5.8 difference in mean flipper length as seen in the original data.

Q7. Include a boxplot of your chosen variable in your report.

Boxplot of Penguin Bill Length
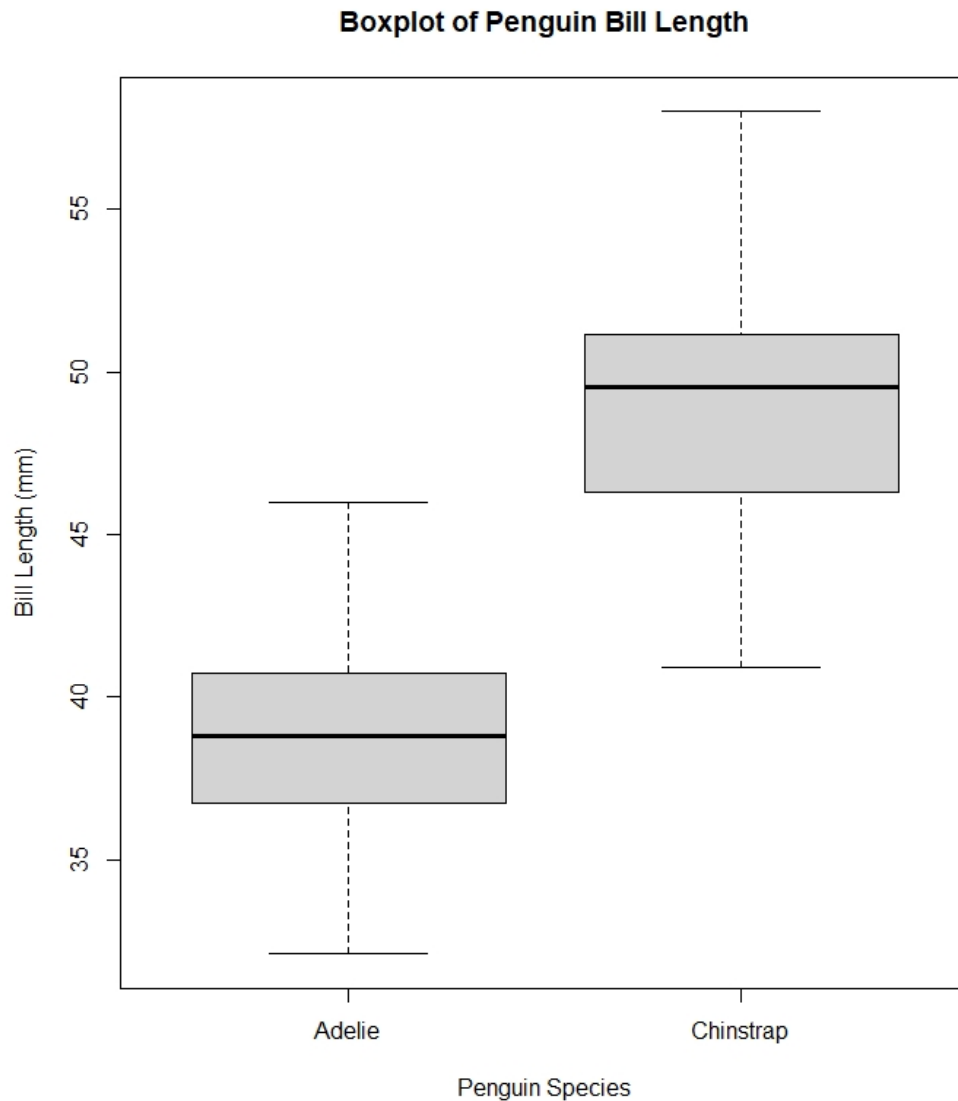
Q8. Report the group means and difference between the means.

See below the different group means of bill length (mm) for each species, Adelie and Chinstrap

> agg_means (Here we are using aggregate() to calculate the group means of bill length for each species)

       species   bill_length_mm

1   Adelie   38.79139

2 Chinstrap   48.83382

> diff_crit (this is the difference between the means of the two species' bill lengths.)

[1] 10.04243.

At first glance, this seems like an impressive number for difference in means, in that you might typically observe Chinstrap penguins to have longer bills.

Q9. Interpret the p-value from the t-test output in plain, non-technical English that a non-statistician would understand.

The reported p-value from our t-test for penguin bill length was a very, very small number:
        p-value < 2.2e-16.

With such a small p-value, we can understand this to mean that our difference in means for penguin bill length based on species is significant. The small p-value demonstrates that the chance is very small that there is NO association between bill length and species. In fact, since the p-value is so small, we would say there IS a great chance there is some sort of association between bill length and species. In other words, a very small p-value means that there is very strong evidence in favor of the alternative hypothesis, (in favor of there being a real difference in bill length between different penguin species).

Q10. How many differences in means were greater than diff_crit? (Remember to treat this as a 2-tailed test.)

0, There are NONE. In simulating two samples of different sample sizes, repeated a 1000 times, there is no observed difference in means that were greater than or equal to the original difference of means, which is the diff_crit value of 10.04242. The resampling we are conducting, which is Monte Carlo resampling, is destroying the structure of our original data and randomizing it. It creates a null distribution for us and shows us all of the plausible values for differences in means assuming the null hypothesis would be true. We can then compare those null distribution values of possible differences of means to the original data and our diff_crit value. We see that 10.04 falls far outside the null distribution values for difference of means.

I used the below code to check this:
two_group_resample = 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)

}

```
n = 1000

mean_differences = c()

for (i in 1:n)

{

  mean_differences = c(

    mean_differences,

    two_group_resample(dat_pen$bill_length_mm, 68, 152)

   )

}

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

We use sum to add up all of the potential difference in means values that were greater than 10.04243. IN this case the sum is 0, in that we have no difference in mean values higher than 10.04243. We took the absolute value because this is a two-sided test, and we don't care which species would have longer bills, just that there is a difference between the species.

*Q11 on next page

Q11. Include a histogram of your simulation results in your report. Make sure it has appropriate title and labels.

**Histogram of Resampled Differences of Means
Bill Length (mm) in Adelie and Chinstrap Penguins**