Data Science for Economists

Lecture 2b: Clean Code

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Prologue



Source: xkcd

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

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_1_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 and next class are about minimizing these struggles through Clean Code and a reproducible workflow

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 -- what makes good programmers great is their ability to 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. Organization of data and files
- 2. Version Control¹
- 3. Automation
- 4. Abstraction
- 5. Documentation
- 6. Time / task management
- 7. Test-driven development (unit testing, profiling, refactoring)
- 8. Pair programming

1a. 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

Untitled 138.00CX Untitled 241.doc Untitled 138 copy.docx Untitled 138 copy 2. docx Untitled 139. docx Untitled 40 MOM ADDRESS. Jpg Untitled 242.doc Untitled 243. doc Untitled 243 IMPORTANT. doc Not tla L H OH MY GOD.

PROTIP: NEVER LOOK IN SOMEONE. ELSE'S DOCUMENTS FOLDER.

Source: xkcd

What is a working directory?

- All the files on your computer are organized in directories or folders
- When you are running a script, you are working from a particular directory
 - This is not necessarily the directory where the script is located
 - Your computer looks for my_data.csv in this directory when you execute read.csv('my_data.csv')
 - 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 double click the .Rproj file to set the working directory to the root of the project
 - You can also change your working directory using the setwd() function (avoid this within scripts)

getwd()

[1] "C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials/lectures/02-empirical-

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, it is:

C:\Users\kgcsp\OneDrive\Documents\Education\ECON368-DSE\big-data-class-materials\lectures\02empirical-workflow\02-empirical-workflow.Rmd¹

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 \setminus or /

This is called an **absolute path**:

• It is long, hard to remember, and not portable across computers

Relative paths solve a lot of this:

using ..

- The path to a file or directory starting from the current working directory
- If my working directory is /big-data-class-materials, then I can write lectures/02-empirical-workflow.Rmd
- This is portable: if you have a copy of the big-data-class-materials repository, this script will ¹ This is a Windows path, Mac and Linux paths use / instead of \. See appendix for slides on how to move between them

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:
 - 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
 - presentations for all presentations a. presentations/slides for slides b.
 presentations/notes for notes
- I'll further more or less as needed
- See the my_project folder on GitHub (in the same folder as this lecture) as an example

What is the value of directories?

• All of the files in a directory are related to each other

Ο

- Can reference a file within the data/raw folder, from the code/build folder without writing out the full path
- If you use file.path() or the **here** package, you can automate the slashes in your file paths
 - file.path('data', 'raw', 'file.csv') will work on Windows, Mac, and Linux
 - here::here('data', 'raw', 'file.csv') will do the same thing (see appendix for more on it)
- Then you do not need to worry about shifting around directories

1b. 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_state	region_county
##	1	36037	NY	3817735	43320903	1	1
##	2	36038	NY	422999	43320903	1	1
##	3	36039	NY	324920	NA	1	1
##	4	36040	<na></na>	143432	43320903	1	1
##	5	NA	NY	NA	43320903	1	1
##	6	37001	VA	3228290	7173000	3	3
##	7	37002	VA	449499	7173000	3	3
##	8	37003	VA	383888	7173000	3	4
##	9	37004	VA	483829	7173000	3	3
##	10	NA	VA	NA	7173000	3	3

Why is RDBM better?

##		county	state	cnty_pop
##	1	36037	NY	3817735
##	2	36038	NY	422999
##	3	36039	NY	324920
##	4	36040	NY	143432
##	5	37001	VA	3228290
##	6	37002	VA	449499
##	7	37003	VA	383888
##	8	37004	VA	483829

##		state	state_pop	region
##	1	NY	43320903	1
##	2	VA	7173000	3

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

3. 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)

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
- This is somewhat aligned with the structure of an essay
 - intro paragraph =/= body paragraph 1 =/= ... =/= conclusion
- Much like essays revisions, modular code makes it easier to debug and revise

Have a main script that runs all scripts in order

- A single script that shows the sequence of steps, i.e. "shows your work"
 - This script will run modular scripts in sequence to exactly reproduce your analysis
- You will rarely run it all at once, but it will be a nice way to organize your thoughts
- A benefit of a well-organized directory: easily see what scripts you need to run in what order $_{20/54}$

#File: main.R.R
#By: Kyle Coombs
#What: Runs the project from start to finish in Python
#Date: 2024-09-0
Instructions:
Run this code from the root directory of your project

#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(paste0(analysis,'/summary_stats.R'))
source(paste0(analysis,'/basic_regression.R'))

#Tables will likely be made with a host of R packages
courses(pasts)(pasts)(pasts)(pasts)(pasts)

Main script with functions

Main script as .Rmd

- In this class, your problem sets will be .Rmd files that you knit
- The .Rmd file will serve as your main script
- You can source() modular code files in code chunks
- It improves chances your code runs from start to finish instead of only when working interactively
 - Means I can run (and grade) your code more easily!

What's a housekeeping file?

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

- 1. Load packages
- 2. Save strings of path directories to use later using the file.path() function to reference elsewhere¹
 - If a folder name changes, you only need to change it in one place in your code
 - Use these strings to reference files in other scripts

```
read.csv(file.path(data_raw,'my_data.csv'))
```

3. Create directories if they don't exist

```
# 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('tidyverse'))
library(tidyverse)
library(haven) # installed by tidyverse
```

```
## Directory objects
```

```
data_dir ← file.path('data')
raw_dir ← file.path(data_dir,'raw')
clean_dir ← file.path(data_dir,'clean')
output_dir ← file.path('output')
code_dir ← file.path('code')
processing_dir ← file.path(code_dir,'processing')
analysis_dir ← file.path(code_dir,'analysis')
documentation_dir ← file.path('documentation')
```

```
# Create directories
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)
```

})

4. Abstraction

- Abstraction: "reducing the complexity of something by hiding unnecessary details from the user"
- e.g. A dishwasher. I mainly need to know how to load it, put in soap, and press start. I don't need to understand the electrical wiring or plumbing.
- In programming, abstraction is usually handled with functions
- Abstraction is usually a good thing
- But it you can go too far: overly abstract code can be "impenetrable" and difficult to modify or debug

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 to accomplish a task

```
# Downloading a sequence of files from 2004 to 2020 gets tedious
```

```
download.file('https://data.nber.org/tax-stats/zipcode/2020/zipcode2020.zip',destfile=paste0(data_dir,
download.file('https://data.nber.org/tax-stats/zipcode/2019/zipcode2019.zip',destfile=paste0(data_dir,
download.file('https://data.nber.org/tax-stats/zipcode/2019/zipcode2019.zip',destfile=paste0(data_dir,
# etc.
```

Notice any problems?

```
# Downloading a sequence of files from 20 wih a loop
lapply(2004:2020,function(y) {
    download.file(paste0('https://data.nber.org/tax-stats/zipcode/',y,'/zipcode',y,'.zip'),destfile=pas
})
```

- We'll learn more about iteration/for loops/appy statements later
- There are many forms of redundancy that can be eliminated with abstraction beyond iteration

Abstract to improve clarity

Say you want to round a number to the nearest of different integers:

- 1. Divide the number by there base integer
- 2. Round the result to the nearest whole number
- 3. Multiply by the base integer

I start coding and copy and paste the code for each integer:

```
rounded_157_nearest_5 \leftarrow round(157/5)*5
rounded 157 nearest 7 \leftarrow round(157/5)*7
```

Notice a problem?

Why not abstract with a function?

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

Otherwise, don't abstract

- 1. Write/use functions for tasks that are repeated
- 2. Write thoughtful variable names (e.g. x100, x101 versus household_income, household_size)
- 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 everything inside of a function (i.e. err on the side of over-abstraction when starting out)
 - And look for opportunities to loop (or use apply functions)

5. Documentation

Documentation gives sufficient information to replicate work, but not so much that it is overwhelming¹

Rules for 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 naming functions and variables thoughtfully

Documentation in R

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

¹ Anyone who has ever built IKEA furniture knows this all too well

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_dir download packages x, y, z
- Changelog (short narrative commit history):
 - 9/23/2023 KGC added function x to do Y

Documentation and problem sets

Documentation inevitably creates a host of issues on assignments.

It is challenging to give narrative technical instructions:

On a blank problem set:

- The reader (you) still needs to engage thoughtfully with the task
- The writer (me) needs to account for many misinterpretations!

On a completed problem set:

- The reader (me) is trying to guess what you were thinking
- The writer (you) may have made a mistake and not realized it

This challenge is a feature, not a bug.

My assignments are a learning experience of the **robustness principle/Postel's law**¹ (for people):

"Be conservative in what you send, be liberal in what you accept." - Jon Postel

He was talking about internet protocols, but I see it as a general principle for communication:

- Conservative: Make instructions instructions as clear s
- Liberal: Give the benefit of the doubt and try to engage thoughtfully with documentation This quote was originally in reference to how to design programs that send and receive data.

6. Time and task management

Time management

- Time management is key to writing clean code¹
- 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

Task management

- When collaborating on code, avoid 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 and milestones for all of my coding projects including developing this class

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
 - Whenever you make a change, check it against the output you expect
 Ideally, check against a small example so it runs fast and is easy to confirm
- What if the code takes too long to check completely? Meet **unit tests**
- **Unit testing** is nearly universally used in professional software development

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 91% of the code base
- **testthat** is a nice step-by-step guide for doing this in R (I use it to autograde exercises)

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

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)

Minimal reproducible example¹

- Related to unit testing are minimal reproducible examples (aka MRE, reprex, minreps,...)
- The best way to isolate bugs is a minimal reproducible example
- If code throws an error, there's likely superfluous lines of code that are irrelevant to the error
 - The superfluous stuff makes it harder to read and replicate 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 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

Min Reprex from RStudio community

- If someone does not have hrbrthemes installed, they will not be able to run the code below
 - 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)
dat ← iris[1:4,]
ggplot(data = dat, 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.
```

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

dput(iris[1:4,]) # copy/paste output of dput into your MRE

```
## structure(list(Sepal.Length = c(5.1, 4.9, 4.7, 4.6), Sepal.Width = c(3.5,
## 3, 3.2, 3.1), Petal.Length = c(1.4, 1.4, 1.3, 1.5), Petal.Width = c(0.2,
## 0.2, 0.2, 0.2), Species = structure(c(1L, 1L, 1L, 1L), levels = c("setosa",
## "versicolor", "virginica"), class = "factor")), row.names = c(NA,
## 4L), class = "data.frame")
```

A complete MRE¹

Summary

When I try to make a scatterplot with ggplot, I am told that geom_point() requires missing aesthetics x and y. But I specified x and y in the ggplot() function. Can you help resolve?

Expected behavior

I expected the code to produce a scatterplot of Sepal.Length and Sepal.Width from the iris dataset.

Data

I used a subset of the iris dataset.

dat \leftarrow iris[1:4,]

Code and error message

```
ggplot(data = dat, x = Sepal.Length, y = Sepal.Width) +
    geom_point()
```

```
## Error in `geom_point()`:
## ! Problem while setting up geom.
```

¹ Every forum has its own approach to MREs. Sometimes session info is not initially needed!

Try to write an MRE!

- Sync your fork of the exercise repository and open the folder for mre-exercise
- The file mre-opatlas.Rmd has a bug in it that has led to a host of problems when you look at the knit output, mre-opatlas.md
- Try to write an MRE
- I have already raised this as a poorly-written issue on GitHub. You can see the issue here
- Tips: https://aosmith16.github.io/spring-r-topics/slides/week09_reprex.html#1

Appendix

Shifting directories

Help! I need to run code from code, but need a file in data/raw/file.csv!

- 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!

Main script with functions

name: main-with-functions

```
#File: main.Rmd or main.R
#Bv: 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 \leftarrow read dta(paste0(raw, 'file3.dta'))
#Clean files
cleaned df1 \leftarrow clean df1(df1)
cleaned df2 \leftarrow clean df2(df2)
cleaned df3 \leftarrow 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)
```

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
```

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

Refactoring

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

after refactoring becomes

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

Alternative to file.path 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/6

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

[1] "C:/Users/kgcsp/OneDrive/Documents/Education/Big Data/big-data-class-materials/lectures/02-empirical-

- Can be less clunky than paste() and sep="/"
- Get lost in your directories? Use file.path() to identify your root directory