Statistics and Data Science Workshop Series

Friday March 3

Today's topic: how to manage your project's files/repository

Motivation

Unless you are working alone, you need a system with which to share files with your team.

Some common file-sharing platforms include:

- GitHub
- Google Drive
- Posit Cloud

Good practices

Agree upon naming conventions for files/variables with your team. Here are some common ones:

- Snakecase: variable one, variable two
- Kebabcase: variable-one, variable-two
- Pascalcase: VariableOne, VariableTwo
- Camelcase: variableOne, variableTwo
- Hungarian Notation—describes variable type or purpose at the beginning
 - 0
 - sUserName 0
- arrDistributeGroup // Array called "Distribute Group"
 - // String called "User Name"
 - // Integer called "Random Seed"

iRandomSeed 0

When referencing other files, do not use your computer's specific filepath. Instead, assume that the main repository file is your working directory. For example, instead of:

data <-

read.csv("/Users/anyamac/Desktop/GitHub/sdsw-project/data/data.csv")

You could write

data <- read.csv("~/data/data.csv")</pre>

The goal is to reduce confusion and make it easier to reproduce your work on other computers.

Miscellaneous tips

- If you're unsure what to do, Google it!
- If you are using randomly generated numbers or data, make sure you are setting a seed for reproducibility.
- Have a groupchat on some platform so that no one works on the same file at the same time. Also just communicate.
- COMMENT YOUR CODE!
- Be consistent with tabbing and whitespace conventions.

README.md files

We will talk about this more later, but your repository should at minimum have a README file. It should give any user a general overview of the purpose and what your project is doing.

Demo: RMarkdown and GitHub