INTRODUCTION TO R

Where did R come from?

- Thank you Ross Ihaka and Robert Gentleman
- Created to help teach statistics
- Successor to S (also named for its co-creators)
- Comprehensive R Archive Network (CRAN) contains source code and user-created packages
- R is commonly used across many disciplines
- Object-oriented programming (OOP)



Why is R so popular?

It's FREE

Generally excellent documentation

Extremely flexible

Peer reviewed, user-created packages that do just about anything you can think of (including telling your fortune)

IT'S A STEP-BY-STEP DOCUMENTATION OF HOW YOU'VE DONE YOUR ANALYSIS



How do you get started?



Think about how you're going to share your analysis when you reach the article/report/posting stage



Archiving data and code is a strong suggestion or requirement of many journals now



Other forms of publication also often require documentation of your analysis



In this class, we will use GitHub, which is often used for research in progress



Ways to archive

Zenodo Dryad

Version control

- Keeping track of changes that you and others have made to your code and data
- Sharing your analysis as it develops, either publicly or privately
- GitHub hosts many R packages, and you can follow them as they update, even make changes yourself
- You can clone* repositories** onto your own machine in R
- GitHub Tutorial: https://docs.github.com/en/get-started/quickstart/hello-world
- Connecting R and Git: https://happygitwithr.com/index.html

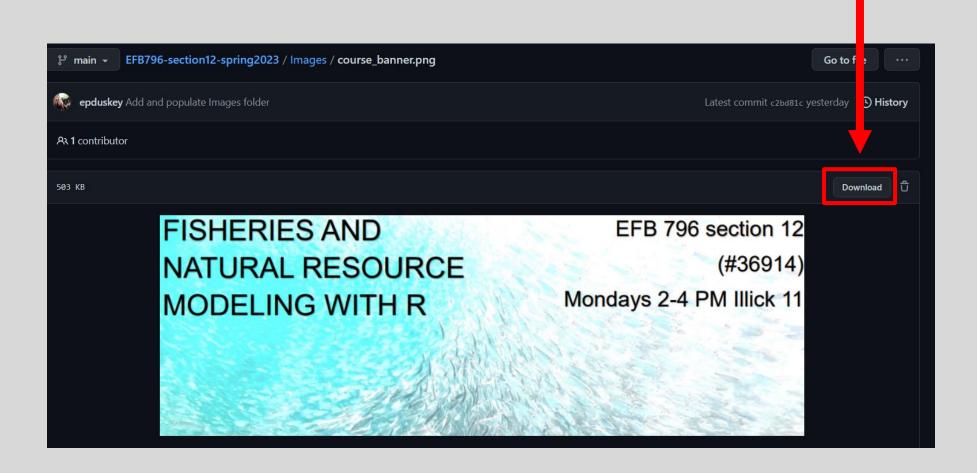


Two options

- Download individual files
- Pros
 - Don't have to bother learning much about GitHub
- Con
 - You will have to copy/paste code into your own script files

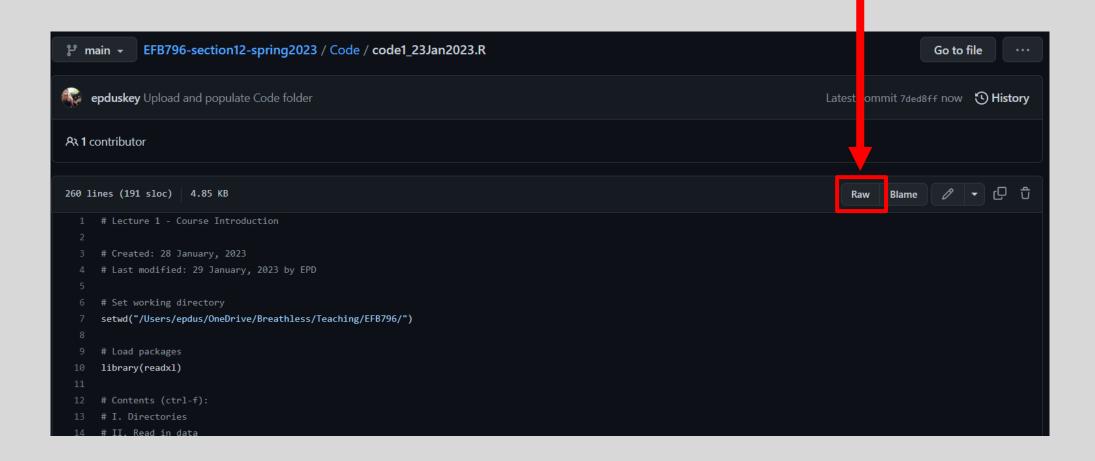
- Clone the repository
- Pros
 - Updates will appear automatically
 - You won't have to learn this stuff later when the journal you've submitted to demands compliance with open research policy
- Cons
 - Learning two things at once!

If NO to GitHub



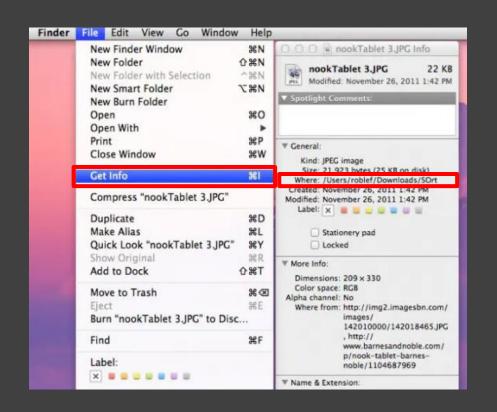
If NO to GitHub

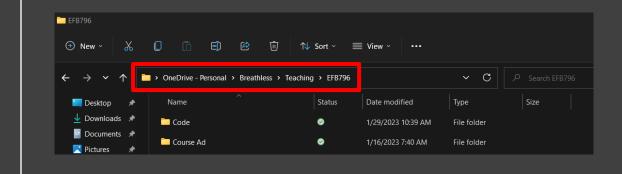
Then right-click and download OR copy/paste



Beginning with R

- General workflow
 - 1. Set your working directory
 - 2. Load the packages you need
 - 3. Load the data you need
 - 4. Manipulate and edit data
 - 5. Perform analysis ↔ debugging
 - 6. Function-ize it
 - 7. Clean-up and organization





HOW TO FIND YOUR WORKING DIRECTORY

Copy file path in file finder on both Windows and Mac

Packages in R

- Find a package
 - Search engine
 - Use a package finder package to find a package
- Use a package
 - See documentation at: https://cran.r-project.org/
 - Search for questions on stack overflow: https://stackoverflow.com/
 - ASK a question on stack overflow, but check it's not been asked before
- Examples
 - Use help() to get documentation and see reproducible examples
 - Modify the code for your own purposes



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How to find data

- Repositories galore!
 - Zenodo
 - Dryad
 - Web of Science
 - Supplemental material on journal website
 - Discipline specific data such as CEFAS

Loading in data



Place data somewhere in your working directory, preferably in a sub-folder



You can also load data from online sources



If you clone a GitHub repository, the data therein will update automatically

Manipulate data

- Adding new rows or columns
 - New calculations result in new columns
 - Combining multiple identically structured data frames results in new rows
- Splitting data into multiple data frames
 - You usually do this when you want a separate data frame for each [value]
- Renaming columns or rows (usually columns)
 - Shorter names are better as they're more efficient and visually less confusing
- Subsetting data
 - There might be certain times/values/species/etc. that you are not interested in
 - You might be interested in everything, but want to look at one [value] at a time



Perform analysis

- This is where the statistics in the base and analytical packages come in
- Let the question you're asking guide the analytical method that you choose
 - Stats/math experts are handy here; we study for years and years to learn these things, so ask us!
- Sometimes you have a tool and you have to use it
 - Check documentation
 - Check stack overflow
 - Look for examples that are like your own, manipulate your data to match, and apply the code

Debugging

- Deal with error messages
- Sometimes you can ignore these, but usually not
- Copy/paste cryptic error messages into a search engine (I still do this all the time)
- Always test your code on one row/chunk of data, knowing what the outcome should be
 - If the result is as expected, it's still a good idea to check a couple more to make sure it's not a fluke

Function-ize it

Make your code more general by turning your analysis into a function

In the future, you may wish to perform a similar analysis on a different species/population/habitat/etc.

Others who wish to use your code will find it much easier

This is not a required step, but it will help