Final Project Practice

2023-04-17

Practicing for the Final Project

This is meant to help you prepare for the final project, which I will be handing out next week. The final project will have about the same amount of guidance (or maybe even a bit more) that I've given you here. If you can work your way through these practice problems, you'll be in good shape!

I'm expecting you to be able to filter and summarize the data in ways you need, choose the appropriate visualization, choose the appropriate analysis, and correctly interpret the analysis for the question I've asked you.

Some important notes:

- For both this and the final project, we are going to use the `palmerpenguins` dataset, which we've used before! You can learn more about it here.
- I will not be giving you an answer key for your final project since part of your grade for the assignment is to choose the correct visualizations and analyses.
- For every plot you make, be sure to clarify and clean up the labels and add a theme.
- Because we are working through this together in class, I will be grading this assignment on completion only! That said, make sure you actually answer ***every question*** that's in here for full credit... there are quite a few!

Set-Up

Let's load our packages and get started!

```
library(tidyverse)
library(palmerpenguins)
```

We will be using the `penguins` data frame. It exists as part of the `palmerpenguins` package, but if you want it to show up in your environment, run the following code chunk.

```
penguins <- penguins
```

Problem Set 1

For this problem set, we are going to look at the difference in flipper lengths for each species on Dream island.

First things first, let's make a dataframe with only penguins on Dream island. We will want to use this dataframe for the rest of this problem set.

```
dream <- penguins %>%
  filter(island == "Dream")
```

Based on our question, which variable is independent and which is dependent? Which is continuous and/or which is categorical?

First, calculate the minimum, maximum, and mean of the flipper lengths for each species

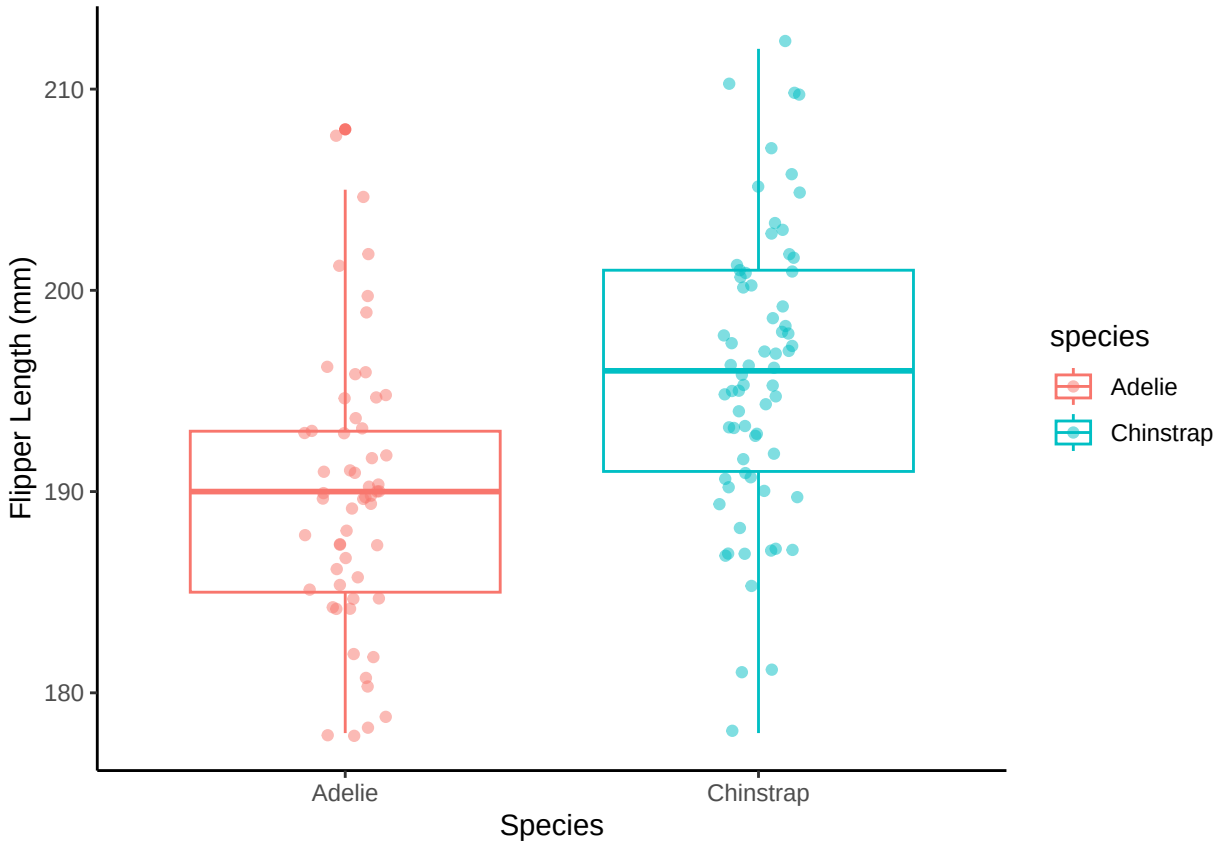
```
flippers <- dream %>%
  group_by(species) %>%
  summarise(min_flipper = min(flipper_length_mm, na.rm = TRUE),
            max_flipper = max(flipper_length_mm, na.rm = TRUE),
            mean_flipper = mean(flipper_length_mm, na.rm = TRUE))
flippers
```

```
## # A tibble: 2 x 4
##   species   min_flipper max_flipper mean_flipper
##   <fct>           <int>       <int>        <dbl>
## 1 Adelie            178         208         190.
## 2 Chinstrap         178         212         196.
```

Choose an effective visualization method for this data. Use `ggplot2`.

```
# boxplot, multiple histogram, or multiple density plot are all acceptable

ggplot(dream, aes(x = species, y = flipper_length_mm, color = species)) +
  geom_boxplot() +
  geom_jitter(width = 0.1, alpha = 0.5) +
  labs(x = "Species",
       y = "Flipper Length (mm)") +
  theme_classic()
```



Write out the null and alternative hypotheses.

Null: there is no difference in the mean flipper length between the two species

Alternative: there is a difference in the mean flipper length between the two species

Run the appropriate statistical test.

```
t.test(data = dream, flipper_length_mm ~ species)
```

```
##
##  Welch Two Sample t-test
##
## data:  flipper_length_mm by species
## t = -4.937, df = 120.37, p-value = 2.581e-06
## alternative hypothesis: true difference in means between group Adelie and group Chinstrap is not equa
## 95 percent confidence interval:
##  -8.534213 -3.648561
## sample estimates:
##    mean in group Adelie mean in group Chinstrap
##                189.7321                 195.8235
```

Interpret the results of your statistical test:

- What is the p-value?
- Is the p-value above or below 0.05?
- What does your answer to the question above mean?
- Should we reject or fail to reject the null hypothesis?

Should we run pairwise comparisons? If yes, do so below and interpret:

Problem Set 2

For this problem set, we want to know if there is a relationship between flipper length and bill length amongst all penguins (we aren't going to worry about species right now).

Are our variables of interest continuous and/or categorical?

Take note that in this example, there is no dependent or independent variable per say. We don't have any reason to think that flipper length influences bill length or vice versa. We just want to determine if there is a relationship or not.

That said, treat flipper length as the *independent* variable (x-axis) and bill length as the *dependent* variable (y-axis).

First, calculate the mean and standard deviation for both bill length and flipper length.

```
bill_flipper <- penguins %>%
  summarise(mean_bill = mean(bill_length_mm, na.rm = TRUE),
            sd_bill = sd(bill_length_mm, na.rm = TRUE),
            mean_flipper = mean(flipper_length_mm, na.rm = TRUE),
            sd_flipper = sd(flipper_length_mm, na.rm = TRUE))
bill_flipper
```

```
## # A tibble: 1 x 4
##   mean_bill sd_bill mean_flipper sd_flipper
##       <dbl>   <dbl>        <dbl>      <dbl>
## 1      43.9    5.46         201.       14.1
```

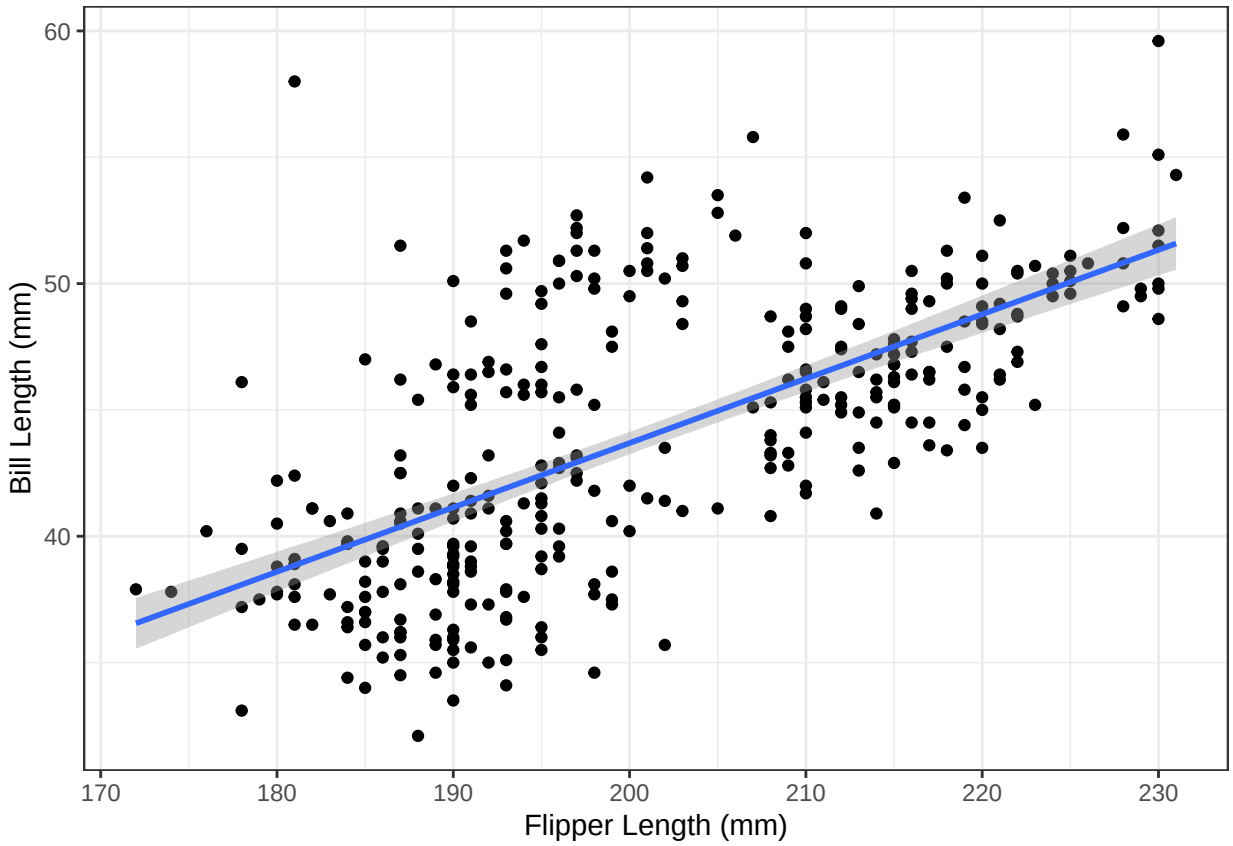
Choose the best way to visualize the relationship between these two variables

```
ggplot(penguins, aes(flipper_length_mm, bill_length_mm)) +
  geom_point() +
  geom_smooth(method = "lm") +
    labs(x = "Flipper Length (mm)",
       y = "Bill Length (mm)") +
  theme_bw()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```



To do the rest of this problem set, the easiest way is to create a new data frame with no NA values. Run the code chunk below and use that new data frame for the rest of the problem set.

```
penguins_noNA <- penguins %>%
  filter(!is.na(bill_length_mm),
         !is.na(flipper_length_mm))
```

Calculate the correlation coefficient and the `r^2` value.

- According to the correlation coefficient, is the relationship positive, negative or is there no relationship?
- According to the `r^2` value, how much of the variation in this relationship is explained? Remember, we usually multiply the `r^2` by 100 to represent this as a percentage.

```
r <- cor(x = penguins_noNA$flipper_length_mm, y = penguins_noNA$bill_length_mm)
r^2
```

```
## [1] 0.430574
```

Run the appropriate model for this data.

```
lm_model <- lm(data = penguins_noNA, bill_length_mm ~ flipper_length_mm)
summary(lm_model)
```

```
##
## Call:
```

```
## lm(formula = bill_length_mm ~ flipper_length_mm, data = penguins_noNA)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.5792 -2.6715 -0.5721  2.0148 19.1518
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -7.26487    3.20016   -2.27   0.0238 *
## flipper_length_mm  0.25477    0.01589   16.03   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.126 on 340 degrees of freedom
## Multiple R-squared:  0.4306, Adjusted R-squared:  0.4289
## F-statistic: 257.1 on 1 and 340 DF,  p-value: < 2.2e-16
```

Using variables and numbers from the summary above, write out the equation of the line

Answer: bill_length_mm = 0.25*flipper_length_mm - 7.26

Interpret the results of your statistical test:

- What is the p-value?
- Is the p-value above or below 0.05?
- What does your answer to the question above mean?

Should we run pairwise comparisons? If yes, do so below and interpret:

Bonus

Let's add in the species variable into our analysis! Keep using the `penguins_noNA` data frame.

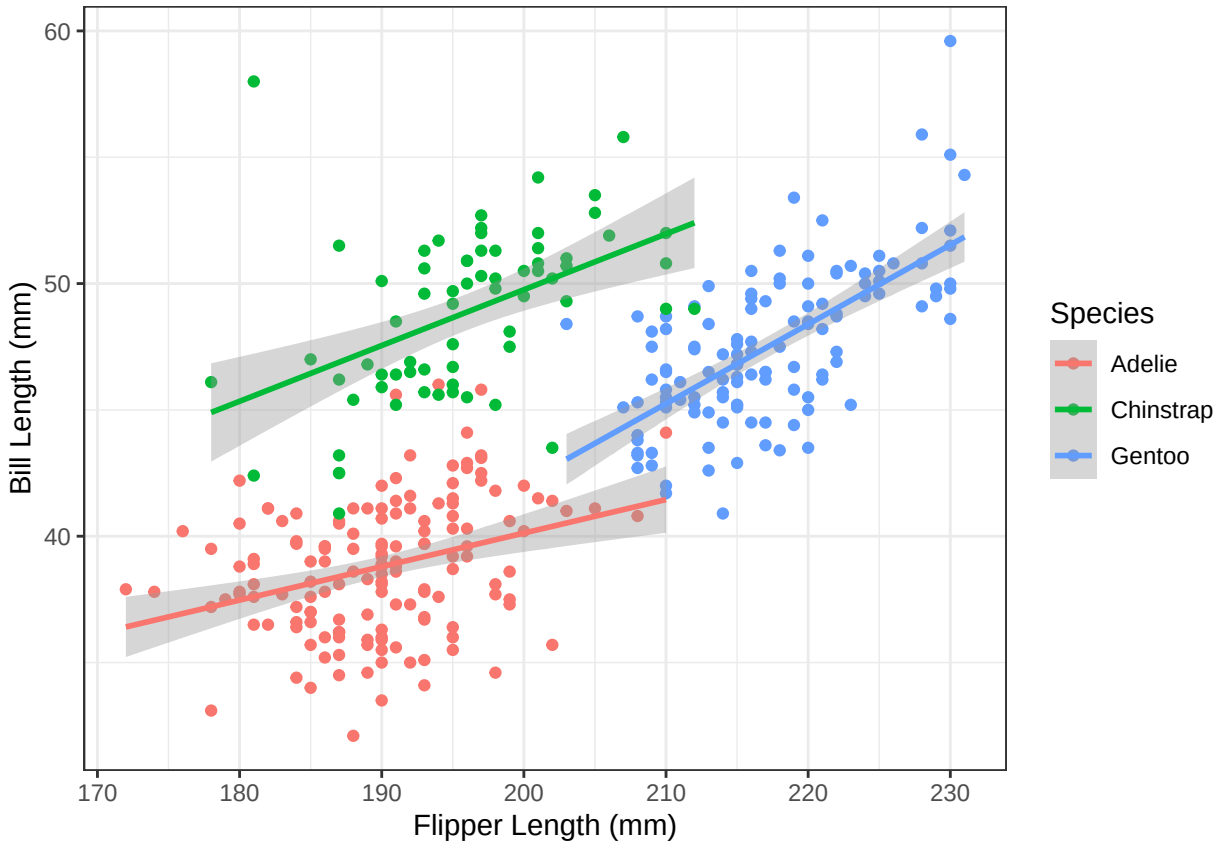
First, plot the data, this time including species as a variable in the plot.

```
ggplot(penguins, aes(flipper_length_mm, bill_length_mm, color = species)) +
  geom_point() +
  geom_smooth(method = "lm") +
  labs(x = "Flipper Length (mm)",
       y = "Bill Length (mm)",
       color = "Species") +
  theme_bw()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 2 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 2 rows containing missing values (`geom_point()`).
```



Run the model again, this time including species and the species interaction with "independent" variable.

```
mlm_model <- lm(data = penguins_noNA, bill_length_mm ~ flipper_length_mm * species)
summary(mlm_model)
```

```
##
## Call:
## lm(formula = bill_length_mm ~ flipper_length_mm * species, data = penguins_noNA)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.6977 -1.7046  0.0596  1.5571 12.4394
##
## Coefficients:
##                                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)                        13.58714    6.05061   2.246 0.025380 *
## flipper_length_mm                   0.13269    0.03183   4.168 3.91e-05 ***
## speciesChinstrap                   -7.99376   10.48117  -0.763 0.446190
## speciesGentoo                     -34.32335    9.81983  -3.495 0.000537 ***
## flipper_length_mm:speciesChinstrap  0.08813    0.05405   1.631 0.103915
## flipper_length_mm:speciesGentoo     0.18152    0.04775   3.801 0.000171 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.55 on 336 degrees of freedom
## Multiple R-squared:  0.7851, Adjusted R-squared:  0.7819
## F-statistic: 245.5 on 5 and 336 DF,  p-value: < 2.2e-16
```

Interpret the results from the model above. Focus on the p-values for the independent variables and/or interaction terms, not the overall model.

Answer:

Problem Set 3

For this problem set, we want to know if there is a difference in the body mass of the penguin species.

Based on our question, which variable is independent and which is dependent? Which is continuous and/or which is categorical?

First, calculate the minimum, maximum, and mean of the body mass for each species.

```
body_mass <- penguins %>%
  group_by(species) %>%
  summarise(min_mass = min(body_mass_g, na.rm = TRUE),
            max_mass = max(body_mass_g, na.rm = TRUE),
            mean_mass = mean(body_mass_g, na.rm = TRUE))
body_mass
```

```
## # A tibble: 3 x 4
##   species   min_mass max_mass mean_mass
##   <fct>        <int>    <int>     <dbl>
## 1 Adelie        2850     4775     3701.
## 2 Chinstrap     2700     4800     3733.
## 3 Gentoo        3950     6300     5076.
```

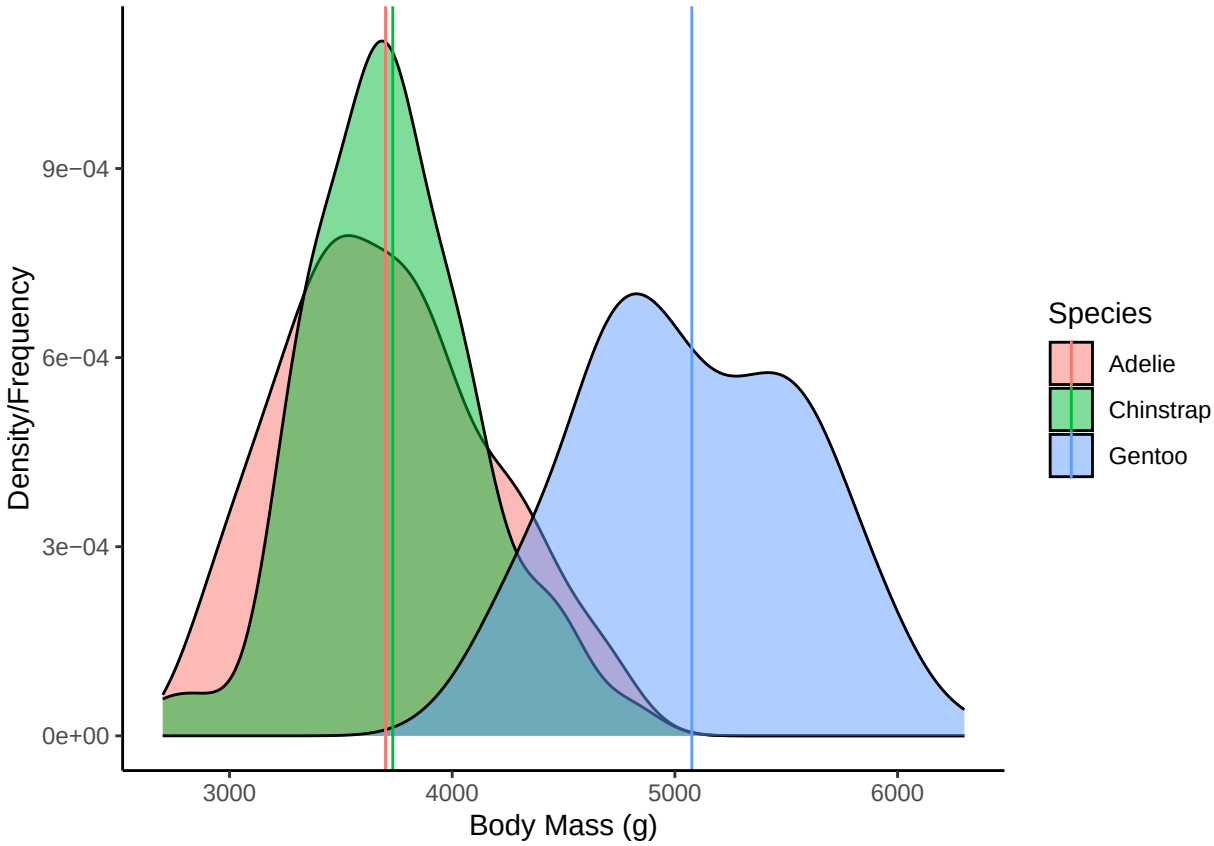
Convert all the columns in the `body_mass` data frame from grams to kilograms. (Hint: I recommend using the `mutate()` function. Remember that you divide grams by 1000 to get kilograms)

```
body_mass_kg <- body_mass %>%
  mutate(min_mass = min_mass / 1000,
         max_mass = max_mass / 1000,
         mean_mass = mean_mass / 1000)
```

Back to the question at hand... choose an effective visualization method for this data (you will want to use the original `penguins` dataframe). Practice adding lines that represent to mean values in the plot. Thinking critically about which columns to use!

```
ggplot(penguins, aes(x = body_mass_g, fill = species)) +
  geom_density(alpha = 0.5) +
  geom_vline(data = body_mass, aes(xintercept = mean_mass, color = species)) +
  labs(x = "Body Mass (g)",
       y = "Density/Frequency",
       fill = "Species",
       color = "Species") +
  theme_classic()
```

```
## Warning: Removed 2 rows containing non-finite values (`stat_density()`).
```



Write out the null and alternative hypotheses.

Run the appropriate statistical test.

```
aov_mod <- aov(data = penguins, body_mass_g ~ species)
summary(aov_mod)
```

```
##              Df    Sum Sq  Mean Sq F value Pr(>F)
## species       2 146864214 73432107   343.6 <2e-16 ***
## Residuals   339  72443483   213698
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 2 observations deleted due to missingness
```

Interpret the results of your statistical test:

- What is the p-value?
- Is the p-value above or below 0.05?
- What does your answer to the question above mean?
- Should we reject or fail to reject the null hypothesis?

Should we run pairwise comparisons? If yes, do so below and interpret:

```
TukeyHSD(aov_mod)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = body_mass_g ~ species, data = penguins)
##
## $species
##                         diff       lwr       upr     p adj
## Chinstrap-Adelie   32.42598 -126.5002  191.3522 0.8806666
## Gentoo-Adelie    1375.35401 1243.1786 1507.5294 0.0000000
## Gentoo-Chinstrap 1342.92802 1178.4810 1507.3750 0.0000000
```