Zooming Through Data

Directions: Follow along with the slides and answer the questions in **BOLDED** font in your journal.

Data with Clarity

- Previously, we've looked at graphs of entire variables (By looking at all of their values).
 - Doing this is helpful to get a big picture idea of our data.
- In this lab, we'll learn how to zoom in on our data by learning how to subset.
 - We'll also learn a few ways to manipulate the plots we've been making to make them easier to use for analyses.
- Import the data from your class' Food Habits campaign and name it food.

Splitting data sets

- In lab 1B, we learned that we can facet (or split) our data based on a categorical variable.
- Use the dotPlot() function to create a dotPlot of the amount of sugar in our food data.
 - The code to create a dotPlot is exactly like you'd use to make a histogram.
 - Make sure to use a capital P in dotPlot.
- Split the dotPlot in two by faceting on our observations' salty/sweet variable.
 - Describe how R decides which observations go into the left or right plot.
 - What does each *dot* in the plot represent?

Altering the layout

- It would be much easier to compare the sugar levels of salty and sweet snacks if the dotPlots were stacked on top of one another.
- We can change the layout of our separated plots by including the layout option in our dotPlot function.
 - Add the following option to the code you used create the dotPlot split by salty_sweet

layout = c(1,2)

• *Hint*: Use your history pane to see how we handled options with the bargraph function. Use a similar syntax to add the layout option to the dotPlot function.

Subsetting

- Subsetting is a term we use to describe the process of looking at only the data that conforms to some set of rules:
 - Geologists may subset earthquake data by looking at only large earthquakes.
 - Stock market traders may subset their trading data by looking only at the previous day's trades.
- There's many ways to subset data using RStudio, we'll focus on learning the most common methods.

The subset function

- Creating two plots, one for salty and one for sweet is useful for comparing salty and sweet But what if we want to examine only one group by itself?
- Start by creating a subset of the data:
 - Fill in the blanks below with the data and variable names needed to subset our food data based on people who ate Salty snacks:

```
food_salty <- subset(____ , ___ == "Salty")</pre>
```

• View food_salty and write down the number of observations in it. Then use the subset data to make a dotPlot of the sodium in our Salty snacks.

So what's really going on?

- Coding in R is really just about supplying directions in a way that R understands.
 - We'll start by focusing on everything to the right of the "<-" symbol

```
food_salty <- subset(____ , ___ == "Salty")
```

- subset() tells R that we're going to look at only the values in our data that follow a rule.
- The first blank should be the data we're going to filter down into a smaller set (Based on our rule).
- salty_sweet == "Salty" is the rule to follow.

3 parts of defining rules

- We can decompose our rule, salty_sweet == "Salty", into 3 parts:
 - (1) salty_sweet, is the particular variable we want to use to select our subset.
 - (2) "Salty", is the *value* of the variable that we want to select. We only want to see data with the value Salty for the variable salty_sweet.
 - (3) == describes how we want to relate our variable (salty_sweet) to our value ("Salty"). In this case, we want values of salty_sweet that are exactly equal to "Salty".
- Notice: Values (that are also words) have quotation marks around them. Variables do not.

More on ==

- We can use the head() function to help us see what's happening when we write salty_sweet == "Salty".
 - head() returns the values of the first 6 observations.
 - The tail() function returns the last 6 observations.
- Run the following code and answer the question below:

```
head(salty_sweet == "Salty", data = food)
```

• What do the values TRUE and FALSE tell us about how our *rule* applies to the first six snacks in our data? Which of the first six observations were Salty?

Saving values

- To use our subset data we need to save it first.
 - When we save something in R what we are really doing is giving a value, or set of values, a specific name for us to use later.
- The arrow <- is called the "assignment" operator. It assigns names (on the left) to values (on the right)
 - We now focus on everything to the left of, and including, the "<-" symbol

```
food_salty <- subset(____ , ___ == "Salty")</pre>
```

Saving our subset

```
food_salty <- subset(____ , ___ == "Salty")</pre>
```

- This code then:
 - takes our subset data, (everything to the right of "<-") ...
 - and assigns the subset data, by using the arrow "<-" ...
 - the name food_salty.
- We can now use food_salty to do anything we could do with the regular food data ...
 - but only including those snacks who reported being Salty.

Put it all together

- Use an appropriate dotPlot to answer each of the following questions:
 - About how much fat does the typical sweet snack have?
 - How does the typical amount of fat compare when healthy_level < 3 and when healthy_level > 3?
- It can sometime be helpful to change the number of intervals, or bins, used in dotPlots and histograms.
 - To change the number of *intervals* in your plots, include the nint option. For instance, to have a plot with 3 bins, use nint = 3. To have a plot with 30 bins, use nint = 30.