Lab 8

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The goal of this lab is learn more about exploring missing data and writing modular code.

The Data

This lab's data concerns mark-recapture data on four species of trout from the Blackfoot River outside of Helena, Montana. These four species are **rainbow trout (RBT)**, **westslope cutthroat trout (WCT)**, **bull trout**, and **brown trout**.

Mark-recapture is a common method used by ecologists to estimate a population's size when it is impossible to conduct a census (count every animal). This method works by *tagging* animals with a tracking device so that scientists can track their movement and presence.

Data Exploration

The measurements of each captured fish were taken by a biologist on a raft in the river. The lack of a laboratory setting opens the door to the possibility of measurement errors.

1a. Let's look for missing values in the dataset. Output ONE table that answers BOTH of the following questions:

- **How many observations have missing values?**
- **What variable(s) have missing values present?**

> You should use `across()`!

```
fish |>
  summarise(across(.cols = 1:7, ~sum(is.na(.))))
```

```
# A tibble: 1 x 7
   trip  mark length weight  year section species
  <int> <int>  <int>  <int> <int>   <int>   <int>
1     0     0      0   1796     0       0       0
```

1b. Using `map_int()`, produce a nicely formatted table of the number of missing values for each variable in the `fish` data that displays the same information as 1a

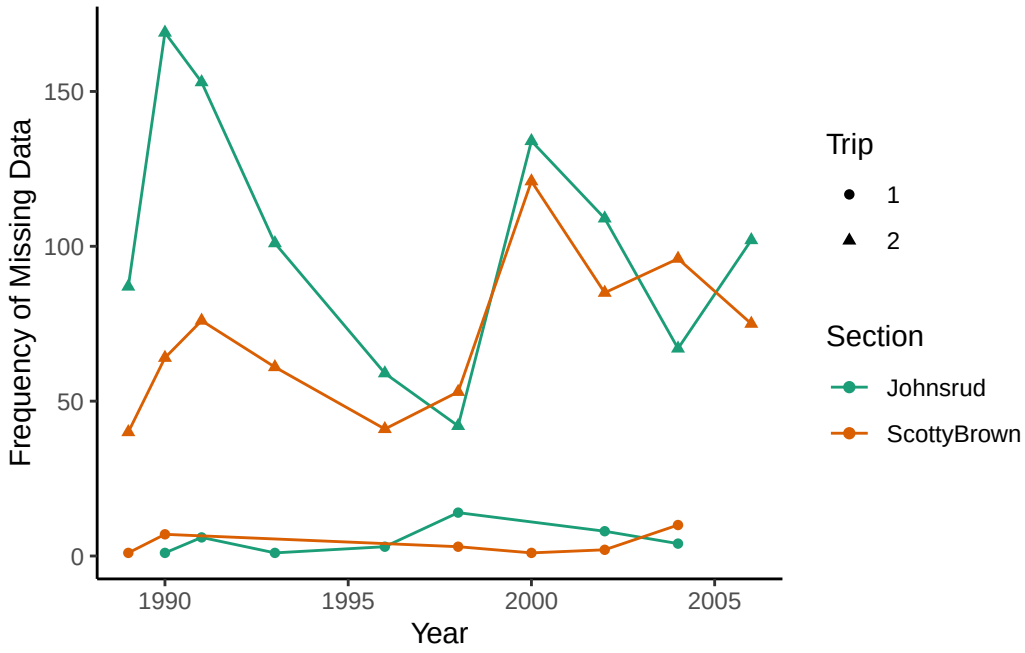
```
fish |>
  map_int(~sum(is.na(.)))
```

```
   trip    mark  length  weight    year section species
      0       0       0    1796       0       0       0
```

2. Create ONE thoughtful visualization that explores the frequency of missing values across the different years, sections, and trips.

```
fish |>
  filter(if_any(.cols = 1:7, is.na)) |>
  group_by(year, section, trip) |>
  summarise(n = n()) |>
  ggplot(aes(x = year, y = n, color = section, shape = factor(trip))) +
  geom_point() +
  geom_line() +
  labs(shape = "Trip", color = "Section", x = "Year", y = "Frequency of Missing Data") +
  scale_color_brewer(palette = "Dark2") +
  theme_classic()
```

```
`summarise()` has grouped output by 'year', 'section'. You can override using
the `.groups` argument.
```



Rescaling the Data

If I wanted to rescale every quantitative variable in my dataset so that they only have values between 0 and 1, I could use this formula:

$$y_{scaled} = \frac{y_i - min\{y_1, y_2, ..., y_n\}}{max\{y_1, y_2, ..., y_n\} - min\{y_1, y_2, ..., y_n\}}$$

I might write the following `R` code to carry out the rescaling procedure for the `length` and `weight` columns of the `BlackfoorFish` data:

```
fish |>
  mutate(length = (length - min(length, na.rm = TRUE)) /
           (max(length, na.rm = TRUE) - min(length, na.rm = TRUE)),
         weight = (weight - min(weight, na.rm = TRUE)) /
           (max(weight, na.rm = TRUE) - min(length, na.rm = TRUE)))
```

This process of duplicating an action multiple times can make it difficult to understand the intent of the process. *Additionally, it can make it very difficult to spot mistakes.*

3. What is the mistake I made in the above rescaling code?

You reassigned the scaled values to the original. Instead a new variable should be created for scaled value.

When you find yourself copy-pasting lines of code, it's time to write a function, instead!

4. Transform the repeated process above into a `rescale_01()` function. Your function should...

- **... take a single vector as input.**
- **... return the rescaled vector.**

```
rescale_01 <- function(x){
  if(!is.numeric(x) | length(x) <= 1) {
    stop(domain = "please enter a numeric vector with length > 1")
    }
  x1 = (x - min(x, na.rm = TRUE)) / (max(x, na.rm = TRUE) - min(x, na.rm = TRUE))
  x1
}
```

> Efficiency
>
> Think about the efficiency of the function you wrote. Are you calling the **same** function multiple times? You might want to look into the `range()` function.

5. Let's incorporate some input validation into your function. Modify your previous code so that the function stops if ...

- **... the input vector is not numeric.**
- **... the length of the input vector is not greater than 1.**

> Modify Previous Code
>
> Do not create a new code chunk here – simply add these stops to your function above!

Test Your Function

6. Run the code below to test your function. Verify that the maximum of your rescaled vector is 1 and the minimum is 0!

```
x <- c(1:25, NA)

rescaled <- rescale_01(x)
min(rescaled, na.rm = TRUE)
```

```
[1] 0
```

```
max(rescaled, na.rm = TRUE)
```

```
[1] 1
```

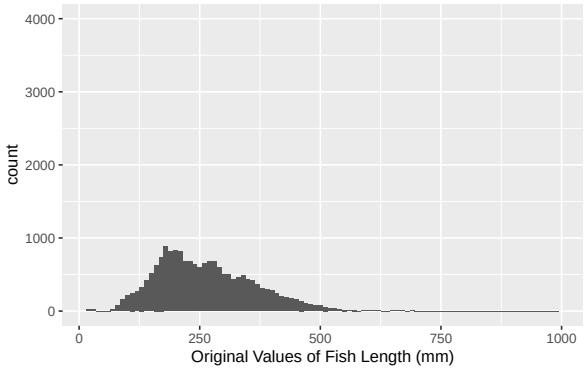
Next, let's test the function on the `length` column of the `BlackfootFish` data.

7. The code below makes a histogram of the original values of `length`. Add a plot of the rescaled values of `length`. Output your plots side-by-side, so the reader can confirm the only aspect that has changed is the scale.

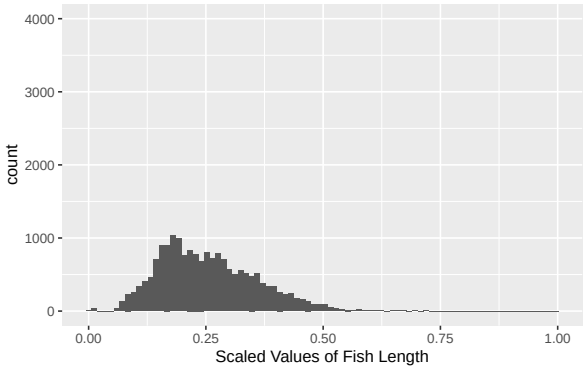
> **Warning**
>
> This will require you to call your `rescale_01()` function within a `mutate()` statement in order to create a `length_scaled` variable.

```
p1 <- fish |>
  ggplot(aes(x = length)) +
  geom_histogram(binwidth = 10) +
  labs(x = "Original Values of Fish Length (mm)") +
  scale_y_continuous(limits = c(0,4000))

# Code for Q7 plot.

p2 <- fish |>
  mutate(length = rescale_01(length)) |>
  ggplot(aes(x = length)) +
  geom_histogram( binwidth = 0.012) +
  labs(x = "Scaled Values of Fish Length") +
  scale_y_continuous(limits = c(0,4000))

p1
p2
```

> **Tip**
>
> 1. Set the y-axis limits for both plots to go from 0 to 4000 to allow for direct comparison across plots.
> 2. Pay attention to `binwidth`!



(a) Original Values



(a) Scaled Values

3. Use a Quarto code chunk option to put the plots side-by-side.

Challenge: Use Variables within a Dataset

Suppose you would like for your `rescale()` function to perform operations on a **variable within a dataset**. Ideally, your function would take in a data frame and a variable name as inputs and return a data frame where the variable has been rescaled.

8. Create a `rescale_column()` function that accepts two arguments:

- **a dataframe**
- **the name(s) of the variable(s) to be rescaled**

The body of the function should call the original `rescale_01()` function you wrote previously. Your solution MUST use one of the `rlang` options from class.

Tip

If you are struggling with this task, I recommend looking back over the data frame functions section of R for Data Science!

```
rescale_column <- function(df, col.names){
  l = length(col.names)
  rows <- dim(df)[1]
  out = matrix(NA, nrow = rows, ncol = l)
  for(i in 1:l){
    col <- col.names[i]
    out[,i] = rescale_01(df[[col]])
```

```
  }
  colnames(out) = col.names
  data.frame(out)
}
```

9. Use your `rescale_column()` function to rescale *both* the `length` and `weight` columns.

> ⚠ Warning
>
> I expect that you carry out this process by calling the `rescale_column()` function only ONE time!

```
head(rescale_column(fish, col.names = c("length", "weight")), 10)
```

```
      length      weight
1  0.2804124 0.037417148
2  0.2804124 0.040624332
3  0.2773196 0.052384007
4  0.3154639 0.058798375
5  0.3051546 0.064143682
6  0.3577320 0.081248664
7  0.2608247 0.036348086
8  0.1484536 0.008552491
9  0.2030928 0.017104982
10 0.1453608 0.007483430
```