Homework 4

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```
#call the packages I want to use
library(tidyverse)
library(here)
library(lterdatasampler)
library(performance)
library(broom)
library(ggeffects)
library(car)
library(naniar)
library(flextable)
```

How does fish length predict fish weight for trout perch (across all sample years)?
This data set, like most observational environmental or ecological data sets, is noisy (i.e. a lot of spread between points). It is also somewhat messy. You are expected to read the metadata, protocols, and all relevant information on the EDI portal before working with the data.

Problem 1

1. Write your null and alternative hypotheses in mathematical and biological terms.

Biological:

H0: Fish length does not predict fish weight for trout perch across all sample years.

HA: Fish length does predict fish weight for trout perch across all sample years.

Mathematical:

H0: $\beta 1 = 0$

HA: $\beta 1 \neq 0$

2. Create a visualization of the missing data for the filtered data set containing the observations you will use.

```
#make an object that reads the CSV file containing the data
fish <- read.csv(here("data/ntl6_v12.csv"))

#filter the data to only include trout
fish_clean <- fish %>%
  filter(spname == "TROUTPERCH")
```

```r
#visualize missing data
gg_miss_var(fish_clean) +
  #add a caption of how missing data affects hypothesis
  labs (caption = str_wrap("Figure 1. There are 200 missing observations for fish weight. This affects our hypothesis to understand if fish length predicts fish weight.")) +
  #space out where I want the caption
  theme(
    plot.caption = element_text(hjust = 0)
  )
```

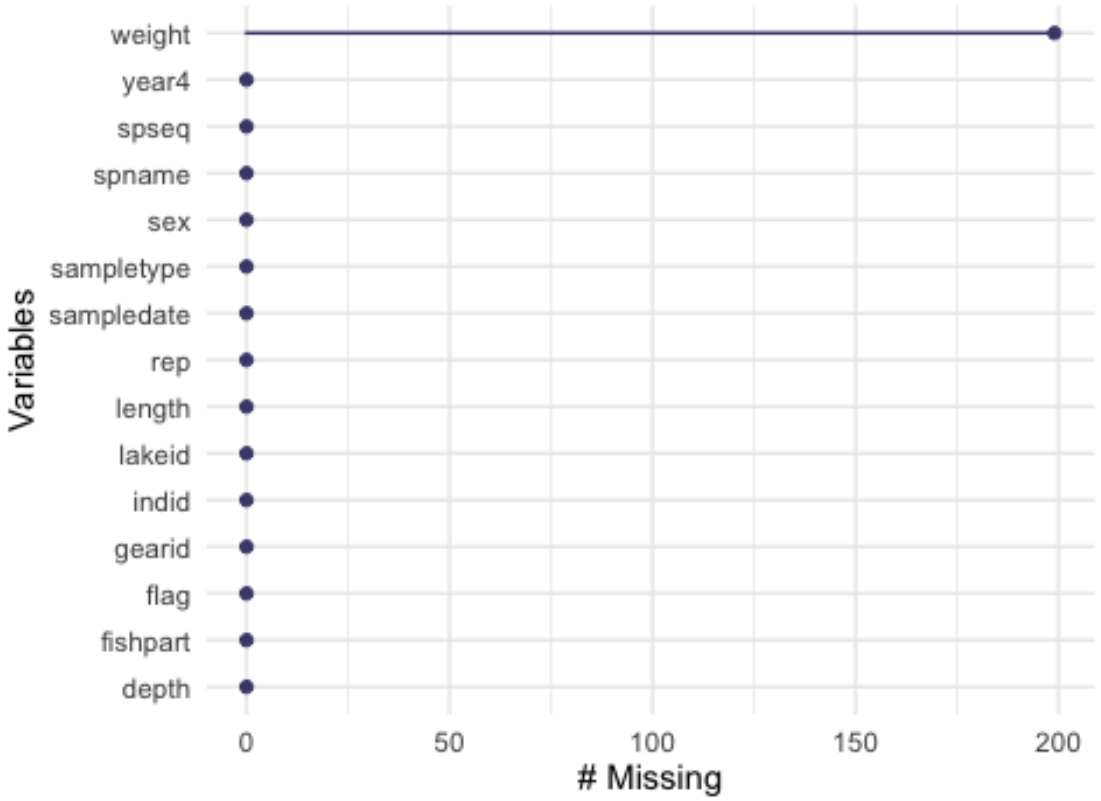


Figure 1. There are 200 missing observations for fish weight. This affects o
hypothesis to understand if fish length predicts fish weight.

a. Write an accompanying caption explaining how/if the missing data is relevant to your hypotheses.

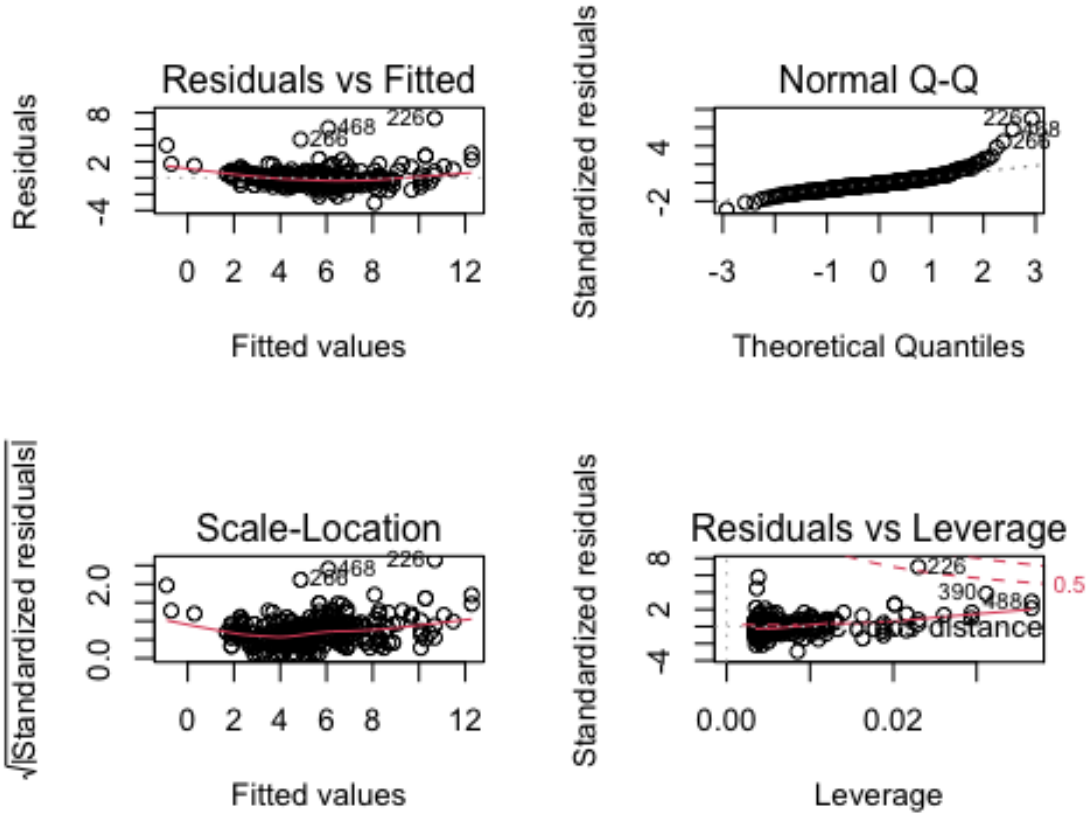
There are 200 observations from the “weight” column are missing. Since it is missing, we will have to delete the null values from the data set, meaning there are less observations to work with. The linear regression is intended to see if fish length can predict fish weight, missing some values of fish weight gives us less data to base our analysis on.

3. Run your test.

```r
#create a model object containing the linear model for if fish length
predicts weight using the filtered data frame
modelobject <- lm(weight ~ length, data = fish_clean)
```

4. Visually check the assumptions of your test. Display your diagnostic plots in a grid.

```r
# makes the viewer pane show a 2x2 grid of plots
# format: par(mfrow = c(number of rows, number of columns))
par(mfrow = c(2, 2))
plot(modelobject)
```




```r
# turns off the 2x2 grid - pop this under the code chunk where you set the
2x2 grid
dev.off()

null device
          1
```

5. For each diagnostic plot, describe in 1-2 sentences what it is showing you, and what you decide after looking at the plot.

Residuals vs Fitted: Tells you about homoscedasticity of variance. In the relationship between errors or residuals there is a cluster in the middle around the red line. The red line is pretty straight meaning they are constant throughout the range of x and y values.

Scale-location: Tells you about homoscedasticity of variance. It uses the square root of standardized residuals. The plot shows the data is more clustered in the middle but around the red line. The line is pretty straight across which means that there is good homoscedasticity.

Normal QQ: Shows us if the errors are normally distributed. The data is pretty clustered around the straight normal line meaning that the data is pretty normally distributed.

Residuals vs Leverage: Shows us if the outliers are influencing the model estimates. It measures the influence of a single observation on the model. There are a good amount of data points labeled meaning there are some outliers present in the data. This is also called the Cook's model.

6. Display the results from summary() using your model object.

```
# store the model summary as an object
model_summary <- summary(modelobject)

model_summary
```

```
Call:
lm(formula = weight ~ length, data = fish_clean)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.0828 -0.4862 -0.1830  0.4128  7.3191 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -11.702476   0.481564  -24.30   <2e-16 ***
length        0.199852   0.005584   35.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.057 on 288 degrees of freedom
  (199 observations deleted due to missingness)
Multiple R-squared:  0.8164,    Adjusted R-squared:  0.8158 
F-statistic:  1281 on 1 and 288 DF,  p-value: < 2.2e-16
```

7. Create a table that summarizes the ANOVA table. Make sure this table has informative column and row names and p-values displayed without scientific notation.

```
# store the ANOVA table as an object
# anova(): special function to get analysis of variance tables for a model
```

```r
model_squares <- anova(modelobject)

model_squares
```

```
Analysis of Variance Table

Response: weight
           Df  Sum Sq Mean Sq F value    Pr(>F)
length      1 1432.29 1432.29  1280.8 < 2.2e-16 ***
Residuals 288  322.05    1.12
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# don't name this chunk! some intricacies with Quarto: do not name chunks with tables in them

model_squares_table <- tidy(model_squares) %>%
  # round the sum of squares and mean squares columns to have 5 digits (could be less)
  mutate(across(sumsq:meansq, ~ round(.x, digits = 2))) %>%
  # round the F-statistic to have 1 digit
  mutate(statistic = round(statistic, digits = 1)) %>%
  # replace the very very very small p value with < 0.001
  mutate(p.value = case_when(
    p.value < 0.001 ~ "< 0.001"
  )) %>%
  # rename the length cell to be meaningful
  mutate(term = case_when(
    term == "length" ~ "Length (mm)",
    TRUE ~ term
  )) %>%
  # make the data frame a flextable object
  flextable() %>%
  # change the header labels to be meaningful
  set_header_labels(df = "Degrees of Freedom",
                    sumsq = "Sum of squares",
                    meansq = "Mean squares",
                    statistic = "F-statistic",
                    p.value = "p-value")

model_squares_table
```

term	Degrees of Freedom	Sum of squares	Mean squares	F-statistic	p-value
Length (mm)	1	1,432.29	1,432.29	1,280.8	< 0.001

term	Degrees of Freedom	Sum of squares	Mean squares	F-statistic	p-value
Residuals	288	322.05	1.12		

8. In 1-2 sentences, describe how the ANOVA table relates to the information you get from the summary() object.

The ANOVA table relates to the information from the summary() object because the it is created using the anova function which extracts summary information from the model object, including the degrees of freedom, sum of squares, mean squares, and the p-value. The ANOVA table uses the summary of the model object to understand if there is a significant relationship between the predictor variable and what you are trying to predict.

9. In 2-3 sentences, summarize your results in prose with in-text references to test results. Include all relevant information.

The results from this linear regression were that fish length can be used to predict fish weight. The null hypothesis was rejected because the p-value was <0.001. The high R^2 value explains 81.58% of the variance all fish weight observations can be predicted by the model. The low mean squared value of 1.12 supports the alternative hypothesis because on average the model only differs from the actual values by 1.12g. The scatter plot visually shows the observations are clustered along the regression line, indicating the regression line is a good fit. Analysis of variance, F(1,288) = 1280 p< 0.001, a = 0.05.

10. Create a visualization with model predictions and confidence intervals on top of the underlying data. Finalize your plot.

```
# extract model predictions using ggpredict
predictions <- ggpredict(modelobject, terms = "length")

predictions

# Predicted values of weight

length | Predicted |         95% CI
-----------------------------------
    50 |     -1.71 | [-2.12, -1.30]
    60 |      0.29 | [-0.02,  0.59]
    65 |      1.29 | [ 1.03,  1.54]
    75 |      3.29 | [ 3.12,  3.45]
    85 |      5.28 | [ 5.16,  5.41]
    95 |      7.28 | [ 7.12,  7.44]
```

```
   105 |      9.28 | [ 9.04,  9.53]
   120 |     12.28 | [11.88, 12.68]

plot_predictions <- ggplot(data = fish_clean,
                           aes(x = length, y = weight)) +
  # first plot the underlying data from fish_clean
  geom_point() +
  # then plot the predictions
  geom_line(data = predictions,
            aes(x = x, y = predicted),
            color = "green", linewidth = 1) +
  # then plot the 95% confidence interval from ggpredict
  geom_ribbon(data = predictions,
              aes(x = x, y = predicted, ymin = conf.low, ymax = conf.high),
              alpha = 0.2) +
  # theme and meaningful labels
  theme_bw() +
  # labeling the x and y axis
  labs(x = "Trout Perch length (mm)",
       y = "Trout Perch weight (g)",
       caption = "Figure 2. An increase in fish length (mm) does predict an
increase in fish weight (g)") +
  #adjusting caption
        theme(
    plot.caption = element_text(hjust = 0))

plot_predictions
```

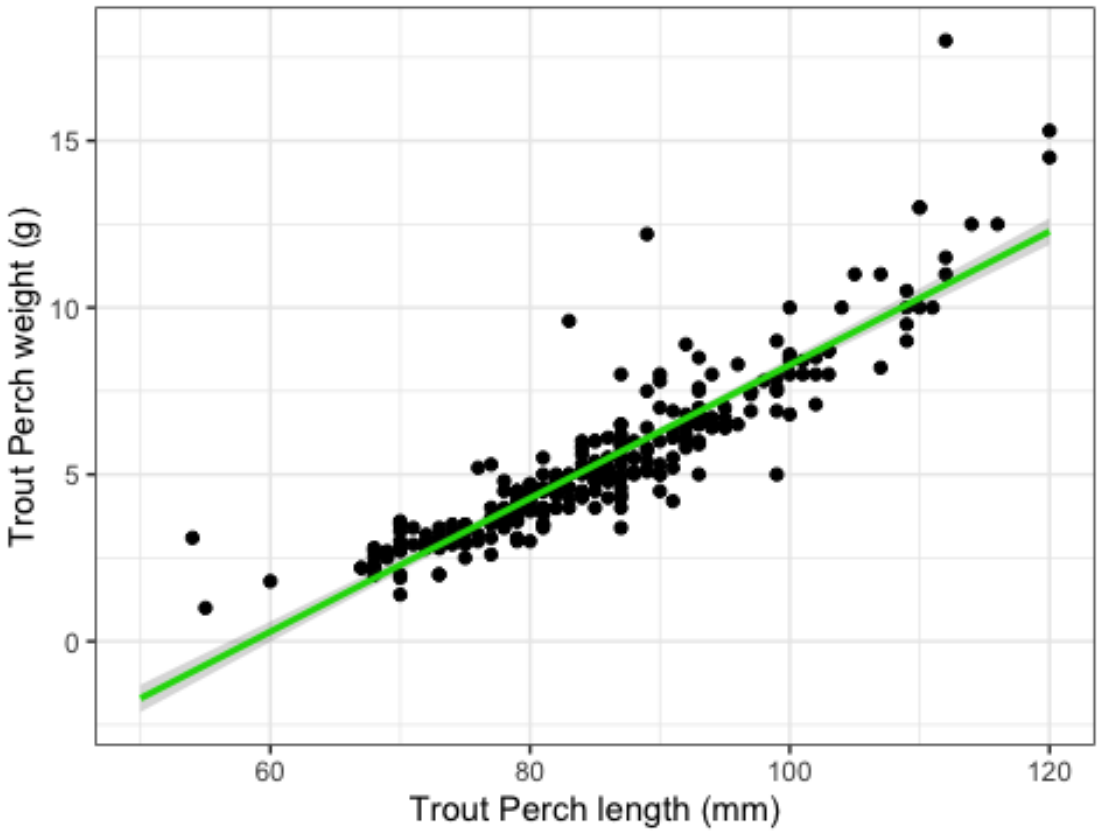


Figure 2. An increase in fish length (mm) does predict an increase in fish weight (g)