Homework 4

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Link to github repository:

https://github.com/v-yc/ENVS-193DS_homework-04_Yang-Victoria

1. Setup

Load in required packages.

```
library(tidyverse)
library(here)
library(performance)
library(broom)
library(flextable)
library(ggeffects)
library(car)
library(naniar)
```

Read in the data and subset data of interest (length and weight of trout perch species).

```
# read in data
fish <- read_csv(here("data", "knb-lter-ntl.6.34", "ntl6_v12.csv")) %>%

  # only include troutperch species
  filter(spname == "TROUTPERCH") %>%

  # select the columns of interest
  select(length, weight)
```

2. Initial data visualization

In mathematical terms:

- The null hypothesis is that the slope of the linear model is 0 ($\beta_1 = 0$).
- The alternative hypothesis is that the slope of the linear model is not 0 ($\beta_1 \neq 0$).

In biological terms,

- The null hypothesis is that fish length is not a good predictor of fish weight for trout perch.
- The alternative hypothesis is that fish length is a good predictor of fish weight for trout perch.

Visualize the missing data:

```
gg_miss_var(fish)
```

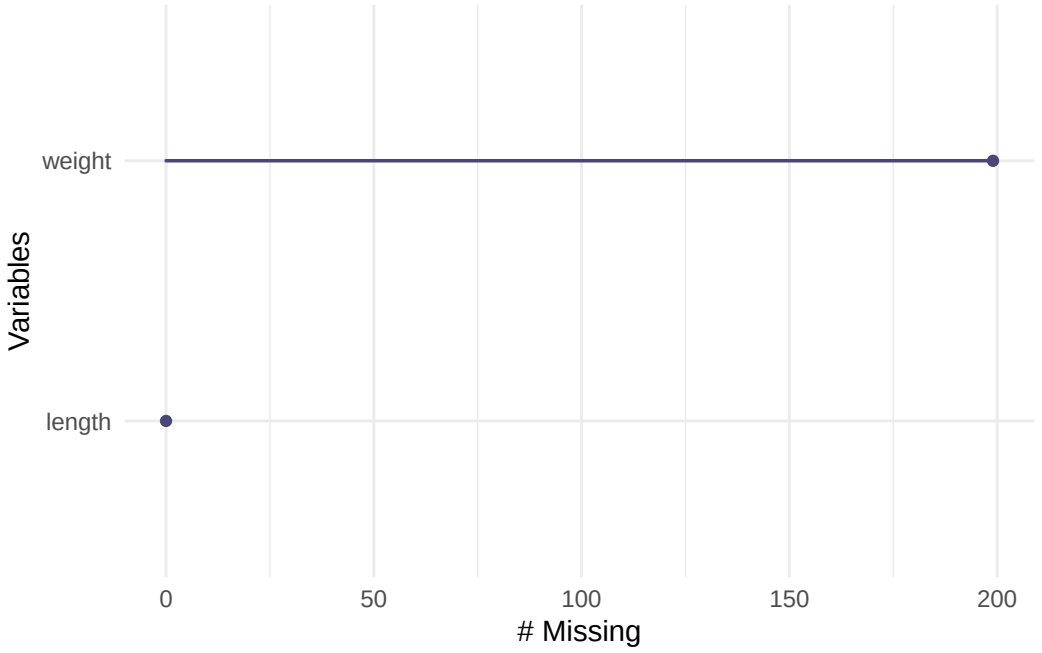


Figure 1: There are about 200 missing data points for the weight variable, which is significant because there are only 489 observations in this dataset. This would mean that about 41% of the data is missing.

However, we do not know why these data points are missing because this is from an online data set. Additionally, there are still 290 observations left if we remove the missing data, which is a large sample size. As a result, I will remove the NA values by subsetting the data for this analysis because there will be enough data points left to make a good model.

```
fish_subset <- fish %>%

  # drops rows with NA values in the columns specified
  drop_na(length, weight)
```

3. Create a linear model and check assumptions

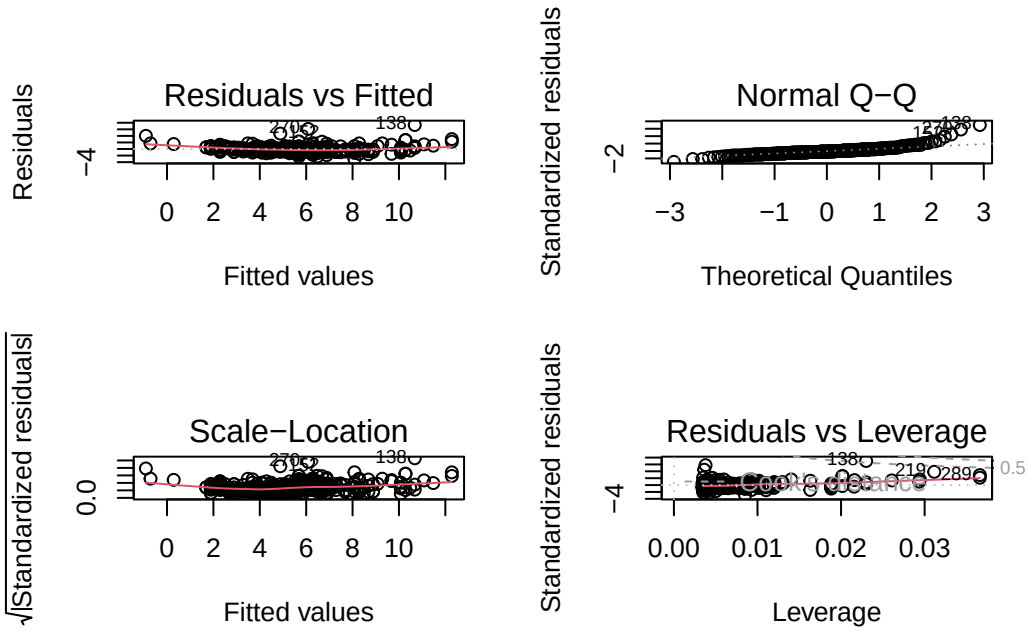
Creating a linear model where fish length is the predictor variable and fish weight is the response variable:

```
modelobject <- lm(weight ~ length, data = fish_subset)
```

Check assumptions by plotting residual diagnostic plots.

```
# display diagnostic plots in a 2x2 grid
par(mfrow = c(2, 2))

# plot diagnostic plots to check linear model assumptions
plot(modelobject)
```



Interpretation of diagnostic plots:

- Residuals vs fitted plot: The red line is mostly straight and the residuals are mostly evenly distributed about the dotted line. Consequently, I would say the residuals look mostly homoskedastic.
- Normal Q-Q plot: The majority of the points fall on the dotted line so I would say the residuals look mostly normally distributed.
- Scale-location plot: The data points are evenly distributed about the red line and the red line looks somewhat straight. Consequently, I would say that the residuals are homoskedastic.
- Residuals vs Leverage: There are 3 points labeled and one of them is outside the dotted line, which suggests that it might be an outlier that influences the model. Since only one data point is outside the dotted lines and I do not know where it came from, I think it would be safer to keep it in the model.

Create a summary table

First, create a model summary to get the information of interest. The summary() function gives us the coefficients (slope and y-intercept) of the linear model, the standard error of the coefficients, multiple R2 (quantifies how well the independent variable predicts the dependent variable), and the p-value for the model fit.

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

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

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
Multiple R-squared:  0.8164,    Adjusted R-squared:  0.8158
F-statistic:  1281 on 1 and 288 DF,  p-value: < 2.2e-16
```

Then, create an ANOVA table and a summary statistics table to report the ANOVA results.

```r
# store the ANOVA table as an object
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
# make the summary statistics table
model_squares_table <- tidy(model_squares) %>%

  # round the sum of squares and mean squares to 2 digits
  mutate(across(sumsq:meansq, ~ round(.x, digits = 1))) %>%

  # round the F-statistic to 1 digit
  mutate(statistic = round(statistic, digits = 1)) %>%

  # replace the small p values with < 0.001
  mutate(p.value = case_when(p.value < 0.001 ~ "< 0.001")) %>%

  # make the data frame a flextable object
  flextable() %>%

  # change header labels
  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-statisticp-value
length	1	1,432.3	1,432.3	1,280.8< 0.001
Residuals	288	322.1	1.1	

The ANOVA has information on the degrees of freedom, f-statistic, and p-value of the model like the summary() object. However, it also includes information on the sum of squares and mean squares values, which is useful for understanding where the F-statistic, p-value and R2 values from the summary() object come from.

Results:

A linear model and F-test with a significance level of 0.05 was used to test the null hypothesis that there is no significant relationship between fish length and fish weight for trout perch. Based on our data with a sample size of 290 observations, fish length is a good predictor of fish weight for trout perch across all sample years ($F_{1,288} = 1280.8$, $p < 0.001$, $R2 = 0.8$).

The equation of the linear model is y = -11.7 + 0.2x so for each 1 mm increase in fish length, we expect a 0.2 g increase in fish weight.

Visualize model

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

# visualize the model and include predictions and confidence intervals

plot_predictions <- ggplot(data = fish_subset, aes(x = length, y = weight)) +

  # plot the underlying data
  geom_point() +

  # plot the predictions
  geom_line(data = predictions,
            aes(x = x, y = predicted),
            color = "red",
            linewidth = 1) +

  # plot the 95% confidence interval
  geom_ribbon(data = predictions,
              aes(x = x, y = predicted, ymin = conf.low, ymax = conf.high),
              alpha = 0.2) +

  # add a theme
  theme_gray() +

  # add labels
  labs(x = "Trout Perch Length (mm)",
       y = "Trout Perch Weight (g)")

plot_predictions
```

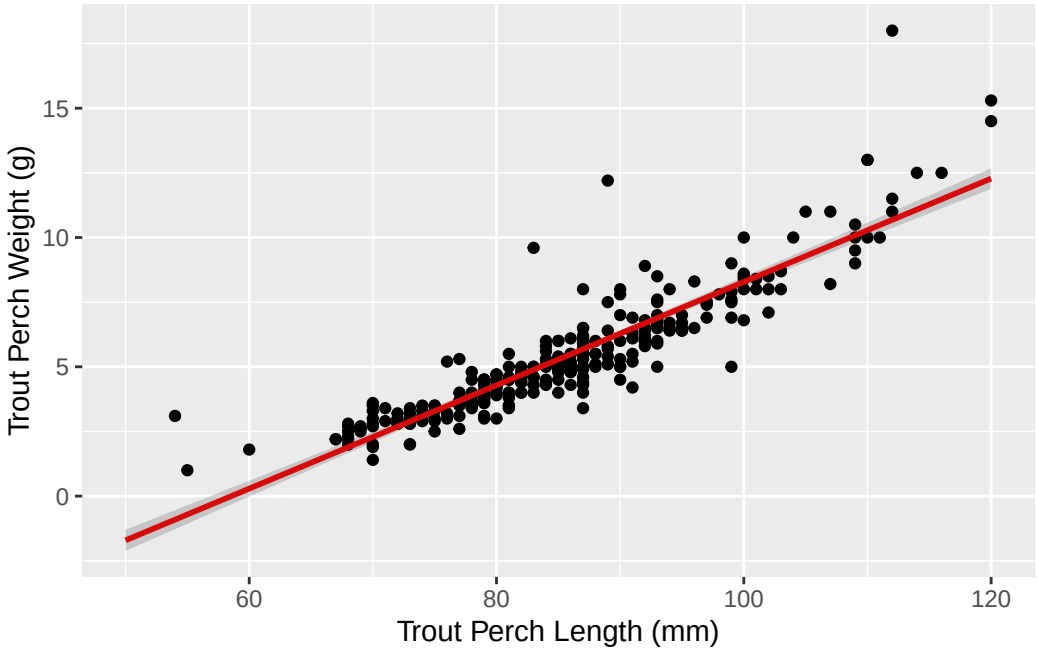


Figure 2: Linear model of trout perch weight as a function of trout perch length. The black dots represent individual data points, the red line represents the linear model, and the gray area around the line represents a 95% confidence interval.