R for Excel Users

Julie Lowndes & Allison Horst

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Chapter 1

Welcome

Hello! This is a workshop taught by Julie Stewart Lowndes and Allison Horst at the RStudio Conference: January 27-28 in San Francisco, California.

We are environmental scientists who use and teach R in our daily work. We both work at the University of California Santa Barbara: Julie is based at the National Center for Ecological Analysis and Synthesis as part of the Ocean Health Index team and leads Openscapes, and Allison is based at the Bren School of Environmental Science and Management as a lecturer of data science & statistics — and is also an Artist in Residence at RStudio.

1.1 Agenda: pilot workshop

Time	Day 1	Day 2
9-10:30	Motivation, R & RStudio, RMarkdown	Charts with `ggplot2`
break		
11-12:30	Intro to GitHub	`dplyr` & Pivot Tables
lunch		
13:00-14:30	Importing data: `readxl`	`dplyr` & VLOOKUPs

From 14:30-15:00 each day we have time for additional help and feedback.

1.2 Prerequisites

Before the training, please make sure you have done the following:

1. Download and install **up-to-date versions** of:
    - R: https://cloud.r-project.org
    - RStudio: http://www.rstudio.com/download
2. Install the Tidyverse
3. Create a an account:
    - https://github.com

1. Get comfortable: if you're not in a physical workshop, be set up with two screens if possible. You will be following along in RStudio on your own computer while also watching a virtual training or following this tutorial on your own.

Chapter 2

Overview

2.1 Welcome!

In this workshop you will learn hands-on how to begin to interoperate between Excel and R. But this workshop is not only about learning R; we will learn R using additional software: RStudio and GitHub. These tools will help us develop good habits for working in a reproducible and collaborative way — critical attributes of the modern analyst.

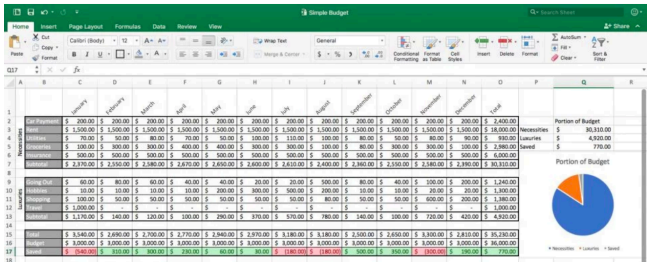
It's going to be fun and empowering!

2.2 Why learn R if I know Excel?

Excel is a widely used and powerful tool for working with data, and it is great for a lot of things. This is convenient and familiar; most of us have had their first experiences with data through Excel or other spreadsheet programs. As Jenny Bryan has said, "Excel is how we learn that we love data analysis".

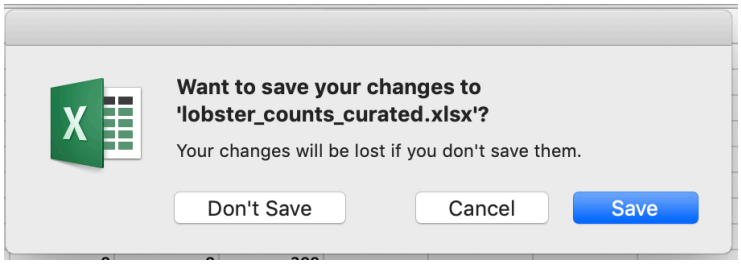
Excel is great for data entry. Can also be good for looking at data and feeling like you can touch it, and creating quick exploratory figures.

Excel can also become problematic with extending to analyses. This is because there aren't firm lines between what is data and what is analyses. For example, in this sheet:



This makes the analytical steps taken are not readily apparent, nor easy to reproduce. Have you ever done forensics on an Excel sheet, trying to understand what happened between columns or sheets? Maybe it was even your own Excel file from the (recent) past.

This also makes them pretty brittle/sensitive to minor changes. Has seeing this ever given you a feeling of horror:



So while it is great how easily you can update different fields and add analytical steps in an Excel sheet, it can also be a bit hard to handle, particularly as projects get more complicated.

So, as automation, reproducibility, collaboration, and frequent reporting become increasingly expected in data analysis, a good option for Excel users is to extend their workflows with R.

2.2.1 What to expect

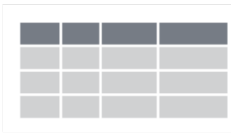
This is going to be a fun workshop.

This workshop will give you hands-on experience and confidence with R, and how to interoperate between Excel and R — it is not about wholesale replacing everything you do in Excel into R. We will learn technical skills that you can incrementally incorporate into your existing workflows. But a big part of interfacing between Excel and R is not only skillsets, it is mindsets. It is the mindset about how we think about data. How we shape data and organize data and analyze data. And how what we do now can make our analytical life better in the future.

A modern R user has a workflow framed around collaboration, and uses an ecosystem of tools and practices. We will be learning three main things all at the same time:

1. coding with best practices (R/RStudio/tidyverse)
2. collaborative bookkeeping (Git/GitHub)
3. reporting and publishing (RMarkdown/GitHub)

R users keep raw data separate from their analyses, which means having data in one file and written computational commands saved as a separate file. We also embrace the concept of **"tidy data"**, where the data has a rectangular shape and each column is a variable and each row is an observation. Tidy data is a way of life.



region	state	code	park_name	type	visitors	year
PW	CA	CHIS	Channel Islands National Park	National Park	1200	1963
PW	CA	CHIS	Channel Islands National Park	National Park	1500	1964
PW	CA	CHIS	Channel Islands National Park	National Park	1600	1965
PW	CA	CHIS	Channel Islands National Park	National Park	300	1966
PW	CA	CHIS	Channel Islands National Park	National Park	15700	1967
PW	CA	CHIS	Channel Islands National Park	National Park	31000	1968
PW	CA	CHIS	Channel Islands National Park	National Park	33100	1969
PW	CA	CHIS	Channel Islands National Park	National Park	32000	1970

We are going to go through a lot in these two days and it's less important that you remember it all. More importantly, you'll have experience with it and confidence that you can do it. The main thing to take away is that there *are* good ways to work between R and Excel; we will teach you to expect that so you can find what you need and use it! A theme throughout is that tools exist and are being developed by real, and extraordinarily nice, people to meet you where you are and help you do what you need to do.

You are all welcome here, please be respectful of one another. Everyone in this workshop is coming from a different place with different experiences and expectations. But everyone will learn something new here, because there is so much innovation in the data science world. Instructors and helpers learn something new every time, from each other and from your questions. If you are already familiar with some of this material, focus on how we teach, and how you might teach it to others. Use these workshop materials not only as a reference in the future but also for talking points so you can communicate the importance of these tools to your communities. A big part of this training is not only for you to learn these skills, but for you to also teach others and increase the value and practice of open data science in science as a whole.

2.3 Guiding principles / recurring themes

"Keep the raw data raw" — A hard line separating raw data and analyses. In R, we have data in one file and written computational commands saved as a separate file.

Scripted analyses — We write analytical logic in code (rather than clicks) so that can be understood, rerun, and built upon.

Learn from data that are not your own — We aren't using your data in this workshop, but you will see similiarities and patterns, and you'll see that these tools and practices apply to your work.

Think ahead for Future You, Future Us. Help make lives easier — first and foremost your own. Create breadcrumbs for yourselves and others: document and share your work.

2.4 Resources

R is not only a language, it is an active community of developers, users, and educators (often these traits are in each person). This workshop and book based on many excellent materials created by other members in the R community, who share their work freely to help others learn. Using community materials is how WE learned R, and each chapter of the book will have Resources listed for further reading into the topics we discuss. And, when there is no better way to explain something (ahem Jenny Bryan), we will quote or reference that work directly.

- What They Forgot to Teach You About R — Jenny Bryan & Jim Hester
- Stat545 — Jenny Bryan & Stat545 TAs
- Where do Things Live in R? REX Analytics
-
- Spreadsheet Drama (Episode 9) — Not So Standard Deviations with Roger Peng & Hilary Parker
- more to come!

Chapter 3

R & RStudio, RMarkdown

3.1 Summary

We'll learn RMarkdown, which helps you tell a story with your data analysis because you can write text alongside the code. We are actually learning two languages at once: R and Markdown.

3.1.1 Objectives

In this lesson we will:

- get oriented to the RStudio interface
- work with R in the console
- be introduced to built-in R functions
- learn to use the help pages
- explore RMarkdown

3.1.2 Resources

- R for Excel Users by Gordon Shotwell (blog)

3.2 Why learn R with RStudio

You are all here today to learn how to code. Coding made me a better scientist because I was able to think more clearly about analyses, and become more efficient in doing so. Data scientists are creating tools that make coding more

intuitive for new coders like us, and there is a wealth of awesome instruction and resources available to learn more and get help.

Here is an analogy to start us off. **Think of yourself as a pilot, and R is your airplane.** You can use R to go places! With practice you'll gain skills and confidence; you can fly further distances and get through tricky situations. You will become an awesome pilot and can fly your plane anywhere.

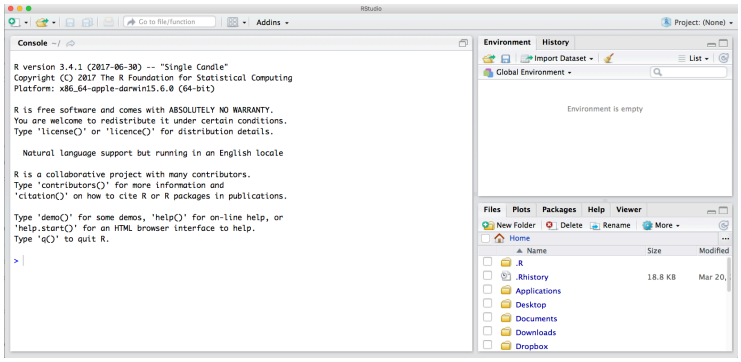
And **if R were an airplane, RStudio is the airport**. RStudio provides support! Runways, communication, community, and other services that makes your life as a pilot much easier. So it's not only the infrastructure (the user interface or IDE), although it is a great way to learn and interact with your variables, files, and interact directly with GitHub. It's also a data science philosophy, R packages, community, and more. So although you can fly your plane without an airport and we could learn R without RStudio, that's not what we're going to do.

> We are learning R together with RStudio and its many supporting features.

3.3 RStudio Orientation

Open RStudio for the first time.

Launch RStudio/R.



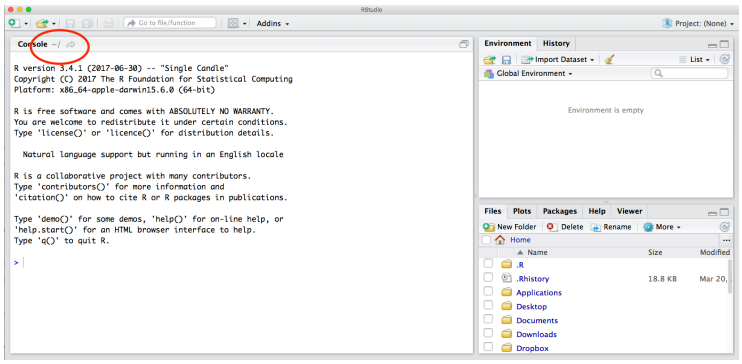
Notice the default panes:

- Console (entire left)
- Environment/History (tabbed in upper right)
- Files/Plots/Packages/Help (tabbed in lower right)

FYI: you can change the default location of the panes, among many other things: Customizing RStudio.

An important first question: **where are we?**

If you've have opened RStudio for the first time, you'll be in your Home directory. This is noted by the `~/` at the top of the console. You can see too that the Files pane in the lower right shows what is in the Home directory where you are. You can navigate around within that Files pane and explore, but note that you won't change where you are: even as you click through you'll still be Home: `~/`.



3.3.1 R Console

OK let's go into the Console, where we interact with the live R process.

We can do math:

```
52*40
365/12
```

But like Excel, the power comes not from doing small operations by hand (like 8*22.3), it's by being able to operate on whole suites of numbers and datasets. In Excel, data are stored in the spreadsheet. In R, they are stored in objects, which are often vectors or dataframes. They are rectangular.

3.3.2 Viewing data in R

Let's have a look at some data in R. Unlike Excel, R comes out-of-the-box with several built-in data sets that we can look at and work with.

One of these datasets is called `cars`. If I write this in the Console, it will print the data in the console.

```
cars
```

This returns data. To me this is not super interesting data, but I can appreciate that there are different variables listed as column headers and then numeric values for each type of row observation. (Unfortunately I don't know if these are different cars or trials or conditions but we won't focus on that for now).

I can also use RStudio's Viewer to see this in a more familiar-looking format. Let's type this — and make sure it's a capital V and open and closed parentheses:

```
View(cars)
```

This opens the fourth pane of the RStudio IDE; when you work in R you will have all four panes open so this will become a very comforting setup for you.

> ***Aside*** The basic R data structure is a vector. You can think of a vector like a column in an Excel spreadsheet with the limitation that all the data in that vector must be of the same type. If it is a character vector, every element must be a character; if it is a logical vector, every element must be TRUE or FALSE; if it's numeric you can trust that every element is a number. There's no such constraint in Excel: you might have a column which has a bunch of numbers, but then some explanatory test intermingled with the numbers. This isn't allowed in R. - Gordon Shotwell

In the Viewer I can do things like filter or sort. This does not do anything to the actual data, it just changes how you are viewing the data. So even as I explore it, I am not editing or manipulating the data.

3.3.3 R functions, help pages

Like Excel, some of the biggest power in R is that there are built-in functions that you can use in your analyses (and, as we'll see, R users can easily create and share functions, and it is this open source developer and contributor community that makes R so awesome).

R has a mind-blowing collection of built-in functions that are used with the same syntax: function name with parentheses around what the function needs to do what it is supposed to do. `function_name(argument1 = value1, argument2 = value2, ...)`. When you see this syntax, we say we are "calling the function".

Let's try using `seq()` which makes regular sequences of numbers and, while we're at it, demo more helpful features of RStudio.

Type `se` and hit TAB. A pop up shows you possible completions. Specify `seq()` by typing more to disambiguate or using the up/down arrows to select. Notice the floating tool-tip-type help that pops up, reminding you of a function's arguments. If you want even more help, press F1 as directed to get the full documentation in the help tab of the lower right pane.

Type the arguments `1, 10` and hit return.

```
seq(1, 10)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

We could probably infer that the `seq()` function makes a sequence, but let's learn for sure. Type (and you can autocomplete) and let's explore the help page:

```
?seq
help(seq) # same as ?seq
```

When I press enter/return, it will open up a help page in the bottom right pane. Help pages vary in detail I find some easier to digest than others. But they all have the same structure, which is helpful to know. The help page tells the name of the package in the top left, and broken down into sections:

- Description: An extended description of what the function does.
- Usage: The arguments of the function and their default values.
- Arguments: An explanation of the data each argument is expecting.
- Details: Any important details to be aware of.
- Value: The data the function returns.
- See Also: Any related functions you might find useful.
- Examples: Some examples for how to use the function.

When I look at a help page, I start with the description, which might be too in-the-weeds for the level of understanding I need at the offset. For the `sum` page, it is pretty straight-forward and lets me know that yup, this is the function I want.

I next look at the usage and arguments, which give me a more concrete view into what the function does. This syntax looks a bit cryptic but what it means is that you use it by writing sum, and then passing whatever you want to it in terms of data: that is what the "..." means. And the "na.rm=FALSE" means that by default, it will not remove NAs (I read this as: "remove NAs? FALSE!")

Then, I usually scroll down to the bottom to the examples. This is where I can actually see how the function is used, and I can also paste those examples into the Console to see their output. Let's try it:

```
seq(from = 1, to = 10) # same as seq(1, 10); R assumes by position
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
seq(from = 1, to = 10, by = 2)
```

```
## [1] 1 3 5 7 9
```

The above also demonstrates something about how R resolves function arguments. You can always specify in `name = value` form. But if you do not, R attempts to resolve by position. So above, it is assumed that we want a sequence `from = 1` that goes `to = 10`. Since we didn't specify step size, the default value of `by` in the function definition is used, which ends up being 1 in this case. For functions I call often, I might use this resolve by position for the first argument or maybe the first two. After that, I always use `name = value`.

The examples from the help pages can be copy-pasted into the console for you

to understand what's going on. Remember we were talking about expecting there to be a function for something you want to do? Let's try it.

3.3.4 Activity

> Exercise: Talk to your neighbor(s) and look up the help file for a function that you know or expect to exist. Here are some ideas: `?getwd()`, `?plot()`, `min()`, `max()`, `?mean()`, `?log()`).

Let's try another. In Excel, there is a "SUM" function to calculate a total. Let's expect that there is the same in R. I will type this into the Console:

```
sum(1, 2, 3)
```

R is case-sensitive. So "sum" is a completely different thing to "Sum" or "SUM". And this is true for the names of functions, data sets, variable names, and data itself ("blue" vs "Blue").

Awesome. Let's try this on our `cars` data

```
sum(cars)
```

Alright. What is this number? It is the sum of ALL of the data in the `cars` dataset. Maybe in some analysis this would be a useful operation, but I would worry about the way your data is set up and your analyses if this is ever something you'd want to do. More likely, you'd want to take the sum of a specific column. In R, you can do that with the `$` operator.

Let's say we want to calculate the total distance:

```
sum(cars$dist)
```

There are many functions that are built into R, and we'll learn more of them shortly.

Not all functions have (or require) arguments:

```
date()
```

```
## [1] "Sat Dec  7 08:22:00 2019"
```

3.3.5 Packages

So far we've been using a couple functions from base R, such as `sum()` and `date()`. But, one of the amazing things about R is that a vast user community is always creating new functions and packages that expand R's capabilities. In R, the fundamental unit of shareable code is the package. A package bundles together code, data, documentation, and tests, and is easy to share with others.

They increase the power of R by improving existing base R functionalities, or by adding new ones.

The traditional place to download packages is from CRAN, the Comprehensive R Archive Network, which is where you downloaded R. You can also install packages from GitHub, which we'll do tomorrow.

You don't need to go to CRAN's website to install packages, this can be accomplished within R using the command `install.packages("package-name-in-quotes")`. Let's install a small, fun package `praise`. You need to use quotes around the package name.

Do this in the Console instead of in your RMarkdown file because we don't want this to load every time:

```
install.packages("praise")
```

Now we've installed the package, but we need to tell R that we are going to use the functions within the `praise` package. We do this by using the function `library()`.

In my mind, this is analogous to needing to wire your house for electricity: this is something you do once; this is `install.packages`. But then you need to turn on the lights each time you need them (R Session).

```
library(praise)
```

Now that we've loaded the `praise` package, we can use the single function in the package, `praise()`, which returns a randomized praise to make you feel better.

```
praise()
```

```
## [1] "You are priceless!"
```

3.3.6 Assigning objects with <-

This might be a really important value that we want to have on hand. We can save this as its own object.

This is a big difference with Excel, where you usually identify data by its location on the grid, like `$A1:D$20`. (You can do this with Excel by naming ranges of cells, but many people don't do this.)

Data can be a variety of formats, like numeric and text.

We do this by writing the name along with the assignment operator `<-`

```
sum_dist <- sum(cars$dist)
```

And we can execute it. In my head I hear "sum_dist gets 2149".

Object names can be whatever you want, although they cannot start with a digit and cannot contain certain other characters such as a comma or a space. Different folks have different conventions; you will be wise to adopt a convention for demarcating words in names.

```
# i_use_snake_case
# other.people.use.periods
# evenOthersUseCamelCase
```

Notice that as I start typing `sum_dist` in the Console, there will be options to auto-fill. This is RStudio helping you out, which is great because we all are prone to typos. I actually have to ignore the help to try to force a typo:

```
sumdist
# Error: object 'sumdist' not found
```

OK this is an error, but I didn't break R — error messages are your friends.

The first thing to do with an error message is read it. Yes it's in angry red text and it's unexpected — but most error messages are doing their best to help you solve the problem. And you'll get more familiar with they way they tell you. By saying "object 'sumdist' not found" alerts me immediately to the fact that this thing I think exists R doesn't think exists — so maybe it's a typo or not loaded?

3.3.7 Error messages are your friends

As Jenny Bryan says:

> Implicit contract with the computer / scripting language: Computer will do tedious computation for you. In return, you will be completely precise in your instructions. Typos matter. Case matters. Pay attention to how you type.

Remember that this is a language, not unsimilar to English! There are times you aren't understood – it's going to happen. There are different ways this can happen. Sometimes you'll get an error. This is like someone saying 'What?' or 'Pardon'? Error messages can also be more useful, like when they say 'I didn't understand what you said, I was expecting you to say blah'. That is a great type of error message. Error messages are your friend. Google them (copy-and-paste!) to figure out what they mean.

And also know that there are errors that can creep in more subtly, when you are giving information that is understood, but not in the way you meant. Like if I am telling a story about suspenders that my British friend hears but silently interprets in a very different way (true story). This can leave me thinking I've gotten something across that the listener (or R) might silently interpreted very differently. And as I continue telling my story you get more and more confused…

Clear communication is critical when you code: write clean, well documented code and check your work as you go to minimize these circumstances!

3.3.8 Logical operators and expressions

A moment about **logical operators and expressions**. We can ask questions about the objects we made. This is not assigning a new value to our `sum_dist` object.

- `==` means 'is equal to'
- `!=` means 'is not equal to'
- `<` means ' is less than'
- `>` means ' is greater than'
- `<=` means ' is less than or equal to'
- `>=` means ' is greater than or equal to'

```
sum_dist == 2
```

```
## [1] FALSE
```

```
sum_dist <= 3000
```

```
## [1] TRUE
```

```
sum_dist != 500
```

```
## [1] TRUE
```

> Shortcuts You will make lots of assignments and the operator `<-` is a pain to type. Don't be lazy and use `=`, although it would work, because it will just sow confusion later. Instead, utilize **RStudio's keyboard shortcut: Alt + - (the minus sign)**. Notice that RStudio automagically surrounds `<-` with spaces, which demonstrates a useful code formatting practice. Code is miserable to read on a good day. Give your eyes a break and use spaces. RStudio offers many handy keyboard shortcuts. Also, Alt+Shift+K brings up a keyboard shortcut reference card.
>
> My most common shortcuts include command-Z (undo), and combinations of arrow keys in combination with shift/option/command (moving quickly up, down, sideways, with or without highlighting.

3.4 Clearing the environment

Now look at the objects in your environment (workspace) – in the upper right pane. The workspace is where user-defined objects accumulate.

For reproducibility, it is critical that you delete your objects and restart your R session frequently. You don't want your whole analysis to only work in whatever way you've been working right now — you need it to work next week, after you upgrade your operating system, etc. Restarting your R session will help you identify and account for anything you need for your analysis.

We will keep coming back to this theme but let's restart our R session together: Go to the top menus: Session > Restart R.

Don't save the workspace!

So this is great, but if we were going to do any kind of real analysis, we need to be able to write it in a document rather than this command line prompt in the Console. Let's do something much more interesting and really start feeling its power.

3.5 Intro to RMarkdown

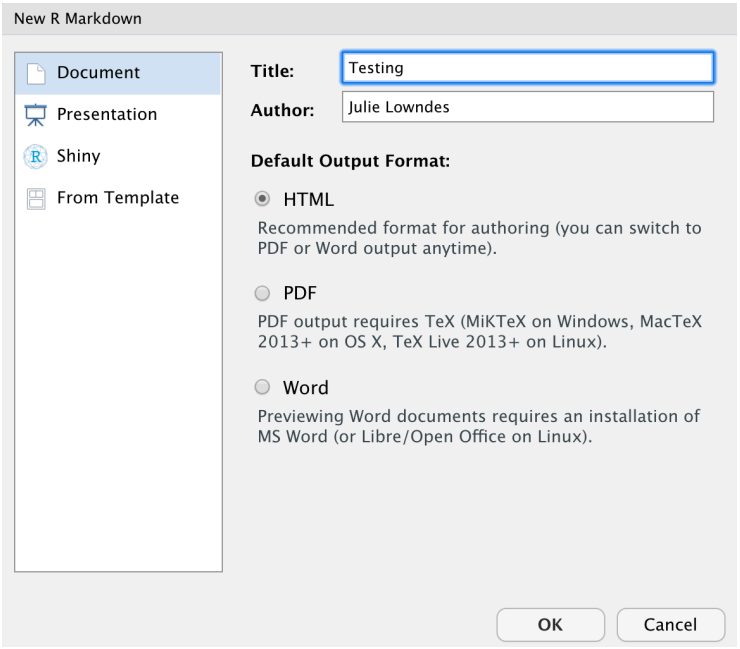
An RMarkdown file is a special type of file for making reports — it allow us to weave markdown text with chunks of R code to be evaluated and output content like tables and plots.

This is really critical to reproducibility, and it also saves time. This document will recreate your figures for you in the same document where you are writing text. So no more doing analysis, saving a plot, pasting that plot into Word, redoing the analysis, re-saving, re-pasting, etc.

Let's experience this a bit ourselves and then we'll talk about it more.

3.5.1 Create an RMarkdown file

File -> New File -> RMarkdown… -> Document of output format HTML, OK.



You can give it a Title like "Testing" (a name that's totally ok to use as you're trying something out). Then click OK.

OK, first off: by opening a file, we are seeing the 4th pane of the RStudio console, which is essentially a text editor. This lets us organize our files within RStudio instead of having a bunch of different windows open.

Let's have a look at this file — it's not blank; there is some initial text is already provided for you. Notice a few things about it:

- Title and Author are auto-filled, and the today's date has been added
- There are white and grey sections. These are the 2 main languages that make up an RMarkdown file.
  - **Grey sections are R code**
  - **White sections are Markdown text**

```
---
title: "Testing"
author: "Julie Lowndes"
date: "11/14/2019"
output: html_document
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
```

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```{r cars}
summary(cars)
```

Including Plots

You can also embed plots, for example:

```{r pressure, echo=FALSE}
plot(pressure)
```

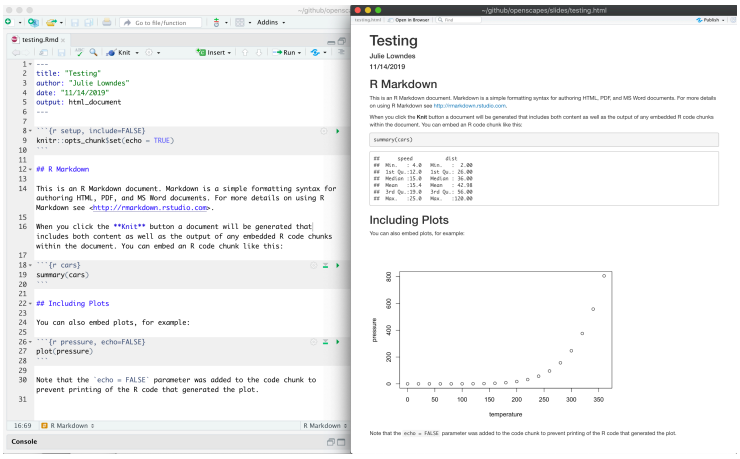
Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.
```

3.5.2 Knit your RMarkdown file

Let's go ahead and "Knit" by clicking the blue yarn at the top of the RMarkdown file. It's going to ask us to save first, I'll name mine "testing.Rmd".

How cool is this, we've just made an html file, a webpage that we are viewing locally on our own computers. Knitting this RMarkdown document has rendered — we also say formatted — both the Markdown text (white) and the R code (grey), and the it also executed — we also say ran — the R code.

Let's have a look at them side-by-side:



Let's take a deeper look at these two files. So much of learning to code is looking for patterns.

3.5.3 R code chunks

Notice how the grey **R code chunks** are surrounded by 3 backticks and `{r LABEL}`. These are evaluated and return the output text in the case of `summary(cars)` and the output plot in the case of `plot(pressure)`.

Notice how the code `plot(pressure)` is not shown in the HTML output because of the R code chunk option `echo=FALSE`.

We can create a new chunk in your RMarkdown first in one of these ways:

- click "Insert > R" at the top of the editor pane
- type by hand "'{r} "'
- if you haven't deleted a chunk that came with the new file, edit that one

Now, let's write some code in R. Earlier we calculated `sum(cars$dist)`. Now let's do the average. In R, this is the `mean()` function

```
mean_dist <- mean(cars$dist)
```

Now, hitting return does not execute this command; remember, it's a text file in the text editor, it's not associated with the R engine. To execute it, we need to get what we typed in the the R chunk (the grey R code) down into the console. How do we do it? There are several ways (let's do each of them):

1. copy-paste this line into the console.
2. select the line (or simply put the cursor there), and click 'Run'. This is available from
   a. the bar above the file (green arrow)
   b. the menu bar: Code > Run Selected Line(s)
   c. keyboard shortcut: command-return
3. click the green arrow at the right of the code chunk

And when we do this, we see the `mean_dist` object appear in he Environment pane.

Cool tip: doesn't have to be only R, other languages supported.

3.5.4 Activity (3 min)

> Calculate the maximum cars distance in your RMarkdown file by typing `max(cars$dist)`. Remember to write your R code within a code chunk (grey)!
> Execute your commands by trying the three ways above. Then, knit your R Markdown file, which will also save the Rmd by default.

3.5.5 Markdown sections

The second language is Markdown. This is a formatting language for plain text, and there are only about 15 rules to know.

Notice the syntax for:

- **headers** get rendered at multiple levels: `#`, `##`
- **bold**: `**word**`

There are some good cheatsheets to get you started, and here is one built into RStudio: Go to Help > Markdown Quick Reference

Learn more: http://rmarkdown.rstudio.com/

3.5.6 Activity

1. In Markdown write some italic text, make a numbered list, and add a few subheaders. Use the Markdown Quick Reference (in the menu bar: Help > Markdown Quick Reference).
2. Reknit your html file.

3.5.7 Restart R

To end our work from this session, save, knit, and then restart R (Go to the top menus: Session > Restart R.)

Notice that now with a clean workspace, if I knit my document instead of sending code to the Console, my objects (like `mean_dist`) don't show up in my Environment. This is because R isn't actually running this in this R session, it is actually spinning up a clean session to knit my document. This is important for reproducible analyses because I don't want the success of this analysis to be dependent on some weird setting I have on my computer that will make Future Me or Future Us not able to run or understand these important analyses. Having RMarkdown be self-contained in this way helps you develop good habits for reproducibility.

3.5.8 What is RMarkdown? (1-minute video)

Let's watch this to demonstrate all the amazing things you can now do:

What is RMarkdown?

3.6 Deep thoughts

Comments! Organization (spacing, subsections, vertical structure, indentation, etc.)! Well-named variables! Also, well-named operations so analyses (select(data, columnname)) instead of data[1:6,5] and excel equivalent. (Ex with strings) Not so brittle/sensitive to minor changes.

3.7 Efficiency Tips

—>

Chapter 4

GitHub

4.1 Summary

We will learn about version control using git and GitHub, and we will interface with this through RStudio. Why use version control? To save time when working with your most important collaborator: you.

4.2 Objectives

Today, we'll interface with GitHub from our local computers using RStudio. There are many other ways to interact with GitHub, including GitHub's Desktop App or the command line (here is Jenny Bryan's list of git clients), but today we are going to work from RStudio. You have the largest suite of options if you interface through the command line, but the most common things you'll do can be done through one of these other applications (i.e. RStudio and the GitHub Desktop App).

Here's what we'll do after we set up git on your computers:

1. create a repository on Github.com
2. clone locally using RStudio
3. learn the RStudio-GitHub workflow by syncing to Github.com: pull, stage, commit, push
4. explore github.com: files, commit history, file history
5. practice the RStudio-GitHub workflow by editing and adding files
6. practice R Markdown

git will track and version your files, GitHub stores this online and enables you to collaborate with others (and yourself). Although git and GitHub are two

different things, distinct from each other, we can think of them as a bundle since we will always use them together. It also helped me to think of GitHub like Dropbox: you make folders that are 'tracked' and can be synced to the cloud. GitHub does this too, but you have to be more deliberate about when syncs are made. This is because GitHub saves these as different versions, with information about who contributed when, line-by-line. This makes collaboration easier, and it allows you to roll-back to different versions or contribute to others' work.

4.3 Resources

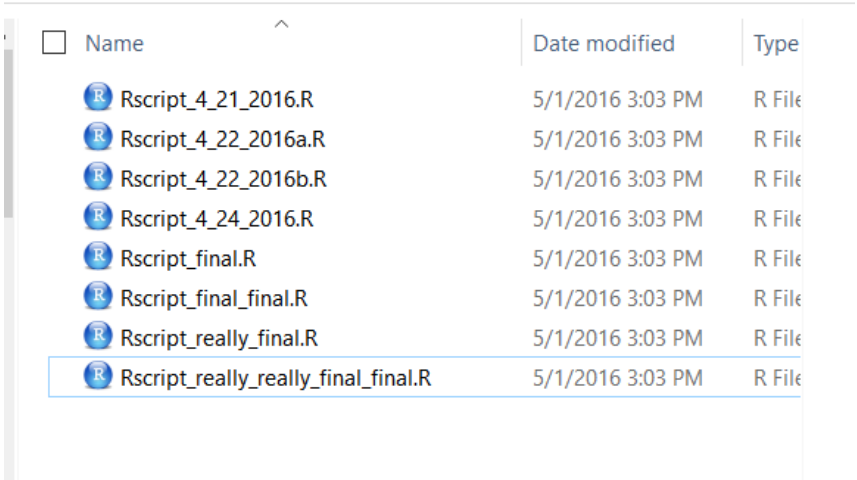
These materials borrow from:

- Jenny Bryan's lectures from STAT545 at UBC: The Shell
- Jenny Bryan's Happy git with R tutorial
- Melanie Frazier's GitHub Quickstart, GitHub Lesson at University of Queensland
- Ben Best's Software Carpentry at UCSB

Today, we'll only introduce the features and terminology that new R users need to learn to begin managing their projects.

4.4 Why should R users use Github?

1. Ends (or, nearly ends) the horror of keeping track of versions. Basically, we get away from this:



When you open your repository, you only see the most recent version. But, it easy to compare versions, and you can easily revert to previous versions.

2. Improves collaborative efforts. Different researchers can work on the same files at the same time!
3. It is easy to share and distribute files through the Github website.
4. Your files are available anywhere, you just need internet connection!

4.4.1 What are Git and Github?

- **Git** is a version control system that lets you track changes to files over time. These files can be any kind of file (eg .doc, .pdf, .xls), but free text differences are most easily visible (eg txt, csv, md).
- **Github** is a website for storing your git versioned files remotely. It has many nice features to be able visualize differences between images, rendering & diffing map data files, render text data files, and track changes in text.

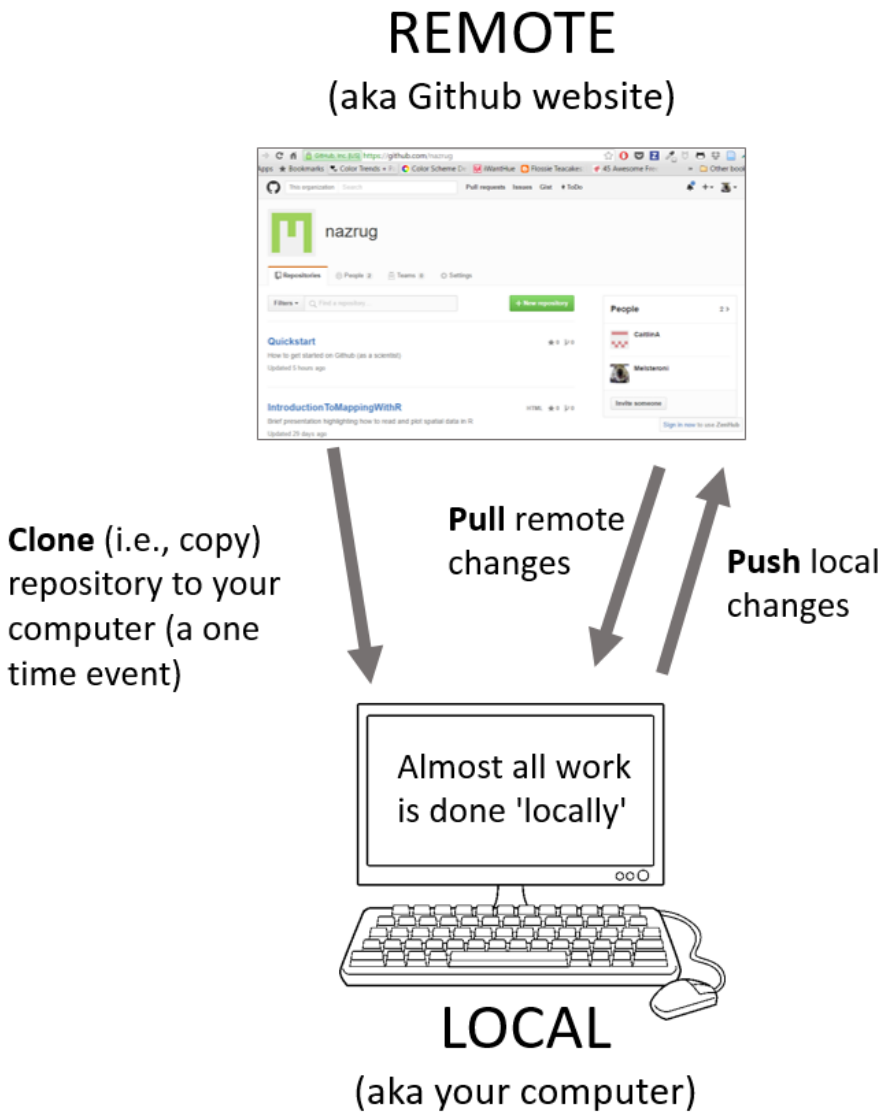
Github was developed for social coding (i.e., sort of like an open source Wikipedia for programmers). Consequently, much of the functionality and terminology of Github (e.g., branches and pull requests) isn't necessary for a new R user getting started.

These concepts are more important for coders who want the entire coding community (and not just people working on the same project) to be able to suggest changes to their code. This isn't how most new R users will use Github.

To get the full functionality of Github, you will eventually want to learn other concepts. But, this can wait.

4.4.2 Some Github terminology

- **User**: A Github account for you (e.g., jules32).
- **Organization**: The Github account for one or more user (e.g., datacarpentry).
- **Repository**: A folder within the organization that includes files dedicated to a project.
- **Local Github**: Copies of Github files located your computer.
- **Remote Github**: Github files located on the https://github.com website.
- **Clone**: Process of making a local copy of a remote Github repository. This only needs to be done once (unless you mess up your local copy).
- **Pull**: Copy changes on the remote Github repository to your local Github repository. This is useful if multiple people are making changes to a repository.
- **Push**: Save local changes to remote Github



4.5 Setup Git & GitHub

We're going to switch gears from R for a moment and set up Git and GitHub, which we will be using along with R and RStudio for the rest of the workshop. This set up is a one-time thing! You will only have to do this once per computer. We'll walk through this together.

1. We will use the `usethis` package to configure **git** with global commands, which means it will apply 'globally' to all files on your computer, rather

than to a specific folder.

```
install.packages("usethis")
library(usethis)

use_git_config(user.name = "jules32", user.email = "jules32@example.org")
```

BACKUP PLAN If `usethis` fails, the following is the classic approach to configuring **git**. Open the Git Bash program (Windows) or the Terminal (Mac) and type the following:

```
# display your version of git
git --version

# replace USER with your Github user account
git config --global user.name USER

# replace NAME@EMAIL.EDU with the email you used to register with Github
git config --global user.email NAME@EMAIL.EDU

# list your config to confirm user.* variables set
git config --list
```

Not only have you just set up git as a one-time-only thing, you have just used the command line. We don't have time to learn much of the command line today, but you just successfully used it following explicit instructions, which is huge! There are great resources for learning the command line, check out this tutorial from SWC at UCSB.

4.5.1 Troubleshooting

If you have problems setting up git, please see the Troubleshooting section in Jenny Bryan's amazing HappyGitWithR.

4.5.1.1 New(ish) Error on a Mac

We've also seen the following errors from RStudio:

`error key does not contain a section --global terminal`

and

`fatal: not in a git directory`

To solve this, go to the Terminal and type: `which git`

Look at the filepath that is returned. Does it say anything to do with Apple?

-> If yes, then the Git you downloaded isn't installed, please redownload if necessary, and follow instructions to install.

-> If no, (in the example image, the filepath does not say anything with Apple) then proceed below:

In RStudio, navigate to: Tools > Global Options > Git/SVN.

Does the **"Git executable"** filepath match what the url in Terminal says?

If not, click the browse button and navigate there.

> *Note*: on my laptop, even though I navigated to /usr/local/bin/git, it then automatically redirect because /usr/local/bin/git was an alias on my computer. That is fine. Click OK.

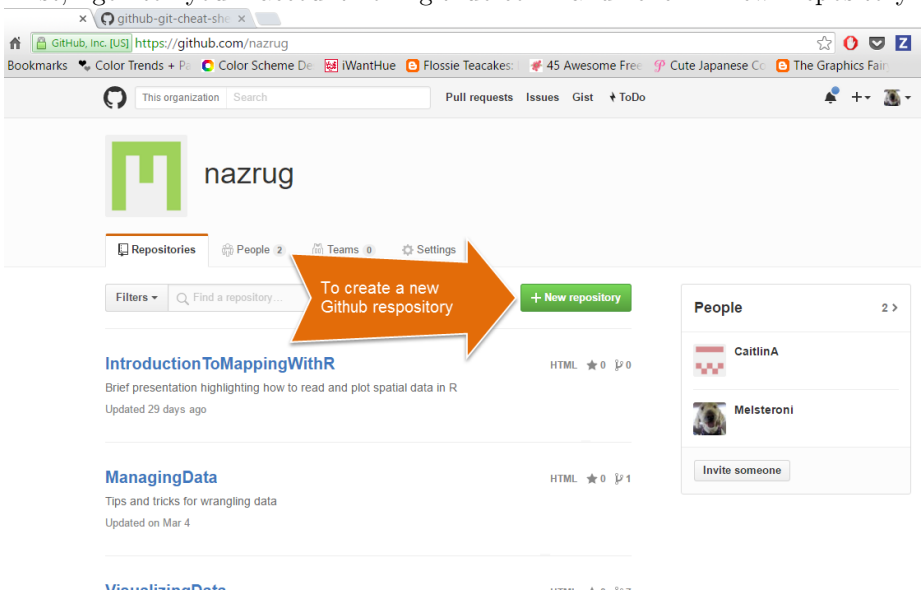
Quit RStudio.

Then relaunch RStudio.

Try syncing or cloning, and if that works and then you don't need to worry about typing into the Terminal, you're all done!

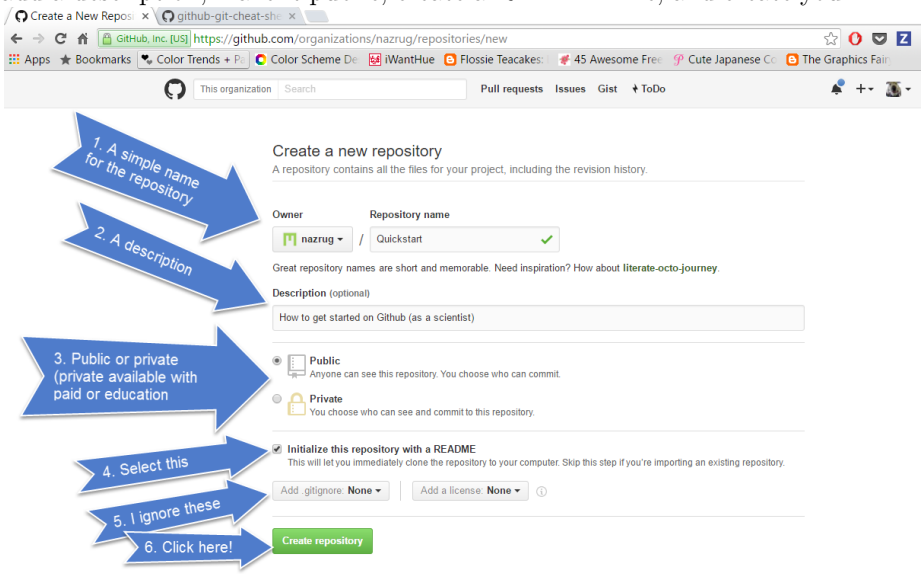
4.6 Create a repository on Github.com

First, go to your account on github.com and click "New repository".



Choose a name. Call it whatever you want (the shorter the better), or follow me for convenience. I will call mine `r-workshop`.

Also, add a description, make it public, create a README file, and create your repo!

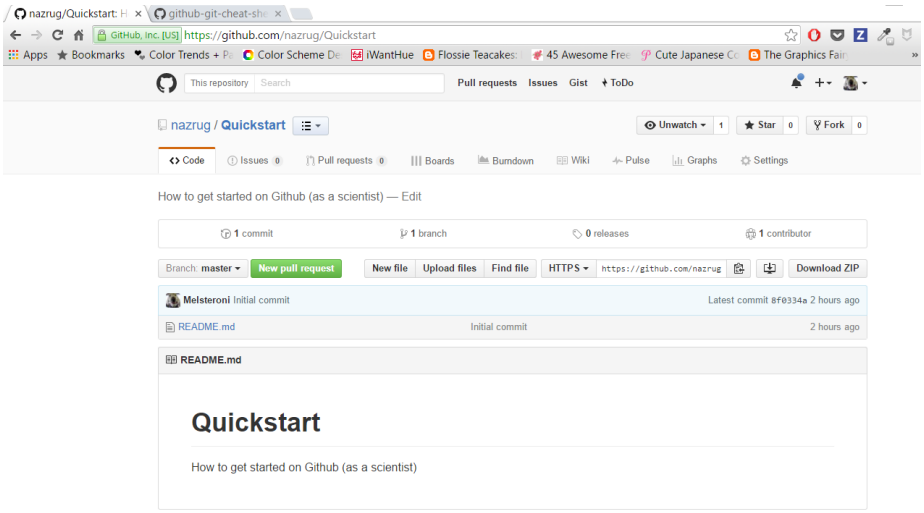


The *Add gitignore* option adds a document where you can identify files or file-types you want Github to ignore. These files will stay in on the local Github folder (the one on your computer), but will not be uploaded onto the web version of Github.

The *Add a license* option adds a license that describes how other people can use your Github files (e.g., open source, but no one can profit from them, etc.). We won't worry about this today.

Check out our new repository!

Notice how the README.md file we created is automatically displayed at the bottom. The .md means that it is Markdown (remember how .Rmd was RMarkdown?) so the formatting we learned in the last lesson apply here.



4.7 Create a gh-pages branch

We aren't going to talk about branches very much, but they are a powerful feature of git/GitHub. I think of it as creating a copy of your work that becomes a parallel universe that you can modify safely because it's not affecting your original work. And then you can choose to merge the universes back together if and when you want. By default, when you create a new repo you begin with one branch, and it is named `master`. When you create new branches, you can name them whatever you want. However, if you name one `gh-pages` (all lowercase, with a `-` and no spaces), this will let you create a website. And that's our plan. So, let's do this to create a `gh-pages` branch:

On the homepage for your repo on GitHub.com, click the button that says "Branch:master". Here, you can switch to another branch (right now there aren't any others besides `master`), or create one by typing a new name.

Let's type `gh-pages`.

Let's also change `gh-pages` to the default branch and delete the master branch: this will be a one-time-only thing that we do here:

First click to control branches:

And then click to change the default branch to `gh-pages`. I like to then delete the `master` branch when it has the little red trash can next to it. It will make you confirm that you really want to delete it, which I do!

From here, you will work locally (on your computer).

4.8 Clone your repository using RStudio

We'll start of by cloning to our local computer using RStudio. We are going to be cloning a copy of our Remote repository on Github.com to our local computers. Unlike downloading, cloning keeps all the version control and user information bundled with the files.

Step 0: Create your `github` folder

This is really important! We need to be organized and deliberate about where we want to keep all of our GitHub repositories (since this is the first of many in your career).

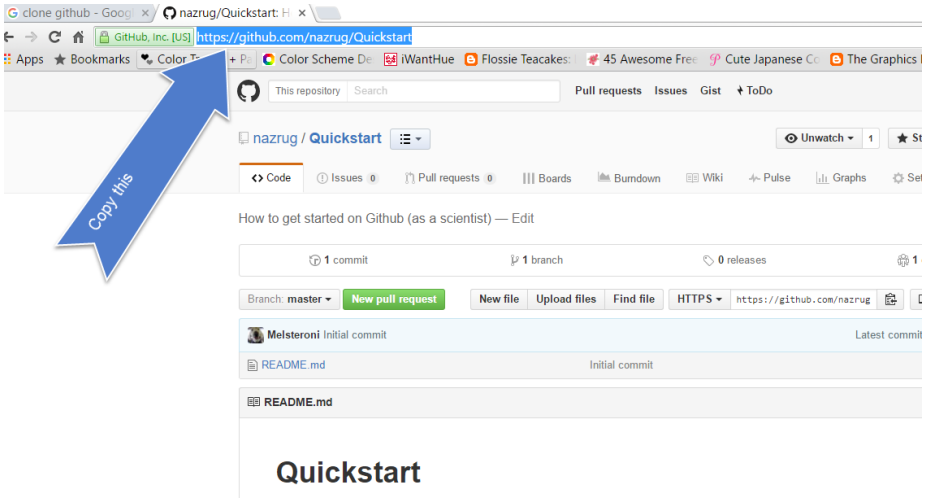
Let's all make a folder called `github` (all lowercase!) in our home directories. So it will look like this:

- Windows: `Users\[User]\Documents\github\`
- Mac: `Users/[User]/github/`

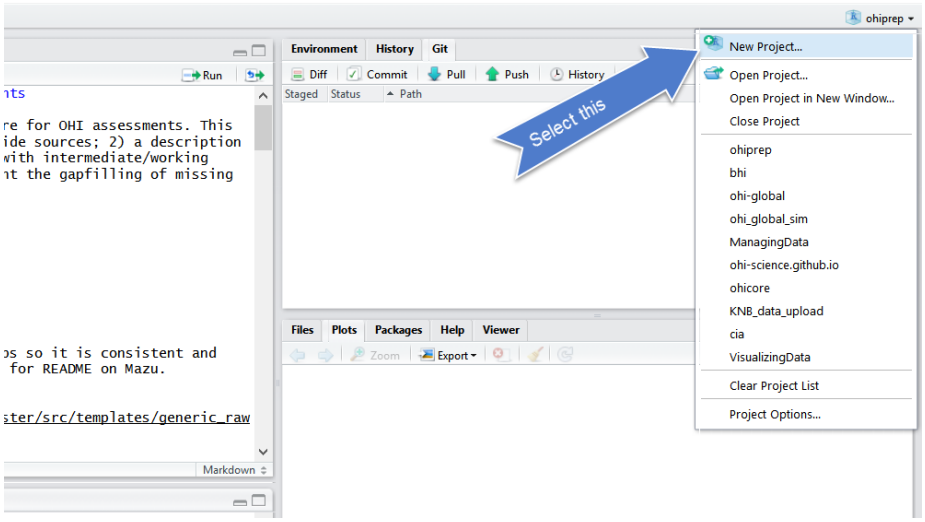
This will let us take advantage of something that is really key about GitHub.com: you can easily navigate through folders within repositories and the urls reflect this navigation. The greatness of this will be evident soon. So let's set ourselves up for easily translating (and remembering) those navigation paths by having a folder called `github` that will serve as our 'github.com'.

So really. Make sure that you have an all-lowercase folder called `github` in your home directory!!

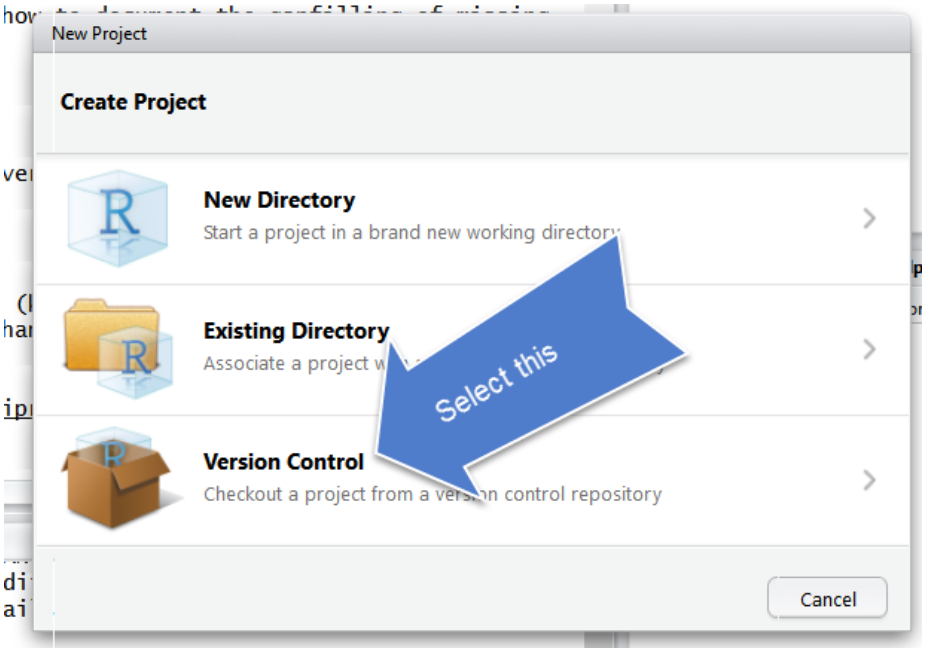
Step 1: Copy the web address of the repository you want to clone.



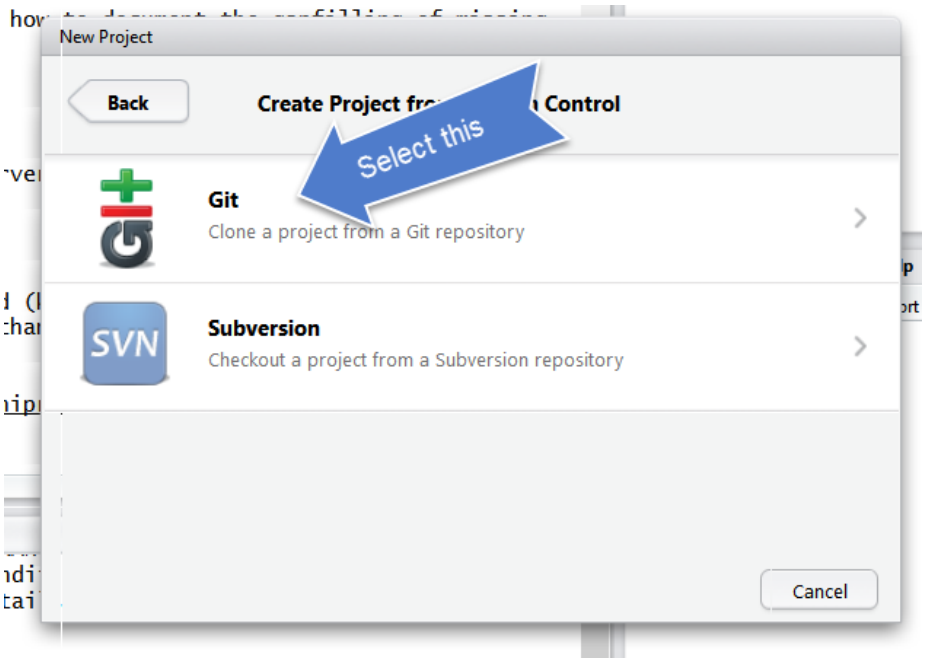
Step 2: from RStudio, go to New Project (also in the File menu).



Step 3: Select Version Control

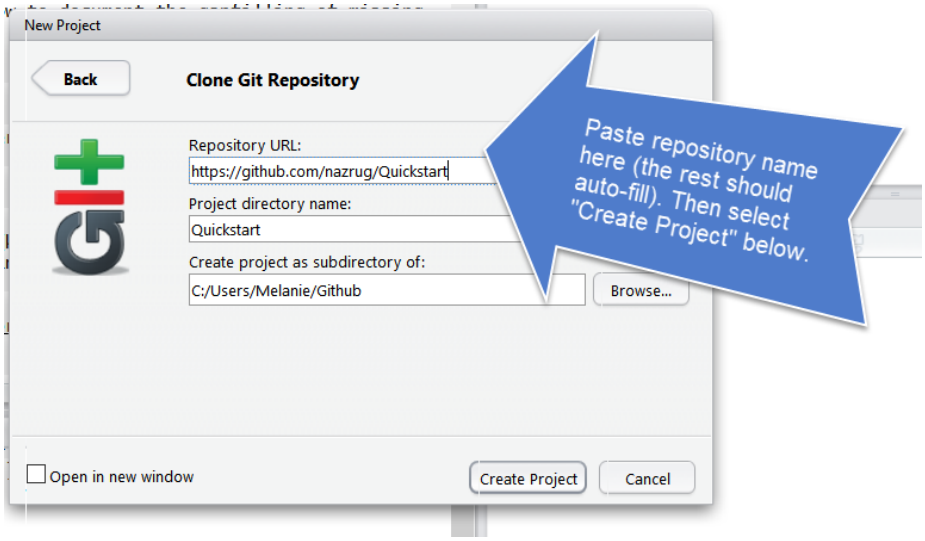


Step 4: Select Git

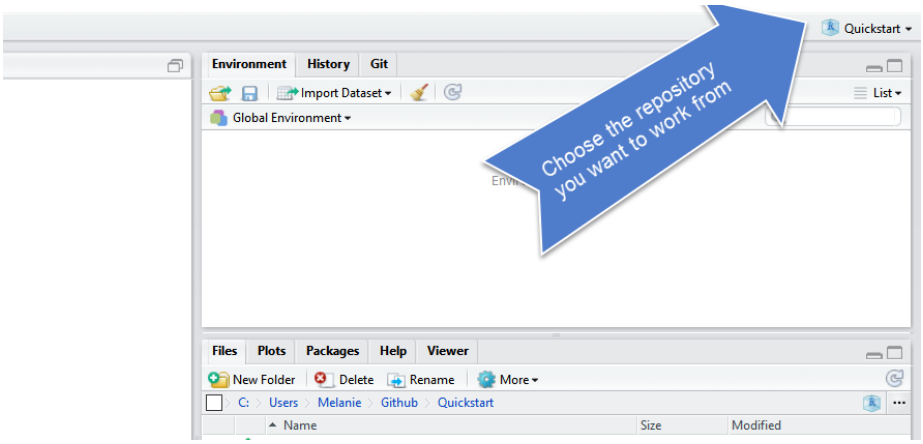


Step 5: Paste it in the Repository URL field, and type **tab** to autofill the Project Directory name. Make sure you keep the Project Directory Name **THE SAME** as the repository name from the URL.

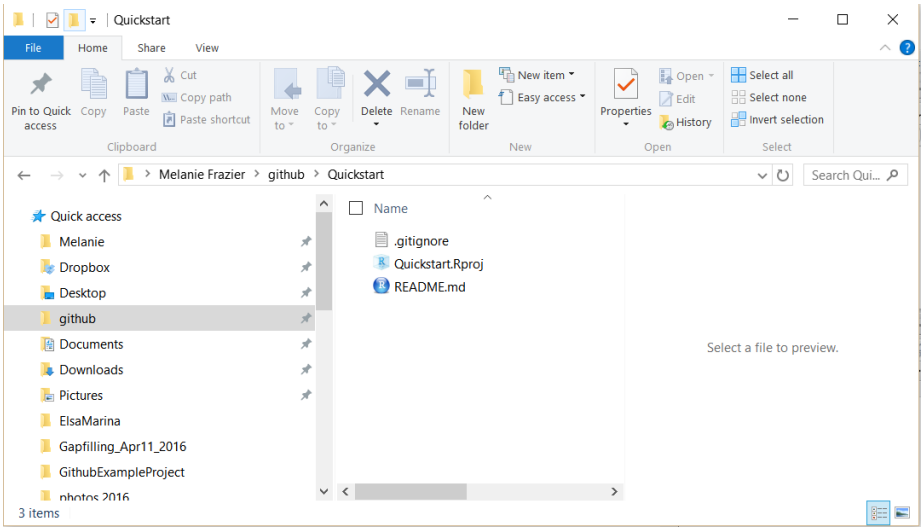
Save it in your github folder (click on Browse) to do this.



If everything went well, the repository will be added to the list located here:



And the repository will be saved to the Github folder on your computer:



Ta da!!!! The folder doesn't contain much of interest, but we are going to change that.

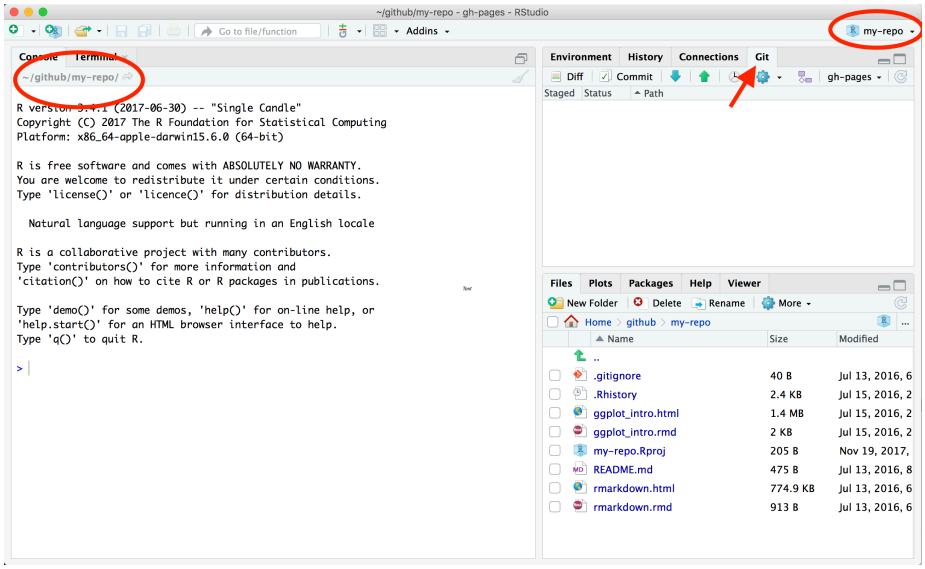
4.9 Inspect your repository

Notice a few things in our repo here:

1. Our working directory is set to `~/github/r-workshop`. This means that I can start working with the files I have in here without setting the filepath. This is that when we cloned this from RStudio, it created an RStudio project, which you can tell because:
    - `.RProj` file, which you can see in the Files pane.

- The project is named in the top right hand corner

2. We have a git tab! This is how we will interface directly to Github.com



When you first clone a repo through RStudio, RStudio will add an `.Rproj` file to your repo. And if you didn't add a `.gitignore` file when you originally created the repo on GitHub.com, RStudio will also add this for you. These will show up with little yellow `?` icons in your git tab. This is GitHub's way of saying: "I am responsible for tracking everything that happens in this repo, but I haven't seen these files yet. Do you want me to track them too?" (We'll see that when you click the box to stage them, they will turn into `A`s because they have been added to the repo.

4.10 Add files to our local repo

The repository will contain:

- .gitignore file
- README.md
- Rproj

Let's create the following:

- folder called "data"
- folder called "figures"

They both show up in your Finder! ...

4.10.1 Get data files into your working directory

In Session 1, we introduced how and why R Projects are great for reproducibility, because our self-contained working directory will be the **first** place R looks for files.

You downloaded several files for this workshop, some comma separate value (CSV) files and some as Excel spreadsheets (.xlsx):

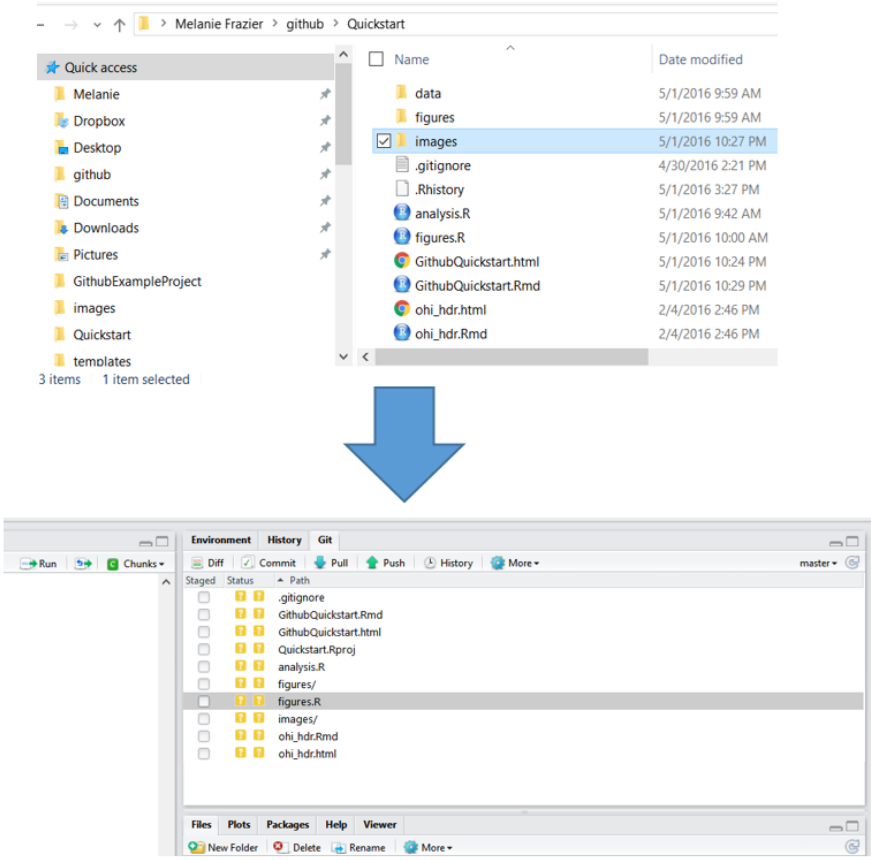
- fish_counts_curated.csv
- invert_counts_curated.xlsx
- kelp_counts_curated.xlsx
- substrate_cover_curated.xlsx
- lobsters.xlsx
- lobsters2.xlsx
- ca_np.csv
- ci_np.xlsx

Copy and paste those files into the 'data' subfolder of your R project. Notice that now these files are in your working directory when you go back to that Project in RStudio (check the 'Files' tab and navigate to the data subfolder). That means they're going to be in the first place R will look when you ask it to find a file to read in.

I'm going to go to the Finder (Windows Explorer on a PC) and copy a file into my repository from there. And then I'm going to go back to RStudio – it shows up in the git tab! So the repository is being tracked, no matter how you make changes to it (changes do not have to be done only through RStudio).

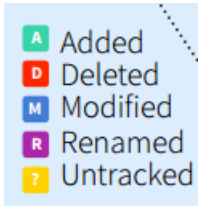
To make changes to the repository, you will work from your computer ("local Github").

When files are changed in the local repository, these changes will be reflected in the Git tab of RStudio:



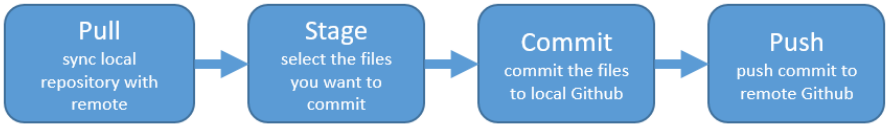
4.10.2 Inspect what has changed

These are the codes RStudio uses to describe how the files are changed, (from the RStudio cheatsheet):



4.11 Sync from RStudio to GitHub

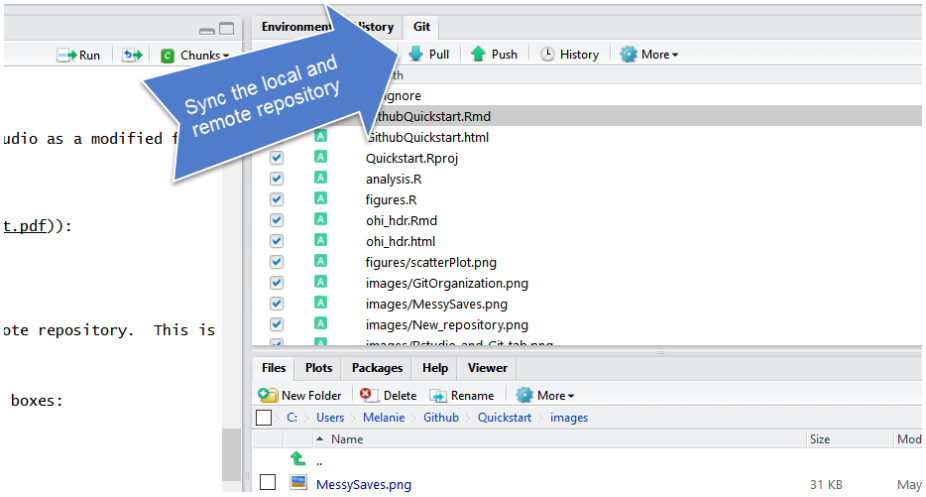
When you are ready to commit your changes, you follow these steps:



We walk through this process below:

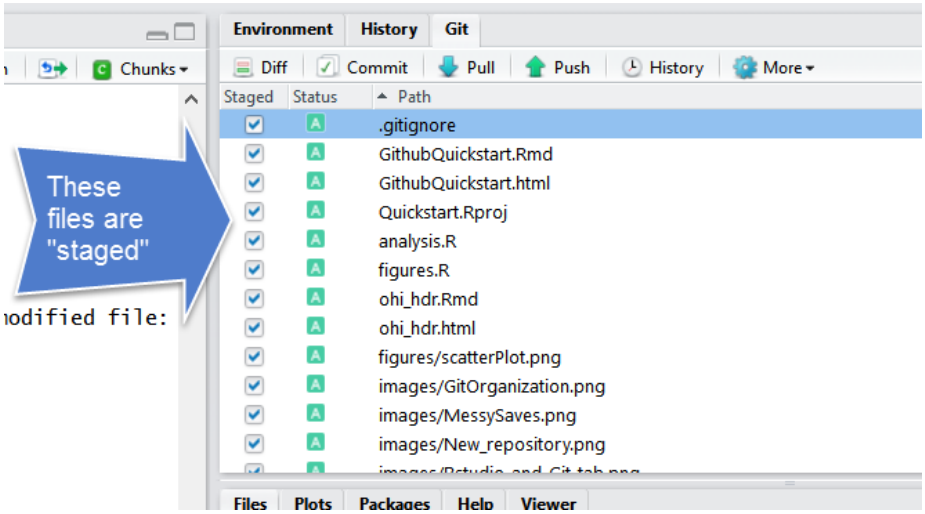
4.11.1 Pull

From the Git tab, "Pull" the repository. This makes sure your local repository is synced with the remote repository. This is very important if other people are making changes to the repository or if you are working from multiple computers.

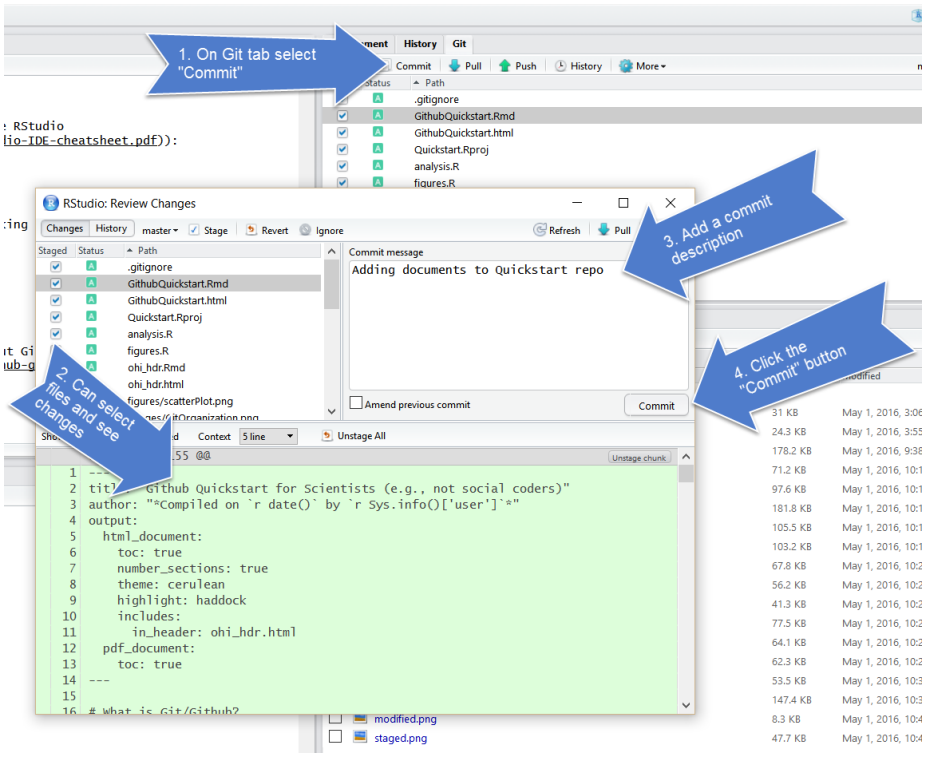


4.11.2 Stage

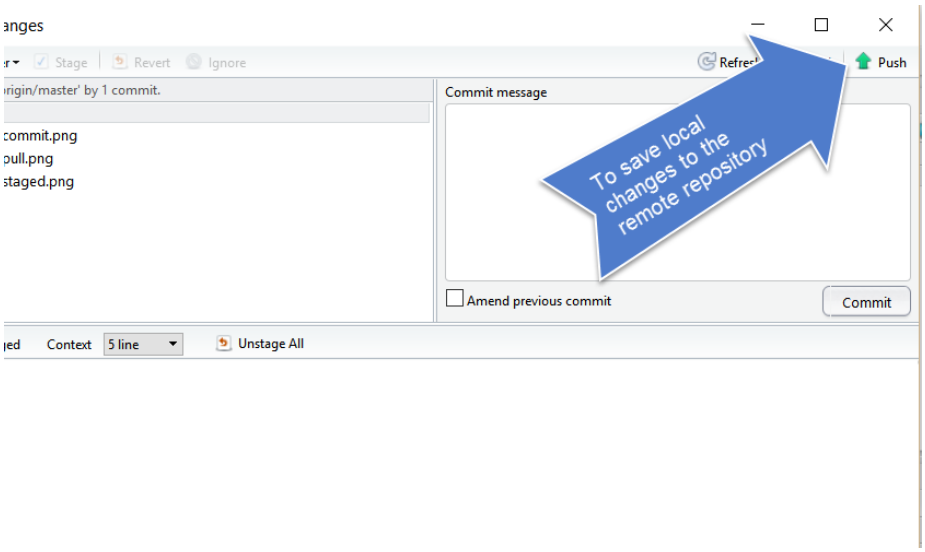
Stage the files you want to commit. In RStudio, this involves checking the "Staged" boxes:


Environment
History
Git
Diff
Commit
Pull
Push
History
More
Staged
Status
Path
.gitignore
GithubQuickstart.Rmd
GithubQuickstart.html
Quickstart.Rproj
analysis.R
figures.R
ohi_hdr.Rmd
ohi_hdr.html
figures/scatterPlot.png
images/GitOrganization.png
images/MessySaves.png
images/New_repository.png
These files are "staged"
Files
Plots
Packages
Help
Viewer

4.11.3 Commit

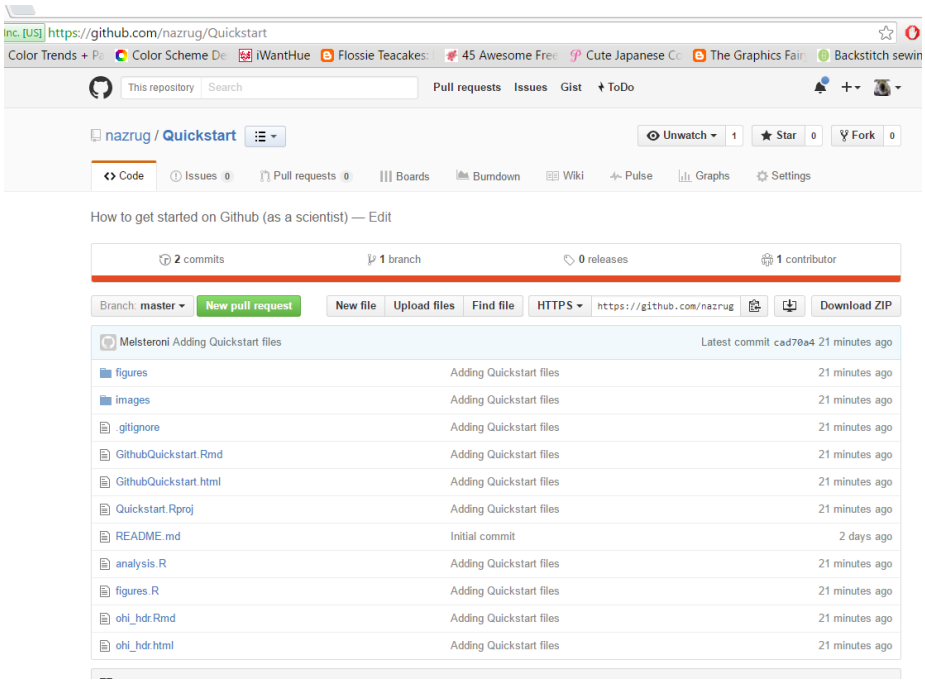

1. On Git tab select "Commit"
RStudio: Review Changes
Commit message
Adding documents to Quickstart repo
3. Add a commit description
2. Can select files and see changes
4. Click the "Commit" button
Amend previous commit
Commit

4.11.4 Push



4.12 Explore remote Github

The files you added should be on github.com:



Let's also explore commit history, file history.

4.12.1 Activity

Go back to RStudio.

This time let's edit an existing file instead of adding something new. Open your README file by clicking on it in the Files pane (lower right corner). Write a few lines of text (like your dog's name), save, and see what happens in your Git Tab. Sync it to your remote repository at Github.com.

4.13 Create a new R Markdown file

Now get ourselves back into learning R. We are going to use R Markdown so that you can write notes to yourself in Markdown, and have a record of all your R code. Writing R commands in the console like we did this morning is great, but limited; it's hard to keep track of and hard to efficiently share with others. Plus, as your analyses get more complicated, you need to be able to see them all in one place.

Go to File > New File > R Markdown … (or click the green plus in the top left corner).

Let's set up this file so we can use it for the rest of the day. I'm going to delete all the text that is already there and write some new text.

Here's what I'm going to write in my R Markdown file to begin:

```
---
title: "Reading data into R with `readxl`"
author: "Julie Lowndes"
date: "12/7/2019"
output: html_document
---

# Learning `readxl`

We are working with data and it's going to be amazing.
```

Now, let's save it. I'm going to call my file `readxl.Rmd`. You can knit it if you'd like.

Then, knit your file, and sync your file to GitHub: commit and pull

What if a file doesn't show up in the Git tab and you expect that it should? Check to make sure you've saved the file. If the filename is red with an asterix, there have been changes since it was saved. Remember to save before syncing to GitHub!

4.14 Explore your webpage

You've just created a webpage!

It will exist at this url: username.github.io/repo-name/filename. Mine is: jules32.github.io/r-workshop/readxl.

> ***ProTip*** Pay attention to URLs. An unsung skill of the modern analyst is to be able to navigate the internet by keeping an eye on patterns.

Troubleshooting:

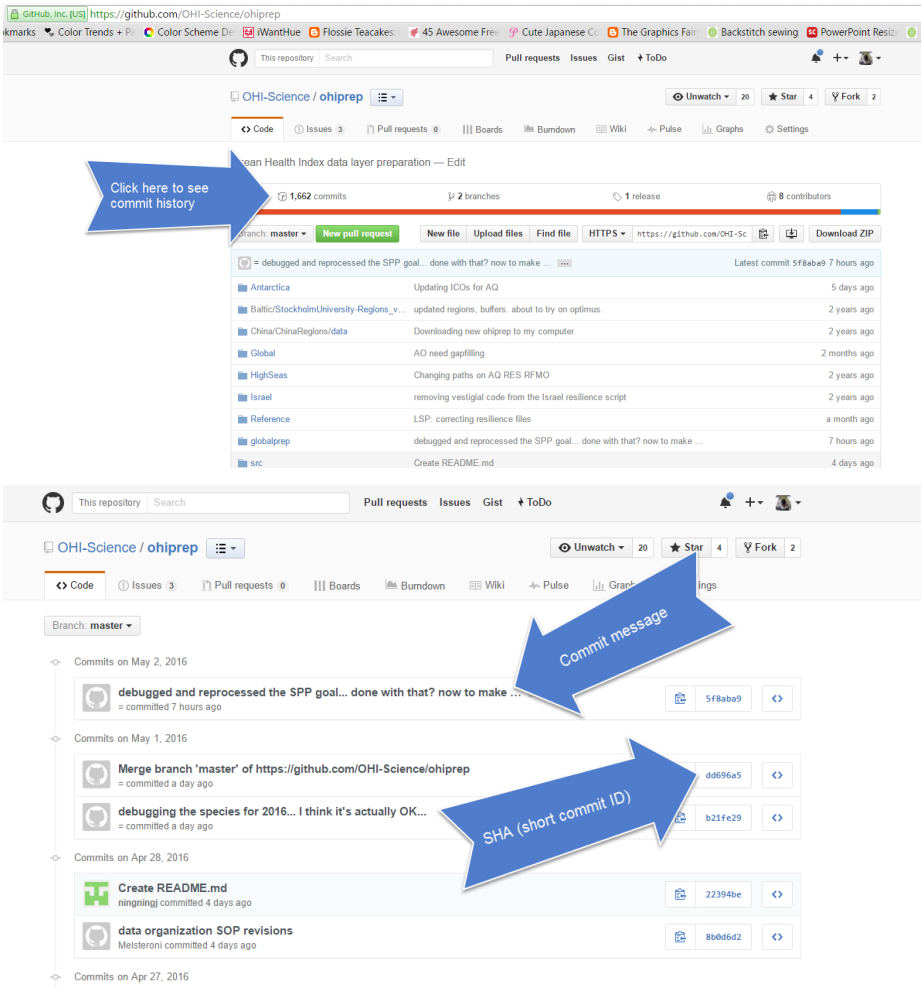
- 404 error? Remove trailing / from the url
- Wants you to download? Remove trailing .Rmd from the url

4.15 Committing - how often? Tracking changes in your files

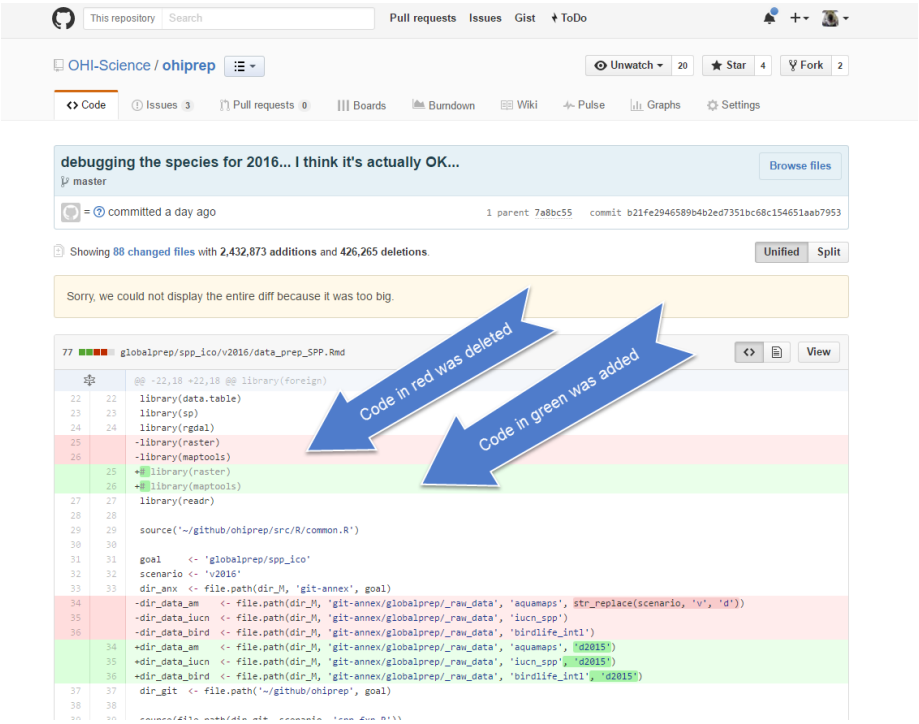
Whenever you make changes to the files in Github, you will walk through the Pull -> Stage -> Commit -> Push steps.

I tend to do this every time I finish a task (basically when I start getting nervous that I will lose my work). Once something is committed, it is very difficult to lose it.

One thing that I love about about Github is that it is easy to see how files have changed over time. Usually I compare commits through github.com:



You can click on the commits to see how the files changed from the previous commit:



4.16 Happy Git with R

If you have problems, we'll help you out using Jenny Bryan's HappyGitWithR, particularly the sections on Detect Git from RStudio and RStudio, Git, GitHub Hell (troubleshooting). So as we are coming around, have a look at it and see if you can help troubleshoot too!

4.17 Efficiency Tips

Chapter 5

`readxl`

5.1 Summary

Check this, may need to be a block quote: The **readxl** package makes it easy to import tabular data from Excel spreadsheets (.xls or .xlsx files) and includes several options for cleaning data during import. **readxl** has no external dependencies and functions on any operating system, making it an OS- and user-friendly package that simplifies getting your data from Excel into R.

5.1.1 Objectives

- Use `read_csv()` to read in a comma separated value (CSV) file
- Use `read_excel()` to read in an Excel worksheet from an Excel workbook
- Replace a specific string/value in a spreadsheet with with `NA`
- Skip n rows when importing an Excel worksheet
- Use `read_excel()` to read in parts of a worksheet (by cell range)
- Specify column names when importing Excel data
- Read and combine data from multiple Excel worksheets into a single df using `purrr::map_df()`
- Write data using `write_csv()` or `write_xlsx()`

5.1.2 Resources

- https://readxl.tidyverse.org/
- readxl Workflows article (from tidyverse.org)

5.2 Lesson

5.2.1 Attach packages

In the .Rmd you just created within your version-controlled `r-workshop` R project, attach the `tidyverse`, `readxl`, `writexl`, and `here` packages.

In this lesson, we'll read in a CSV file with the `read_csv()` function, so we need to have the `readr` package attached. Since it's part of the `tidyverse`, we'll go ahead and attach the `tidyverse` package below our script header using `library(package_name)`. It's a good idea to attach packages within the set-up chunk in R Markdown, so we'll also attach the `readxl`, `writexl`, and `here` packages there.

Here's our first code chunk:

```
{r setup, eval = FALSE}
knitr::opts_chunk$set(echo = TRUE)

# Attach the tidyverse, readxl, writexl and here packages:
library(tidyverse)
library(readxl)
library(writexl)
library(here)
```

Now, all of the packages and functions within the `tidyverse` and `readxl`, including `read_csv()` and `read_excel()`, are available for use.

5.2.2 Use `read_csv()` to read in data from a CSV file

There are many types of files containing data that you might want to work with in R. A common one is a comma separated value (CSV) file, which contains values with each column entry separated by a comma delimiter. CSVs can be opened, viewed, and worked with in Excel just like an .xls or .xlsx file - but let's learn how to get data directly from a CSV into R where we can work with it more reproducibly.

The CSV we'll read in here is called "fish_counts_curated.csv", and contains observations for "the abundance and size of fish species as part of SBCLTER's kelp forest monitoring program to track long-term patterns in species abundance and diversity" from the Santa Barbara Channel Long Term Ecological Research program.

Source: Reed D. 2018. SBC LTER: Reef: Kelp Forest Community Dynamics: Fish abundance. Environmental Data Initiative. https://doi.org/10.6073/pasta/dbd1d5f0b225d903371ce89b09ee7379. Dataset accessed 9/26/2019.

Read in the "fish_counts_curated.csv" file `read_csv("file_name.csv")`, and store it in R as an object called *fish_counts*:

```
fish_counts <- read_csv(here("data", "fish_counts_curated.csv"))
```

Notice that the name of the stored object (here, *fish_counts*) will show up in our Environment tab in RStudio.

Click on the object in the Environment, and R will automatically run the `View()` function for you to pull up your data in a separate viewing tab. Now we can look at it in the spreadsheet format we're used to.

Here are a few other functions for quickly exploring imported data:

- `summary()`: summary of class, dimensions, `NA` values, etc.
- `names()`: variable names (column headers)
- `ls()`: list all objects in environment
- `head()`: Show the first x rows (default is 6 lines)
- `tail()`: Show the last x rows (default is 6 lines)

Now that we have our fish counts data ready to work with in R, let's get the substrate cover and kelp data (both .xlsx files). In the following sections, we'll learn that we can use `read_excel()` to read in Excel files directly.

5.2.3 Use `read_excel()` to read in a single Excel worksheet

First, take a look at *substrate_cover_curated.xlsx* in Excel, which contains a single worksheet with substrate type and percent cover observations at different sampling locations in the Santa Barbara Channel.

A few things to notice:

- The file contains a single worksheet
- There are multiple rows containing text information up top
- Where observations were not recorded, there exists '-9999'

Let's go ahead and read in the data. If the file is in our working directory, we can read in a single worksheet .xlsx file using `read_excel("file_name.xlsx")`. *Note: read_excel() works for both .xlsx and .xls types.*

Like this:

```
substrate_cover <- read_excel(here("data", "substrate_cover_curated.xlsx"))
```

Tada? Not quite.

Click on the object name (*substrate_cover*) in the Environment to view the data in a new tab. A few things aren't ideal:

```
substrate_cover
```

```
## # A tibble: 23,942 x 9
##    `Substrate cover dataset,~ ...2  ...3   ...4  ...5  ...6  ...7  ...8   ...9
##    <chr>                      <chr> <chr>  <chr> <chr> <chr> <chr> <chr>  <chr>
##  1 Source: https://portal.ed~ <NA>  <NA>   <NA>  <NA>  <NA>  <NA>  <NA>   <NA>
##  2 Accessed: 9/28/2019        <NA>  <NA>   <NA>  <NA>  <NA>  <NA>  <NA>   <NA>
##  3 <NA>                       <NA>  <NA>   <NA>  <NA>  <NA>  <NA>  <NA>   <NA>
##  4 year                       month date   site  tran~ quad  side  subst~ perce~
##  5 -9999                      -9999 -9999  carp  1     20    i     b      -9999
##  6 2000                       9     -9999  carp  1     20    o     b      -9999
##  7 2000                       9     9/8/00 carp  1     20    i     b      100
##  8 2000                       9     9/8/00 carp  1     20    o     b      100
##  9 2000                       9     9/8/00 carp  1     40    i     b      100
## 10 2000                       9     9/8/00 carp  1     40    o     b      100
## # ... with 23,932 more rows
```

- The top row of text has automatically become the (messy) column headers
- There are multiple descriptive rows before we actually get to the data
- There are -9999s that we want R to understand as `NA` instead

We can deal with those issues by adding arguments within `read_excel()`. Like:

- Add `skip = n` to skip the first 'n' rows when importing data
- Add `na = "this"` to replace "this" with `NA` when reading in spreadsheet data

```
substrate_cover <- read_excel(here("data", "substrate_cover_curated.xlsx, skip = 4, na
```

```
substrate_cover
```

```
## # A tibble: 23,938 x 9
##    year  month date   site  transect quad  side  substrate_type percent_cover
##    <chr> <chr> <chr>  <chr> <chr>    <chr> <chr> <chr>          <chr>
##  1 <NA>  <NA>  <NA>   carp  1        20    i     b              <NA>
##  2 2000  9     <NA>   carp  1        20    o     b              <NA>
##  3 2000  9     9/8/00 carp  1        20    i     b              100
##  4 2000  9     9/8/00 carp  1        20    o     b              100
##  5 2000  9     9/8/00 carp  1        40    i     b              100
##  6 2000  9     9/8/00 carp  1        40    o     b              100
##  7 2000  9     9/8/00 carp  2        20    i     b              90
##  8 2000  9     9/8/00 carp  2        20    o     b              80
##  9 2000  9     9/8/00 carp  2        40    i     b              80
## 10 2000  9     9/8/00 carp  2        40    o     b              85
## # ... with 23,928 more rows
```

Check out *substrate_cover*, and see that the first row *after* the 4 skipped are the column names, and all -9999s have been updated to `NA`. Hooray!

5.2.4 Use `read_excel()` to read in only *part* of an Excel worksheet

We always advocate for leaving the raw data raw, and writing a complete script containing all steps of data wrangling & transformation. But in *some* situations (be careful), you may want to specify a range of cells to read in from an Excel worksheet.

You can specify a range of cells to read in using the `range =` argument in `read_excel()`. For example, if I want to read in the rectangle from D12:I15 in *substrate_cover_curated.xlsx* - only observations for Carpenteria Beach (Transect 2) in September 2000 - I can use:

```
carp_cover_2000 <- read_excel(here("data", "substrate_cover_curated.xlsx", range = "D12:I15")
```

But yuck. Look at *carp_cover_2000* and you'll notice that the first row *of that range* is automatically made the column headers. To keep all rows within a range and **add your own column names**, add a `col_names =` argument:

```
carp_cover_2000 <- read_excel(here("data", "substrate_cover_curated.xlsx", range = "D12:I15", col
```

```
carp_cover_2000
```

```
## # A tibble: 4 x 6
##   site_name transect quad  plot_side type  coverage
##   <chr>     <chr>    <chr> <chr>     <chr> <chr>
## 1 carp      2        20    i         b     90
## 2 carp      2        20    o         b     80
## 3 carp      2        40    i         b     80
## 4 carp      2        40    o         b     85
```

So far we've read in a single CSV file using `read_csv()`, and an Excel file containing a single worksheet with `read_excel()`. Next, let's read in data from an Excel workbook that contains multiple worksheets.

5.2.5 Use `read_excel()` to read in selected worksheets from a workbook

Now, we'll read in the kelp fronds data from file *kelp_counts_curated.xlsx*. Open the file in Excel, and notice see that it contains multiple worksheets with giant kelp observations in the Santa Barbara Channel during July 2016, 2017, and 2018, with data collected at each *site* in a separate worksheet.

To read in a single Excel worksheet from a workbook we'll again use `read_excel("file_name.xlsx")`, but we'll need to let R know which worksheet to get.

Let's read in the kelp data just like we did above, as an object called *kelp_counts*.

```
kelp_counts <- read_excel(here("data", "kelp_counts_curated.xlsx")
```

You might be thinking, "Hooray, I got all of my Excel workbook data!" But remember to always look at your data - you will see that actually only the first worksheet was read in. The default in `read_excel()` is to read in the **first worksheet** in a multi-sheet Excel workbook.

To check the worksheet names in an Excel workbook, use `excel_sheets()`:

```
excel_sheets(here("data", "kelp_counts_curated.xlsx")
```

If we want to read in data from a worksheet other than the first one in an Excel workbook, we can specify the correct worksheet by name or position by adding the `sheet` argument.

Let's read in data from the worksheet named *golb* (Goleta Beach) in the *kelp_counts_curated.xlsx* workbook:

```
kelp_golb <- read_excel(here("data", "kelp_counts_curated.xlsx", sheet = "golb"))
```

Note that you can also specify a worksheet by position: since *golb* is the 6th worksheet in the workbook, we could also use the following:

```
kelp_golb <- read_excel(here("data", "kelp_counts_curated.xlsx", sheet = 6))
```

```
kelp_golb
```

```
## # A tibble: 3 x 4
##   year  month site  total_fronds
##   <chr> <chr> <chr>        <dbl>
## 1 2016  7     golb          2557
## 2 2017  7     golb          1575
## 3 2018  7     golb          1629
```

5.2.6 Read in and combine data from multiple worksheets into a data frame simultaneously with `purrr::map_df()`

So far, we've read in entire Excel worksheets and pieces of a worksheet. What if we have a workbook (like *kelp_counts_curated.xlsx*) that contains worksheets that contain observations for the same variables, in the same organization? Then we may want to read in data from *all* worksheets, and combine them into a single data frame.

We'll use `purrr::map_df()` to loop through all the worksheets in a workbook, reading them in & putting them together into a single data frame in the process.

The steps we'll go through in the code below are:

1. Set a pathway so that R knows where to look for an Excel workbook
2. Get the names of all worksheets in that workbook with `excel_sheets()`
3. Set names of a vector with `set_names()`
4. Read in all worksheets, and put them together into a single data frame with `purrr::map_df()`

Aside: the pipe operator (`%>%`)

There are many ways to use R functions in sequence. One way, that follows the order that we think about steps in sequence, is using the **pipe operator** (`%>%`). We can use the pipe operator between steps in a sequence, each place we think "and then do this."

For example, if I would like to **walk my dog** and *then* **eat a burrito**, in code that might be: `walk(dog) %>% eat(burrito, type = "California")`

Here, we'll use the pipe operator to complete steps 1 - 4 above in sequence:

```
kelp_path <- here("data", "kelp_counts_curated.xlsx")

kelp_all_sites <- kelp_path %>%
  excel_sheets() %>%
  set_names() %>%
  purrr::map_df(read_excel, kelp_path)
```

Check out *kelp_all_sites*, and notice that now the data from all 11 sites is now collected into a single data frame:

```
kelp_all_sites
```

```
## # A tibble: 32 x 4
##    year  month site  total_fronds
##    <chr> <chr> <chr>        <dbl>
##  1 2016  7     abur           307
##  2 2017  7     abur           604
##  3 2018  7     abur          3532
##  4 2016  7     ahnd          2572
##  5 2017  7     ahnd            16
##  6 2018  7     ahnd            16
##  7 2016  7     aque         11152
##  8 2017  7     aque          9194
##  9 2018  7     aque          7754
## 10 2016  7     bull          6706
## # ... with 22 more rows
```

5.2.7 Save data frames as .csv or .xlsx with `write_csv()` or `write_xlsx()`

There are a number of reasons you might want to save (/export) data in a data frame as a .csv or Excel worksheet, including:

- To store raw data within the project you're working in
- To store copies of intermediate data frames
- To convert your data back to a format that your coworkers/clients/colleagues will be able to use it more easily

Use `write_csv(object, "file_name.csv")` to write a data frame to a CSV, or `write_xlsx(object, "file_name.xlsx")` to similarly export as a .xlsx (or .xls) worksheet.

In the previous step, we combined all of our kelp frond observations into a single data frame. Wouldn't it make sense to store a copy?

As a CSV:

```
write_csv(kelp_all_sites, here("data", "kelp_all_sites.csv"))
```

A cool thing about `write_csv()` is that it just quietly *works* without wrecking anything else you do in a sequence, so it's great to add at the end of a piped sequence.

For example, if I want to read in the range cells C1:D3 'ivee' worksheet from kelp_counts_curated.xlsx, then write that new subset to a .csv file, I can pipe all the way through:

```
kelp_ivee_subset <- read_excel(here("data", "kelp_counts_curated.xlsx"),
                               sheet = "ivee",
                               range = "C1:D3") %>%
  write_csv(here("data", "kelp_ivee.csv"))
```

Now I've created *kelp_ivee_subset.csv*, but the object *kelp_ivee_subset* also exists as an object for me to use in R.

If needed, I can also export a data frame as an Excel (.xlsx) worksheet:

```
write_xlsx(kelp_all_sites, here("data", "kelp_all_sites.xlsx"))
```

5.3 Activity: Import some invertebrates!

There's one dataset we haven't imported or explored yet: invertebrate counts for 5 popular invertebrates (California cone snail, California spiny lobster, orange cup coral, purple urchin and rock scallops) at 11 sites in the Santa Barbara

Channel. Take a look at the *invert_counts_curated.xlsx* data by opening it in Excel

- Read in the *invert_counts_curated.xlsx* worksheet as object 'inverts_july', only retaining **site**, **common_name**, and **2016** and setting the existing first row in the worksheet as to column headers upon import
- Explore the imported data frame using View, names, head, tail, etc.
- Write 'inverts_july' to a CSV file in your working directory called "inverts_july.csv"

```
# Importing only 'site' through '2016' columns:

inverts_july <- read_excel(here("data", "invert_counts_curated.xlsx"), range = "B1:D56")

# Do some basic exploring (why might we want to do this in the Console instead?):

View(inverts_july)
names(inverts_july)
head(inverts_july)
tail(inverts_july)
ls()

# Writing a csv "inverts_july.csv":
write_csv(inverts_july, here("data", "inverts_july.csv"))
```

5.4 Efficiency Tips

- Add an assignment arrow in (<-): Alt + minus (-)
- Undo shortcut: Command + Z
- Redo shortcut: Command + Shift + Z

5.5 Additional thoughts

- Economist article about gene > dates issue in Excel
- Mine: data frame of bike casualities in NC, column names are age ranges but some of them import as dates
- Excel makes some wrong assumptions and doesn't give you a heads up about its decision making

Chapter 6

Graphs with ggplot2

6.1 Summary

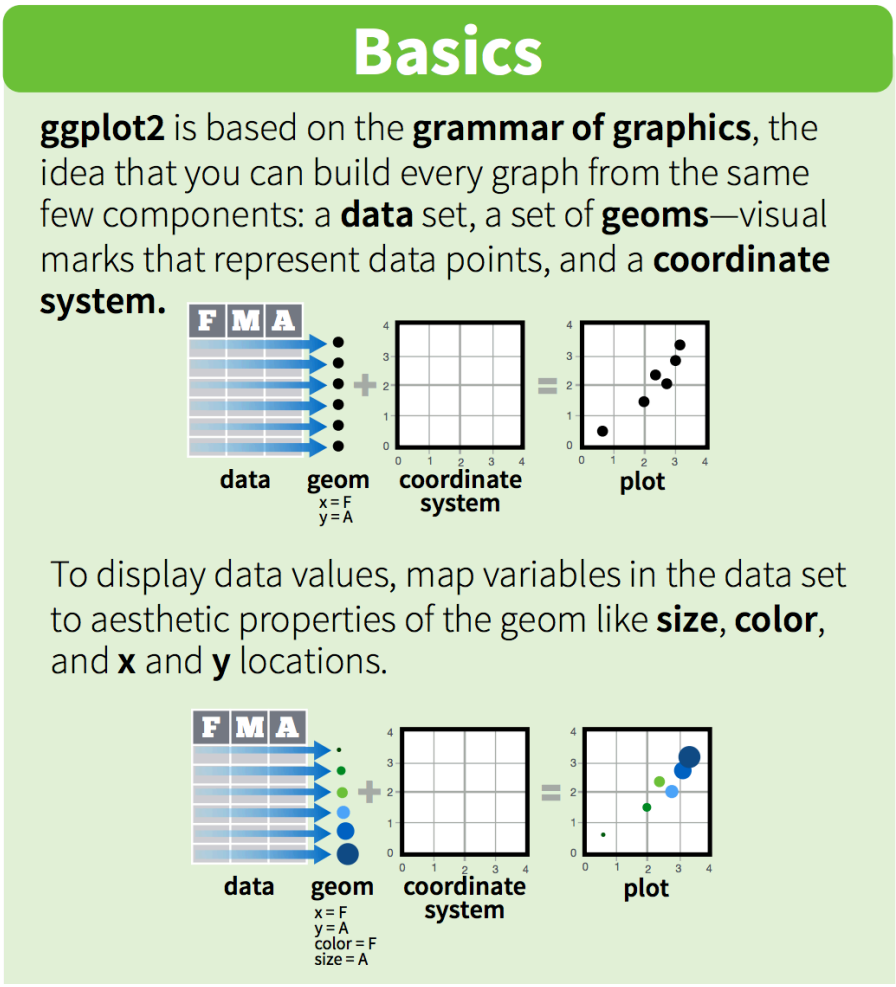
Now that we know how to *get* some data, the next thing we'll probably want to do is *look* at it. In Excel, graphs are made by manually selecting options - which, as we've discussed previously, may not be the best option for reproducibility. Also, if we haven't built a graph with reproducible code, then we might not be able to easily recreate a graph *or* use that code again to make the same style graph with different data.

Using `ggplot2`, the graphics package within the `tidyverse`, we'll write reproducible code to manually and thoughtfully build our graphs.

> "ggplot2 implements the grammar of graphics, a coherent system for describing and building graphs. With ggplot2, you can do more faster by learning one system and applying it in many places." - R4DS

So yeah...that `gg` is from "grammar of graphics" - original source

We'll use the `ggplot2` package, but the function we use to initialize a graph will be `ggplot`, which works best for data in tidy format (i.e., a column for every variable, and a row for every observation). Graphics with `ggplot` are built step-by-step, adding new elements as layers with a plus sign (`+`) between layers (note: this is different from the pipe operator, `%>%`. Adding layers in this fashion allows for extensive flexibility and customization of plots.



6.1.1 Objectives

- Build several common types of graphs (scatterplot, column, line) in ggplot2
- Customize gg-graph aesthetics (color, style, themes, etc.)
- Update axis labels and titles
- Combine compatible graph types (geoms)
- Build multiseries graphs
- Split up data into faceted graphs
- Exporting figures with `ggsave()`

6.1.2 Resources

- https://r4ds.had.co.nz/data-visualisation.html
- ggplot2-cheatsheet-2.1.pdf

- Graphs with ggplot2 - Cookbook for R

- "Why I use ggplot2" - David Robinson Blog Post

6.2 Lesson

6.2.1 Getting started - Create a new .Rmd, attach packages & get data

Within your existing version-controlled R project, create a new R Markdown document with title "Data visualization with ggplot2." Remove everything below the first code chunk. Knit and save the .Rmd file within your project working directory as "my_ggplot2".

The `ggplot2` package is part of the `tidyverse`, so we don't need to attach it separately. Attach the `tidyverse`, `readxl` and `here` packages in the top-most code chunk of your .Rmd.

```
library(tidyverse)
library(readxl)
library(here)
```

In this session, we'll use data for parks visitation from two files:

- A comma-separated-value (CSV) file containing visitation data for all National Parks in California (ca_np.csv)
- A single Excel worksheet containing only visitation for Channel Islands National Park (ci_np.xlsx)

Add a new code chunk to read in the data from the **data** subfolder within your working directory.

```
ca_np <- read_csv(here("data", "ca_np.csv"))
ci_np <- read_xlsx(here("data", "ci_np.xlsx"))
```

Let's take a quick look at the data to see what it contains. For example:

- `View()`: to look at the object in spreadsheet format
- `names()`: to see the variable (column) names
- `summary()`: see a quick summary of each variable

6.2.2 Our first ggplot graph: Visitors to Channel Islands NP

To create a bare-bones ggplot graph, we need to tell R three basic things:

1. We're using `ggplot`
2. Data we're using & variables we're plotting (i.e., what is x and/or y?)
3. What type of graph we're making (the type of *geom*)

Generally, that structure will look like this:

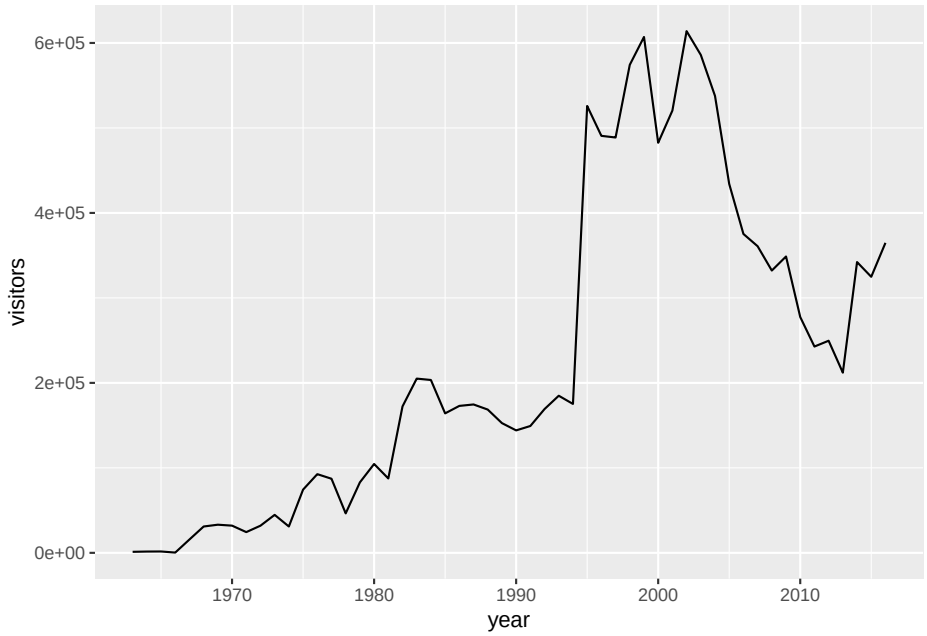
```
ggplot(data = df_name, aes(x = x_var_name, y = y_var_name)) +
  geom_type()
```

Breaking that down:

- First, tell R you're using `ggplot()`
- Then, tell it the object name where variables exist (`data = df_name`)
- Next, tell it the aesthetics `aes()` to specify which variables you want to plot
- Then add a layer for the type of geom (graph type) with `geom_*()` - for example, `geom_point()` is a scatterplot, `geom_line()` is a line graph, `geom_col()` is a column graph, etc.

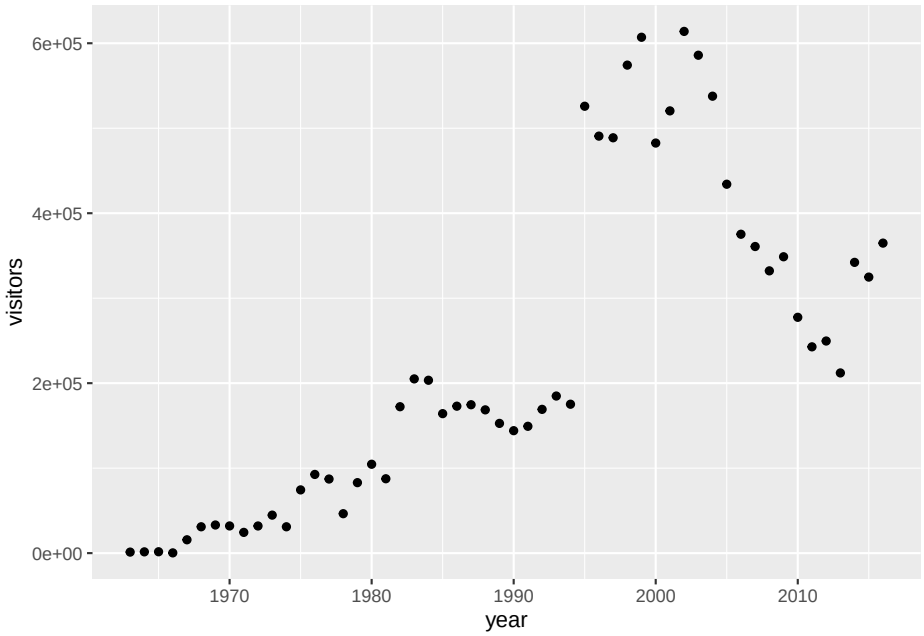
Let's do that to create a line graph of visitors to Channel Islands National Park:

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_line()
```



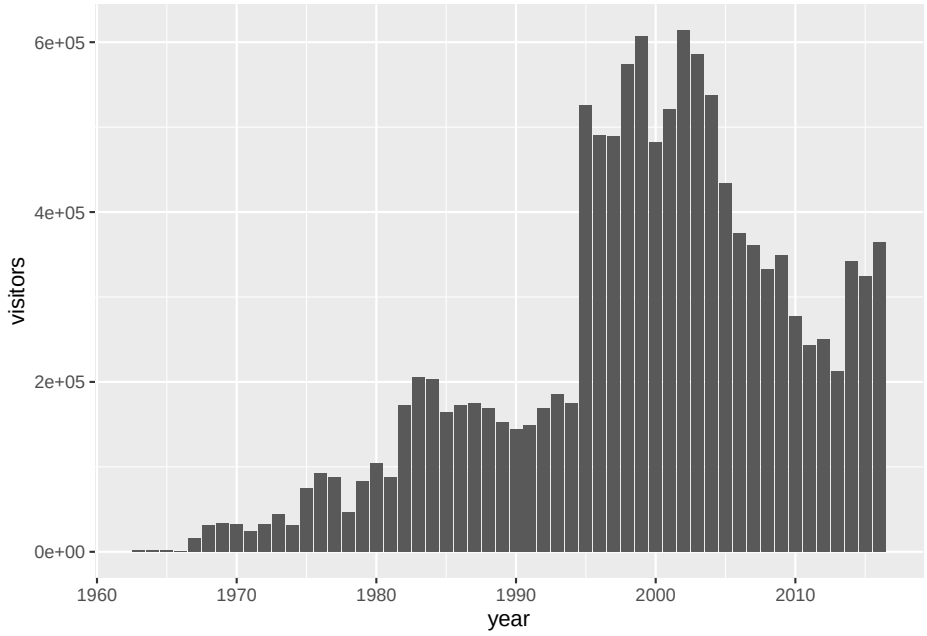
Or, we could change that to a scatterplot just by updating the `geom_*`:

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_point()
```



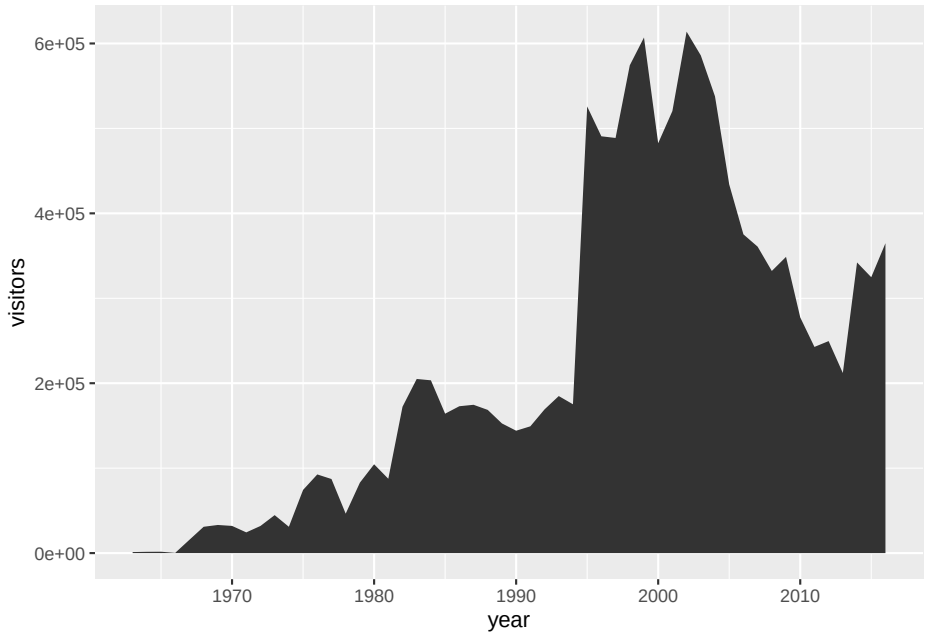
We could even do that for a column graph:

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_col()
```



Or an area plot...

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_area()
```



We can see that updating to different `geom_*` types is quick, so long as the types

of graphs we're switching between are compatible.

The data are there, now let's do some data viz customization.

6.2.3 Intro to customizing ggplot graphs

First, we'll customize some aesthetics (e.g. colors, styles, axis labels, etc.) of our graphs based on non-variable values.

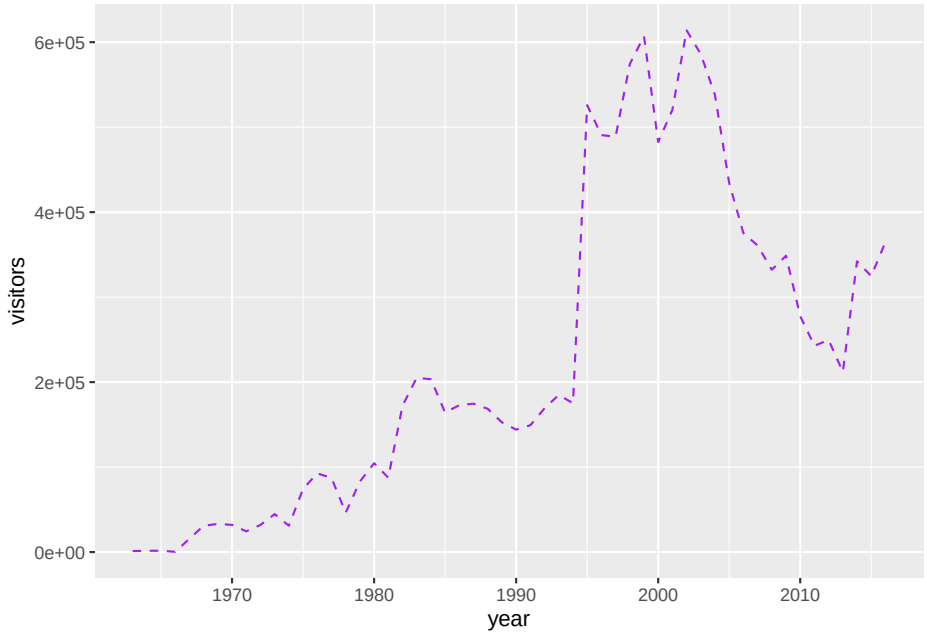
> We can change the aesthetics of elements in a ggplot graph by adding arguments within the layer where that element is created.

Some common arguments we'll use first are:

- `color =` or `colour =`: update point or line colors
- `fill =`: update fill color for objects with areas
- `linetype =`: update the line type (dashed, long dash, etc.)
- `pch =`: update the point style
- `size =`: update the element size (e.g. of points or line thickness)
- `alpha =`: update element opacity (1 = opaque, 0 = transparent)

Building on our first line graph, let's update the line color to "purple" and make the line type "dashed":

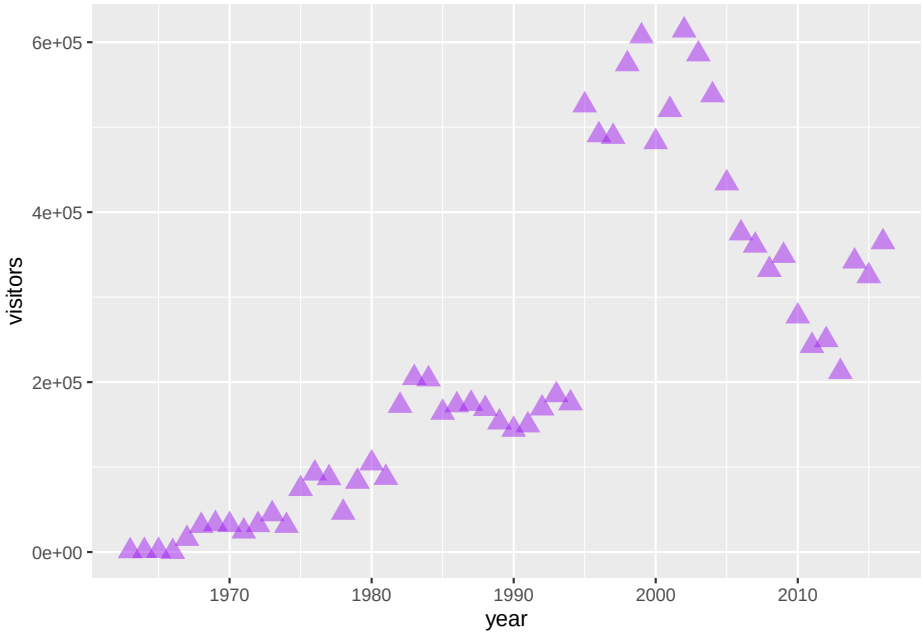
```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_line(
    color = "purple",
    linetype = "dashed"
  )
```



How do we know which color names ggplot will recognize? If you google "R colors ggplot2" you'll find a lot of good resources. Here's one: SAPE ggplot2 colors quick reference guide

Now let's update the point, style and size of points on our previous scatterplot graph using `color =`, `size =`, and `pch =` (see `?pch` for the different point styles, which can be further customized).

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_point(color = "purple",
             pch = 17,
             size = 4,
             alpha = 0.5)
```



6.2.3.1 Activity: customize your own ggplot graph

Update one of the example graphs you created above to customize **at least** an element color and size!

6.2.4 Mapping variables onto aesthetics

In the examples above, we have customized aesthetics based on constants that we input as arguments (e.g., the color / style / size isn't changing based on a variable characteristic or value). Sometimes, however, we **do** want the aesthetics of a graph to depend on a variable. To do that, we'll **map variables onto graph aesthetics**, meaning we'll change how an element on the graph looks based on a variable characteristic (usually, character or value).

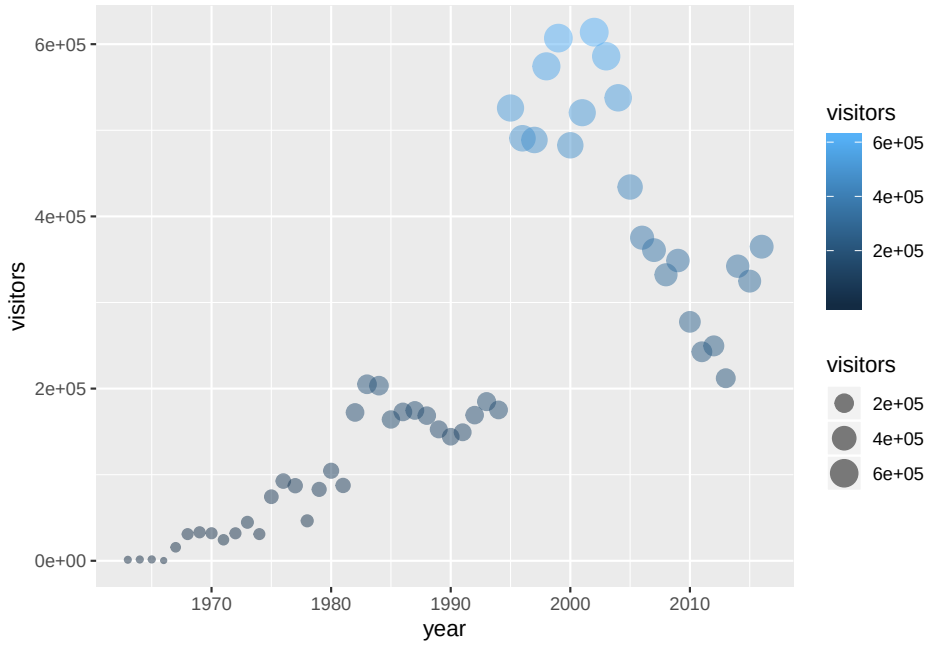
> When we want to customize a graph element based on a variable's characteristic or value, add the argument within `aes()` in the appropriate `geom_*()` layer

In short, if updating aesthetics based on a variable, make sure to put that argument inside of `aes()`.

Example: Create a ggplot scatterplot graph where the **size** and **color** of the points change based on the **number of visitors**, and make all points the same level of opacity (`alpha = 0.5`). Notice the `aes()` around the `size =` and `color =` arguments.

Also: this is overmapped and unnecessary. Avoid excessive / overcomplicated aesthetic mapping in data visualization.

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_point(
    aes(size = visitors,
        color = visitors),
    alpha = 0.5
  )
```

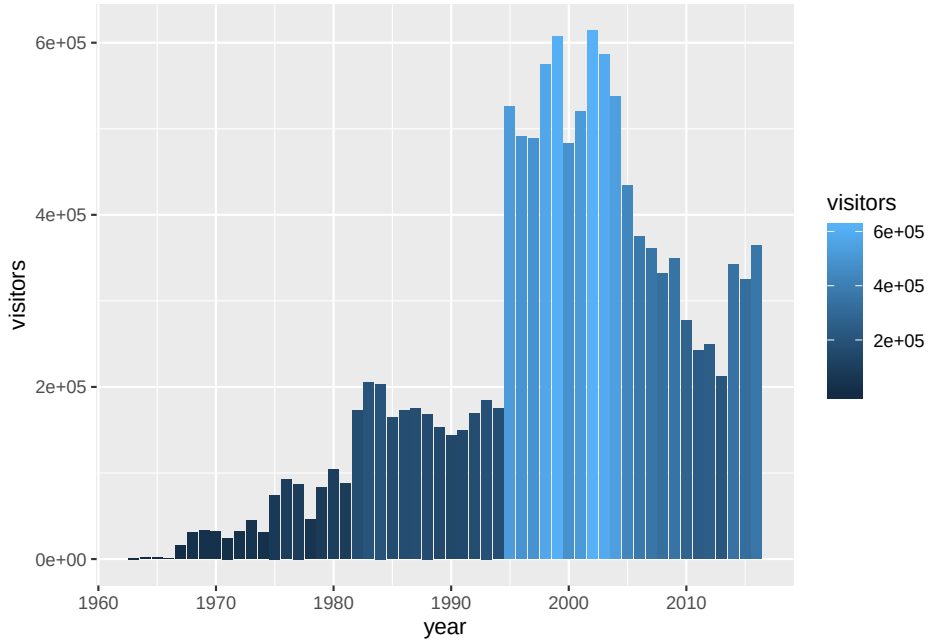


In the example above, notice that the two arguments that **do** depend on variables are within `aes()`, but since `alpha = 0.5` doesn't depend on a variable then it is *outside the `aes()` but still within the `geom_point()` layer.*

6.2.4.1 Activity: map variables onto graph aesthetics

Create a column plot of Channel Islands National Park visitation over time, where the **fill color** (argument: `fill =`) changes based on the number of **visitors**.

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_col(aes(fill = visitors))
```



Sync your project with your GitHub repo.

6.2.5 ggplot2 complete themes

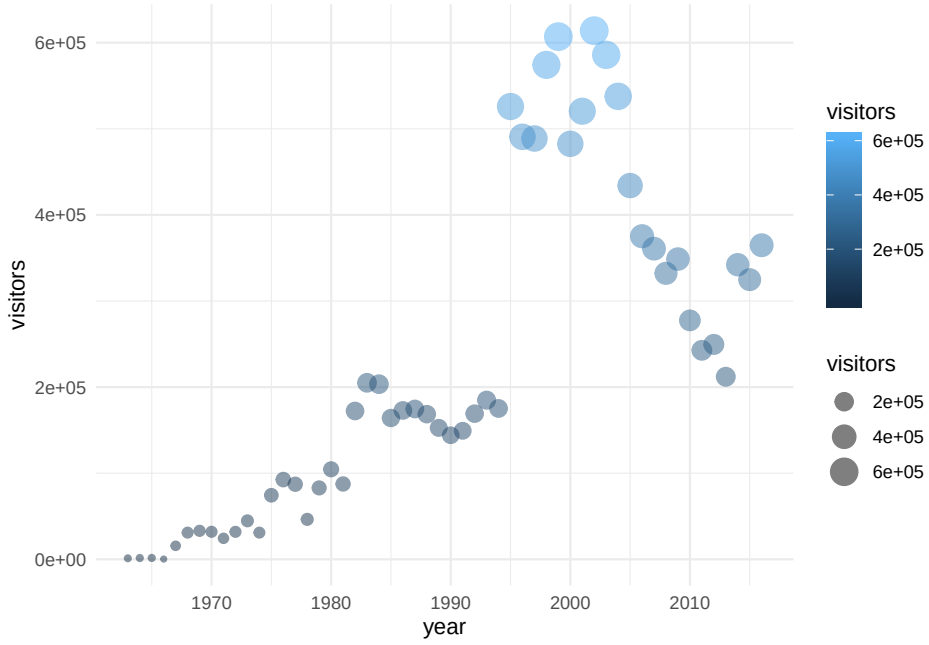
While every element of a ggplot graph is manually customizable, there are also built-in themes (`theme_*()`) that you can add to your ggplot code to make some major headway before making smaller tweaks manually.

Here are a few to try today (but also notice all the options that appear as we start typing `theme_` into our ggplot graph code!):

- `theme_light()`
- `theme_minimal()`
- `theme_bw()`

Here, let's update our previous graph with `theme_minimal()`:

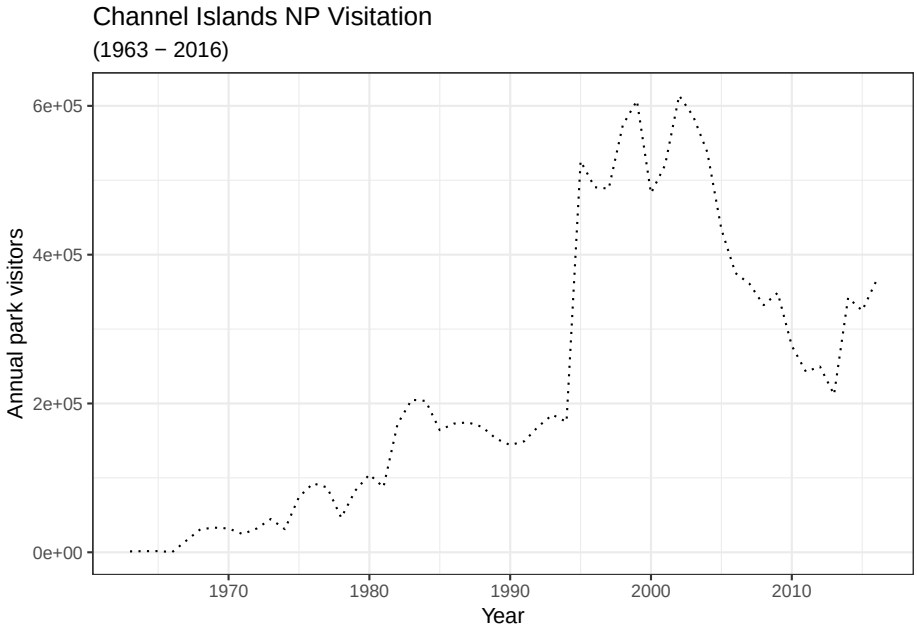
```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_point(
    aes(size = visitors,
        color = visitors),
    alpha = 0.5
  ) +
  theme_minimal()
```



6.2.6 Updating axis labels and titles

Use `labs()` to update axis labels, and add a title and/or subtitle to your ggplot graph.

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_line(linetype = "dotted") +
  theme_bw() +
  labs(
    x = "Year",
    y = "Annual park visitors",
    title = "Channel Islands NP Visitation",
    subtitle = "(1963 - 2016)"
  )
```



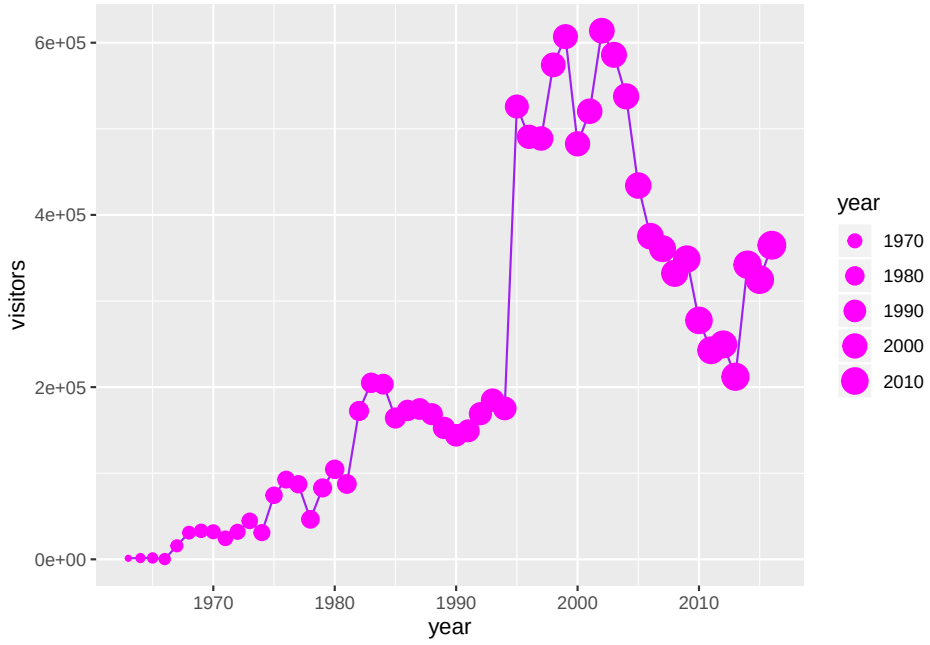
Note: If you want to update the formatting of axis values (for example, to convert to comma format instead of scientific format above), you can use the `scales` package options (see more from the R Cookbook).

6.2.7 Combining compatible geoms

As long as the geoms are compatible, we can layer them on top of one another to further customize a graph.

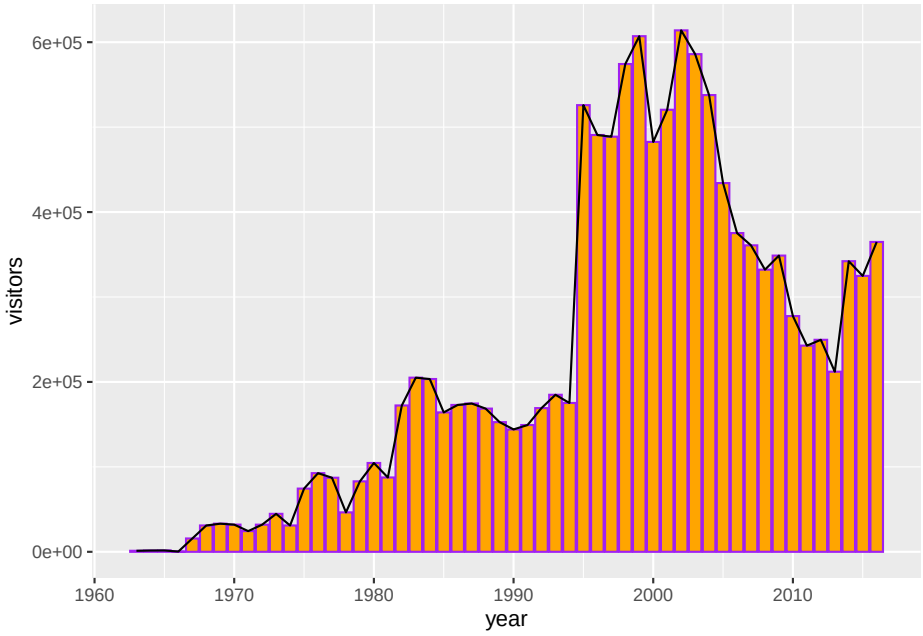
For example, adding points to a line graph:

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_line(color = "purple") +
  geom_point(color = "magenta",
             aes(size = year))
```



Or, combine a column and line graph (not sure why you'd want to do this, but you can):

```
ggplot(data = ci_np, aes(x = year, y = visitors)) +
  geom_col(fill = "orange",
           color = "purple") +
  geom_line()
```

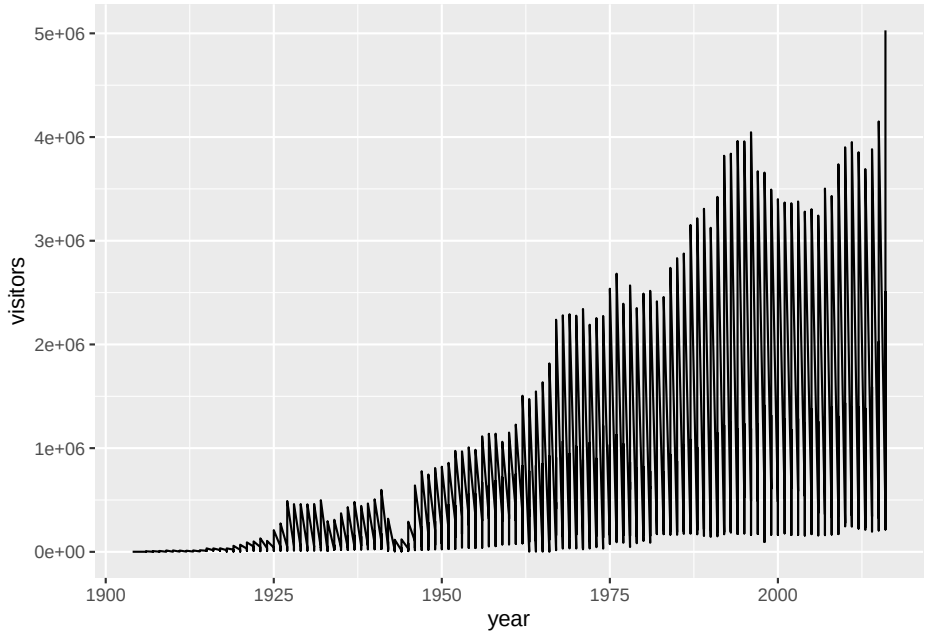


6.2.8 Multi-series ggplot graphs

In the examples above, we only had a single series - visitation at Channel Islands National Park. Often we'll want to visualize multiple series. For example, from the `ca_np` object we have stored, we might want to plot visitation for *all* California National Parks.

To do that, we need to add an aesthetic that lets `ggplot` know how things are going to be grouped. A demonstration of why that's important - what happens if we *don't* let ggplot know how to group things?

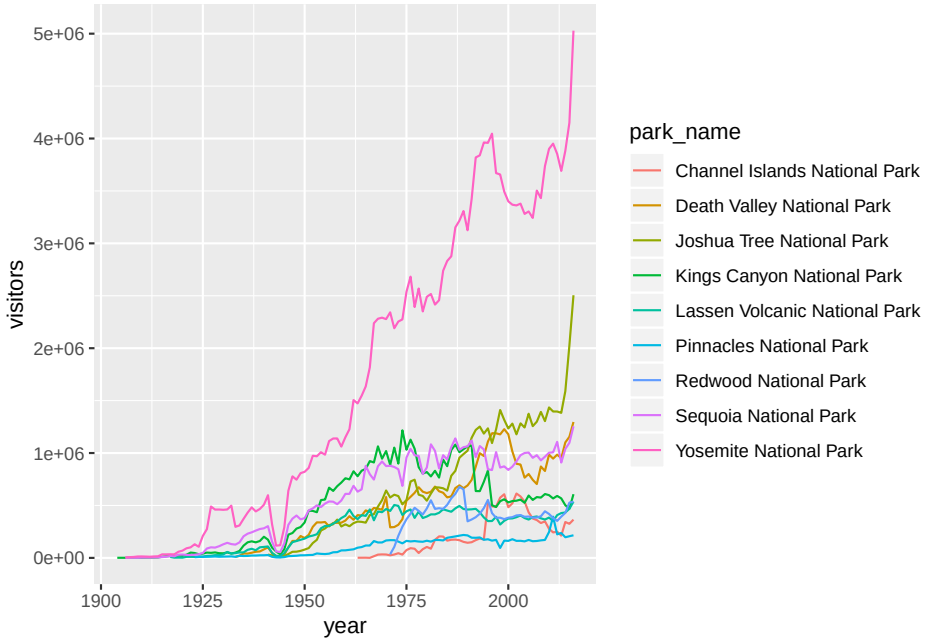
```
ggplot(data = ca_np, aes(x = year, y = visitors)) +
  geom_line()
```



Well that's definitely a mess, and it's because ggplot has no idea that these **should be different series based on the different parks that appear in the 'park_name' column**.

We can make sure R does know by updating an aesthetic based on *park_name*:

```
ggplot(data = ca_np, aes(x = year, y = visitors, color = park_name)) +
  geom_line()
```



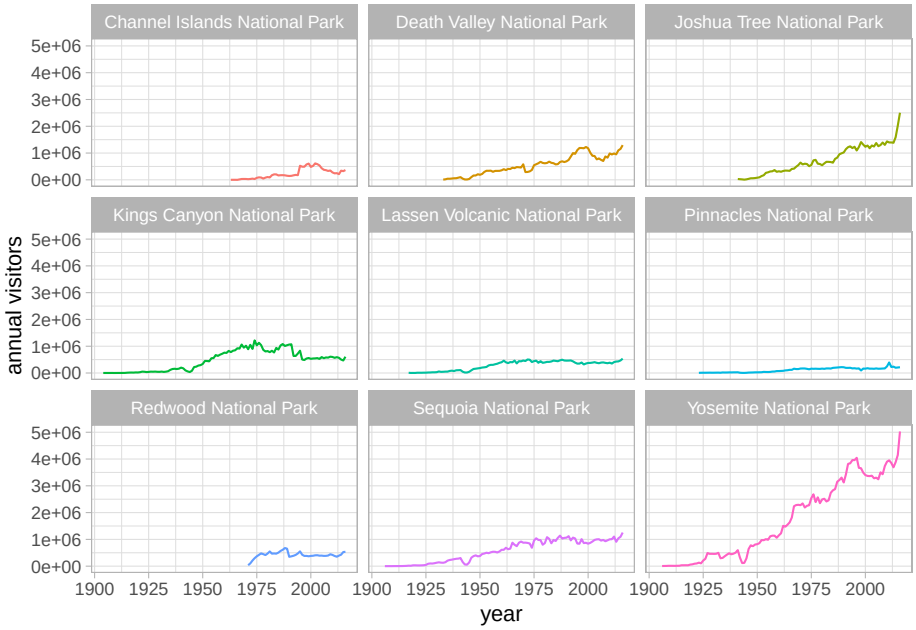
Note: You could also add that aesthetic (`color = park_name`) in the `geom_line()` layer, instead of in the topmost `ggplot()` layer.

6.2.9 Faceting ggplot graphs

When we facet graphs, we split them up into multiple plotting panels, where each panel contains a subset of the data. In our case, we'll split the graph above into different panels, each containing visitation data for a single park.

Also notice that any general theme changes made will be applied to *all* of the graphs.

```
ggplot(data = ca_np, aes(x = year, y = visitors, color = park_name)) +
  geom_line(show.legend = FALSE) +
  theme_light() +
  labs(x = "year", y = "annual visitors") +
  facet_wrap(~ park_name)
```



6.2.10 Exporting a ggplot graph with `ggsave()`

If we want our graph to appear in a knitted html, then we don't need to do anything else. But often we'll need a saved image file, of specific size and resolution, to share or for publication.

`ggsave()` will export the *most recently run* ggplot graph by default (`plot = last_plot()`), unless you give it the name of a different saved ggplot object. Some common arguments for `ggsave()`:

- `width =`: set exported image width (default inches)
- `height =`: set exported image height (default height)
- `dpi =`: set dpi (dots per inch)

So to export the faceted graph above at 180 dpi, width a width of 8" and a height of 7", we can use:

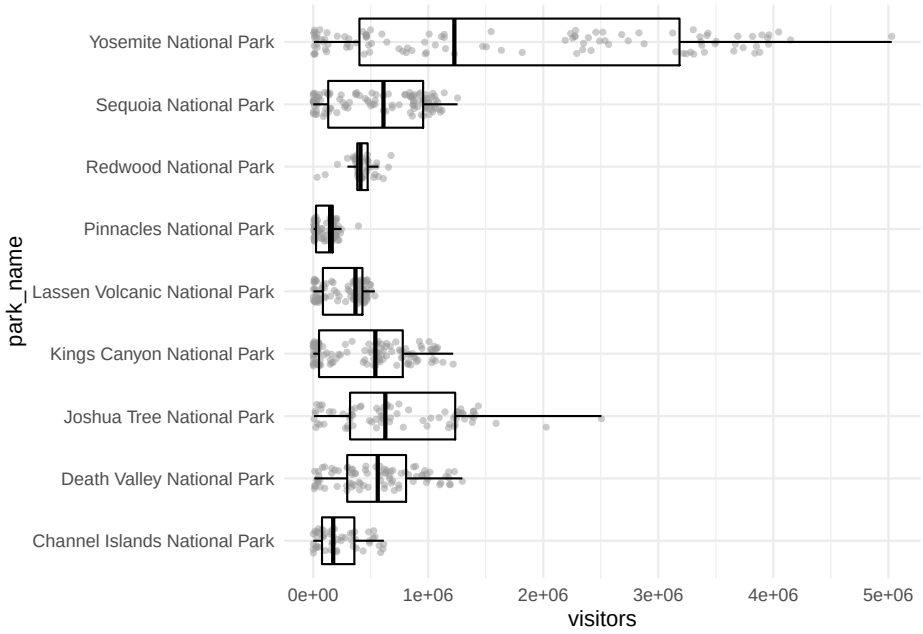
```
ggsave(here("figures", "np_graph.jpg"), dpi = 180, width = 8, height = 7)
```

Notice that a .jpg image of that name and size is now stored in your project working directory. You can change the type of exported image, too (e.g. pdf, tiff, eps, png, mmp, svg).

6.2.11 One final graph example: jitter and boxplots

For the record: this is not a good option for showing the visitation data because values are not independent observations of a random variable. But, for the purposes of showing a graph, we'll use visitation as our continuous measured variable in a jitter + boxplot anyway.

```
ggplot(data = ca_np, aes(x = park_name, y = visitors)) +
  geom_jitter(alpha = 0.5,
              color = "gray60",
              width = 0.2,
              size = 1) +
  geom_boxplot(fill = NA,
               color = "black",
               outlier.color = NA) +
  coord_flip() +
  theme_minimal()
```



Sync your project with your GitHub repo.

Chapter 7

`dplyr` and Pivot Tables

7.1 Summary

Pivot tables are powerful tools in Excel for summarizing data in different ways. We will create these tables using the `group_by` and `summarize` functions from the `dplyr` package (part of the Tidyverse). We will also learn how to format tables and practice creating a reproducible report using RMarkdown and sharing it with GitHub.

7.2 Objectives

In R, we can use dplyr for pivot tables by using 2 main verbs in combination: `group_by` and `summarize`. We will also continue to emphasize reproducibility in all our analyses.

- Discuss pivot tables in Excel
- Introduce `group_by() %>% summarize()` from the `dplyr` package
- Format tables with the `DT` and `knitr` packages
- Practice our reproducible workflow with RMarkdown and GitHub

7.3 Resources

- dplyr.tidyverse.org
- R for Data Science: Transform Chapter
- Intro to Pivot Tables I-III by Excel Campus (YouTube)

7.4 Pivot table overview

Wikipedia describes a pivot table as a "table of statistics that summarizes the data of a more extensive table…This summary might include sums, averages, or other statistics, which the pivot table groups together in a meaningful way." Fun fact: it also says that "Although pivot table is a generic term, Microsoft trademarked PivotTable in the United States in 1994."

Pivot tables are a really powerful tool for summarizing data, and we can have similar functionality in R — as well as nicely automating and reporting these tables. We will learn about this using data about lobsters and will go back and forth between R and Excel as we learn.

Let's start off in R, and have a look at the data.

7.5 RMarkdown setup

Let's start a new RMarkdown file in our repo, at the top-level (where it will be created by default in our Project). I'll call mine `pivot_lobsters.Rmd`.

In the setup chunk, let's attach our libraries and read in our lobster data. In addition to the `tidyverse` package we will also use the `skimr` package. You will have to install it, but don't want it to be installed every time you write your code. The following is a nice convention for having the install instructions available (on the same line) as the `library()` call.

```
## attach libraries
library(tidyverse)
library(readxl)
library(here)
library(skimr) # install.packages('skimr')

## read in data
lobsters <- read_xlsx(here("data/lobsters.xlsx"))
```

Let's add a code chunk and explore the data in a few ways.

```
# explore data
head(lobsters) # year and month as well as a column for date
```

```
## # A tibble: 6 x 7
##    year month date    site  transect replicate size_mm
##   <dbl> <dbl> <chr>   <chr>    <dbl> <chr>       <dbl>
## 1  2012     8 8/20/12 ivee         3 A              70
## 2  2012     8 8/20/12 ivee         3 B              60
## 3  2012     8 8/20/12 ivee         3 B              65
## 4  2012     8 8/20/12 ivee         3 B              70
```

```
## 5  2012     8 8/20/12 ivee          3 B              85
## 6  2012     8 8/20/12 ivee          3 C              60
```

`head()` gives us a look at the first rows of the data (6 by default). I like this because I can see the column names and get a sense of the shape of the data. I can also see the class of each column (double or character)

In this data set, every row is a unique observation. This is called "uncounted" data; you'll see there is no row for how many lobsters were seen because each row is an observation, or an "n of 1".

```
# explore data
summary(lobsters)
```

```
##       year          month           date               site
##  Min.   :2012   Min.   :8.000   Length:2893        Length:2893
##  1st Qu.:2014   1st Qu.:8.000   Class :character   Class :character
##  Median :2015   Median :8.000   Mode  :character   Mode  :character
##  Mean   :2015   Mean   :8.037
##  3rd Qu.:2016   3rd Qu.:8.000
##  Max.   :2016   Max.   :9.000
##
##     transect      replicate            size_mm
##  Min.   :1.000   Length:2893        Min.   : 18.00
##  1st Qu.:2.000   Class :character   1st Qu.: 62.00
##  Median :3.000   Mode  :character   Median : 72.00
##  Mean   :3.723                      Mean   : 71.38
##  3rd Qu.:5.000                      3rd Qu.: 81.00
##  Max.   :9.000                      Max.   :165.00
##                                     NA's   :5
```

`summary` gives us summary statistics for each variable (column). I like this for numeric columns, but it doesn't give a lot of useful information for non-numeric data. To have a look there I like using the skimr package:

```
# explore data
skimr::skim(lobsters)
```

Data summary

Name

lobsters

Number of rows

2893

Number of columns

7

Column type frequency:

character

3

numeric

4

Group variables

None

Variable type: character

skim_variable

n_missing

complete_rate

min

max

empty

n_unique

whitespace

date

0

1

6

7

0

28

0

site

0

1

4

4

0

5

0

replicate

0

1

1

1

0

4

0

Variable type: numeric

skim_variable

n_missing

complete_rate

mean

sd

p0

p25

p50

p75

p100

hist

year

0

1

2014.70

1.19

2012

2014

2015

2016

2016

month

0

1

8.04

0.19

8

8

8

8

9

transect

0

1

3.72

2.30

1

2

3

5

9

size_mm

5

1

71.38

14.75

18

62

72

81

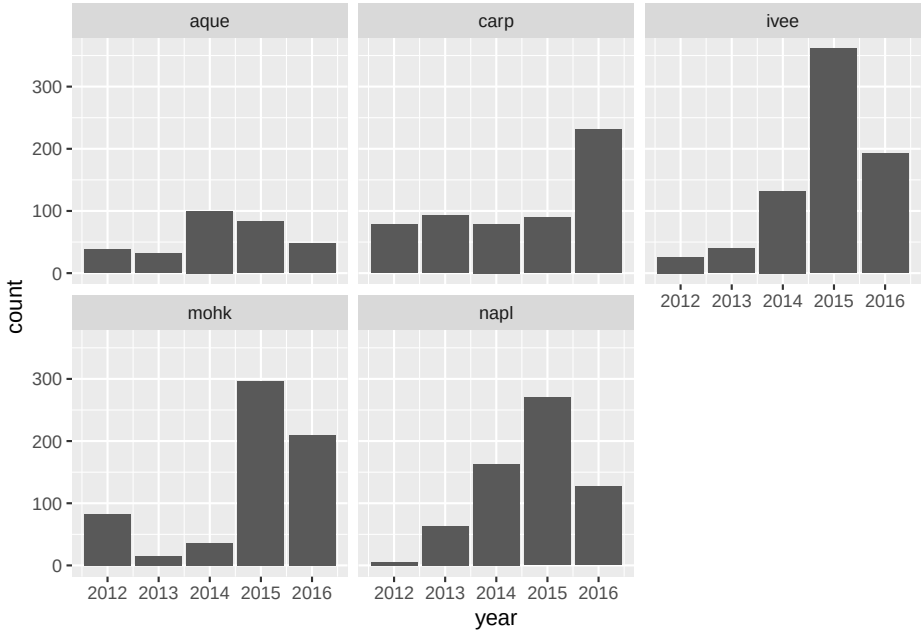
165

This `skimr::` notation is a reminder to me that `skim` is from the `skimr` package. It is a nice convention: it's a reminder to others (especially you!).

`skim` lets us look more at each variable. I particularly like looking at missing data. There are 6 missing values in the `size_mm` variable.

We can also make a quick plot to have a look at these data, and use our new ggplot2 skills. Let's make a bar chart by year for each site

```
ggplot(lobsters, aes(x = year)) +
  geom_bar() +
  facet_wrap(~site)
```



(geom_bar() counts things and geom_col() is for values within the data (mean))

7.5.1 Our task

So this is all great to get a quick look. But what if we needed to report to someone about how the average size of lobsters has changed over time across

sites?

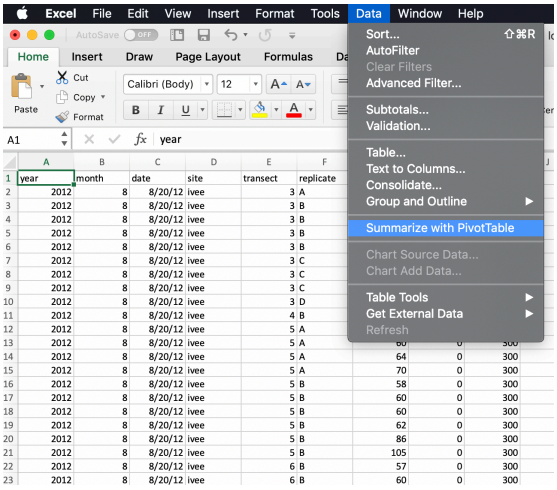
To answer this we need to do a pivot table in Excel, or data wrangling in R.

Let's start by having a quick look at what pivot tables can do in Excel.

7.6 Pivot table demo

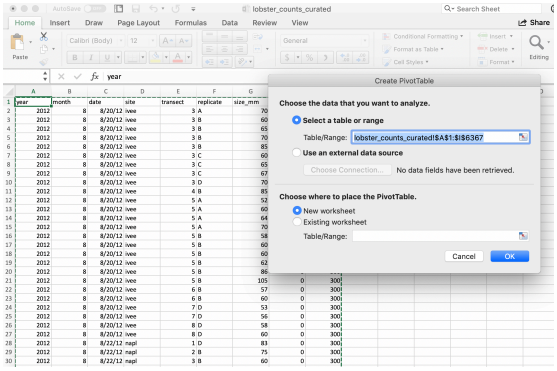
Let's make a pivot table with our lobster data.

Let's start off with how many lobsters were counted each year. I want a count of rows by year So to do this in Excel we would initiate the Pivot Table Process:



	year	month	date	site	transect	replicate			
2	2012	8	8/20/12	ivee	3	A			
3	2012	8	8/20/12	ivee	3	B			
4	2012	8	8/20/12	ivee	3	B			
5	2012	8	8/20/12	ivee	3	B			
6	2012	8	8/20/12	ivee	3	B			
7	2012	8	8/20/12	ivee	3	C			
8	2012	8	8/20/12	ivee	3	C			
9	2012	8	8/20/12	ivee	3	C			
10	2012	8	8/20/12	ivee	3	D			
11	2012	8	8/20/12	ivee	4	B			
12	2012	8	8/20/12	ivee	5	A			
13	2012	8	8/20/12	ivee	5	A			
14	2012	8	8/20/12	ivee	5	A	64	0	300
15	2012	8	8/20/12	ivee	5	A	70	0	300
16	2012	8	8/20/12	ivee	5	B	58	0	300
17	2012	8	8/20/12	ivee	5	B	60	0	300
18	2012	8	8/20/12	ivee	5	B	60	0	300
19	2012	8	8/20/12	ivee	5	B	62	0	300
20	2012	8	8/20/12	ivee	5	B	86	0	300
21	2012	8	8/20/12	ivee	5	B	105	0	300
22	2012	8	8/20/12	ivee	6	B	57	0	300
23	2012	8	8/20/12	ivee	6	B	60	0	300

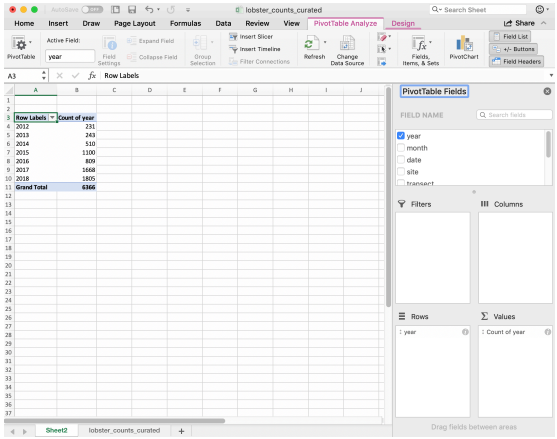
And it will do its best to find the data I would like to include in my Pivot Table (it can have difficulty with non-rectangular or "non-tidy" data), and suggest we make this in a new sheet:



And then we'll get a little wizard to help us create the Pivot Table.

7.6.1 pivot one variable

I want to summarize by year, so I drag "year" down into the "Rows" box, and to get the counts by year I actually drag the same variable, "year" into the "Values" box. And it will create a Pivot Table for me! But "sum" as the default summary statistic, so I can click the little "I" icon to change this to count.



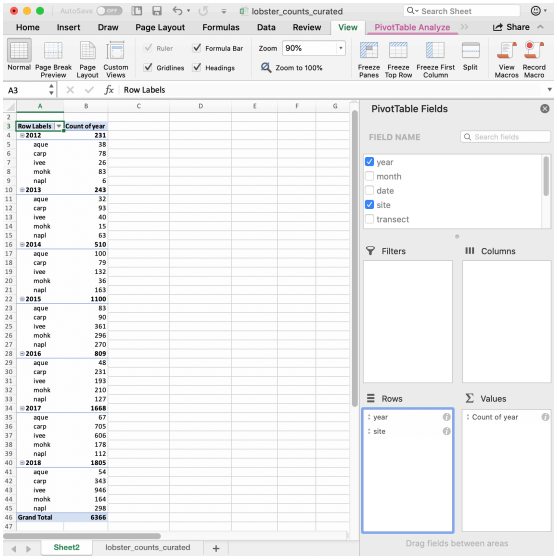
A few things to note:

- The pivot table is separate entity from our data (it's on a different sheet); the original data has not been affected
- The pivot table only shows the variables we requested; we don't see other columns (like date, month, or site).

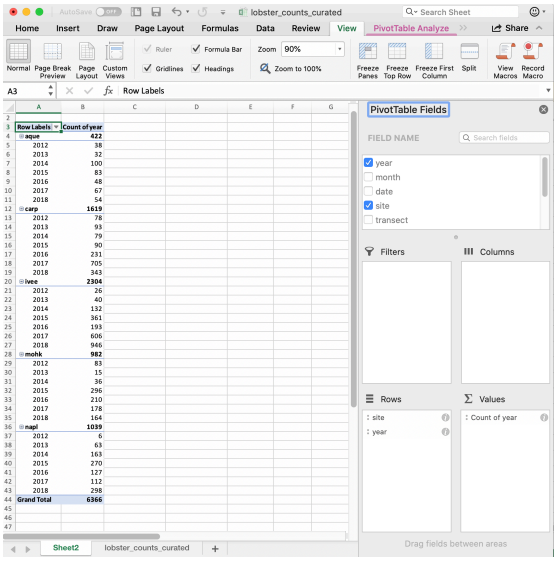
So pivot tables are great because they summarize the data and keep the raw data raw — they even promote good pratice because they by default ask you if you'd like to present the data in a new sheet rather than in the same sheet.

7.6.2 pivot two variables

We can also add site as a second variable by dragging it:



And then can reverse the order by dragging:



So in terms of our final interest of average size by site and year, we are on our way! I'm going to stop here because we want to be able to do this in R.

The power of R is in the automation, and in keeping that raw data truly raw.

Let's talk about how this looks like in R.

7.7 group_by() %>% summarize()

In R, we can create the functionality of pivot tables by using 2 main `dplyr` verbs in combination: `group_by` and `summarize`.

Say it with me: "pivot tables are group_by and then summarize". And just like pivot tables, you have flexibility with how you are going to summarize. For example, we can calculate an average, or a total.

I think it's incredibly powerful to visualize what we are talking about with our data when do do these kinds of operations. It looks like this (from RStudio's cheatsheet; all cheatsheets available from https://rstudio.com/resources/cheatsheets):

When we were reporting by year or site, we were essentially modifying what we were grouping by (the different colors here in this figure.

Let's do this in R.

7.7.1 group_by one variable

Let's try this on our `lobsters` data, just like we did in Excel. We will count the the total number of lobster by year. In R vocabulary, we will group_by year and then summarize by counting using `n()`, which is a function from `dplyr`. `n()` counts the number of times an observation shows up, and since this is uncounted data, this will count each row. We'll also use the pipe operator `%>%`, which you can read as "and then".

This to me reads: "take the lobsters data and then group_by year and then summarize by count in a new column called 'count' "

```
lobsters %>%
  group_by(year) %>%
  summarize(count_by_year = n())
```

```
## # A tibble: 5 x 2
##    year count_by_year
##   <dbl>         <int>
## 1  2012           231
## 2  2013           243
```

```
## 3  2014           510
## 4  2015          1100
## 5  2016           809
```

Notice how together, `group_by` and `summarize` minimize the amount of information we see. We also saw this with the pivot table. We lose the other columns that aren't involved here.

Question: What if you *don't* group_by first? Let's try it and discuss what's going on.

```
lobsters %>%
  summarize(count =  n())
```

```
## # A tibble: 1 x 1
##   count
##   <int>
## 1  2893
```

So if we don't `group_by` first, we will get a single summary statistic (sum in this case) for the whole dataset.

Notice that in Excel we retain the overall totals for each site (in bold, on the same line with the site name). This is nice for communicating about data. But it can be problematic for further analyses, because it could be easy to take a total of this column and introduce errors.

7.7.2 RStudio Viewer

Let's now check the `lobsters` variable. We can do this by clicking on `lobsters` in the Environment pane in RStudio.

We see that we haven't changed any of our original data that was stored in this variable. (Just like how the pivot table didn't affect the raw data on the original sheet).

> ***Aside***: You'll also see that when you click on the variable name in the Environment pane, `View(lobsters)` shows up in your Console. `View()` (capital V) is the R function to view any variable in the viewer. So this is something that you can write in your RMarkdown script, although RMarkdown will not be able to knit this view feature into the formatted document. So, if you want include `View()` in your RMarkdown document you will need to either comment it out `#View()` or add `eval=FALSE` to the top of the code chunk so that the full line reads `{r, eval=FALSE}`.

7.7.3 group_by multiple variables

Great. Now let's summarize by both year and site like we did in the pivot table. We are able to `group_by` more than one variable. Let's do this together:

```
lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n())
```

```
## # A tibble: 25 x 3
## # Groups:   site [5]
##    site   year count_by_siteyear
##    <chr> <dbl>             <int>
##  1 aque   2012                38
##  2 aque   2013                32
##  3 aque   2014               100
##  4 aque   2015                83
##  5 aque   2016                48
##  6 carp   2012                78
##  7 carp   2013                93
##  8 carp   2014                79
##  9 carp   2015                90
## 10 carp   2016               231
## # ... with 15 more rows
```

text.

7.7.4 summarize multiple variables

We can summarize multiple variables at a time. So far we've done the count of lobster observations. Let's also do the mean and standard deviation. First let's use the `mean()` function to calculate the mean. We do this within the same summarize() function, but we can add a new line to make it easier to read. Notice how when you put your curser within the parenthesis and hit return, the indentation will automatically align.

```
lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n(),
            mean_size_mm = mean(size_mm))
```

```
## # A tibble: 25 x 4
## # Groups:   site [5]
##    site   year count_by_siteyear mean_size_mm
##    <chr> <dbl>             <int>        <dbl>
##  1 aque   2012                38         71
##  2 aque   2013                32         72.1
```

```
##  3 aque   2014               100         76.9
##  4 aque   2015                83         68.5
##  5 aque   2016                48         68.7
##  6 carp   2012                78         74.4
##  7 carp   2013                93         76.6
##  8 carp   2014                79         NA
##  9 carp   2015                90         70.7
## 10 carp   2016               231         68.9
## # ... with 15 more rows
```

Aside Command-I will properly indent selected lines.

Great! But this will actually calculate some of the means as NA because one or more values in that year are NA. So we can pass an argument that says to remove NAs first before calculating the average. Let's do that, and then also calculate the standard deviation with the `sd()` function:

```
lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n(),
            mean_size_mm = mean(size_mm, na.rm=TRUE),
            sd_size_mm = sd(size_mm, na.rm=TRUE))
```

```
## # A tibble: 25 x 5
## # Groups:   site [5]
##    site   year count_by_siteyear mean_size_mm sd_size_mm
##    <chr> <dbl>             <int>        <dbl>      <dbl>
##  1 aque   2012                38         71        10.2
##  2 aque   2013                32         72.1      12.3
##  3 aque   2014               100         76.9       9.32
##  4 aque   2015                83         68.5      12.6
##  5 aque   2016                48         68.7      12.5
##  6 carp   2012                78         74.4      14.6
##  7 carp   2013                93         76.6       8.71
##  8 carp   2014                79         79.1       8.57
##  9 carp   2015                90         70.7      14.6
## 10 carp   2016               231         68.9      12.5
## # ... with 15 more rows
```

So we can make the equivalent of Excel's pivot table in R with `group_by` and then `summarize`. But a powerful thing about R is that maybe we want this information to be used in further analyses. We can make this easier for ourselves by saving this as a variable. So let's add a variable assignment to that first line:

```
siteyear_summary <- lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n(),
            mean_size_mm = mean(size_mm, na.rm = TRUE),
```

```
            sd_size_mm = sd(size_mm, na.rm = TRUE))

siteyear_summary
```

```
## # A tibble: 25 x 5
## # Groups:   site [5]
##    site   year count_by_siteyear mean_size_mm sd_size_mm
##    <chr> <dbl>             <int>        <dbl>      <dbl>
##  1 aque   2012                38         71        10.2
##  2 aque   2013                32         72.1      12.3
##  3 aque   2014               100         76.9       9.32
##  4 aque   2015                83         68.5      12.6
##  5 aque   2016                48         68.7      12.5
##  6 carp   2012                78         74.4      14.6
##  7 carp   2013                93         76.6       8.71
##  8 carp   2014                79         79.1       8.57
##  9 carp   2015                90         70.7      14.6
## 10 carp   2016               231         68.9      12.5
## # ... with 15 more rows
```

7.7.5 Activity

Calculate the median `size_mm` (Hint: ?median) and create a

Then, save, commit, and push your RMarkdown file.

Solution (no peeking):

```
siteyear_summary <- lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n(),
            mean_size_mm = mean(size_mm, na.rm = TRUE),
            sd_size_mm = sd(size_mm, na.rm = TRUE),
            median_size_mm = median(size_mm, na.rm = TRUE), )

siteyear_summary

## a ggplot option:
ggplot(data = siteyear_summary, aes(x = year, y = median_size_mm, color = site)) +
  geom_line()

## another option:
ggplot(siteyear_summary, aes(x = year, y = median_size_mm)) +
  geom_col() +
  facet_wrap(~site)
```

Don't forget to knit, commit, and push!

Nice work everybody.

7.8 Oh no, our colleague sent the wrong data!

Oh no! After all our analyses and everything we've done, our colleague just emailed us at 4:30pm on Friday that he sent the wrong data and we need to redo all our analyses with a new .xlsx file: `lobsters2.xlsx`, not `lobsters.xlsx`. Aaaaah!

If we were doing this in Excel, this would be a bummer; we'd have to rebuild our pivot table and click through all of our logic again.

But, since we did it in R, we are much safer. We can go back to the top of our RMarkdown file, and read in the updated dataset, and then re-knit. We will still need to check that everything outputs correctly, (and that column headers haven't been renamed), but our first pass will be to update the filename and re-knit:

```
## read in data
lobsters <- read_xlsx(here("data/lobsters2.xlsx"))
```

And now we can see that our plot updated as well:

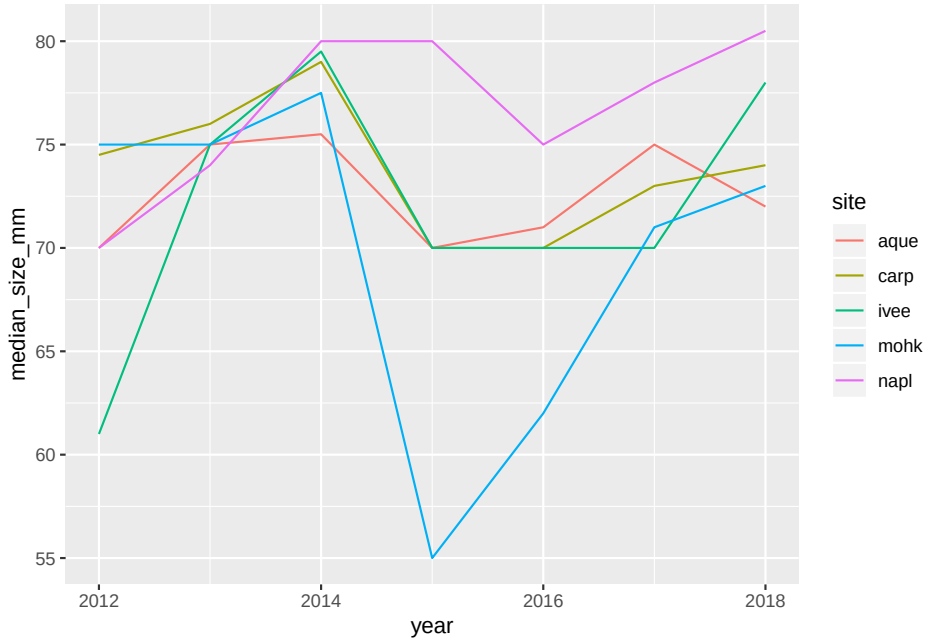
```
siteyear_summary <- lobsters %>%
  group_by(site, year) %>%
  summarize(count_by_siteyear =  n(),
            mean_size_mm = mean(size_mm, na.rm = TRUE),
            sd_size_mm = sd(size_mm, na.rm = TRUE),
            median_size_mm = median(size_mm, na.rm = TRUE), )

siteyear_summary
```

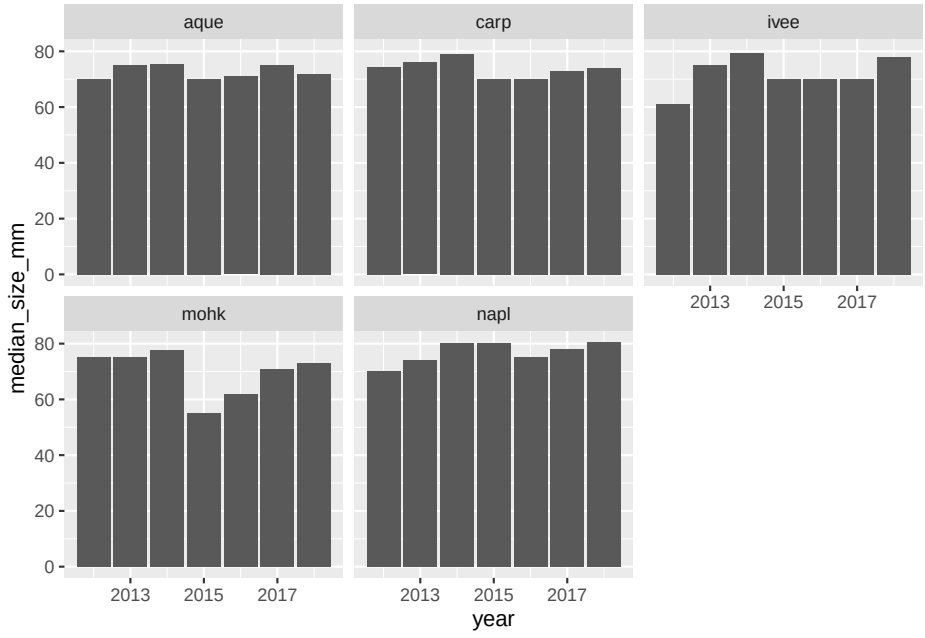
```
## # A tibble: 35 x 6
## # Groups:   site [5]
##    site   year count_by_siteyear mean_size_mm sd_size_mm median_size_mm
##    <chr> <dbl>             <int>        <dbl>      <dbl>          <dbl>
##  1 aque   2012                38         71        10.2            70
##  2 aque   2013                32         72.1      12.3            75
##  3 aque   2014               100         76.9       9.32           75.5
##  4 aque   2015                83         68.5      12.6            70
##  5 aque   2016                48         68.7      12.5            71
##  6 aque   2017                67         73.9      11.9            75
##  7 aque   2018                54         71.7       8.14           72
##  8 carp   2012                78         74.4      14.6            74.5
##  9 carp   2013                93         76.6       8.71           76
```

```
## 10 carp   2014                79         79.1       8.57           79
## # ... with 25 more rows
```

```
## a ggplot option:
ggplot(data = siteyear_summary, aes(x = year, y = median_size_mm, color = site)) +
  geom_line()
```




```
## another option:
ggplot(siteyear_summary, aes(x = year, y = median_size_mm)) +
  geom_col() +
  facet_wrap(~site)
```



7.8.1 dplyr::count()

Now that we've spent time with group_by %>% summarize, there is a shortcut if you only want to summarize by count. This is with a function called `count()`, and it will group_by your selected variable, count, and then also ungroup. It looks like this:

```
lobsters %>%
  count(site, year)

## This is the same as:
lobsters %>%
  group_by(site, year) %>%
  summarize(n = n()) %>%
  ungroup()
```

Switching gears...

7.9 mutate()

There are a lot of times where you don't want to summarize your data, but you do want to operate beyond the original data. This is often done by adding a column. We do this with the `mutate()` function from `dplyr`. Let's try this with our original lobsters data. The sizes are in millimeters but let's say it was important for them to be in meters. We can add a column with this calculation:

```
# quick reminder what this looks like
head(lobsters)
```

```
## # A tibble: 6 x 7
##    year month date    site  transect replicate size_mm
##   <dbl> <dbl> <chr>   <chr>    <dbl> <chr>       <dbl>
## 1  2012     8 8/20/12 ivee         3 A              70
## 2  2012     8 8/20/12 ivee         3 B              60
## 3  2012     8 8/20/12 ivee         3 B              65
## 4  2012     8 8/20/12 ivee         3 B              70
## 5  2012     8 8/20/12 ivee         3 B              85
## 6  2012     8 8/20/12 ivee         3 C              60
```

```
lobsters %>%
  mutate(size_m = size_mm / 1000)
```

```
## # A tibble: 6,366 x 8
##     year month date    site  transect replicate size_mm size_m
##    <dbl> <dbl> <chr>   <chr>    <dbl> <chr>       <dbl>  <dbl>
##  1  2012     8 8/20/12 ivee         3 A              70  0.07
##  2  2012     8 8/20/12 ivee         3 B              60  0.06
##  3  2012     8 8/20/12 ivee         3 B              65  0.065
##  4  2012     8 8/20/12 ivee         3 B              70  0.07
##  5  2012     8 8/20/12 ivee         3 B              85  0.085
##  6  2012     8 8/20/12 ivee         3 C              60  0.06
##  7  2012     8 8/20/12 ivee         3 C              65  0.065
##  8  2012     8 8/20/12 ivee         3 C              67  0.067
##  9  2012     8 8/20/12 ivee         3 D              70  0.07
## 10  2012     8 8/20/12 ivee         4 B              85  0.085
## # ... with 6,356 more rows
```

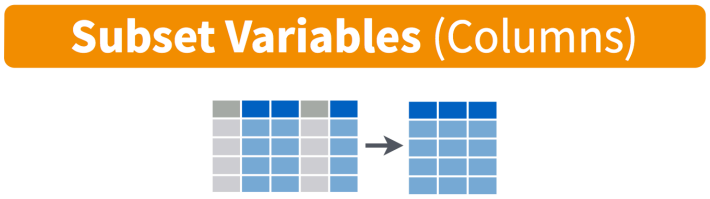
If we want to add a column that has the same value repeated, we can pass it just one value, either a number or a character string (in quotes). And let's save

this as a variable called `lobsters_detailed`

```
lobsters_detailed <- lobsters %>%
  mutate(size_m = size_mm / 1000,
         millenia = 2000,
         observer = "Allison Horst")
```

7.10 select()

We will end with one final function, `select`. This is how to choose, retain, and move your data by columns:



Let's say that we want to present this data finally with only columns for date, site, and size in meters. We would do this:

```
lobsters_detailed %>%
  select(date, site, size_m)
```

```
## # A tibble: 6,366 x 3
##    date    site  size_m
##    <chr>   <chr>  <dbl>
##  1 8/20/12 ivee   0.07
##  2 8/20/12 ivee   0.06
##  3 8/20/12 ivee   0.065
##  4 8/20/12 ivee   0.07
##  5 8/20/12 ivee   0.085
##  6 8/20/12 ivee   0.06
##  7 8/20/12 ivee   0.065
##  8 8/20/12 ivee   0.067
##  9 8/20/12 ivee   0.07
## 10 8/20/12 ivee   0.085
## # ... with 6,356 more rows
```

One last time, let's knit, save, commit, and push to GitHub.

7.11 Deep thoughts

Highly recommended read: Broman & Woo: Data organization in spreadsheets. Practical tips to make spreadsheets less error-prone, easier for computers to process, easier to share

Great opening line: "Spreadsheets, for all of their mundane rectangularness, have been the subject of angst and controversy for decades."

7.12 Efficiency Tips

arrow keys with shift, option, command

Chapter 8

Tidying

TODO: janitor: adorn and kable

8.1 Summary

In previous sessions, we learned to read in data, do some wrangling, and create a graph and table. Here, we'll continue by *reshaping* data frames (converting from long-to-wide, or wide-to-long format), *separating* and *uniting* variable (column) contents, converting between *explicit* and *implicit* missing (`NA`) values, and cleaning up our column names with the `janitor` package.

8.2 Objectives

- Reshape data frames with `tidyr::pivot_wider()` and `tidyr::pivot_longer()`
- Convert column names with `janitor::clean_names()`
- Combine or separate information from columns with `tidyr::unite()` and `tidyr::separate()`
- Make implicit missings *explicit* with `tidyr::complete()`
- Make explicit missings *implicit* with `tidyr::drop_na()`
- Use our new skills as part of a bigger wrangling sequence
- Make a customized table (TODO: or introduce Kable if not time in pivot tables chapter)

8.3 Resources

– Ch. 12 *Tidy Data*, in R for Data Science by Grolemund & Wickham - `tidyr` documentation from tidyverse.org - `janitor` repo / information from Sam Firke

8.4 Lesson

8.4.1 Lesson Prep

8.4.1.1 Create a new R Markdown and attach packages

Within your day 2 R Project, create a new .Rmd. Attach the `tidyverse`, `janitor` and `readxl` packages with `library(package_name)`. Knit and save your new .Rmd within the project folder.

```
# Attach packages
library(tidyverse)
library(janitor)
library(readxl)
```

8.4.1.2 Read in data

Use `readxl::read_excel()` to import the "invert_counts_curated.xlsx" data:

```
inverts_df <- readxl::read_excel("invert_counts_curated.xlsx")
```

Be sure to explore the imported data a bit:

- `View()`
- `names()`
- `summary()`

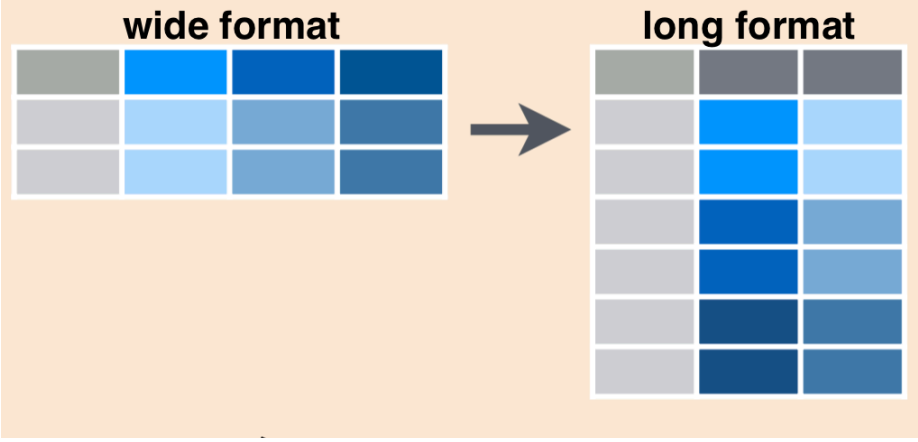
8.4.2 Reshaping with `tidyr::pivot_longer()` and `tidyr::pivot_wider()`

8.4.2.1 Wide-to-longer format with `tidyr::pivot_longer()`

In *tidy format*, each variable is contained within a single column. If we look at *inverts_df*, we can see that the *year* variable is actually split over 3 columns, so we'd say this is currently in **wide format**.

There may be times when you want to have data in wide format, but often with code it is more efficient to convert to **long format** by gathering together observations for a variable that is currently split into multiple columns.

Schematically, converting from wide to long format looks like this:



Generally, the code to gather wide columns together using `tidyr::pivot_longer()` looks like this:

TODO: Add pivot_longer() schematic

We'll use `tidyr::pivot_longer()` to gather data from all years in *inverts_df* into two columns: one called *year*, which contains the year (as a number), and another called *sp_count* that contains the number of each species observed. The new data frame will be stored as *inverts_long*:

```
inverts_long <- tidyr::pivot_longer(data = inverts_df,
                                    cols = '2016':'2018',
                                    names_to = "year",
                                    values_to = "sp_count")
```

The outcome is the new long-format *inverts_long* data frame:

```
inverts_long
```

```
## # A tibble: 165 x 5
##    month site  common_name              year  sp_count
##    <chr> <chr> <chr>                    <chr>    <dbl>
##  1 7     abur  california cone snail    2016       451
##  2 7     abur  california cone snail    2017        28
##  3 7     abur  california cone snail    2018       762
##  4 7     abur  california spiny lobster 2016        17
##  5 7     abur  california spiny lobster 2017        17
##  6 7     abur  california spiny lobster 2018        16
##  7 7     abur  orange cup coral         2016        24
##  8 7     abur  orange cup coral         2017        24
##  9 7     abur  orange cup coral         2018        24
## 10 7     abur  purple urchin            2016        48
```

```
## # ... with 155 more rows
```

Hooray, long format!

One thing that isn't obvious at first (but would become obvious if you continued working with this data) is that since those year numbers were initially column names (characters), when they are stacked into the *year* column, their class wasn't auto-updated to numeric.

Explore the class of *year* in *inverts_long*:

```
class(inverts_long$year)
```

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

We'll use `dplyr::mutate()` in a different way here: to create a new column (that's how we've used `mutate()` previously) that has the same name of an existing column, in order to update and overwrite the existing column.

In this case, we'll `mutate()` to add a column called *year*, which contains an `as.numeric()` version of the existing *year* variable:

```
# Coerce "year" class to numeric:

inverts_long <- inverts_long %>%
  mutate(year = as.numeric(year))
```

Checking the class again, we see that *year* has been updated to a numeric variable:

```
class(inverts_long$year)
```

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

8.4.2.2 Long-to-wider format with `tidyr::pivot_wider()`

In the previous example, we had information spread over multiple columns that we wanted to *gather*. Sometimes, we'll have data that we want to *spread* over multiple columns.

For example, imagine that starting from *inverts_long* we want each species in the *common_name* column to exist as its **own column**. In that case, we would be converting from a longer to a wider format, and will use `tidyr::pivot_wider()` as follows:

TODO: Add pivot_wider() schematic

Specifically for our data, we write code to spread the *common_name* column as follows:

```
inverts_wide <- inverts_long %>%
  tidyr::pivot_wider(names_from = common_name,
                     values_from = sp_count)
```

```
inverts_wide
```

```
## # A tibble: 33 x 8
##    month site   year `california con~ `california spi~ `orange cup cor~
##    <chr> <chr> <dbl>            <dbl>            <dbl>             <dbl>
##  1 7     abur   2016              451               17                24
##  2 7     abur   2017               28               17                24
##  3 7     abur   2018              762               16                24
##  4 7     ahnd   2016               27               16                24
##  5 7     ahnd   2017               24               16                24
##  6 7     ahnd   2018               24               16                24
##  7 7     aque   2016             4971               48              1526
##  8 7     aque   2017             1752               48              1623
##  9 7     aque   2018             2616               48              1859
## 10 7     bull   2016             1735               24                36
## # ... with 23 more rows, and 2 more variables: `purple urchin` <dbl>, `rock
## #   scallop` <dbl>
```

We can see that now each *species* has its own column (wider format). But also notice that those column headers (since they have spaces) might not be in the most coder-friendly format…

8.4.2.3 Meet the `janitor` package

The `janitor` package by Sam Firke is a brilliant collection of functions for some quick data cleaning. We recommend that you explore the different functions it contains. Like:

- `janitor::clean_names()`: update column headers to a case of your choosing
- `janitor::get_dupes()`: see all rows that are duplicates within variables you choose
- `janitor::remove_empty()`: remove empty rows and/or columns
- `janitor::andorn_*()`: jazz up frequency tables of counts (we'll return to this for a table example in TODO: Session 8)
- …and more!

Here, we'll use `janitor::clean_names()` to convert all of our column headers to a more convenient case - the default is **lower_snake_case**, which means all spaces and symbols are replaced with an underscore (or a word describing the symbol), all characters are lowercase, and a few other nice adjustments.

For example, `janitor::clean_names()` would update these nightmare column names into much nicer forms:

- `My...RECENT-income!` becomes `my_recent_income`
- `SAMPLE2.!test1` becomes `sample2_test1`
- `ThisIsTheName` becomes `this_is_the_name`
- `2015` becomes `x2015`

If we wanted to then use these columns (which we probably would, since we created them), we could clean the names to get them into more coder-friendly lower_snake_case with `janitor::clean_names()`:

```
inverts_wide <- inverts_wide %>%
  janitor::clean_names()
```

```
names(inverts_wide)
```

```
## [1] "month"                    "site"
## [3] "year"                     "california_cone_snail"
## [5] "california_spiny_lobster" "orange_cup_coral"
## [7] "purple_urchin"            "rock_scallop"
```

And there are other options for the case, like:

- "snake" produces snake_case
- "lower_camel" or "small_camel" produces lowerCamel
- "upper_camel" or "big_camel" produces UpperCamel
- "screaming_snake" or "all_caps" produces ALL_CAPS
- "lower_upper" produces lowerUPPER
- "upper_lower" produces UPPERlower

8.4.3 Combine or separate information in columns with `tidyr::unite()` and `tidyr::separate()`

Sometimes we'll want to *separate* contents of a single column into multiple columns, or *combine* entries from different columns into a single column.

For example, the following data frame has *genus* and *species* in separate columns:

id

genus

species

common_name

1

Scorpaena

guttata

sculpin

2

Sebastes

miniatus

vermillion

We may want to combine the genus and species into a single column, *scientific_name*:

id

scientific_name

common_name

1

Scorpaena guttata

sculpin

2

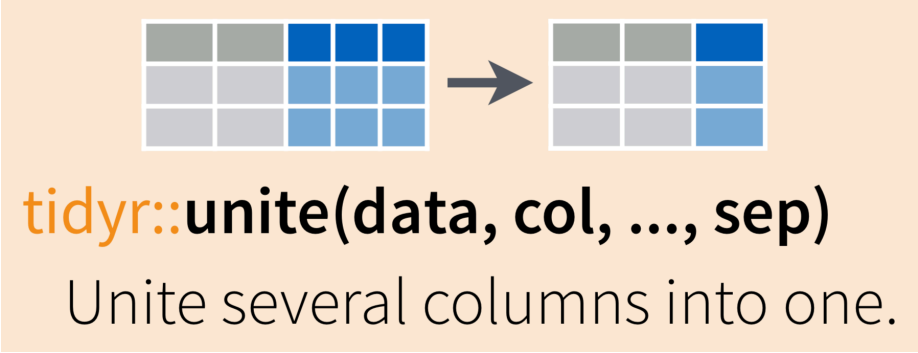
Sebastes miniatus

vermillion

Or we may want to do the reverse (separate information from a single column into multiple columns). Here, we'll learn `tidyr::unite()` and `tidyr::separate()` to help us do both.

8.4.3.1 `tidyr::unite()` to merge information from separate columns

Use `tidyr::unite()` to combine (paste) information from multiple columns into a single column (as for the scientific name example above)



To demonstrate uniting information from separate columns, we'll make a single column that has the combined information from *site* abbreviation and *year* in *inverts_wide*.

We need to give `tidyr::unite()` several arguments:

- **data:** the data frame containing columns we want to combine (or pipe into the function from the data frame)
- **col:** the name of the new "united" column
- the **columns you are uniting**
- **sep:** the symbol, value or character to put between the united information from each column

```
inverts_unite <- inverts_wide %>%
  tidyr::unite(col = "site_year", # What to name the new united column
               c(site, year), # The columns we'll unite (site, year)
               sep = "_") # How to separate the things we're uniting
```

```
## # A tibble: 6 x 7
##   month site_year california_cone~ california_spin~ orange_cup_coral
##   <chr> <chr>                <dbl>            <dbl>            <dbl>
## 1 7     abur_2016              451               17               24
## 2 7     abur_2017               28               17               24
## 3 7     abur_2018              762               16               24
## 4 7     ahnd_2016               27               16               24
## 5 7     ahnd_2017               24               16               24
## 6 7     ahnd_2018               24               16               24
## # ... with 2 more variables: purple_urchin <dbl>, rock_scallop <dbl>
```

Try updating the separator from "_" to "*hello!*" to see what the outcome column contains.

`tidyr::unite()` can also combine information from *more* than two columns. For example, to combine the *site*, *common_name* and *year* columns from *inverts_long*, we could use:

```
# Uniting more than 2 columns:

inverts_triple_unite <- inverts_long %>%
  tidyr::unite(col = "year_site_name",
               c(year, site, common_name),
               sep = "-")
```

```
head(inverts_triple_unite)
```

```
## # A tibble: 6 x 3
##   month year_site_name                    sp_count
##   <chr> <chr>                                <dbl>
## 1 7     2016-abur-california cone snail        451
```

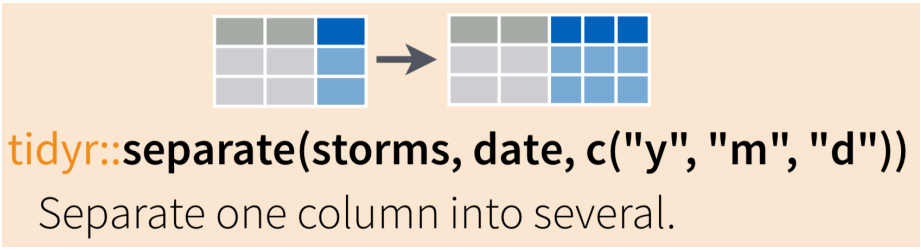
```
## 2 7     2017-abur-california cone snail          28
## 3 7     2018-abur-california cone snail         762
## 4 7     2016-abur-california spiny lobster       17
## 5 7     2017-abur-california spiny lobster       17
## 6 7     2018-abur-california spiny lobster       16
```

8.4.3.2 `tidyr::separate()` to separate information into multiple columns

While `tidyr::unite()` allows us to combine information from multiple columns, it's more likely that you'll *start* with a single column that you want to split up into pieces.

For example, I might want to split up a column containing the *genus* and *species* (*Scorpaena guttata*) into two separate columns (*Scorpaena* | *guttata*), so that I can count how many *Scorpaena* organisms exist in my dataset at the genus level.

Use `tidyr::separate()` to "separate a character column into multiple columns using a regular expression separator."



Let's start again with *inverts_unite*, where we have combined the *site* and *year* into a single column called *site_year*. If we want to **separate** those, we can use:

```
inverts_sep <- inverts_triple_unite %>%
  tidyr::separate(year_site_name, into = c("my_year", "my_site_name"))
```

```
## Warning: Expected 2 pieces. Additional pieces discarded in 165 rows [1, 2, 3, 4,
## 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].
```

What is that warning `Expected 2 pieces...` telling us? If we take a look at the resulting data frame *inverts_sep*, we see that it only keeps the first **two** pieces, and gets rid of the third (name). Which is a bit concerning, because we rarely want to just throw away information in a data frame.

```
head(inverts_sep)
```

```
## # A tibble: 6 x 4
##   month my_year my_site_name sp_count
##   <chr> <chr>   <chr>           <dbl>
```

```
## 1 7     2016    abur              451
## 2 7     2017    abur               28
## 3 7     2018    abur              762
## 4 7     2016    abur               17
## 5 7     2017    abur               17
## 6 7     2018    abur               16
```

That's problematic. How can we make sure we're keeping as many different elements as exist in the united column?

We have a couple of options:

1. Create the *number* of columns that are needed to retain as many elements as exist (in this case, 3, but we only created two new columns in the example above)

```
inverts_sep3 <- inverts_triple_unite %>%
  tidyr::separate(year_site_name, into = c("the_year", "the_site", "the_name"))
```

```
## Warning: Expected 3 pieces. Additional pieces discarded in 165 rows [1, 2, 3, 4,
## 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, ...].
```

Another warning. What is that about? Let's take a look at the resulting data frame and think about what's missing (what are the "pieces discarded"?):

```
head(inverts_sep3)
```

```
## # A tibble: 6 x 5
##   month the_year the_site the_name   sp_count
##   <chr> <chr>    <chr>    <chr>         <dbl>
## 1 7     2016     abur     california      451
## 2 7     2017     abur     california       28
## 3 7     2018     abur     california      762
## 4 7     2016     abur     california       17
## 5 7     2017     abur     california       17
## 6 7     2018     abur     california       16
```

Aha! Only the *first word* of the common name was retained, and anything else was trashed. We want to keep everything after the second dash in the new *the_name* column.

That's because the **default is `extra = "warn"`**, which means that if you have more pieces than columns you're separating into, it will populate the columns that have been allotted (in our case, just 3) then drop any additional information, giving you a warning that pieces have been dropped.

To keep the extra pieces that have been dropped, add the `extra = "merge"` argument within `tidyr::separate()` to override:

```
inverts_sep_all <- inverts_triple_unite %>%
  separate(year_site_name,
```

```
            into = c("sample_year", "location", "sp_name"),
            extra = "merge")
```

No warning there about things being discarded. Explore *inverts_sep_all*:

```
## # A tibble: 165 x 5
##    month sample_year location sp_name                  sp_count
##    <chr> <chr>       <chr>    <chr>                        <dbl>
##  1 7     2016        abur     california cone snail          451
##  2 7     2017        abur     california cone snail           28
##  3 7     2018        abur     california cone snail          762
##  4 7     2016        abur     california spiny lobster        17
##  5 7     2017        abur     california spiny lobster        17
##  6 7     2018        abur     california spiny lobster        16
##  7 7     2016        abur     orange cup coral                24
##  8 7     2017        abur     orange cup coral                24
##  9 7     2018        abur     orange cup coral                24
## 10 7     2016        abur     purple urchin                   48
## # ... with 155 more rows
```

We see that the resulting data frame has split *year_site_name* into three separate columns, *sample_year*, *location*, and *sp_name*, but now everything after the second break ("-") remains together in *sp_name* instead of dropping pieces following the third word.

8.4.4 Convert between explicit and implicit missings (`NA`s)

An *explicit missing* is when every possible outcome actually appears in a data frame as a row, even if a variable of interest for that row is missing (`NA`).

Conversely, an *implicit missing* is when an observation (row) does *not* appear in the data frame because a variable of interest contains an `NA` missing value.

Consider the following data:

day

animal

food_choice

Monday

eagle

fish

Monday

mountain lion

squirrel

Monday

toad

NA

Tuesday

eagle

fish

Tuesday

mountain lion

deer

Tuesday

toad

flies

Notice that the row for **toad** still appears in the dataset for **Tuesday**, despite having a missing food choice for that day. This is an *explicit missing* because the row still appears in the data frame.

If that row was removed, the resulting dataset would look like this:

```
df_missings %>%
  drop_na(food_choice) %>%
  kable()
```

day

animal

food_choice

Monday

eagle

fish

Monday

mountain lion

squirrel

Tuesday

eagle

fish

Tuesday

mountain lion

deer

Tuesday

toad

flies

...and if your reaction is "But then how do I know there's a toad from **MONDAY**?", then you can see how it can be a bit risky to have *implicit missings* instead of *explicit missings*.

Whichever we choose, we can convert between the two forms using `tidyr::drop_na()` or `tidyr::complete()`:

- `tidyr::drop_na()`: removes observations (rows) that contain `NA` for variable(s) of interest
- `tidyr::complete()`: turns implicit missing values into explicit missing values by completing a data frame with missing combinations of data

We'll use both here, starting with the *inverts_long* data frame we created above.

Looking through *inverts_long*, we'll see that there are `NA` observations for every species at site **bull** in 2018 - but those `NA` counts do show up. First, we'll use `tidyr::drop_na()` to make those missings implicit (invisible) instead:

```
inverts_implicit_NA <- inverts_long %>%
  drop_na(sp_count)
```

See that now, the rows that contained an `NA` in the *sp_count* column from *inverts_long* have been removed.

WAIT, I want them back! We can ask R to create explicit missings (by identifying which combinations of groups currently don't appear in the data frame) using `tidyr::complete()`:

```
inverts_explicit_NA <- inverts_implicit_NA %>%
  complete(month, site, common_name, year)
```

Now you'll see `inverts_explicit_NA` has those 5 "missing" observations shown in the data frame.

8.4.5 Activities

TODO

8.4.6 Fun facts / insights

TODO

Chapter 9

Dplyr and vlookups

9.1 Summary

In previous sessions, we've learned to do some basic wrangling and find summary information with functions in the `dplyr` package, which exists within the `tidyverse`. We've used:

- `count()`: get counts of observations for groupings we specify
- `mutate()`: **add** a new column, while keeping the existing ones
- `group_by()`: let R know that **groups** exist within the dataset, by variable(s)
- `summarize()`: calculate a value (that you specify) for each group, then report each group's value in a table

In this session, we'll expand our data wrangling toolkit using:

- `filter()` to conditionally subset our data by **rows**, and
- `*_join()` functions to merge data frames together

The combination of `filter()` and `*_join()` - to return rows satisfying a condition we specify, and merging data frames by like variables - is analogous to the useful VLOOKUP function in Excel.

9.1.1 Objectives

- Use `filter()` to subset data frames, returning **rows** that satisfy variable conditions
- Use `full_join()`, `left_join()`, and `inner_join()` to merge data frames, with different endpoints in mind
- Use `filter()` and `*_join()` as part of a wrangling sequence

9.1.2 Resources

- `filter()` documentation from tidyverse.org
- `join()` documentation from tidyverse.org
- Chapters 5 and 13 in *R for Data Science* by Garrett Grolemund and Hadley Wickham

9.2 Lessons

9.2.1 Getting started - Create a new .Rmd, attach packages & get data

Create a new R Markdown document in your r-workshop project and knit to save as **filter_join.Rmd**. Remove all the example code (everything below the set-up code chunk).

In this session, we'll use three packages:

- `tidyverse`
- `readxl`
- `here`

Attach the packages in the setup code chunk in your .Rmd:

```
# Attach packages:
library(tidyverse)
library(readxl)
library(here)
```

Then create a new code chunk to read in three files from your 'data' subfolder:

- invert_counts_curated.xlsx
- fish_counts_curated.csv
- kelp_counts_curated.xlsx

```
# Read in data:
invert_counts <- read_excel(here("data", "invert_counts_curated.xlsx"))
fish_counts <- read_csv(here("data", "fish_counts_curated.csv"))
kelp_counts_abur <- read_excel(here("data", "kelp_counts_curated.xlsx"))
```

We should always explore the data we've read in using functions like `View()`, `names()`, `summary()`, `head()` and `tail()` to ensure that the data we *think* we've read in is *actually* the data we've read in.

Now, let's use `filter()` to decide which observations (rows) we'll keep or exclude in new subsets, similar to using Excel's VLOOKUP function.

9.2.2 `filter()` to conditionally subset by rows

Use `filter()` to let R know which **rows** you want to keep or exclude, based whether or not their contents match conditions that you set for one or more variables.

Some examples in words that might inspire you to use `filter()`:

- "I only want to keep rows where the temperature is greater than 90°F."
- "I want to keep all observations **except** those where the tree type is listed as **unknown**."
- "I want to make a new subset with only data for mountain lions (the species variable) in California (the state variable)."

When we use `filter()`, we need to let R know a couple of things:

- What data frame we're filtering from
- What condition(s) we want observations to **match** and/or **not match** in order to keep them in the new subset

Here, we'll learn some common ways to use `filter()`.

9.2.2.1 Filter rows by matching a single character string

Let's say we want to keep all observations from the fish_counts data frame where the common name is "garibaldi." Here, we need to tell R to only *keep rows* from the **fish_counts** data frame when the common name (**common_name** variable) exactly matches **garibaldi**. Use `==` to ask R to look for matching strings:

```
fish_garibaldi <- filter(fish_counts, common_name == "garibaldi")
```

Check out the **fish_garibaldi** object to ensure that only *garibaldi* observations remain.

You could also do this using the pipe operator `%>%`:

```
fish_garibaldi <- fish_counts %>%
  filter(common_name == "garibaldi")
```

9.2.2.2 Activity

Task: Create a subset from the **fish_counts** data frame, stored as object **fish_abur**, that only contains observations from Arroyo Burro (site 'abur').

Solution:

```
fish_abur <- fish_counts %>%
  filter(site == "abur")
```

Explore the subset you just created to ensure that only Arroyo Burro observations are returned.

9.2.2.3 Filter rows based on numeric conditions

Use expected operators (>, <, >=, <=, ==) to set conditions for a numeric variable when filtering. For this example, we only want to retain observations when the **total_count** column value is >= 50:

```
fish_over50 <- filter(fish_counts, total_count >= 50)
```

Or, using the pipe:

```
fish_over50 <- fish_counts %>%
  filter(total_count >= 50)
```

9.2.2.4 Filter to return rows that match *this* OR *that* OR *that*

What if we want to return a subset of the fish_counts df that contains *garibaldi*, *blacksmith* OR *black surfperch*?

There are several ways to write an "OR" statement for filtering, which will keep any observations that match Condition A *or* Condition B *or* Condition C. In this example, we will create a subset from **fish_counts** that only contains rows where the **common_name** is *garibaldi* or *blacksmith* or *black surfperch*.

Use `%in%` to ask R to look for *any matches* within a combined vector of strings:

```
fish_3sp <- fish_counts %>%
  filter(common_name %in% c("garibaldi", "blacksmith", "black surfperch"))
```

Alternatively, you can indicate **OR** using the vertical line operator `|` to do the same thing (but you can see that it's more repetitive when looking for matches within the same variable):

```
fish_3sp <- fish_counts %>%
  filter(common_name == "garibaldi" | common_name == "blacksmith" | common_name == "bla
```

9.2.2.5 Filter to return rows that match conditions for multiple variables

In the previous examples, we set filter conditions based on a single variable (e.g. common_name). What if we want to return observations that satisfy conditions for multiple variables?

For example: We want to create a subset that only returns rows from 'invert_counts' where the **site** is "abur" or "mohk" *and* the **common_name** is "purple urchin." In `filter()`, add a comma (or ampersand, &) between arguments for multiple *AND* conditions:

```
urchin_abur_mohk <- invert_counts %>%
  filter(site %in% c("abur","mohk"), common_name == "purple urchin")
```

```
head(urchin_abur_mohk)
```

```
## # A tibble: 2 x 6
##   month site  common_name   `2016` `2017` `2018`
##   <chr> <chr> <chr>          <dbl>  <dbl>  <dbl>
## 1 7     abur  purple urchin     48     48     48
## 2 7     mohk  purple urchin    620    505    323
```

Like most things in R, there are other ways to do the same thing. For example, you could do the same thing using `&` (instead of a comma) between "and" conditions:

```
# Use the ampersand (&) to add another condition "and this must be true":

urchin_abur_mohk <- invert_counts %>%
  filter(site %in% c("abur","mohk") & common_name == "purple urchin")
```

Or you could just do two filter steps in sequence:

```
# Written as sequential filter steps:

urchin_abur_mohk <- invert_counts %>%
  filter(site %in% c("abur", "mohk")) %>%
  filter(common_name == "purple urchin")
```

9.2.2.5.1 Activity: combined filter conditions

Task: Create a subset from the **fish_counts** data frame, called **low_gb_wr** that only contains:

- Observations of *garibaldi* and *rock wrasse*
- Where the *total_count* is *less than or equal to 10*

Solution:

```
low_gb_wr <- fish_counts %>%
  filter(common_name %in% c("garibaldi", "rock wrasse"),
         total_count <= 10)
```

Sync your local project to your repo on GitHub.

9.2.2.6 Filter to return rows that *do not* match conditions

Sometimes we might want to exclude observations. Here, let's say we want to make a subset that contains all rows from **fish_counts** except those recorded at the Mohawk Reef site ("mohk" in the *site* variable).

We use `!=` to return observations that **do not match** a condition.

Like this:

```
fish_no_mohk <- fish_counts %>%
  filter(site != "mohk")
```

This similarly works to exclude observations by a value.

For example, if we want to return all observations *except* those where the total fish count is 1, we use:

```
fish_more_one <- fish_counts %>%
  filter(total_count != 1)
```

What if we want to exclude observations for multiple conditions? For example, here we want to return all rows where the fish species **is not** garibaldi **or** rock wrasse.

We can use `filter(!variable %in% c("apple", "orange"))` to return rows where the variable does **not** match "apple" or "orange". For our fish example, that looks like this:

```
fish_subset <- fish_counts %>%
  filter(!common_name %in% c("garibaldi", "rock wrasse"))
```

Which then only returns observations for the other fish species in the dataset.

```
head(fish_subset)
```

```
## # A tibble: 6 x 4
##    year site  common_name     total_count
##   <dbl> <chr> <chr>                 <dbl>
## 1  2016 abur  black surfperch            2
## 2  2016 abur  blacksmith                1
## 3  2016 abur  senorita                 58
## 4  2016 aque  black surfperch            1
## 5  2016 aque  blacksmith                1
```

```
## 6  2016 aque  senorita                57
```

9.2.2.7 Example: combining `filter()` with other functions using the pipe operator (%>%)

We can also use `filter()` in combination with the functions we previously learned for wrangling. If we have multiple sequential steps to perform, we can string them together using the *pipe operator* (`%>%`).

Here, we'll start with the `invert_counts` data frame and create a subset that:

- Converts to long(er) format with `pivot_longer()`
- Only keeps observations for rock scallops
- Calculates the total count of rock scallops by site only

```
# Counts of scallops by site (all years included):
scallop_count_by_site <- invert_counts %>%
  pivot_longer(cols = '2016':'2018',
               names_to = "year",
               values_to = "sp_count") %>%
  filter(common_name == "rock scallop") %>%
  group_by(site) %>%
  summarize(tot_count = sum(sp_count, na.rm = TRUE))
```

```
scallop_count_by_site
```

```
## # A tibble: 11 x 2
##    site  tot_count
##    <chr>     <dbl>
##  1 abur         48
##  2 ahnd         48
##  3 aque        152
##  4 bull         48
##  5 carp       2519
##  6 golb         48
##  7 ivee        169
##  8 mohk        346
##  9 napl       6416
## 10 scdi       2390
## 11 sctw       1259
```

9.2.3 Merging data frames with `*_join()`

Excel's `VLOOKUP` can also be used to merge data from separate tables or worksheets. Here, we'll use the `*_join()` functions to merge separate data frames in R.

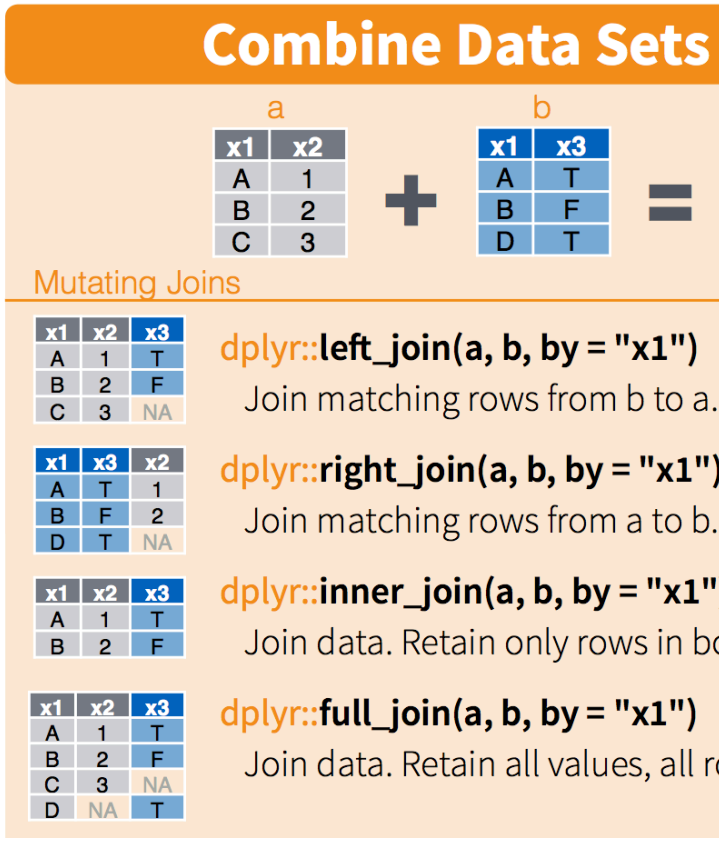
There are a number of ways to merge data frames in R. We'll use `full_join()`, `left_join()`, and `inner_join()` in this session.

From R Documentation (`?join`):

- `full_join()`: "returns all rows and all columns from both x and y. Where there are not matching values, returns NA for the one missing." Basically, nothing gets thrown out, even if a match doesn't exist - making `full_join()` the safest option for merging data frames. When in doubt, `full_join()`.

- `left_join()`: "return all rows from x, and all columns from x and y. Rows in x with no match in y will have NA values in the new columns. If there are multiple matches between x and y, all combinations of the matches are returned."

- `inner_join()`: "returns all rows from x where there are matching values in y, and all columns from x and y. If there are multiple matches between x and y, all combination of the matches are returned." This will drop observations that don't have a match between the merged data frames, which makes it a riskier merging option if you're not sure what you're trying to do.



Schematic (from RStudio data wrangling cheat sheet):

To clarify what the different joins are doing, let's first make a subset of the *fish_counts* data frame that only contains observations from 2016 and 2017.

```
fish_2016_2017 <- fish_counts %>%
  filter(year == 2016 | year == 2017)
```

Take a look to ensure that only those years are included with `View(fish_2016_2017)`. Now, let's merge it with our kelp fronds data in different ways.

9.2.3.1 `full_join()` to merge data frames, keeping everything

When we join data frames in R, we need to tell R a couple of things (and it does the hard joining work for us):

- Which data frames we want to merge together
- Which variables to merge by

Note: If there are **exactly matching** column names in the data frames you're merging, the `*_join()` functions will assume that you want to join by those

columns. If there are *no* matching column names, you can specify which columns to join by manually. We'll do both here.

```
# Join the fish_counts and kelp_counts_abur together:
abur_kelp_join <- fish_2016_2017 %>%
  full_join(kelp_counts_abur, by = c("year", "site")) # Uh oh. An error message.
```

When we try to do that join, we get an error message: `Error: Can't join on 'year' x 'year' because of incompatible types (character / numeric)`

Let's google this. That means copying this from the console and pasting it into Google.

What's going on here? First, there's something fishy (ha) going on with the class of the *year* variable in `kelp_counts_abur`. Use the `class()` function to see how R understands that variable (remember, we use `$` to return a specific column from a data frame).

```
class(kelp_counts_abur$year)
```

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

So the variable is currently stored as a character. Why?

If we go back to the kelp_counts_curated.xlsx file, we'll see that the numbers in both the year and month column have been stored as *text*. There are several hints Excel gives us:

- Cells are left aligned, when values stored as numbers are right aligned
- The green triangles in the corner indicate some formatting
- The warning sign shows up when you click on one of the values with text formatting, and lets you know that the cell has been stored as text. We are given the option to reformat as numeric in Excel, but we'll do it here in R so we have a reproducible record of the change to the variable class.

There are a number of ways to do this in R. We'll use `mutate()` to overwrite the existing `year` column while coercing it to class *numeric* using the `as.numeric()` function.

```
# Coerce the class of 'year' to numeric
kelp_counts_abur <- kelp_counts_abur %>%
  mutate(year = as.numeric(year))
```

Now if we check the class of the *year* variable in `kelp_counts_abur`, we'll see that it has been coerced to 'numeric':

```
class(kelp_counts_abur$year)
```

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

Question: Isn't it bad practice to overwrite variables, instead of just making a new one? Great question, and usually the answer is yes. Here, we feel fine with "overwriting" the year column because we're not changing anything about what's contained within the column, we're only changing how R understands it. Always use caution if overwriting variables, and if in doubt, add one instead!

OK, so now the class of *year* in the data frames we're joining is the same. Let's try that `full_join()` again:

```
abur_kelp_join <- fish_2016_2017 %>%
  full_join(kelp_counts_abur, by = c("year", "site"))
```

Let's look at the merged data frame with `View(abur_kelp_join)`. A few things to notice about how `full_join()` has worked:

1. All columns that existed in **both data frames** still exist.
2. All observations are retained, even if they don't have a match. In this case, notice that for other sites (not 'abur') the observation for fish still exists, even though there was no corresponding kelp data to merge with it. The kelp frond data from 2018 is also returned, even though the fish counts dataset did not have 'year == 2018' in it.
3. The kelp frond data is joined to *all observations* where the joining variables (*year*, *site*) are a match, which is why it is repeated 5 times for each year (once for each fish species).

Because all data (observations & columns) are retained, `full_join()` is the safest option if you're unclear about how to merge data frames. #### `left_join()` to merge data frames, keeping everything in the 'x' data frame and only matches from the 'y' data frame

Now, we want to keep all observations in *fish_2016_2017*, and merge them with *kelp_counts_abur* while only keeping observations from *kelp_counts_abur* that match an observation within *fish_2016_2017*. So when we use `left_join()`, any information on kelp counts from 2018 should be dropped.

```
fish_kelp_2016_2017 <- fish_2016_2017 %>%
  left_join(kelp_counts_abur)
```

```
## Joining, by = c("year", "site")
```

Notice when you look at `fish_kelp_2016_2017`, the 2018 data that **does** exist in `kelp_counts_abur` does **not** get joined to the `fish_2016_2017` data frame, because `left_join(df_a, df_b)` will only keep observations from `df_b` if they have a match in `df_a`!

9.2.3.2 `inner_join()` to merge data frames, only keeping observations with a match in both

When we used `left_join(df_a, df_b)`, we kept all observations in `df_a` but *only observations from `df_b` that matched an entry in `df_a`* (in other words, some entries from `df_b` were excluded).

Use `inner_join()` if you know that you **only** want to retain observations when they match across **both data** frames. Caution: this is built to exclude any observations that don't match across data frames by joined variables - double check to make sure this is actually what you want to do!

For example, if we use `inner_join()` to merge fish_counts and kelp_counts_abur, then we are asking R to **only return observations where the joining variables (*year* and *site*) have matches in both data frames.** Let's see what the outcome is:

```
abur_kelp_inner_join <- fish_counts %>%
  inner_join(kelp_counts_abur)
```

```
## Joining, by = c("year", "site")
```

```
abur_kelp_inner_join
```

```
## # A tibble: 15 x 6
##     year site  common_name     total_count month total_fronds
##    <dbl> <chr> <chr>                 <dbl> <chr>        <dbl>
##  1  2016 abur  black surfperch            2 7              307
##  2  2016 abur  blacksmith                1 7              307
##  3  2016 abur  garibaldi                 1 7              307
##  4  2016 abur  rock wrasse               2 7              307
##  5  2016 abur  senorita                 58 7              307
##  6  2017 abur  black surfperch            4 7              604
##  7  2017 abur  blacksmith                1 7              604
##  8  2017 abur  garibaldi                 1 7              604
##  9  2017 abur  rock wrasse              57 7              604
## 10  2017 abur  senorita                 64 7              604
## 11  2018 abur  black surfperch            1 7             3532
## 12  2018 abur  blacksmith                1 7             3532
## 13  2018 abur  garibaldi                 1 7             3532
## 14  2018 abur  rock wrasse               1 7             3532
## 15  2018 abur  senorita                  1 7             3532
```

Here, we see that only observations where there is a match for *year* and *site* in both data frames are returned.

9.2.3.3 `*_join()` in a sequence

We can also merge data frames as part of a sequence of wrangling steps.

As an example: Starting with the `invert_counts` data frame, we want to:

- First, use `pivot_longer()` to get year and counts each into a single column
- Convert the class of *year* to numeric (so it can join with another numeric year variable)
- Then, only keep observations for "california spiny lobster"
- Next, join the `kelp_counts_abur` to the resulting subset above, **only keeping observations that have a match in both data frames**

That might look like this:

```
abur_lobster_kelp <- invert_counts %>%
  pivot_longer('2016':'2018', names_to = "year", values_to = "total_counts") %>%
  mutate(year = as.numeric(year)) %>%
  filter(common_name == "california spiny lobster") %>%
  inner_join(kelp_counts_abur)
```

```
## Joining, by = c("month", "site", "year")
```

```
abur_lobster_kelp
```

```
## # A tibble: 3 x 6
##   month site  common_name              year total_counts total_fronds
##   <chr> <chr> <chr>                   <dbl>        <dbl>        <dbl>
## 1 7     abur  california spiny lobster  2016           17          307
## 2 7     abur  california spiny lobster  2017           17          604
## 3 7     abur  california spiny lobster  2018           16         3532
```

9.2.3.3.1 Activity

Now let's combine what we've learned about piping, filtering and joining!

Task: Complete the following as part of a single sequence (remember, check to see what you've produced after each step) to create a new data frame called `my_fish_join`:

- Start with `fish_counts` data frame
- Filter to only including observations for 2017 at Arroyo Burro
- Join the `kelp_counts_abur` data frame to the resulting subset using `left_join()`
- Add a new column that contains the 'fish per kelp fronds' density (total_count / total_fronds)

Solution:

Sync your project with your repo on GitHub.

9.3 Fun / kind of scary facts

How is this similar to `VLOOKUP` in Excel? How does it differ?

From Microsoft Office Support, "use VLOOKUP when you need to find things in a table or a range by row."

So, both `filter()` and `VLOOKUP` look through your data frame (or spreadsheet, in Excel) to look for observations that match your conditions. But they also differ in important ways:

(1) By default `VLOOKUP` looks for and returns an observation for *approximate* matches (and you have to change the final argument to FALSE to look for an exact match). In contrast, by default `filter()` will look for exact conditional matches.

(2) `VLOOKUP` will look for and return information from the *first observation* that matches (or approximately matches) a condition. `filter()` will return all observations (rows) that exactly match a condition.

9.4 Interludes (deep thoughts/openscapes)

- Not overusing the pipe in really long sequences. What are other options? Why is that a concern? What are some ways to always know that what's happening in a sequence is what you EXPECT is happening in a sequence? tidylog, check intermediate data frames, sometimes write intermediate data frames, etc.
- The risk of partial joins (& a case for full_join + drop_na instead?)

9.5 Efficiency Tips

- Comment out multiline code with Command + Shift + C
- Knit with Command + Shift + K

Chapter 10

Synthesis

10.1 Summary

In this session, we'll pull together the skills that we've learned so far. We'll create a new GitHub repo and R project, wrangle and visualize data from spreadsheets in R Markdown, communicate between RStudio (locally) and GitHub (remotely) to keep our updates safe, then share our outputs in a nicely formatted GitHub ReadMe. And we'll learn a few new things along the way!

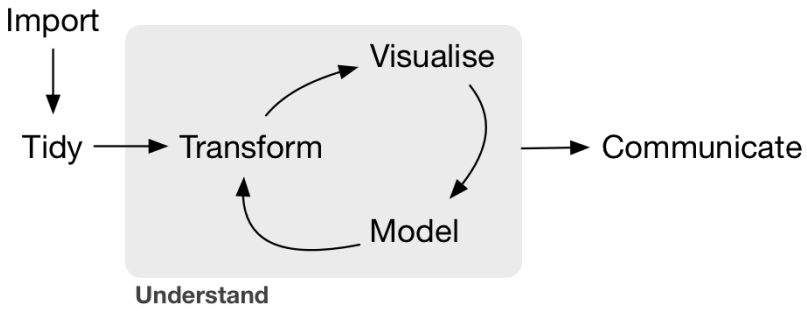


Figure 10.1: Grolemund & Wickham R4DS Illustration

10.2 Objectives

- Create a new repo on GitHub
- Start a new R project, connected to the repo
- Create a new R Markdown document

- Attach necessary packages (`googlesheets4`, `tidyverse`, `here`)
- Use `here::here()` for simpler (and safer) file paths
- Read in data from a Google sheet with the `googlesheets4` package in R
- Basic data wrangling (`dplyr`, `tidyr`, etc.)
- Data visualization (`ggplot2`)
- Publish with a useful ReadMe to share

10.3 Resources

- The `here` package
- googlesheets4 information
- Project oriented workflows by Jenny Bryan

10.4 Lesson

10.4.1 Set-up:

- Log in to your GitHub account and create a new repository called `sea-creature-synthesis`
- Clone the repo to create a version controlled project (remember, copy & paste the URL from the GitHub Clone / Download)
- In the local project folder, create a subfolder called 'data'
- Copy and paste the `fish_counts_curated.csv` and `lobster_counts.csv` into the 'data' subfolder
- Create a new R Markdown document within your `sea-creature-synthesis` project
- Knit your .Rmd to html, saving as `sb_sea_creatures.Rmd`

10.4.2 Attach packages and read in the data

Attach (load) packages with `library()`:

```
library(tidyverse)
library(googlesheets4)
library(here)
library(janitor)
```

Now we'll read in our files with `readr::read_csv()`, but our files aren't in our **project root**. They're in the `data` subfolder.

Use `here::here()` to direct R where to look for files, if they're not in the project root. Not sure where that is? Type `here()` in the Console, and it will tell you!

```
here::here()
```

```
"/returns/your/project/root/"
```

Go ahead, find your project root!

Then use `here::here()` *again* to easily locate a file somewhere outside of the exact project root. In our case, the files we want to read in are in the `data` subfolder - so we have to tell R how to get there from the root:

```
# Read in CSV files
fish_counts <- readr::read_csv(here::here("data", "fish_counts_curated.csv"))
lobster_counts <- readr::read_csv(here::here("data", "lobster_counts.csv"))
```

Check out the two data frames (`fish_counts` and `lobster_counts`).

The `fish_counts` data frame is in pretty good shape. But the `lobster_counts` df could use some love, because there are "-99999" entries indicating `NA` values, and the column names would be difficult to write code with.

When reading in the lobster data, let's:

- convert every "-99999" to an `NA`
- get the column names into lower snake case using `janitor::clean_names()`

```
lobster_counts <- read_csv(here::here("curation", "lobster_counts.csv"),
                           na = "-99999") %>%
                  clean_names()
```

Look at it again to check (always look at your data) - now both data frames seem pretty coder-friendly to work with.

10.4.3 Data wrangling

- join?
- filter?
- unite/separate
- Read in lobster data
- Join with another existing data frame (or 2?)
- Pivoting
- Transforming / subsetting
- Grouping & summarizing (for means, sd, count)
- Make a table
- Make a graph

Possible new things: complete()

10.5 Fun facts (quirky things) - making a note of these wherever possible for interest (little "Did you know?" sections)

10.6 Interludes (deep thoughts/openscapes)

10.7 Efficiency Tips