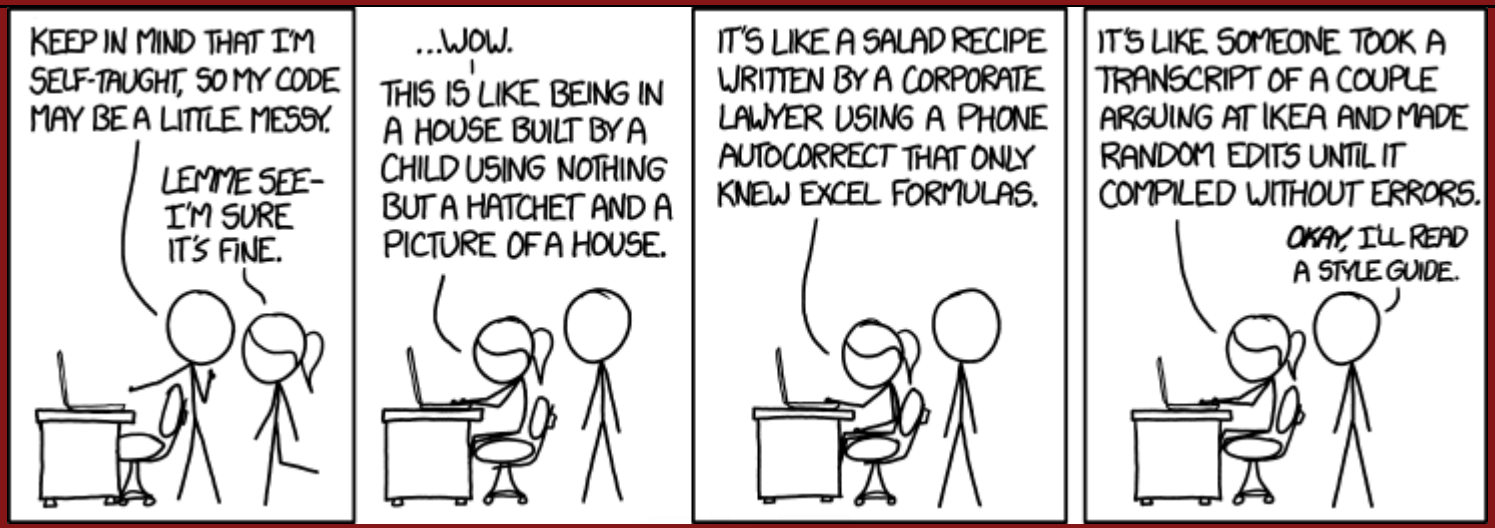
Big Data and Economics

Lecture 2b: The Empirical Workflow and Clean Code

Kyle Coombs (adapted from Tyler Ransom + Scott Cunningham)
Bates College | EC/DCS 368

Table of contents

Prologue



Source: xkcd

Housekeeping

- **Presentations:** Sign-up in the Presentations github repository
- **Problem Set 1:** due on Sunday, January 29th at 11:59pm
- **Final Project Proposal:** due on Sunday, January 25th at 11:59pm
    - Create a fork of the Final Project repository and add me as a collaborator
    - List the names of you and your partner in the README.md file

Attribution

- Today's material comes from these sources:

1. Clean Code by Tyler Ransom
2. *Code and Data for the Social Sciences: A Practitioner's Guide*, by Gentzkow and Shapiro
3. Causal Inference and Research Design by Scott Cunningham
4. Jenny Bryan's UseR 2018 keynote address

Also a small contribution from here and other sundry internet pages

Jargon

- There is a jargon in this class that won't make sense at first, I'll try to flag it as it comes
    - If I don't flag a term, look it up on ChatGPT
    - If it still doesn't make sense, ask me -- could be I'm using it idiosyncratically
- Here's a few terms:
    - **Local machine:** Your personal (or any) computer that isn't a server accessed via the internet
    - **Version Control:** Keep track of different iterations of a project/code
    - **Repository:** The location on GitHub of all project files and (commented) file revision history
    - **GUI:** A Graphical User Interface -- what you're used to pointing and clicking to navigate a computer and execute programs
    - **Command line:** Removes the "graphical" from GUI, instead you type all commands to navigate a computer and execute programs
        - R operates via the Command line, RStudio is a GUI
        - On Mac, this is called Terminal
        - Windows has Powershell, but it Powershell uses quite user-unfriendly commands
        - If you installed Git for Windows, you got *Git Bash*, which uses Bash (Linux) commands
        - You can also install Windows Subsystem for Linux to run Linux on a Windows machine

Reducing empirical chaos

Sad story

- Once upon a time there was a boy who was writing a job market paper on unemployment insurance during the pandemic
- This boy presented the findings a half dozen times, spoke to the media some, and generally thought he had cool results
- Several people suggested he look at a handful of other outcome series and try changing his analysis unit frequency from monthly to weekly
- He also knew that he needed to restrict his sample to reduce noise

The horror!

- But then after making these changes and re-running his code that took two days, his new sample dropped by 50 percent!
- He was, understandably, terrified.
- The young boy spent a week looking for the fix weeding through six different versions of the .do, .R, .dta, .csv, .sh, .py files with suffixes like *_v1* and *_test* and *_test2* and *_final_I_swear* and *_okay_i_lied*
- Finally he discovered the phrase:

```
df %>% filter(insample_new==0)
```

instead of

```
df %>% filter(insample_new==1)
```

- The boy was very frustrated and decided to work on these slides while re-running his code.
- Today I'll present to approaches to avoid this situation:

1. Empirical Workflow
2. Clean Code

Empirical Workflow

The Cunningham Empirical Workflow Conjecture

- The cause of most of your errors is **not** due to insufficient knowledge of syntax in your chosen programming language
- The cause of most of your errors is due to a poorly designed **Empirical Workflow**
- .[Empirical Workflow]: A fixed set of routines you always follow to identify the most common errors
    - Think of it as your morning routine: alarm goes off, go to wash up, make your coffee/tea, put pop tart in toaster, contemplate your existence in the universe until **ding**, eat pop tart repeat *ad infinitum*
- Finding weird errors is a different task; empirical workflows catch typical and common errors
- Empirical workflows follow a checklist

Why do we use checklists?

- I got engaged in July and am planning a wedding in Princeton for next July
- I also moved to New England in August and am still unpacking (in ME and MA)
- I am teaching two upper-level electives
- I am trying to submit several papers to conferences/journals this year
- Each of these gets a checklist:

- **Wedding:**

  ☐ Pick invitation design

  ☐ Send invitations

- **Unpacking:**

  ☐ Put books on shelves

  ☐ Buy dresser

- **AEJ: Policy submission**

  ☐ Write 5-page submission report

  ☐ Submit

- **ECON 368**

  ☐ Write Problem Set 1 solutions

  ☐ Rewrite data tips

- **Senior Thesis:**

  ☐ Create FAQs

  ☐ Develop data guidance

- **Census shocks and racial integration paper**

  ☐ Replicate census shocks results

  ☐ Acquire data on employment, racial wage gap

To remember the obvious stuff

- When I stop to think, I know I need to do everything on my checklists
- But then I forget when I move onto the next task
- Programming is the same, except you have an **empirical checklist**:
- The **empirical checklist**:
  - Covers the intermediate step between "getting the data" and "analyzing the data"
  - It largely focuses on ensuring data quality for the most common, easy to identify problems
  - It'll make you a better coauthor

Simple data checklist items

- Simple, yet non-negotiable, programming commands and exercises to check for data errors
- Here I'll present a few using a messy dataset of blood pressure measurements by race
- Open the raw data and look at it: "Real eyes realize real lies"[1]

```
bp ← read_csv('data/messier_bp.csv',
  show_col_types= FALSE) # Don't tell me the column types
head(bp)
```

```
## # A tibble: 6 × 13
##   STOP.Blood.Pressure.St…¹ X2    X3    X4    X5    X6    X7    X8    X9    X10
##   <chr>                    <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr> <chr>
## 1 <NA>                     <NA>  <NA>  <NA>  <NA>  <NA>  <NA>  Visi… <NA>  Visi…
## 2 pat_id                   Mont… Day … Year… Race  Sex   Hisp… BP    HR    BP
## 3 1                        11    30    1967  White Male  Hisp… 167/… 89    156/…
## 4 2                        12    12    1990  Cauc… Fema… Not … 158/… 77    147/…
## 5 3                        5     4     1989  White Male  Hisp… 171/… 88    161/…
## 6 3                        3     8     1977  Other Fema… Not … 155/… 69    143/…
## # ℹ abbreviated name: ¹STOP.Blood.Pressure.Study
## # ℹ 3 more variables: X11 <chr>, X12 <chr>, X13 <chr>
```

- Oh weird, the first few rows are junk, let's skip them and give more informative names

```
bp ← read_csv('data/messier_bp.csv',skip=2,
  col_names=c('pat_id','birth_month','birth_day','birth_year','race','sex','hispanic',
  'bp_visit1','hr_visit1','bp_visit2','hr_visit2','bp_visit3','hr_visit3'), # Column names
  show_col_types = FALSE) # Don't tell me the column types
head(bp)
```

```
## # A tibble: 6 × 13
##   pat_id birth_month birth_day birth_year race  sex   hispanic bp_visit1
```

[1] Attributed to Ray Charles, Woody Guthrie, Tupac Shakur, Machine Head, and others

Look at summaries of variables

Do factor variables have multiple spellings?

```
table(bp$race,bp$sex)
```

```
##
##             F Female M Male Sex
##   Asian     0      1 0    1   0
##   Black     1      2 1    3   0
##   Caucasian 0      3 0    1   0
##   Other     0      1 0    1   0
##   Race      0      0 0    0   1
##   White     0      2 0    3   0
##   WHITE     0      1 0    1   0
```

The `skimr` package is great for this!

```
skimr::skim(bp)
```

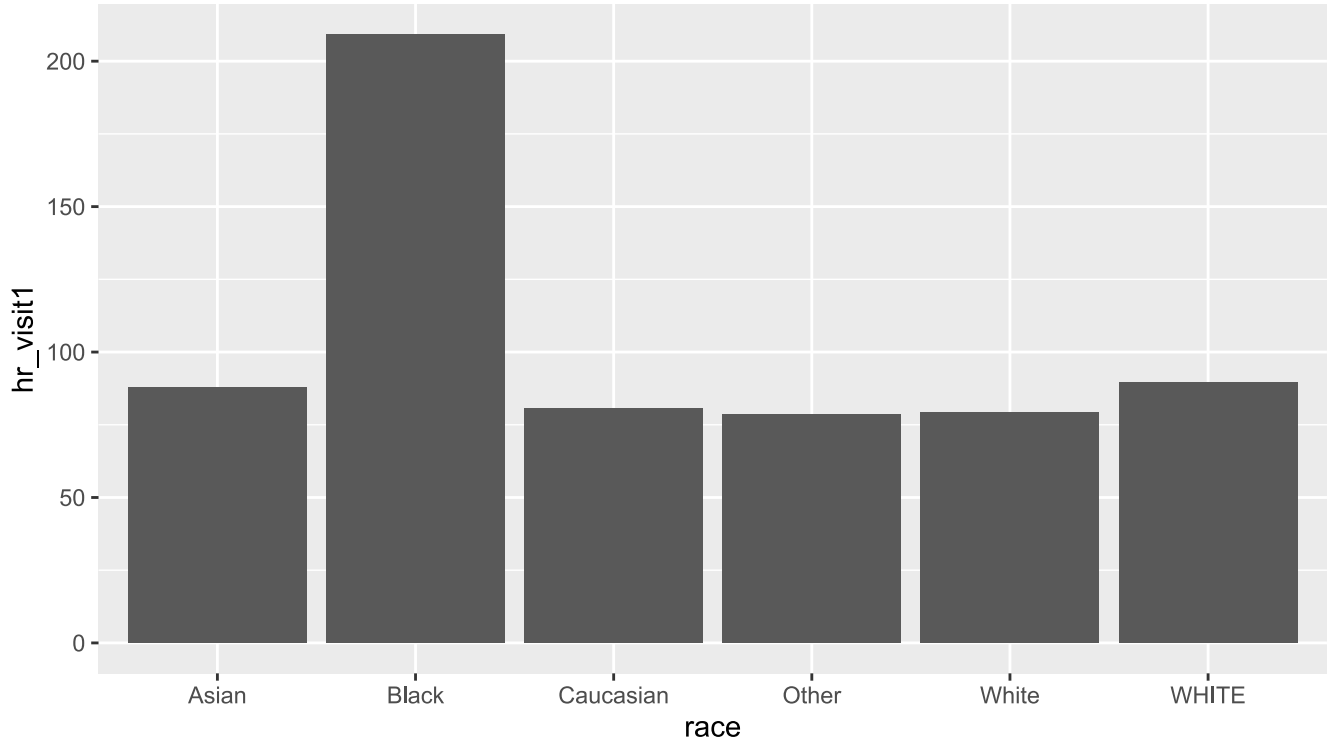
Table: Data summary

Name	bp
Number of rows	24
Number of columns	13

Visualize key facets of the data

```
bp ← read_csv('data/messier_bp.csv',skip=4,
    col_names=c('pat_id','birth_month','birth_day','birth_year','race','sex','hispanic','bp_visit1','hr_visit1','bp_visit2','hr_visit

ggplot(data=bp,aes(y=hr_visit1,x=race)) + geom_bar(stat='summary',fun='mean')
```



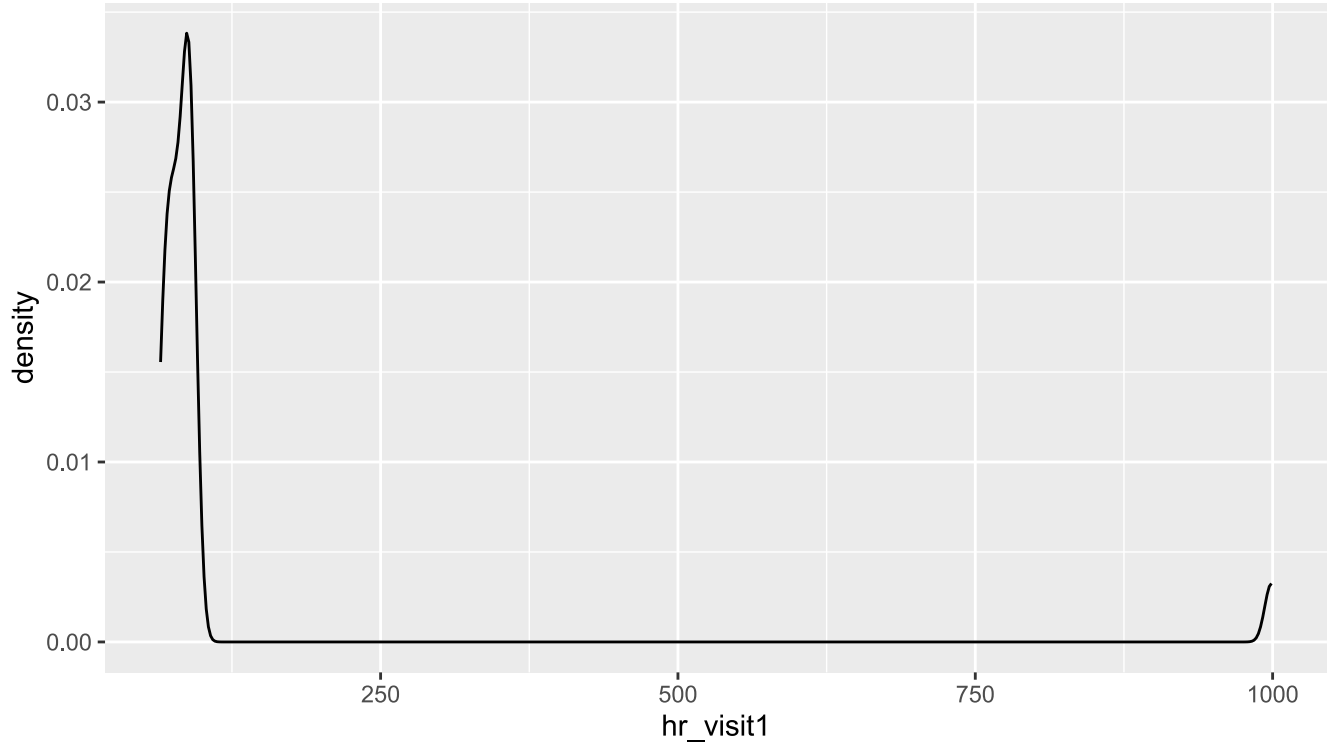
- Are Black people's heart rates really more than twice as high?

Visualize the raw data

- Go beyond the eyeball and graph the data

```
# Get the first three rows of the data frame (or as many rows as needed)

#Make a density of the heart rate on visit 1:
ggplot(data=bp,aes(x=hr_visit1))+geom_density()
```

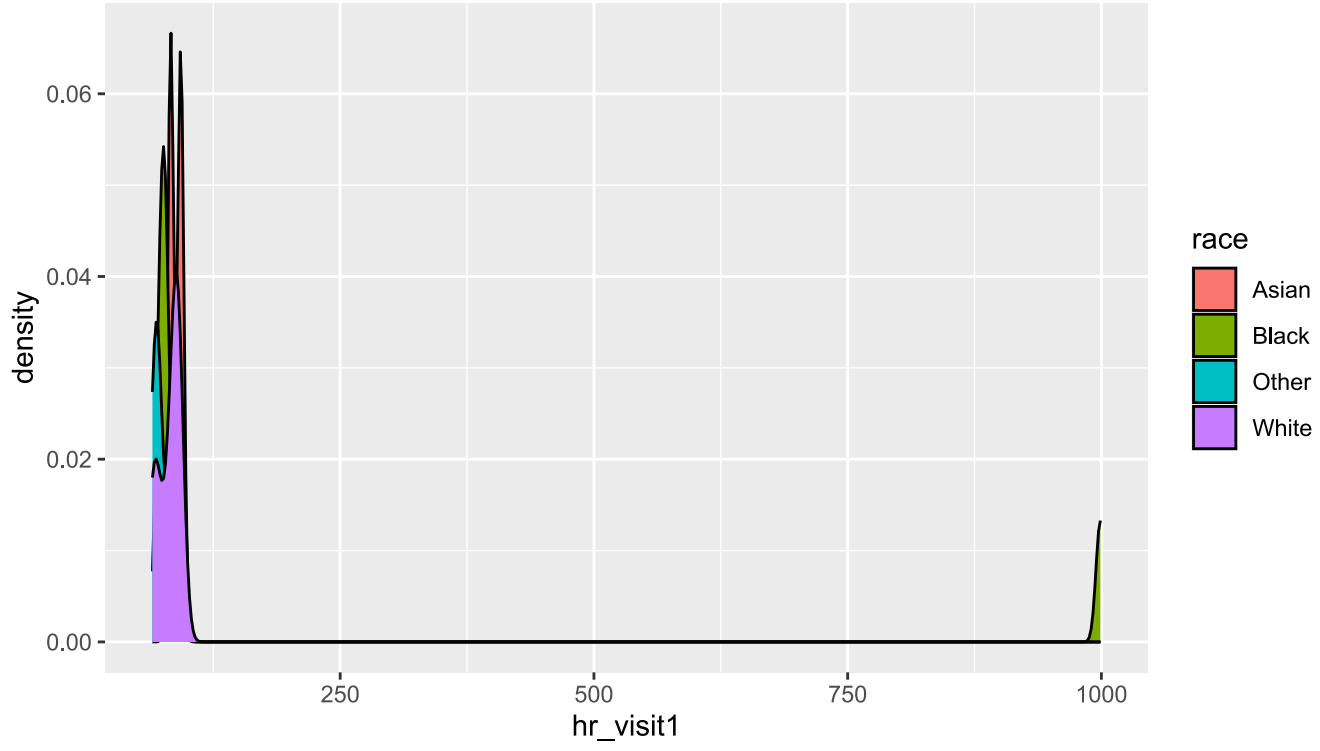


What might be going on here?

Visualize by group

```
# Get the first three rows of the data frame (or as many rows as needed)

#Make a density of the heart rate on visit 1:
ggplot(data=bp %>% mutate(race=ifelse(race=='WHITE' | race=='Caucasian','White',race)),aes(x=hr_visit1,fill=race))+geom_density()
```



- Oh! I bet 999 means NA and a few Black patients have missing heart rates

Other tricks:

- Check if the data are the right-size
- If you have a panel dataset is 50 states over 20 years, check if there are 1000 observations
- If not, find out why! Maybe there are 1020 because DC is (rightfully) included
- Search for outliers or oddities and work out possible explanations using:
  - Codebooks
  - Intuition
  - Emails to the source/creator of data

Clean Code

What is Clean Code?

Clean Code: Code that is easy to understand, easy to modify, and hence easy to debug

Clean code advances scientific progress

- Good science uses careful observations to iteratively test hypotheses/make predictions
- Scientific progress is impeded if
  - mistaken previous results are erroneously given authority
  - previous hypothesis tests are not reproducible
  - previous methods and results are not transparent
- Thus, for science that involves computer code, clean code is a must
- Reduces "the influence of hidden researcher decisions" (Huntington-Klein et al. 2021)

Clean code increases personal/team sanity

- You will always make a mistake while coding -- hat makes good programmers great is their ability to quickly identify and correct mistakes
- Clean code makes it easier to identify and correct mistakes
- Saves you stress in the long-run and makes your collaborative relationships more pleasant

Why clean code is under-produced

- If clean code is so beneficial and important, why isn't there more of it?

1. **Competitive pressure** to produce research/products as quickly as possible
2. **End user** (journal editor, reviewer, reader, dean) **doesn't care what the code looks like**, just that the product works
3. In the moment, clean code **takes longer to produce** while seemingly conferring no benefit

How does one produce clean code?

1. Automation
2. Version Control[1]
3. Organization of data and software files
4. Abstraction
5. Documentation
6. Time / task management
7. Test-driven development (unit testing, profiling, refactoring)
8. Pair programming

[1] Skipped today cause we covered it last class.

1. Automation

- Gentzkow & Shapiro's two rules for automation:

1. Automate everything that can be automated

2. Write a single script that executes all code from beginning to end

- There are two reasons automation is so important
    - Reproducibility (helps with debugging and revisions)
    - Efficiency (having a code base saves you time in the future)
- A single script that shows the sequence of steps taken is the equivalent to "showing your work"

How to write scripts

Keep them modular

- Each script should do one thing and one thing only
- e.g. It takes an input in, it returns an output
    - Taking in a raw file and returning a cleaned version
    - Taking in two files and merging them
    - Taking in a cleaned file and returning a figure

Have a main script that runs all scripts in order

- This is the script that you run to reproduce your results
- You will rarely run it all at once, but it will be a nice way to organize your thoughts
- This is a further benefit of a well-organized directory -- you can easily see what scripts you need to run in what order
- Use `source('rscript.R')` to run an external script

--

- A main script could be a `.Rmd`, a `.R`, a `.sh`, a `.py`, a `.do` etc.

Main script

```r
#File: main.Rmd or main.R
#By: Kyle Coombs
#What: Runs the project from start to finish in Python
#Date: 2023/09/12

#Install packages with housekeeping. Also put together paths.
source('housekeeping.R')
#User written functions can be sourced -- or you could write a package, your call
source(paste0(build,'clean_functions.R'))
source(paste0(analysis,'analysis_functions.R'))

#Import files
source(paste0(build,'import_census.R'))
source(paste0(build,'import_admin_data.R'))

#Clean files
source(paste0(build,'clean_census.R'))
source(paste0(build,'clean_admin_data.R'))

#Merge files 1 to 2
source(paste0(build,'merge_census_admin.R'))

#Analysis
source('analysis/summary_stats.R')
source('analysis/basic_regression.R')

#Tables will likely be made with a host of R packages
source('analysis/make_sum_figures.R')
source('analysis/make_reg_figures.R')
source('analysis/make_sum_tables.R')
source('analysis/make_reg_tables.R')
```

Main script with functions

Main script as .Rmd

- In this class, your problem sets will be .Rmd files that you knit to PDF/HTML
- The .Rmd file will serve as your main script
- You can `source()` modular code files in code chunks
- PS1 will show you examples of doing this
- This guarantees your code runs from start to finish instead of only when you are working interactively

What's a housekeeping file?

A housekeeping file automates several tasks and goes at the start of every file in your project

```
# Housekeeping.R
# By: Your Name
# Date: YYYY-MM-DD
# What: This script loads the packages and data needed for the analysis.

## Package installation -- uncomment if running for the first time
#install.packages(c('here','tidyverse'))
library(here)
library(tidyverse)
library(haven)

## Directory creation

here::i_am('housekeeping.R')

data_dir <- here::here('data')
raw_dir <- here::here(data_dir,'raw')
clean_dir <- here::here(data_dir,'clean')
output_dir <- here::here('output')
code_dir <- here::here('code')
processing_dir <- here::here(code_dir,'processing')
analysis_dir <- here::here(code_dir,'analysis')
documentation_dir <- here::here('documentation')

suppressWarnings({
    dir.create(data_dir)
    dir.create(raw_dir)
    dir.create(clean_dir)
    dir.create(documentation_dir)
    dir.create(code_dir)
    dir.create(processing_dir)
    dir.create(analysis_dir)
    dir.create(output_dir)
})
```

3a. File organization

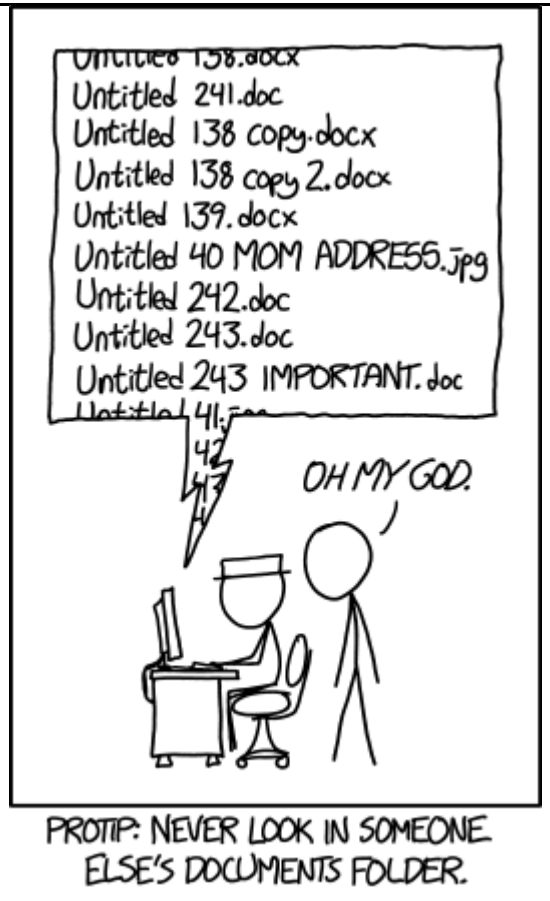
1. Separate directories by function

2. Separate files into inputs and outputs

3. Make directories portable

- To see how professionals do this, check out the source code for R's dplyr package
    - There are separate directories for source code (`/src`), documentation (`/man`), code tests (`/test`), data (`/data`), examples (`/vignettes`), and more
- When you use version control, it forces you to make directories portable (otherwise a collaborator will not be able to run your code)
    - use **relative** file paths, not absolute file paths

Don't be like this



Source: xkcd

What is a directory?

- All the files on your computer are organized in directories or folders
- When you are running a script, you are running it from a particular directory
  - This is *not necessarily* the directory where the script is located
  - It is the directory that your console is in
  - That means if you say `read.csv('my_data.csv')`, your computer looks for `my_data.csv` in that particular directory
  - If that file is not in that directory, you will get a `FileNotFound` error
  - In **R**, you can see what directory you are in using the `getwd()` function
  - It is also above the console in RStudio
  - You can change your working directory using the `setwd()` function

```
getwd()
## [1] "C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials/lectures/02-empirical-workflow"
#setwd('lectures/02-empirical-workflow')
```

What is a directory path?

A path defines the location of a file or directory in a file system tree.

If I navigate to this file in my computer, the path is `C:\Users\kgcsp\OneDrive\Documents\Education\Big Data\big-data-class-materials\lectures\02-empirical-workflow\02-empirical-workflow.Rmd`

The name separates folders that chart the path from the **root** to the file

- **root**: the start of the file system tree (above that is `C:\`)
- Each folder along the tree is separated by a `\` or `/`

This is called an **absolute path**:

- It is long
- It is hard to remember
- It is not portable -- if I send this file to you, it won't work on your computer

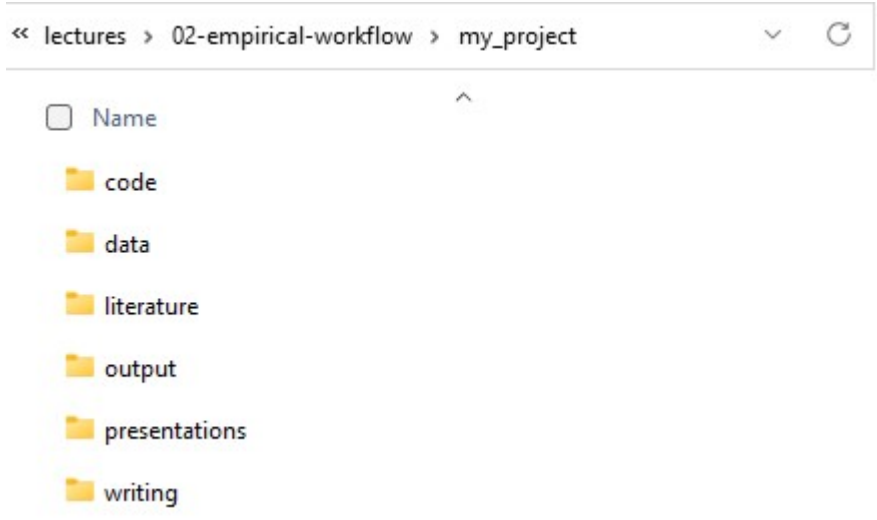
Relative paths solve a lot of this:

- The path to a file or directory starting from the current working directory
- If my current working directory is `/big-data-class-materials`, then I can use `lectures/02-empirical-workflow/02-empirical-workflow.Rmd`
- **This is portable** -- if I send this file to you and you have a copy of the `big-data-class-materials` repository on your computer, it will work on your computer

How I organize research projects

- Entire projects should *ideally* live within the same directory
- I have a folder called (`my_project`)
  - Within that folder I have subfolders:
    1. `data` for all data files a. `raw` for raw data files b. `clean` or `work` for cleaned data files c. `temp` for temporary data files
    2. `code` for all code files, and sometimes: a. `code/analysis` for code files that build/clean code a. `code/build` for code files that do analysis
    3. `output` for all output files a. `output/figures` for code files that make figures b. `output/tables` for code files that make tables
    4. `literature` or `articles` for all relevant literature
    5. `writing` for all writing files a. `writing/notes` for notes b. `writing/drafts` for drafts c. `writing/edits` for edits
    6. `presentations` for all presentations a. `presentations/slides` for slides b. `presentations/notes` for notes
- I'll further more or less as needed
- See GitHub folder for this lecture as an example
  - I also include a script `make_directory.sh` that automates this process

How I organize research projects



Source: My computer

What is the value of directories?

- All of the files in a directory are related to each other
- Can reference a file within the `data/raw` folder, from the `code/build` folder without writing out the full path `C:/Users/kylec/Documents/my_project/data/raw/my_data.csv`
- Can save objects of strings of path directories to use later using the `paste()` function

```
my_project ← 'my_project'
data ← paste(my_project,'data',sep='/')
data_raw ← paste(data,'raw',sep='/')
data_clean ← paste(data,'clean',sep='/')
data_temp ← paste(data,'temp',sep='/')
code ← paste(my_project,'code',sep='/')
code_analysis ← paste(code,'analysis',sep='/')
code_build ← paste(code,'build',sep='/')

print(paste(data_raw,'my_data.csv',sep='/'))
```

```
## [1] "my_project/data/raw/my_data.csv"
```

```
read.csv(paste(data_raw,'my_data.csv',sep='/'))
```

```
##   this is my data
## 1    1  1  1    1
## 2    2  2  2    2
```

- This is a good way to make sure that your code is portable
- If you move your project to a different computer, you can just change the `my_project` variable and all the other paths will update automatically

Alternative to all the pastes is here()

- Better yet is the here
  - `here()` will find the root directory of your project and then you can navigate from there

```
#install.packages('here')
library(here)
```

```
## here() starts at C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials
```

```
here::i_am('my_project/code/build/.placeholder')
```

```
## here() starts at C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials/lectures/02-empirical-workflow
```

```
here('data/raw','my_data.csv')
```

```
## [1] "C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials/lectures/02-empirical-workflow/data/raw/my_data.csv"
```

- Can be less clunky than `paste()` and `sep="/"`
- Get lost in your directories? Use `here::here()` to identify your root directory
- Alternatively, double-click the `.Rproj` file to be redirected to the root directory of your project folder

Help! I am in code/, but I need

- You can use relative paths to navigate between directories
- `..` means "go up one directory"
  - `../data/raw` means "go up one directory, then down into `data/raw`"
- `.` means "stay in the current directory"
  - `./code/build` means "stay in the current directory, then down into `code/build`"
- `../..` means "go up two directories"
  - `../../data/raw` means "go up two directories, then down into `data/raw`

Play around with them yourself!

3b. Data organization

- The key idea is to practice **relational data base management**
- A relational database consists of many smaller data sets
- Each data set is tabular and has a unique, non-missing key
- Data sets "relate" to each other based on these keys
- You can implement these practices in any modern statistical analysis software (R, Stata, SAS, Python, Julia, SQL, ...)
- Gentzkow & Shapiro recommend not merging data sets until as far into your code pipeline as possible

What problems would this create?

county	state	cnty_pop	state_pop	region
36037	NY	3817735	43320903	1
36038	NY	422999	43320903	1
36039	NY	324920	.	1
36040	.	143432	43320903	1
.	NY	.	43320903	1
37001	VA	3228290	7173000	3
37002	VA	449499	7173000	3
37003	VA	383888	7173000	4
37004	VA	483829	7173000	3

Source: Code and Data for the Social Sciences (p. 19)

What's RDBM look like?

county	state	population
36037	NY	3817735
36038	NY	422999
36039	NY	324920
36040	NY	143432
37001	VA	3228290
37002	VA	449499
37003	VA	383888
37004	VA	483829

state	population	region
NY	43320903	1
VA	7173000	3

Source: Code and Data for the Social Sciences (p. 19)

4. Abstraction

- What is abstraction? It means "reducing the complexity of something by hiding unnecessary details from the user"
- e.g. A dishwasher. All I need to know is how to put dirty dishes into the machine, and which button to press. I don't need to understand how the electrical wiring or plumbing work.
- In programming, abstraction is usually handled with functions
- Abstraction is usually a good thing
- But it can be taken to a harmful extreme: overly abstract code can be "impenetrable" which makes it difficult to modify or debug

Rules for Abstraction

- Gentzkow & Shapiro give three rules for abstraction:

1. Abstract to eliminate redundancy

2. Abstract to improve clarity

3. Otherwise, don't abstract

- In the context of R, abstraction means:
  - Write functions
  - Name your objects sensibly

Abstract to eliminate redundancy

- Sometimes you might find yourself repeating lines of code:

```
names_thrice ← c('kyle','alex','charlie','sadie','laila','aidan','alice','ethan','ian','jaden','john','maggie','rawson','sam','sean'
  'kile','alex','charlie','sadie','laila','aidan','alice','ethan','ian','jaden','john','maggie','rawson','sam','sean','tyler','will',
  'alex','charlie','sadie','laila','aidan','alice','ethan','ian','jaden','john','maggie','rawson','sam','sean','tyler','will','yun','
```

Notice any problems?

```
#Better
names_short ← c('kyle','alex','charlie','sadie','laila','aidan','alice','ethan','ian','jaden','john','maggie','rawson','sam','sean',
c(names_short,names_short,names_short)
```

```
##  [1] "kyle"    "alex"    "charlie" "sadie"   "laila"   "aidan"   "alice"
##  [8] "ethan"   "ian"     "jaden"   "john"    "maggie"  "rawson"  "sam"
## [15] "sean"    "tyler"   "will"    "yun"     "yuna"    "kyle"    "alex"
## [22] "charlie" "sadie"   "laila"   "aidan"   "alice"   "ethan"   "ian"
## [29] "jaden"   "john"    "maggie"  "rawson"  "sam"     "sean"    "tyler"
## [36] "will"    "yun"     "yuna"    "kyle"    "alex"    "charlie" "sadie"
## [43] "laila"   "aidan"   "alice"   "ethan"   "ian"     "jaden"   "john"
## [50] "maggie"  "rawson"  "sam"     "sean"    "tyler"   "will"    "yun"
## [57] "yuna"
```

R anticipated repetition and created an in-built function

```
#Even better use rep function
rep(names_short, times = 3)
```

```
##  [1] "kyle"    "alex"    "charlie" "sadie"   "laila"   "aidan"   "alice"
##  [8] "ethan"   "ian"     "jaden"   "john"    "maggie"  "rawson"  "sam"
## [15] "sean"    "tyler"   "will"    "yun"     "yuna"    "kyle"    "alex"
## [22] "charlie" "sadie"   "laila"   "aidan"   "alice"   "ethan"   "ian"
## [29] "jaden"   "john"    "maggie"  "rawson"  "sam"     "sean"    "tyler"
```

Abstract to improve clarity

- Consider the example of obtaining OLS estimates from a vector `y` and covariate matrix `X` that already exist on our workspace
- We could code this in two ways:

```
Bhat = (t(X)%*%X)^(-1)%*%t(X)%*%y
Bhat2 = (t(X)%*%X2)^(-1)%*%t(X2)%*%y
```

or

```
estimate_ols ← function(yvar, Xmat) {
    Bhat = (t(Xmat)%*%Xmat)^(-1)%*%t(Xmat)%*%yvar
    return(Bhat)
}
Bhat = estimate_ols(y,X)
Bhat2 = estimate_ols(y,X2)
```

The second approach is easier to read and understand what the code is doing

Otherwise, don't abstract

- One could argue that the examples on the previous slides are overly abstract
- OLS is a simple operation that only takes one line of code
- If we're only doing it once in our script, then it may not make sense to use the function version
- This discussion points out that it can be difficult to know if one has reached the optimal level of abstraction
- As you're starting out programming, I would advise doing almost every inside of a function (i.e. err on the side of over-abstraction when starting out)

5. Documentation

1. Don't write documentation you will not maintain

2. Code should be self-documenting

- Generally speaking, commented code is helpful
- However, sometimes it can be harmful if, e.g. code comments contain dynamic information
- It may not be helpful to have to rewrite comments every time you change the code
- Code can be "self-documenting" by leveraging abstraction: function arguments make it easier to understand what is a variable and what is a constant

A README is documentation

- A README gives high-level information about the repository or data file:
  - This repository contains code that does X task
  - Simple use case: use this repository to replicate paper X in journal Y
- Onboarding instructions:
  - Add your name to this file in repository folder `the/folder/file.md`
  - Fork the repository and pull request changes
  - Configure your computer settings in this way to run this project
  - Guidelines/rules for contributing to the project
- Licensing information:
  - You can just take this code!
  - This is proprietary and we will sue you if you haven't paid us
- Dependencies:
  - To use this code or package or data, download packages `X`, `Y`, `Z`
- Changelog (short narrative commit history):
  - 9/23/2023 - KGC - added function `X` to do `Y`

Documentation in R

- **R Help System:** access using `?function_name`
- **Package vignettes:** access using `vignette("vignette_name")`
- **Cheatsheets:** access at Posit Cheatsheets

Make your own documentation

- R has excellent built-in documentation called `Roxygen2`
- These make great documents above functions to increase readability
- Here's an example:

```
library(roxygen2)
#' This is a sample function
#'
#' This function does something amazing.
#'
#' @param x A numeric input.
#' @return The result of the amazing operation.
#' @examples
#' amazing_function(5)
amazing_function ← function(x) {
  # function implementation
}
```

- Use `roxygen::roxygenise()` to generate documentation for all functions in a file
- Read more here

6a. Time management

- Time management is key to writing clean code[2]
- It is foolish to think that one can write clean code in a strained mental state
- Code written when you are groggy, overly anxious, or distracted will come back to bite you
- Schedule long blocks of time (1.5 hours - 3 hours) to work on coding where you eliminate distractions (email, social media, etc.)
- Stop coding when you feel that your focus or energy is dissipating

[2] Your professor needs this lecture too

6b. Task management

- When collaborating on code, it is essential to not use email or Slack threads to discuss coding tasks
- Rather, use a task management system that has dedicated messages for a particular point of discussion (bug in the code, feature to develop, etc.)
- I use GitHub issues for all of my coding projects
- For my personal task management, I use Trello to take all tasks out of my email inbox and put them in Trello's task management system
- GitHub and Trello also have Kanban-style boards where you can easily visually track progress on tasks

7. Test-driven development

- The only way to know that your code works is to test it!
- Test-driven development (TDD) consists of a suite of tools for writing code that can be automatically tested
- Simplest test is to check if the code gives you the output you expected
- More complicated is to write a unit test
- **Unit testing** is nearly universally used in professional software development
- Unit testing is to software developers what washing hands is to surgeons

Unit testing

- Unit tests are scripts that check that a piece of code does everything it is supposed to do
- When professionals write code, they also write unit tests for that code at the same time
- If code doesn't pass tests, then bugs are caught immediately
- R's dplyr package shows that all unit tests are passing and that tests cover 88% of the code base
- testthat is a nice step-by-step guide for doing this in R

Assertions

- Assert statements are extremely useful for basic unit tests
- They exist in every langage
- In R it is called stopifnot()

```
x ← TRUE
stopifnot(x)

y ← FALSE
stopifnot(y)
```

```
## Error: y is not TRUE
```

Troubleshooting tips

- Sometimes you've made several changes to your code and suddenly it stops running
    - Was it the new `if` statement?
    - That sick new vectorized function to replace the `for` loop?
    - A stray typo?
- How do you find the bug in hundreds of lines of code?
- Read your code to see if there is an obvious mistake
- **Binary search**: Comment[1] half your code, run the script, and see if the bug persists
    - If it does, the bug is in the other half
    - If it doesn't, the bug is in the commented half
    - Use `#` to comment out lines of code in R, or highlight and press `Ctrl+Shift+C`
- Repeat on each half until you narrow to set of lines
- If you can solve the bug from that line, great!
- If not, make a **Minimal reproducible example**!

[1] Comment in R with `#`. Comment in RMarkdown with `<!-- code -->`. Or highlight and press `Ctrl+Shift+C` in RStudio.

Minimal reproducible example (MRE)

- There's likely a ton of superfluous stuff in your code that is not relevant to the error
- Minimal reproducible examples (reprex) are a great way to isolate the error
    - **Minimal**: Use as little code as possible that still produces the same problem
    - **Complete**: Provide all parts needed to reproduce your problem in the question itself
    - **Reproducible**: Test the code you'll provide to make sure it reproduces the problem
- That means you should be able to copy and paste the code into R and run it yourself
    - Name all packages and data needed to reproduce error
    - Cut out irrelevant packages, steps, and data that are not relevant to the error
- Sometimes writing one will help you find the bug, sometimes it'll help a stranger find the bug in your code faster, and sometimes it'll identify a very real bug in the package itself
- MREs also help you refactor and profile your code

Min Reprex from RStudio community

- If someone does not have `hrbrthemes` installed, they will not be able to run your code.
  - You can remove this package from your code and still reproduce the error.

```
library(ggplot2) #For ggplot
library(datasets) #To load irs
library(hrbrthemes) #For the theme
data(iris)
df ← iris %>%
    mutate(Sepal.Length = Sepal.Length * 1000,
           Sepal.Width = Sepal.Width * 1000)

ggplot(data = df,x = Sepal.Length, y = Sepal.Width) +
    theme_modern_rc() +
    geom_point() +
    scale_x_log10() +
    labs(title = "Iris Sepal Width vs. Sepal Length",
         subtitle = "Log10 Scaled X Axis")
```

```
## Error in `geom_point()`:
## ! Problem while setting up geom.
## ℹ Error occurred in the 1st layer.
## Caused by error in `compute_geom_1()`:
## ! `geom_point()` requires the following missing aesthetics: x and y
```

How to write MREs

- Cut out the unnecessary steps

```
library(ggplot2)

df ← data.frame(stringsAsFactors = FALSE,
                Sepal.Length = c(5.1, 4.9, 4.7, 4.6, 5),
                Sepal.Width = c(3.5, 3, 3.2, 3.1, 3.6)
)
ggplot(data = df, x = Sepal.Length, y = Sepal.Width) +
    geom_point()
```

```
## Error in `geom_point()`:
## ! Problem while setting up geom.
## ℹ Error occurred in the 1st layer.
## Caused by error in `compute_geom_1()`:
## ! `geom_point()` requires the following missing aesthetics: x and y
```

```
#> Error: geom_point requires the following missing aesthetics: x, y
```

- You can use reprex to make sure that your code is reproducible by others.
- You can use dput to make sure that your data is reproducible by others.

Troubleshooting tips (cont.)

- Step back and ask if you're solving the right problem
  - e.g. I'm trying to make a plot, but I'm getting an error about a missing variable. Maybe I should check if I'm loading the right data
  - e.g. I have to create a long data set and I have annual files, but my code is merging instead of appending...
- Check for superfluous things you can remove
  - e.g. Wait, I don't need to include absolute file paths, I can use relative paths
  - Bonus: I'll make fewer typos!
- Try small fixes, then apply broadly
  - e.g. I think the problem is with how I wrote my file paths, let me try to get just one file path to work
- Change one thing at a time
  - e.g. The problem is either with my `paste0()` statement or the `ggsave` function, let me try to get the `paste0()` statement to work first

Troubleshooting tips (cont.)

- Embrace GitHub committing
  - When you have code that works, stage, commit and push it -- even if it is only a small piece of the puzzle
  - If it breaks, revert
  - This minimizes how much you need to re-do/keep track of
- Sometimes it is easier to change things on yourside than it is to force a programming language to work a certain way
  - e.g. Rmarkdown doesn't like the character `#` in filepaths, but I can change the filepaths rather than trying to force Rmarkdown to accept it
- There's more than one way to skin a cat
  - e.g. If I can't get `read.csv()` to work, I'll try `read.table()`
  - e.g. This `googlesheets4` package doesn't seem to work -- what about `gsheet` or `googledrive`?
- With ChatGPT or Google, make very specific asks
  - e.g. "How do I get a file named `/my/path/name/my_file.pdf` into `other/folder/name/file.Rmd`?"

8. Pair programming - work with a buddy

- An essential part of clean code is reviewing code
- An excellent way to review code is to do so at the time of writing
- **Pair programming** involves sitting two programmers at one computer
- One programmer does the writing while the other reviews
- This is a great way to spot silly typos and other issues that would extend development time
- It's also a great way to quickly refactor code at the start
- **I strongly encourage you to do pair programming on problem sets in this course!**
    - (Sometimes I will require it)

Next lecture: R basics, data wrangling, tidyverse and data.table

Appendix

Main script with functions

name: main-with-functions

```
#File: main.Rmd or main.R
#By: Kyle Coombs
#What: Runs the project from start to finish in Python
#Date: 2023/09/12

#Install packages with housekeeping. Also put together paths.
source('housekeeping.R')
#User written functions can be sourced -- or you could write a package, your call
source(paste0(build,'clean_functions.R'))
source(paste0(analysis,'analysis_functions.R'))

#Import files
df1 <- read_csv(paste0(raw,'file1.csv'))
df2 <- read_parquet(paste0(raw,'file2.parquet'))
df3 <- read_dta(paste0(raw,'file3.dta'))

#Clean files
cleaned_df1  <- clean_df1(df1)
cleaned_df2  <- clean_df2(df2)
cleaned_df3  <- cf.clean_df3(df3)

#Merge files 1 to 2
merged_df1_df2 = merge(cleaned_df1, cleaned_df2, on=c('merge','vars'))

#Append file 1 to
append_df1_df2_df3 = rbind(merged_df1_df2, cleaned_df2)

#Analysis
sum_stats=summary_stats(append_df1_df2_df3,stats=c('mean','median','max'))
reg_results=basic_regression(append_df1_df2_df3)

#Tables will likely be made with a host of R packages
make_sum_figures(sum_stats)
make_figures(reg_results)
make_sum_tables(sum_stats)
make_tables(reg_results)
```

Textbooks: Smarter people than me

- Cunningham (2021) Causal Inference: The Mixtape (Also, free version on his website)
- Huntington-Klein (2022) The Effect
- Angrist and Pischke (2009) Mostly Harmless Econometrics (MHE)
- Morgan and Winship (2014) Counterfactuals and Causal Inference (MW)
- Sweigart (2019) Automate The Boring Stuff With Python
- Wickham (2023) Advanced R
- Wickham and Grolemund (2023) R for Data Science
- Peng (2022) R Programming for Data Science

Non-textbook readings

- The help documentation associated with your language (no really)
- Jesse Shapiro's "How to Present an Applied Micro Paper"
- Gentzkow and Shapiro's coding practices manual
- Ljubica "LJ" Ristovska's language agnostic guide to programming for economists
- Grant McDermott on Version Control using Github Link

Helpful for troubleshooting

- The help documentation associated with your language (no really)
- All languages: Stack Overflow, Stack Exchange
- Stata-specific (all hail Nick Cox): Statalist
- Cheatsheets: Stata, RStudio, Python
- Me: Sign up for office hours

Learn by Immersion

- Just like learning a real language, no amount of talking today will teach you how to use any program.
    - You have to need to use it (immersion) to learn it.
    - Google is your dictionary.
    - Help files are your grammar books.
    - ChatGPT is your phrasebook.
    - A great way to start coding is to see lots of other people's code and copy what you read.
- You must learn how to ask the “right” question:
    - Never: "Importing csv file into R not working."
    - Better: "read_csv R [specific error message]."
    - Better still: "read_csv tidyverse [specific error message]."

Abstract to eliminate redundancy (cont.)

What if you can't find an R function? Write your own!

```
set.seed(16)
prod1  = rnorm(1, 0, 1)*rnorm(1,4,6)
prod2  = rnorm(2, 0, 1)*rnorm(2,0,1)
prod3  = rnorm(3, 0, 1)*rnorm(3,15,78)
print(prod1)
## [1] 1.547257
print(prod2)
## [1] 1.2582691 0.6764943
print(prod3)
## [1] -60.06036  10.11156  24.32342
```

```
set.seed(16)
multiply_normals = function(count,mean1=0,sd1=1,mean2=0,sd2=1) {
    prod = rnorm(count,mean1,sd1)*rnorm(count,mean2,sd2)
    return(prod)
}
prod1=multiply_normals(1,mean2=4,sd2=6)
prod2=multiply_normals(2,mean2=0,sd2=1)
prod3=multiply_normals(3,mean2=15,sd2=78)

print(prod1)
## [1] 1.547257
print(prod2)
## [1] 1.2582691 0.6764943
print(prod3)
## [1] -60.06036  10.11156  24.32342
```

Note on seeds

- When randomizing in any language, you aren't really randomizing
- You're producing pseudo-random numbers that return in a deterministic ordered list
- If you set the seed, you can reproduce the same "random" numbers
- This is useful for debugging and sharing code
- Use `set.seed` in R

```
set.seed(0)
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 17.26652
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 15.14712
# New seed
set.seed(1)
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 13.72156
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 16.10432
# Reset seed
set.seed(0)
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 17.26652
print(rnorm(1)+rnorm(1,5)+rnorm(1,10))
## [1] 15.14712
```

Refactoring

- Refactoring refers to the action of restructuring code without changing its external behavior or functionality. Think of it as "reorganizing"

```
get_some_data ← function(config, outfile) {
  if (config_ok(config)) {
    if (can_write(outfile)) {
      if (can_open_network_connection(config)) {
        data ← parse_something_from_network()
        if(makes_sense(data)) {
          data ← beautify(data)
          write it(data, outfile)
```

after refactoring becomes

```
get_some_data ← function(config, outfile) {
  if (config_bad(config)) {
    stop("Bad config")
  }

  if (!can_write(outfile)) {

    stop("Can't write outfile")
```

- Nothing changed in the code except the number of characters in the function
- The new version may run faster, is more readable. The output is unchanged.
- Refactoring could also mean reducing the number of input arguments
- Jenny Bryan gave a great talk on refactoring

Profiling

- Profiling refers to checking the resource demands of your code
- How much processing time does your script take? How much memory?
- Clean code should be highly performant: it uses minimal computational resources
- Profiling and refactoring go hand in hand, along with unit testing, to ensure that code is maximally optimized
- Here are two intro guides to profiling in R:
  - Using `system.time` and `Rprofs` from R Programming for Data Science[https://bookdown.org/rdpeng/rprogdatascience/profiling-r-code.html]
  - Using `lineprof` from Advanced R[http://adv-r.had.co.nz/Profiling.html]

Back to MREs

Neat R functions to help reduce

```
set.seed(16)
list1 = list() # Make an empty list to save output in
for (i in 1:3) { # Indicate number of iterations with "i"
    list1[[i]] = multiply(i) # Save output in list for each iteration
}
list1
```

```
## [[1]]
## [1] 1.547257
##
## [[2]]
## [1] 11.934479 -1.717951
##
## [[3]]
## [1] -7.4831177  0.9587218  4.7882622
```

A better way to eliminate this redundancy is to use the `map` function:

```
set.seed(16)
map(1:3, multiply)
```

```
## [[1]]
## [1] 1.547257
##
## [[2]]
## [1] 11.934479 -1.717951
##
## [[3]]
## [1] -7.4831177  0.9587218  4.7882622
```