GITting started with reproducibility: An introduction to git and knitr

Biostatistics Student Association Computing Workshop

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Why do I care about reproducibility?

Reproducible research is a hallmark of the scientific method, but we're pretty bad at it.

> *In 2012, a researcher then at the biotechnology company Amgen wrote in Nature that when his team tried to reproduce 53 landmark cancer studies, they could replicate just six. And according to a news report in Nature, a project aiming to reproduce the findings of 100 psychology papers has managed to replicate results for only 39 of them (the project's findings are still under peer review).*

"What Science Can Tell Us About Bad Science", *The Atlantic*, September 2015. `http://www.theatlantic.com/magazine/archive/2015/09/a-scientific-look-at-bad-science/399371/`

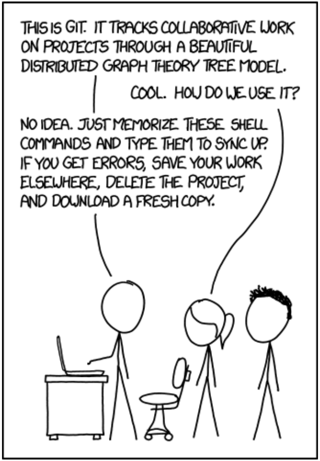
But I'm a Biostatistician!

- Reproducibility is important in both science AND statistics!
- As statisticians, we need to be able to reproduce our results on the same data set
    - This means we have to write reports in a way that minimizes error and write code so that we can get the same results years later.

Agenda

1. Git: A “version control” tool used for collaborating and maintaining different versions of a file, typically for code.
    - Great for collaborating, or just saving your own ass.
    - Often used in conjunction with *GitHub*, an online repository storage service.
2. knitr: An R package that lets you create documents containing R code and output.
    - Keep everything you need to generate a report (e.g., for research, homework, or 699) in one place!
    - My favorite part: Update code without having to re-create tables! (This is where errors creep in!)

A brief warning


THIS IS GIT. IT TRACKS COLLABORATIVE WORK ON PROJECTS THROUGH A BEAUTIFUL DISTRIBUTED GRAPH THEORY TREE MODEL.
COOL. HOW DO WE USE IT?
NO IDEA. JUST MEMORIZE THESE SHELL COMMANDS AND TYPE THEM TO SYNC UP. IF YOU GET ERRORS, SAVE YOUR WORK ELSEWHERE, DELETE THE PROJECT, AND DOWNLOAD A FRESH COPY.

Source: `https://xkcd.com/1597/`

Setup

Create a GitHub account, then download either Git or GitHub Desktop.

- Pure Git (i.e., just command-line tools): `https://git-scm.com/downloads`
- GitHub Desktop (GUI & command-line tools): `https://desktop.github.com/`

Forking a Repository

A *fork* is a copy of a repository. Forks let you

- make changes to an existing repo without affecting the original project
- use the existing project as a starting point for your own

One of the benefits of open source!

Exercise: Fork my `bsa-computing` repository.

Cloning a Repository

- To create a local copy of an existing git repository, use `git clone [url] [directory-name]`.
- In a terminal (Mac, Linux) or the Git Shell (Windows), navigate to the folder you want to clone the repository into.
- **Exercise:** Clone your forked `bsa-computing` repository onto your computer. The URL will be of the form `https://github.com/[username]/bsa-computing.git`

Make Changes!

- You now have a copy of both the current version of `bsa-computing` *and* access to every previous version.
- This clone is NOT automatically synced, à la Dropbox
  - Anything you break is completely isolated from the pristine copy on GitHub and your previous "commits".
- **Exercise:** Add to `food-exercise.md`, and save your changes.

Making Commits and Pushing

- Once you've accomplished a relatively small, but still significant task, you'll want to "commit" your code to the repository.
- This creates a labeled snapshot of the directory at the time of the commit.
- Syncing your commits with the existing remote repository is called "pushing".

Shell Commands for Commits and Push/Pull

- To *pull* down the most recent version of the remote repository, use `git pull`
- To make and push commits
  - Check what you've changed with `git status` and `git diff`.
  - Add files to the commit using `git add [files]`.
  - Create a commit using `git commit -m [message]`
  - Push your commit to the remote repository using `git push`

Merging Your Fork with the Original

On GitHub, create a *pull request* to merge your changes into my repository. The owner (me) will be able to look at and accept/decline them.

What is knitr?

- knitr lets you embed code and output from R into LaTeX, HTML, RMarkdown, etc. I'll be using LaTeX.
- Might require a bit more thought with R code to get the correct output, but it's worth it.

The knitr Bible: http://yihui.name/knitr/

Chunks

knitr separates R code from LaTeX using structures called "chunks".

Chunk Syntax

```
<<list(chunkname, eval=FALSE>>= @
```

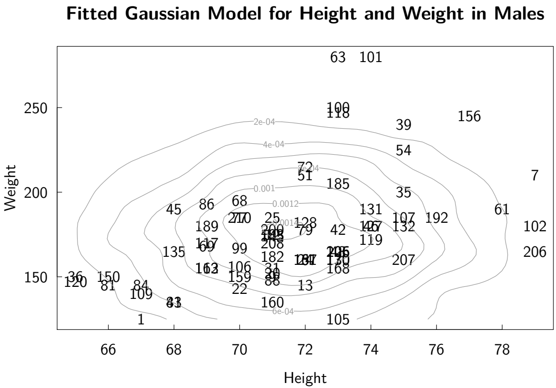
Chunk Options

When you define a chunk, you also can include a number of options that tell `knitr` how to interpret the R code inside. Some basic important options are:

- `echo (TRUE)`: Whether or not to include the R code itself in the document.
- `results`: How to display results. Default is in a LaTeX `verbatim` environment.
    - `asis`: Write raw results into the document (e.g., with `xtable`)
- `include (TRUE)`: Whether to include the chunk output in the document. The code is still run. Useful for data steps.
- `cache (FALSE)`: Stashes the output of a chunk to avoid running it every time you compile.

More options and more details at `http://yihui.name/knitr/options/`.

Example: Figure


Fitted Gaussian Model for Height and Weight in Males

Example: Tables

There are 137 women in this dataset, out of 210 total individuals.

	Mean	Std. Dev.	Median
Height	67.36	4.46	67.00
Weight	145.66	32.69	140.00

Table: Summary Statistics for All Individuals

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
1	65.00	70.00	72.00	71.66	73.00	79.00
2	125.00	155.00	170.00	175.60	185.00	280.00

Table: Summary Statistics for Men