Intro to R

Introduction

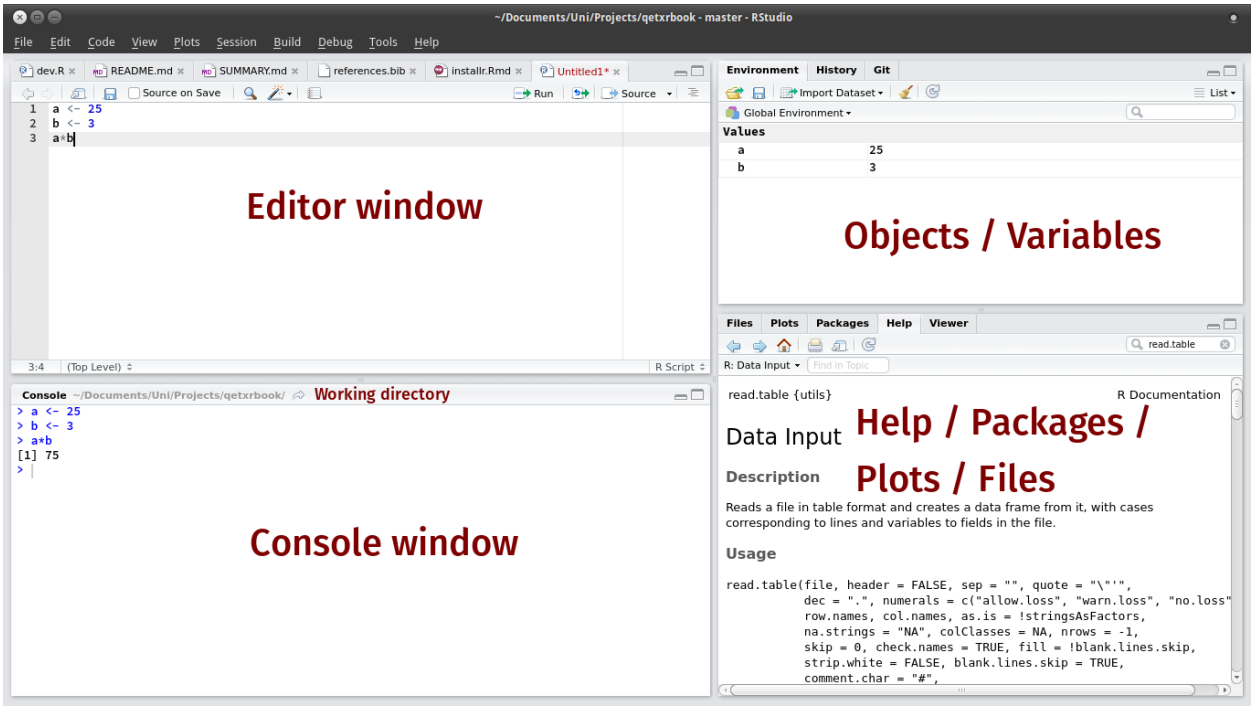
The term `R` is used to refer to both the programming language as well as the software that interprets the scripts written using it. The learning curve may be steeper than with other statistical software, but with `R` the results of your analysis or your plot does not rely on remembering what order you clicked on things, but instead on the written commands you generated. In `R` you will work in scripts or with dynamic documents, with scripts within them (Rmd or Rnw files). Scripts may feel strange at first, but they make the steps you used in your analysis clear for both you and for someone who wants to give you feedback.

RStudio is a free computer application that allows you access to the resources of `R`, while providing you with a comfortable working environment. There are many ways you can interact with `R`, but for many reasons RStudio has become the most popular. To function correctly, RStudio uses `R` behind the scenes, hence both need to be installed on your computer. Both `R` and `RStudio` are cross-platform, so that everyone's versions look and operate the same regardless of their operating system!

For our use of RStudio the desktop version will suffice. There are many videos and guides for installation. See the Stat 217 textbook (pages 12-14) here: https://scholarworks.montana.edu/xmlui/bitstream/handle/1/2999/Greenwood_Book.pdf?sequence=3&isAllowed=y_

RStudio has a panel of 4 windows, where each can be viewed at the same time and has multiple tabs available.

- the **Editor** for your scripts and documents (top-left)
- the `R` **Console** (bottom-left)
- your **Environment (Objects/Variables)/History** (top-right)
- and your **Files/Plots/Packages/Help/Viewer** (bottom-right).



Work Flow in R

It is good code writing and file storage practice to keep a set of all related data, analysis, plots, documents, etc. in the same folder. When all the pieces are in the same folder, it allows for a clean workflow and working directory. When you are executing code for a document/script R will search for things (such as data) in the same folder as the document/script, which is called a *relative path*. If you are having trouble loading your data into RStudio and you have saved your files in this way, it is possible that R is searching in the wrong location and you need to change your working directory.

The easiest way to do this is,

- click on the **Session** drop-down from the top of the screen,
- select the **Set Working Directory** tab,
- select **To Source File Location**.

After this process R will be searching for objects (such as data) in the same folder that the document/script you're working on is saved in.

Working in R

RStudio allows for you to execute commands directly from the code chunk in the document by using the **Ctrl + Enter** (on Macs, **Cmd + Return**) shortcut. If you place your curser on the line in the code chunk that you would like to run and hit this shortcut, R will execute that line(s) of code for you. Alternatively, you can also execute code in the console (where the output of the commands pops up). The difference between running code in the console and in the document is that any code you execute in the console will be lost once you close your R session. If you type code into the document's code chunks, it will be saved when you close your R session. Because we want to be able to go back and re-run our code after today's workshop, it is better to type the command we want R to run in the document and save it!

If R is ready to accept commands, the R console (in the bottom-left) will show a > prompt. When R receives a command (by typing, copy-pasting, or using the shortcut), it will execute it, and when finished will display the results and show the > symbol once again.
If R is still waiting for you to provide it with additional instructions, a + will appear in the console. This should tell you that you didn't finish your command. You could have forgotten to close your parenthesis or a quotation. If this happens and you are unsure of what went wrong, click inside the console and hit the Esc key. Then you can start over and figure out where you went wrong!

Calculator

Practice: Enter each of the following commands and confirm that the response is the correct answer.

```
1 + 2

16*9

sqrt(2)

20/5

18.5 - 7.21
```

```r
3 %% 2 ## what is this doing?
```

Creating Objects

These operations, however, are not very interesting. To do more useful things in R, we need to assign values to an object. To create an object, we tell R the object's name, followed by an assignment arrow (<-), and finally the value of the object. This would look something like this:

```r
x <- 6
```

Once we execute/run this line of code, we notice that a new object appears in our environment window. This window shows all of the objects that you have created during your R session. The value of x appears next to it, since it is a scalar.

Remarks:

- In the above code <- is the assignment operator. It assigns values on the right to objects on the left. So, after executing `year <- 3`, the value of `year` is 6. The arrow can be read as 3 goes into year. For historical reasons, you can also use = for assignments, but not in every context. Because of the slight differences in syntax, it is good practice to always use <- for assignments.
  - In RStudio, typing Alt at the same time as the - key will write <- in a single keystroke. Neat! ==
- There are a few simple rules that apply when creating the same of a new object (like we did above):
  - R is case sensitive, so if you name your variable `cat` but then try to run the code `Cat + 2`, you will get an error saying that `Cat` does not exist
  - You also want your object's name to be explanatory, but not too long. Think `current_temperature` verses `current_temp`. Do you really want to type out temperature every time?
  - Finally, you cannot begin any object's name with a number. You can end a name with a number (e.g. clean_data2), but does that give you much information about what is in the contents of `clean_data2` relative to `clean_data`?
  - The name cannot contain any punctuation symbols, except for `.` and `_` (`.` is not recommended)
  - You should not name your object the same as any common functions you may use (`mean`, `sd`, etc.)

Clean Code

Yes, writing code may be completely new to you, but there is a difference between code that looks nice and code that does not. Generally, object names should be nouns and function names should be verbs. It is also important that your code looks presentable, so that a friend/college/professor can read it and understand what you are doing. For these reasons, there are syle guides for writing code in R. The two main style guides are Google's (link) and the slightly more comprehensive Tidyverse style guide (link). Optionally, you can install `lintr` to automatically check and correct for issues in your code styling. More on packages to come!

Working with Objects

When you assign a value to an object (like we did previously) R does not output anything by default. If you enclose the code you wrote in parenthesis, then R will output the value of the object you created.

```
(x <- 6)
```

```
## [1] 6
```

Once the object has been created, you can use it! Run the following lines of code:

```
2.2 * x
```

```
## [1] 13.2
```

```
4 + x
```

```
## [1] 10
```

```
x %% 3
```

```
## [1] 0
```

We can also overwrite an object's value, so that it has a new value. In the code below we give `x` a new value of 2 and use that to create a new object `y`.

```
x <- 2

y <-  x + 6
```

Exercise 1: Change the value of `x` to back to 6 and see what the value of `y` is. Did it change from before? Is the value of `y` 8 or 12?

Working with Different Data Types

A vector is the basic data type in `R`. A vector is a series of values, which can be either numbers or characters. `R` can tell that you are building a vector when you use the `c()` function, which concatinates a series of numbers or characters together.

```
temps <- c(50, 55, 60, 65)
temps
```

```
## [1] 50 55 60 65
```

To make a vector of characters, you are required to use quotation marks (" ") to indicate to `R` that the value you are using is not an object.

```
animals <- c("cat", "dog", "bird", "fish")
animals
```

```
## [1] "cat"  "dog"  "bird" "fish"
```

Important features of a vector is the type of data they store. Run the following lines of code and decide what type of data the vectors contain.

```
class(temps)
```

```
## [1] "numeric"
```

```
class(animals)
```

```
## [1] "character"
```

Exercise 2: Create a vector that contains decimal valued numbers. Then check what data type does that vector contain?

```
# Exercise 2 code here!
```

Another possible data type is a logical (boolean) value. This type of vector takes on values of `TRUE` and `FALSE`. But, we said that vectors could only be numbers or characters. If `TRUE` and `FALSE` don't have quotations around them, then they aren't characters. So, then they must be numbers. What numbers do you think they are?

```
logic <- c(TRUE, FALSE, FALSE, TRUE)

class(logic)
```

```
## [1] "logical"
```

Exercise 3: What happens when we try to mix different data types into one vector? Speculate what will happen when we run each of the following lines of code:

```
num_char <- c(1, 2, 3, "a")

num_logic <- c(1, 2, 3, FALSE)

char_logic <- c("a", "b", "c", TRUE)

guess <- c(1, 2, 3, "4")
```

In each of these vectors, the two types of data were *coerced* into a single data type. This happens in a hierarchy, where some data types get preference over others. Can we draw a diagram of the hierarchy?

Importing Data

- Use the **Import Dataset** button in the **Environment** tab
- Choose the **From CSV** option
- Click on the **Browse** button
- Direct the computer to where you saved the BlackfootFish data file, click **open**
- It will bring up a preview of the data
- Click on the **Import** button

Notice the code that outputs in the console (the bottom left square). This is the code that you could have typed in the code chunk below to import the data yourself. Copy and paste the code that was output in the code chunk below.

```
# copy and paste the code that was used by R to import the data
# be careful to only copy the code that is next to the > signs!
```

Structure of Data

The data we will use is organized into data tables. When you imported the BlackfootFish data into RStudio was saved as an object. You are able to inspect the structure of the BlackfootFish object using functions built in to `R` (no packages necessary).

Run the following code. What is output from each of the following commands?

```
class(BlackfootFish)
```

```
## [1] "data.frame"
```

```
dim(BlackfootFish)
```

```
## [1] 18352     7
```

```
## What is the first number represent? What about the second number?

names(BlackfootFish)
```

```
## [1] "trip"    "mark"    "length"  "weight"  "year"    "section" "species"
```

```
str(BlackfootFish)
```

```
## 'data.frame':    18352 obs. of  7 variables:
##  $ trip   : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ mark   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ length : num  288 288 285 322 312 363 269 160 213 157 ...
##  $ weight : num  175 190 245 275 300 380 170 40 80 35 ...
##  $ year   : int  1989 1989 1989 1989 1989 1989 1989 1989 1989 1989 ...
##  $ section: chr  "Johnsrud" "Johnsrud" "Johnsrud" "Johnsrud" ...
##  $ species: chr  "RBT" "RBT" "RBT" "RBT" ...
```

```
summary(BlackfootFish)
```

```
##       trip            mark             length          weight
```

```
##  Min.   :1.000   Min.   :0.00000   Min.   : 16.0   Min.   :   0.0
##  1st Qu.:1.000   1st Qu.:0.00000   1st Qu.:186.0   1st Qu.:  65.0
##  Median :2.000   Median :0.00000   Median :250.0   Median : 150.0
##  Mean   :1.501   Mean   :0.09285   Mean   :262.3   Mean   : 246.2
##  3rd Qu.:2.000   3rd Qu.:0.00000   3rd Qu.:330.0   3rd Qu.: 330.0
##  Max.   :2.000   Max.   :1.00000   Max.   :986.0   Max.   :4677.0
##                                                    NA's   :1796
##       year        section            species
##  Min.   :1989   Length:18352       Length:18352
##  1st Qu.:1991   Class :character   Class :character
##  Median :1996   Mode  :character   Mode  :character
##  Mean   :1997
##  3rd Qu.:2002
##  Max.   :2006
##
## What is the data type of each variable in our dataset?
```

When we inspect dataframes, or other objects in `R`, there are some general functions that are useful to check the content/structure of the data. Here are some:

- size:
  - `dim(data)`: rows and columns
  - `nrow(data)`: number of rows
  - `ncol(data)`: number of columns
- content:
  - head(data): first 6 rows
  - tail(data): last 6 rows
  - View(data): opens viewer window in separate tab
- names:
  - colnames(data): column names of dataframe
  - rownames(data): row names of dataframe
- summary of content:
  - `str(data)`: structure of object and information about the columns
  - `glimpse(data)`: similar imformation to `str`, but neater output
  - `summary(data)`: summary statistics for each column

Dataframes

What is a dataframe? A dataframe is a type of `R` object and is the *de facto* structure of tabular data. You can create dataframes by hand, but most of us do not use `R` to input our data by hand. Instead, we import our data using `R` commands that read in spreadsheets (`read.csv`, `read_xls`, etc.). A dataframe is a set of columns, where each column is a vector. Thus, columns have the same data type *within* the column, but potentially different data types *across* columns.

For example, the columns `trip`, `mark`, and `year` are integers (whole numbers), `weight` and `length` are numeric (numbers with decimals), and `section` and `species` are characters.

Extracting Data

If we were interested in accessing a specific variable in our dataset, we can use the `$` command. This command extracts the specified variable (on the right of the `$` sign) from the dataset. When this is extracted, `R` views the variable as a vector of entries, which is what the [1:18352] refers to.

```
years <- BlackfootFish$year
## extracts year from the dataset and saves it into a new variable named year

str(years) ## using the new variable (remember case matters!)
```

```
##  int [1:18352] 1989 1989 1989 1989 1989 1989 1989 1989 1989 1989 ...
```

```
## How would you determine how long the vector is?
```

Another method for accessing data in the dataset is using matrix notation ([row, column]). If you look to your right in the **Environment** window, you notice that RStudio tells you the dimensions of the BlackfootFish data. You can (roughly) view the dataset as a matrix of entries, with variable names for each of the columns. I could instead use bracket notation to perform the same task as above, using the following code.

```
years <- BlackfootFish[, 5] ## This takes ALL rows of data but only the fifth column
## Same as years <- BlackfootFish[1:18352, 5]

str(years)
```

```
##  int [1:18352] 1989 1989 1989 1989 1989 1989 1989 1989 1989 1989 ...
```

Practice:

The following is a preview of the matrix `x`:

```
##      [,1] [,2] [,3] [,4]
## [1,]    1    2    3    4
## [2,]    5    6    7    8
## [3,]    9   10   11   12
## [4,]   13   14   15   16
```

What would be output if you entered: `x[3, ]`?

What would you input to get an output of 4?

The following is a preview of the dataframe `df`:

```
##   x   y    z
## 1 H May 2010
## 2 N Oct 2015
## 3 T Mar 2018
## 4 W Aug 2017
## 5 V Feb 2019
```

What would you input to get an output of `2015`? Can you think of two ways to do it?

How would you pull off only columns `x` and `z`? Can you think of two ways to do it?

How would you modify the script below, to get an output of `[1] 22 24`?

```
s <- c(22, 24, 49, 18, 1, 6)
s[]
```

What would be output if you entered: `s[3, ]`?

What would you input to get an output of `[1] 22 49`? ?

Changing Data Type

The species and section variables were saved as characters, but they are actually factors. In the data section has two levels (Johnsrud and ScottyBrown) and species has four levels (RBT, WCT, Bull, and Brown). If we want R to view these variables as factors, we need to convert them to factors!

```
unique(BlackfootFish$species)
```

```
## [1] "RBT"   "WCT"   "Bull"  "Brown"
```

```
## tells you the unique values of species

unique(BlackfootFish$section)
```

```
## [1] "Johnsrud"    "ScottyBrown"
```

```
## tells you the unique values of section

BlackfootFish$species <- as.factor(BlackfootFish$species)
BlackfootFish$section <- as.factor(BlackfootFish$section)
```

There is also a function that will allow for you to specify the order of the levels of a factor! As we saw before, the `as.factor` function chooses the levels alphabetically. Suppose you would like for the species to be in the following order: Bull, Brown, RBT, and WCT.

Using the `factor` function this would look like:

```
BlackfootFish$species <- factor(BlackfootFish$species,
                                levels = c("Bull", "Brown", "RBT", "WCT"))
```

Practice:

Year was saved as an integer data type (1989 - 2006), but it is a categorical variable (a factor). Write the R code to convert year to a factor (as you did with section and species).

Now, verify that year is now viewed as a categorical variable, with the same levels as before. (hint: you have already used three functions that would do this for you)

What if you decide that you don't want year to be a factor and want to change it back to numeric? What happens if you use the `as.numeric()` function on the year variable?

Packages

As we mentioned previously, `R` has many packages, which people around the world work on to provide and maintain new software and new capabilities for `R`. You will slowly accumulate a number of packages that you use often for a variety of purposes. In order to use the elements (data, functions) of the packages, you have to first install the package (only once) and then load the package (every time).

We're going to install a few packages that are often used.

- Use the **Install** button in the **Packages** tab
- Type in `car` and `mosaic` into the blank line (separated by a comma)
- Check the **Install dependencies** box
- Click on the **Import** button

There will be a large amount of output coming out of the console. This output is `R` trying to download the package(s) you requested by contacting the mirror you chose for it to use when downloading (I chose Northern Michigan University). Once the computer has downloaded the packages, it will tell you that "`The downloaded binary packages are in`", followed by the location of the files.

Now that the files are downloaded, we need to load them in order to use them. The following code will load each package, please run it!

```
library(car)
```

```
## Loading required package: carData
```

```
library(mosaic)
```

```
## Loading required package: dplyr
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:car':
##
##     recode
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
## Loading required package: lattice
```

```
## Loading required package: ggformula
```

```
## Loading required package: ggplot2
```

```
## Loading required package: ggstance
```

```
##
## Attaching package: 'ggstance'
```

```
## The following objects are masked from 'package:ggplot2':
##
##     geom_errorbarh, GeomErrorbarh
```

```
##
## New to ggformula?  Try the tutorials:
##  learnr::run_tutorial("introduction", package = "ggformula")
##  learnr::run_tutorial("refining", package = "ggformula")
## Loading required package: mosaicData
## Loading required package: Matrix
## Registered S3 method overwritten by 'mosaic':
##   method                           from
##   fortify.SpatialPolygonsDataFrame ggplot2
##
## The 'mosaic' package masks several functions from core packages in order to add
## additional features.  The original behavior of these functions should not be affected by this.
##
## Note: If you use the Matrix package, be sure to load it BEFORE loading mosaic.
##
## Attaching package: 'mosaic'
## The following object is masked from 'package:Matrix':
##
##     mean
## The following object is masked from 'package:ggplot2':
##
##     stat
## The following objects are masked from 'package:dplyr':
##
##     count, do, tally
## The following objects are masked from 'package:car':
##
##     deltaMethod, logit
## The following objects are masked from 'package:stats':
##
##     binom.test, cor, cor.test, cov, fivenum, IQR, median,
##     prop.test, quantile, sd, t.test, var
## The following objects are masked from 'package:base':
##
##     max, mean, min, prod, range, sample, sum
```

Notice that when loading the `mosaic` package that there is a large amount of output. This output is telling you all of the other packages that are loaded with the `mosaic` package, because `mosaic` is dependent on them (`dplyr`, `lattice`, `ggformula`, `ggplot2`, etc.).

Finding Help

One of the chief reasons for `R`'s religious following is its wonderful documentation. If you know a function does what you want (say find the variance), but are not quite sure how it's spelled, what arguments it takes, or what package it lives in, don't fret! The `?` and `help()` commands are very powerful. For functions, placing the `?` before the name, will tell `R` to search for that name in all of the functions, in all of the packages you have installed.

- If it finds *one* **identical match**, it will display the help file for that function in the Help tab in the bottom-right corner.

- If it finds *more than one* **identical match**, it will display the functions, in their respective packages, that you have to choose from.

- If it find *no* **identical match**, it will tell you that "`No documentation for ____ in specified packages and libraries:,`" and suggests you use a `??` instead.
  - A `??` in front of the function name will search **all** of `R` for named functions similar to what you typed.
  - The output will tell you what package the function is in, as well as the function's name (`package::function`).

```
?str
help(str)

?Levels ##incorrect function name, case sensitive
??Levels ##looks through all installed packages for a match
```

If you would like help on a particular package, say one that you just downloaded, then you can use the same command(s) to get help.

```
?mosaic

help(mosaic)
```

Functions

In `R` there are both functions that are built in (require no package to be loaded), as well as functions that are housed within specific packages. You have already used a few built in functions to inspect the structure of the BlackfootFish data (`str`, `class`, `summary`). As we know, a function transforms an input into an output. You have to provide `R` with the inputs (arguments) required for the function to generate an output. The argument(s) inside a function happen after the `(` symbol. You know an object is a function when it is immediately followed by a `(` and the corresponding closing `)` comes after the arguments are complete. The output of a function does not have to be numerical and it doesn't have to be singular, it can be a set of things or a dataset.

Arguments describe the details of what a function is to do. Many functions take named arguments, but the arguments are assumed to follow the order the function expects (stated in the help file), if they are not named. When naming an argument, the name of the argument is followed by an `=` sign and then the value of the argument. Notice that here we are using the `=` to declare what value each argument is taking on, we **are not** creating a new variable with that value assigned to it.

Suppose we wanted to create a vector of 10 zeros. To do this, we would use both the `rep` function and the `c` function:

```
rep(0, times = 10) ## repeating 0 three times
```

```
##  [1] 0 0 0 0 0 0 0 0 0 0
```

```
rep(times = 10, 0) ## switching order of arguments
```

```
##  [1] 0 0 0 0 0 0 0 0 0 0
```

```r
rep(0, 10) ## no named arguments
```

```
##  [1] 0 0 0 0 0 0 0 0 0 0
```

```r
rep(10, 0) ## not what we wanted!
```

```
## numeric(0)
```

Now let's look over some other functions that are often used:

```r
mean(BlackfootFish$weight)  ## takes a numerical input, but there are NA's in our data

mean(BlackfootFish$weight, argument here! )  ## add in the argument that removes the NA's

median(BlackfootFish$species) ## gives an error because the input is not the correct data type

cor(BlackfootFish$length, BlackfootFish$weight) ## takes multiple inputs separated by a comma

## Does cor have an option to remove NA's?
```

As seen in the functions above, some functions have *optional* arguments. If they are not specified by the user, then they take on their default value (`FALSE` for `na.rm`). These options control the behavior of the functions, such as whether it includes/excludes NA values.

Cleaning Data

In many instances, you will deal with data that are not "clean". Based on the output we received from the `mean()` function, we know that there are NA's in the BlackfootFish data, possibly across a variety of variables. Before we used `na.rm` as an option to remove NA's *within* a function, but the `na.omit` function takes a dataframe and removes any NA's from that dataset. Based on the output below, how many rows in the BlackfootFish data have an NA present?

```r
dim(BlackfootFish) ## gives the dimensions of the dataset in (row, column) format
```

```
## [1] 18352     7
```

```r
dim(na.omit(BlackfootFish))
```

```
## [1] 16556     7
```

```r
## na.omit takes dataframes, matricies, and vectors and returns the object with incomplete cases remove
```

Remark: The computer is using an algorithm to return a dataset with no NA values anywhere in it. This algorithm goes through every row of the dataset and (roughly) has the following steps,

- Inspect the row to see if there is an NA anywhere in that row
- If there is an NA in that row, the logical (`is.na`) evaluates to TRUE, and the row is deleted
- If there is not any NA's in that row, the logical evaluates to FALSE, and the row is retained
- Once it has stepped through every row, the function outputs the "cleaned" dataframe

Subsetting Data

If we wish to remove all of the NA's from the dataset, we can simply use the `na.omit` command from above. We can save the new "clean" dataset under a new name (creating a new object) or under the same name as before (replacing the old object with the new object).

```
BlackfootFish2 <- na.omit(BlackfootFish)
## Creates a new dataframe, where the NA's have all been removed
```

Data Visualization

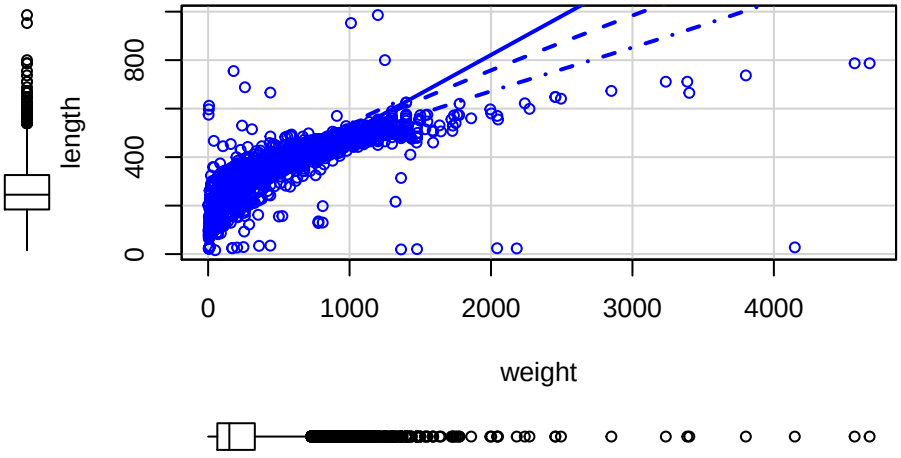
There are many different genres of data graphics, with many different variations on each genre. Here are some commonly encountered kinds:

- **scatterplots**: showing relationships between two quantitative variables
- **distributions**: showing distributions of a single quantitative variable
- **bar charts**: displaying frequencies or densities of a single categorical variable

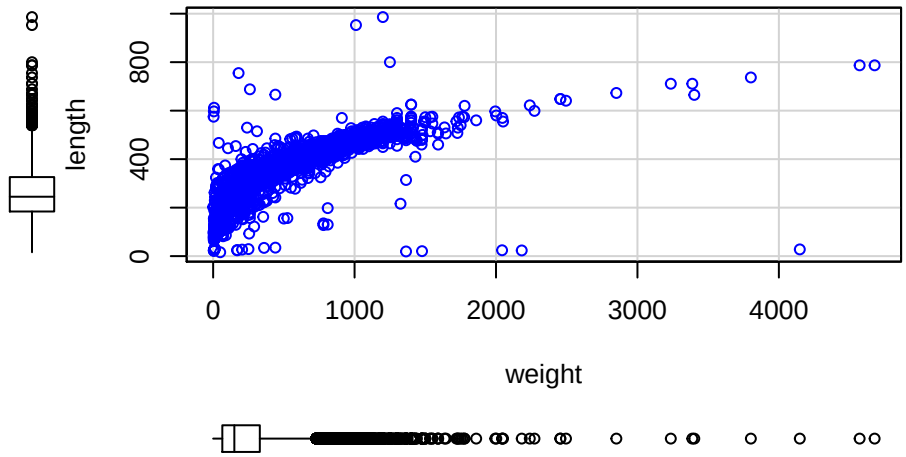
Scatterplots

The main purpose of the scatterplot is to show the relationship between two variables across several or many cases. Most often, there is a Cartesian coordinate system in which the x-axis represents one variable and the y-axis the second variable.

```
#?scatterplot()
scatterplot(length ~ weight, data = BlackfootFish2)
```




```
scatterplot(length ~ weight, data = BlackfootFish2, regLine = FALSE, smooth = FALSE)
```

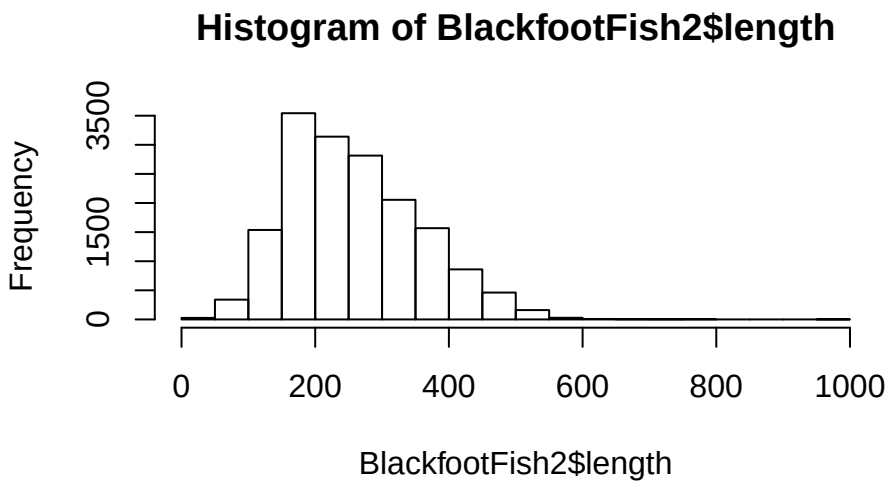



```
## taking out the trend line (smoother) and 95% CI
```

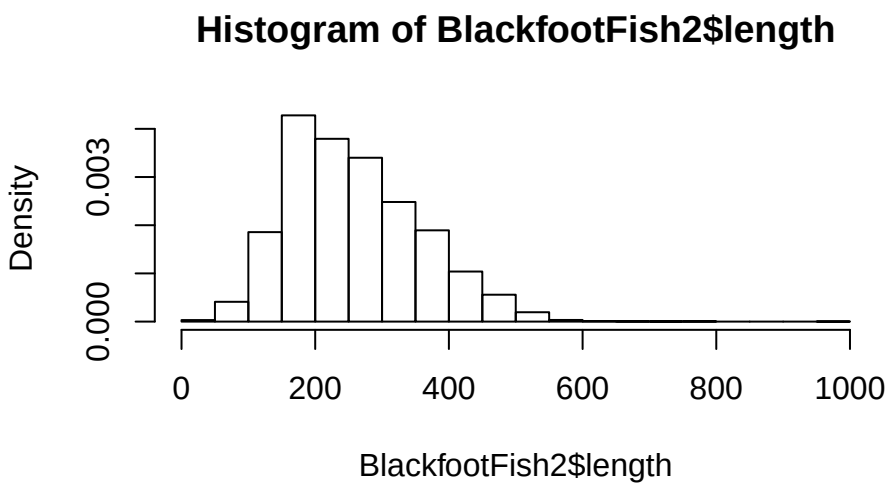
Distribution

A histogram shows how many observations fall into a given range of values of a variable.

```
hist(BlackfootFish2$length)
```

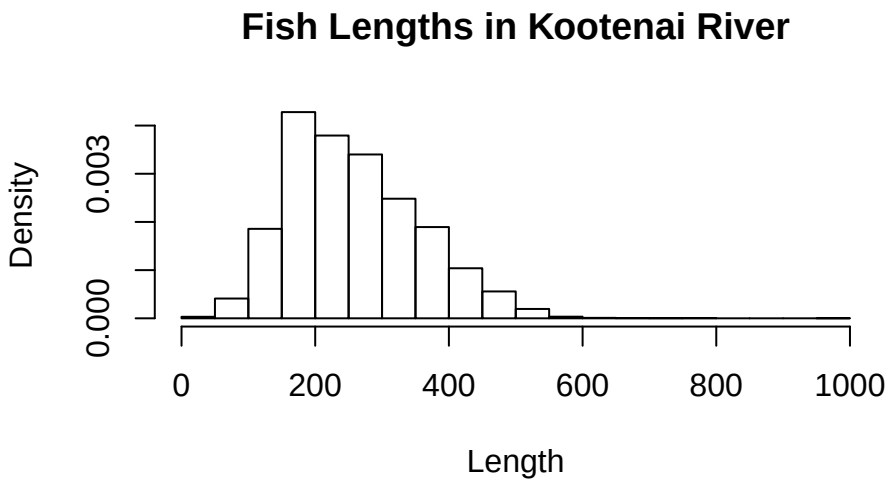



```
hist(BlackfootFish2$length, freq = F) ## converts to a density plot (area adds to 1)
```



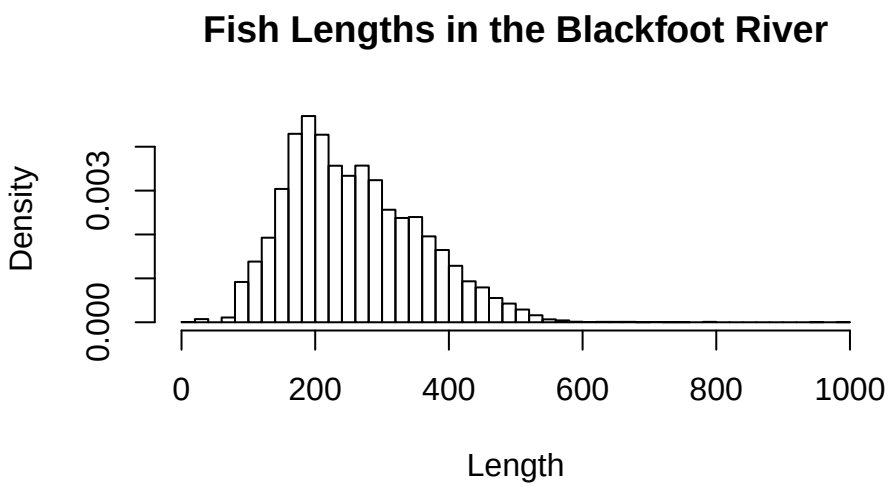

```
## Does freq need to be named?
hist(BlackfootFish2$length, FALSE)
## Why is there an error about the "number of breaks"?
```

```
hist(BlackfootFish2$length, freq = F, xlab = "Length",
     main = "Fish Lengths in Kootenai River")
```




```
## adds x-axis label AND title to plot
```

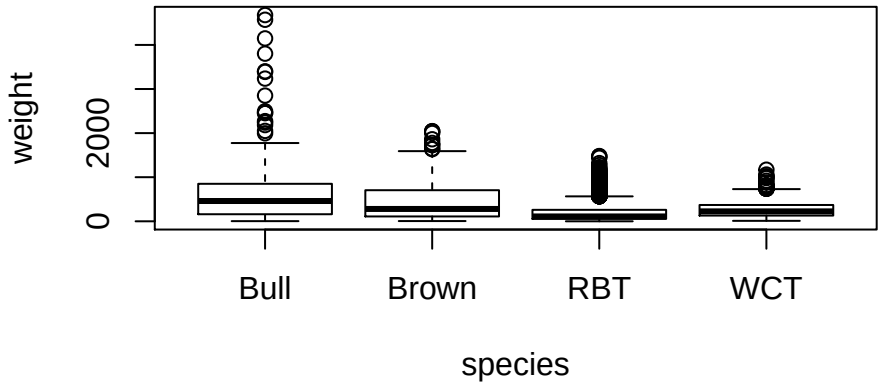
```
hist(BlackfootFish2$length, freq = F, nclass = 50,
     xlab = "Length", main = "Fish Lengths in the Blackfoot River")
## changes the number of bins

## If you put the arguments in the correct order, you don't need to name them, like:
hist(BlackfootFish2$length, 50, FALSE, xlab = "Length",
     main = "Fish Lengths in the Blackfoot River")
```



Side-by-Side Boxplots

The familiar boxplot is effective when the objective is to compare the distribution of a quantitative variable across different levels of a categorical variable.

```
boxplot(weight ~ species, data = BlackfootFish2)
```

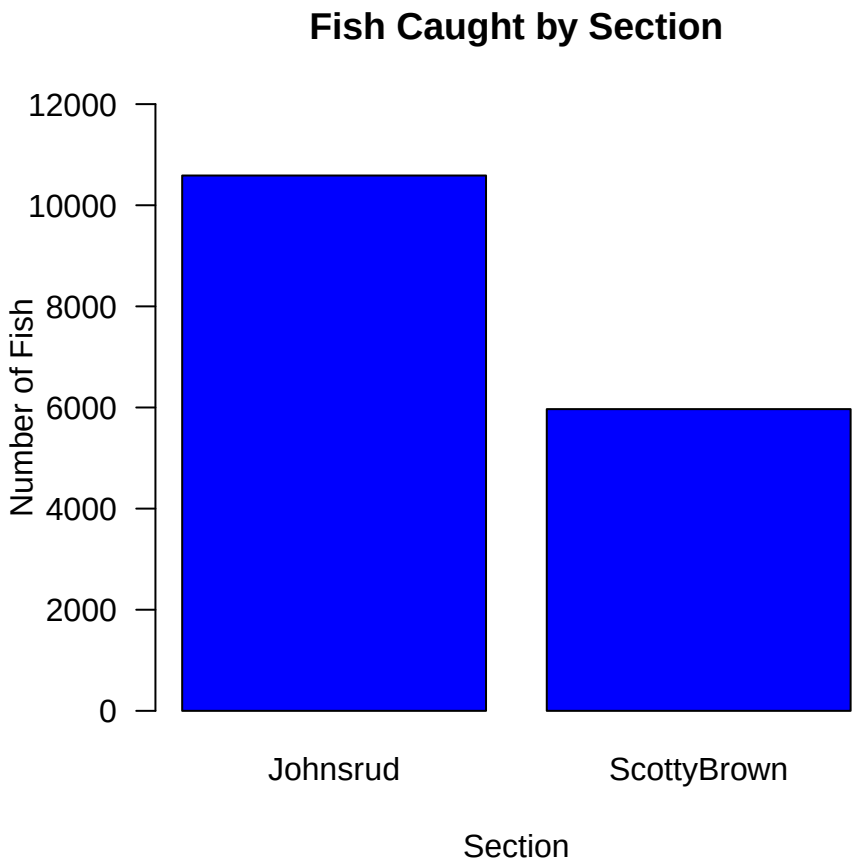



```
## What other options are available to add to your boxplot?
```

Bar Charts

Bar charts are an effective way to compare the frequencies of levels of a categorical variable.

```
section <- table(BlackfootFish2$section)
## tables the number of fish that were caught in each section

barplot(section, xlab = "Section", ylab = "Number of Fish", main = "Fish Caught by Section",
        las = 1, col = "blue", ylim = c(0, 12000))
```



Practice: Using statistics or graphics, which year in our dataset had the most fish caught?

Practice: Make a boxplot of the fish weights over the different years in the dataset.

Workshop Materials Available:

- through RStudio Cloud at: https://rstudio.cloud/project/46123
- through Allison's personal website at: http://www.math.montana.edu/graduate/pages/atheobold/

How to Learn More About `R`

This material is intended to provide you with an introduction to using `R` for scientific analyses of data. The best way for you to continue to learn more about `R` is to use it in your research! This may sound daunting, but writing `R` scripts is the best way to become familiar with the syntax. This will help you progress through more advanced operations, such as cleaning your data, using statistical methods, or creating graphics.

The best place to start is playing around with the code from today's workshop. Change parts of the code and see what happens! Better yet, use the code from the workshop to investigate your own data!