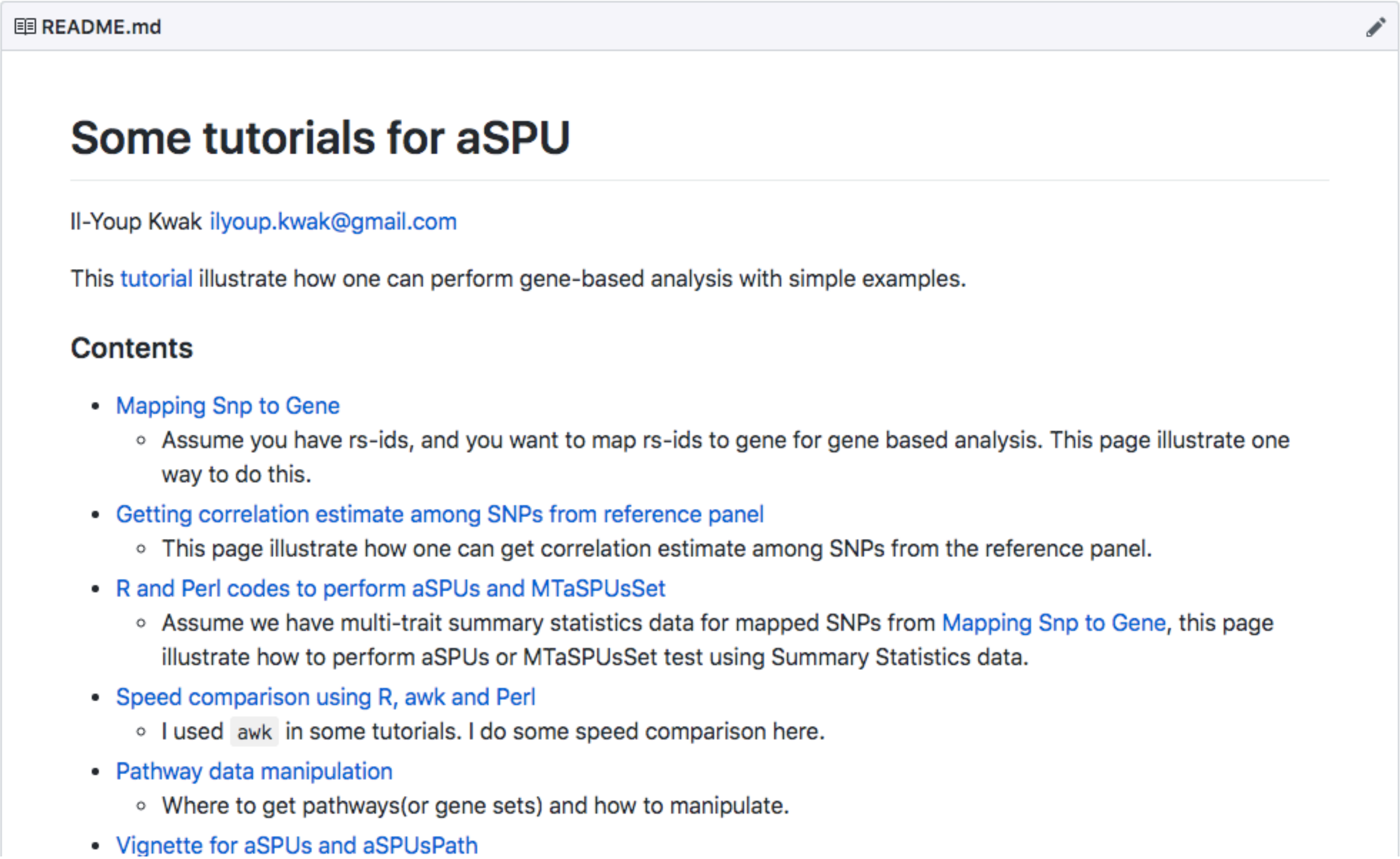
Markdown and Github

Il-Youp Kwak

Markdown

1. Easy to write a html report
2. Language for Jupyter notebook, github reedme
3. Use rmarkdown for reproducible research

Markdown in Github



README.md

Some tutorials for aSPU

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This tutorial illustrate how one can perform gene-based analysis with simple examples.

Contents

- Mapping Snp to Gene
  - Assume you have rs-ids, and you want to map rs-ids to gene for gene based analysis. This page illustrate one way to do this.
- Getting correlation estimate among SNPs from reference panel
  - This page illustrate how one can get correlation estimate among SNPs from the reference panel.
- R and Perl codes to perform aSPUs and MTaSPUsSet
  - Assume we have multi-trait summary statistics data for mapped SNPs from Mapping Snp to Gene, this page illustrate how to perform aSPUs or MTaSPUsSet test using Summary Statistics data.
- Speed comparison using R, awk and Perl
  - I used `awk` in some tutorials. I do some speed comparison here.
- Pathway data manipulation
  - Where to get pathways(or gene sets) and how to manipulate.
- Vignette for aSPUs and aSPUsPath

Markdown Practice using Jupyter notebook

https://heropy.blog/2017/09/30/markdown/

Markdown

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R Markdown

1. A variant of Markdown, developed at RStudio.com

   https://yihui.name/knitr/options/#chunk_options

2. Markdown + knitr + extra

3. LateX equations with $$

Chunk options

echo=FALSE	Don’t include the code
results=“hide”	Don’t include the output
include=FALSE	Don’t show code or output
eval=FALSE	Don’t evaluate the code at all
warning=FALSE	Don’t show R warnings
message=FALSE	Don’t show R messages
fig.width= #	Width of figure
fig.height= #	Height of figure

A lot more at: https://yihui.name/knitr/options/#chunk_options

Global chunk options

~~~
```{r global_options, include=FALSE}
knitr::opts_chunk$set(fig.width=12, fig.height=4, fig.path='Figs/',
                      warning=FALSE, message=FALSE,
                      include=FALSE, echo=FALSE)
set.seed(123123)
```
~~~

- **Use global chunk options rather than repeat the same options over and over**

Global chunk options

~~~
```{r global_options, include=FALSE}
knitr::opts_chunk$set(fig.width=12, fig.height=4, fig.path='Figs/',
                      warning=FALSE, message=FALSE,
                      include=FALSE, echo=FALSE)
set.seed(123123)
```
~~~

- **Use global chunk options rather than repeat the same options over and over**

In-line code

```
Iris data have `r nrow(iris)` obersvations with `r ncol(iris)` columns.
```

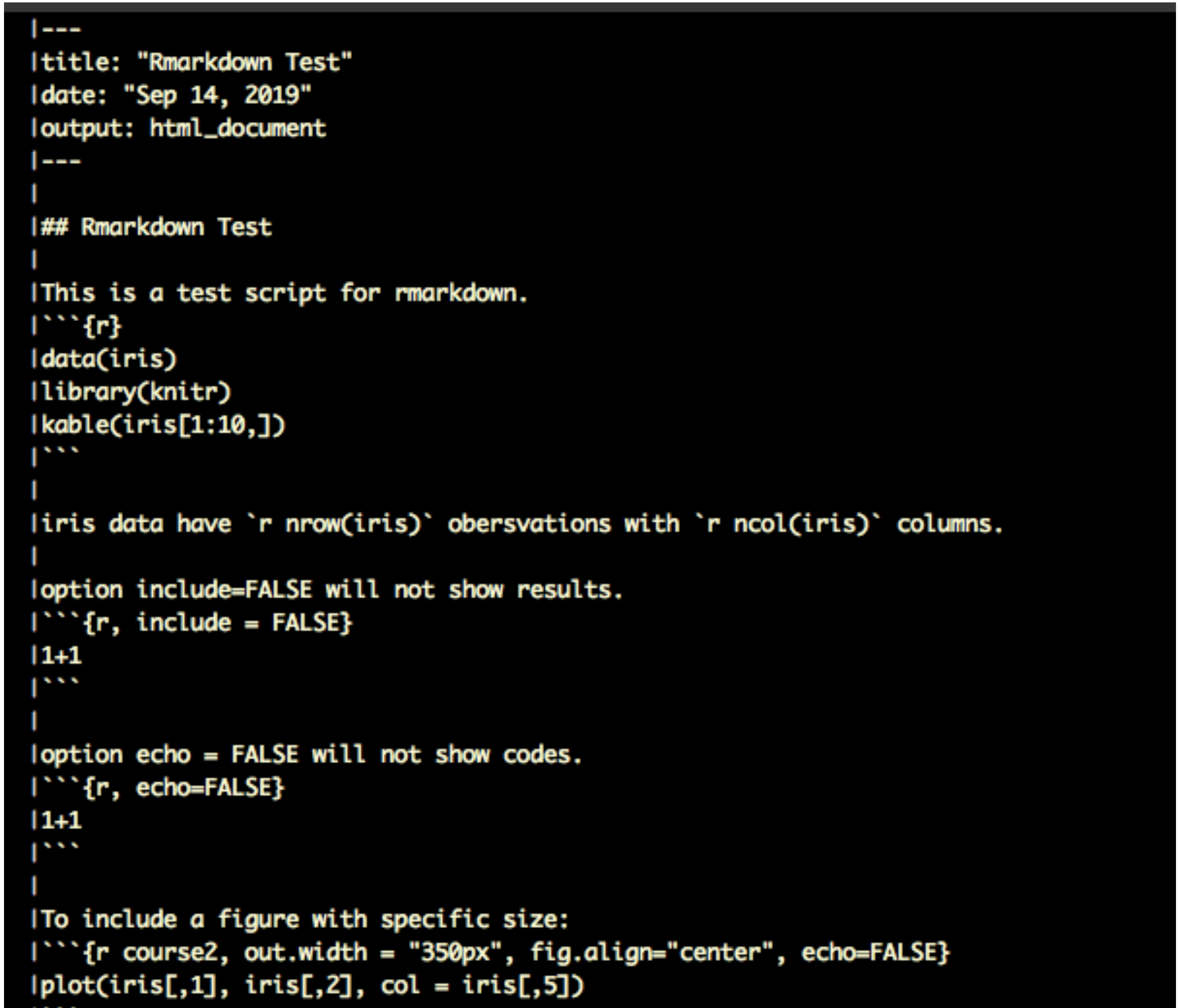
- **Good for automatic updates**

YAML (Yet Another Markup Language) header

```
---
title: "Rmarkdown Test”
author: Il-Youp Kwak
date: "Sep 14, 2019”
output: html_document
---
```

```
---
title: "Rmarkdown Test”
author: Il-Youp Kwak
date: ”`r Sys.Date()`”
output: pdf_document
---
```

Input



~~~
---
title: "Rmarkdown Test"
date: "Sep 14, 2019"
output: html_document
---

## Rmarkdown Test

This is a test script for rmarkdown.
```{r}
data(iris)
library(knitr)
kable(iris[1:10,])
~~~

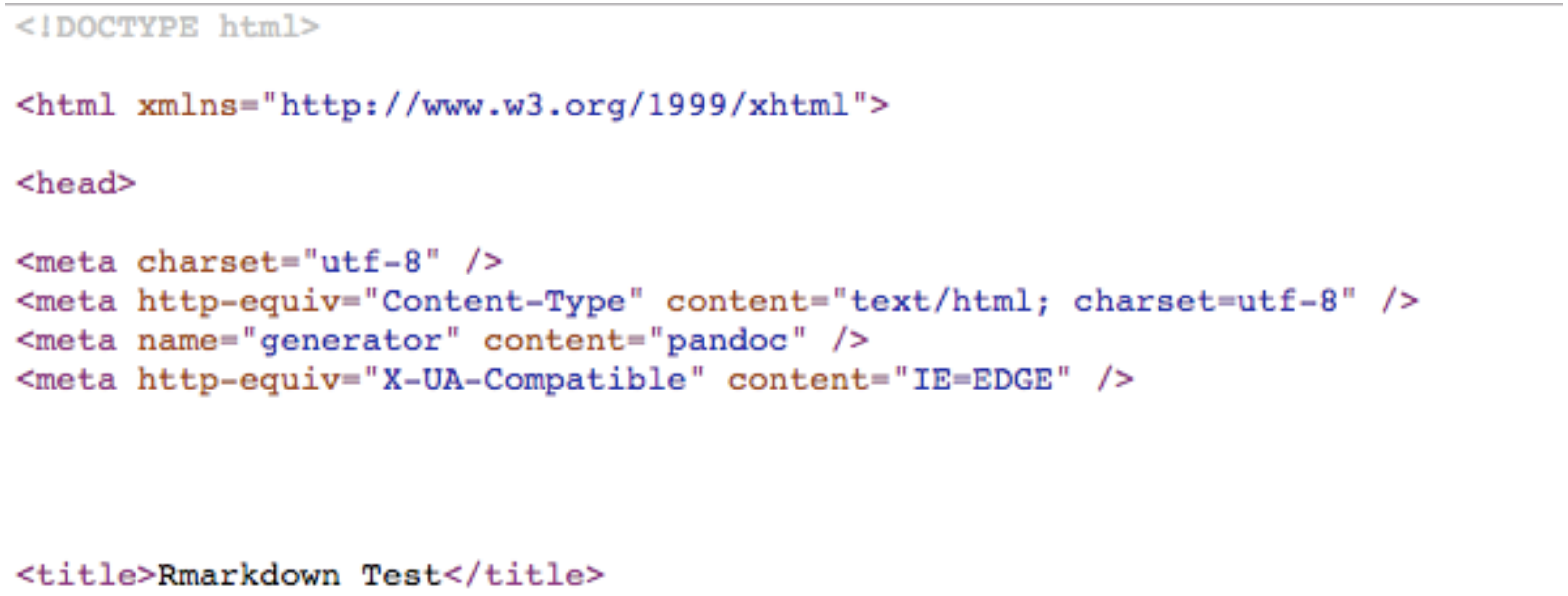
iris data have `r nrow(iris)` obersvations with `r ncol(iris)` columns.

option include=FALSE will not show results.
```{r, include = FALSE}
1+1
```

option echo = FALSE will not show codes.
```{r, echo=FALSE}
1+1
```

To include a figure with specific size:
```{r course2, out.width = "350px", fig.align="center", echo=FALSE}
plot(iris[,1], iris[,2], col = iris[,5])
```

Html output



```
<!DOCTYPE html>

<html xmlns="http://www.w3.org/1999/xhtml">

<head>

<meta charset="utf-8" />
<meta http-equiv="Content-Type" content="text/html; charset=utf-8" />
<meta name="generator" content="pandoc" />
<meta http-equiv="X-UA-Compatible" content="IE=EDGE" />




<title>Rmarkdown Test</title>
```

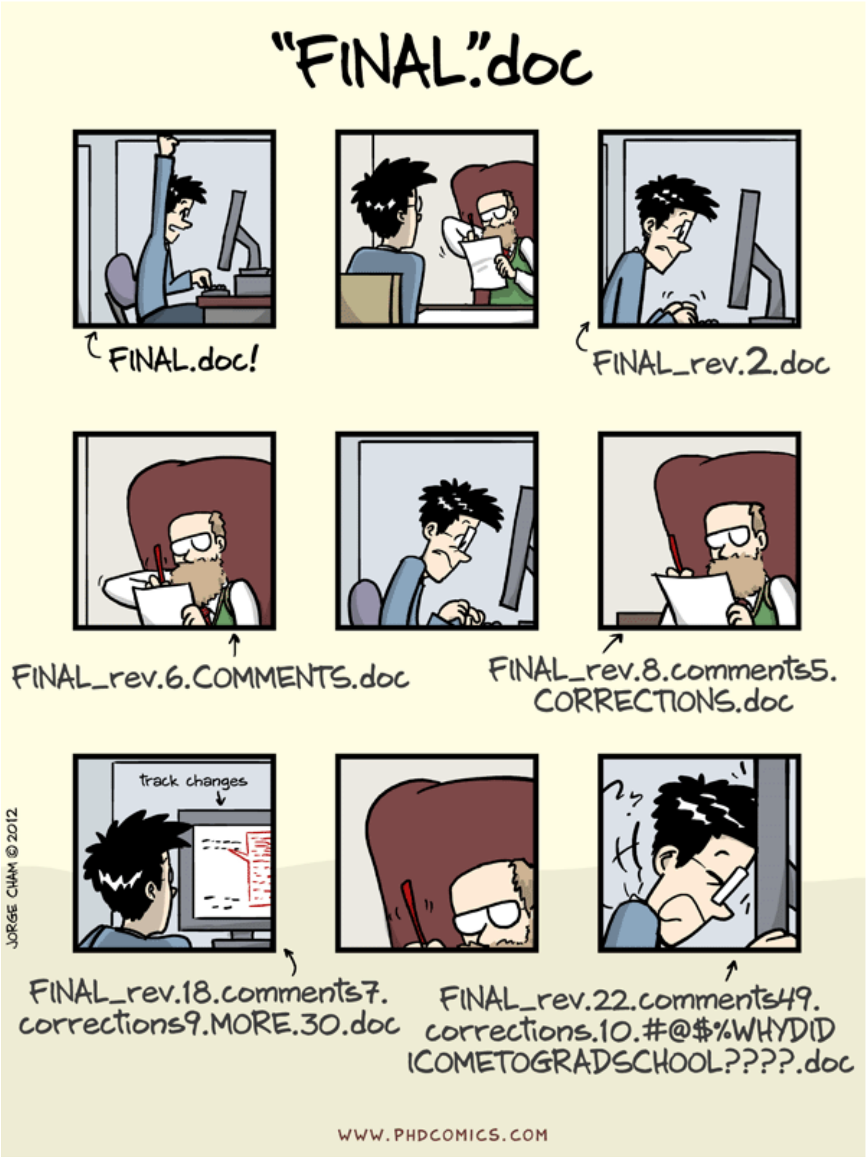
Need pandoc in your PATH

MAC: /Applications/RStudio.app/Contents/MacOS/pandoc

WINDOWS: c:\Program Files\RStudio\bin\pandoc

Rmarkdown Practice

Version control with Github



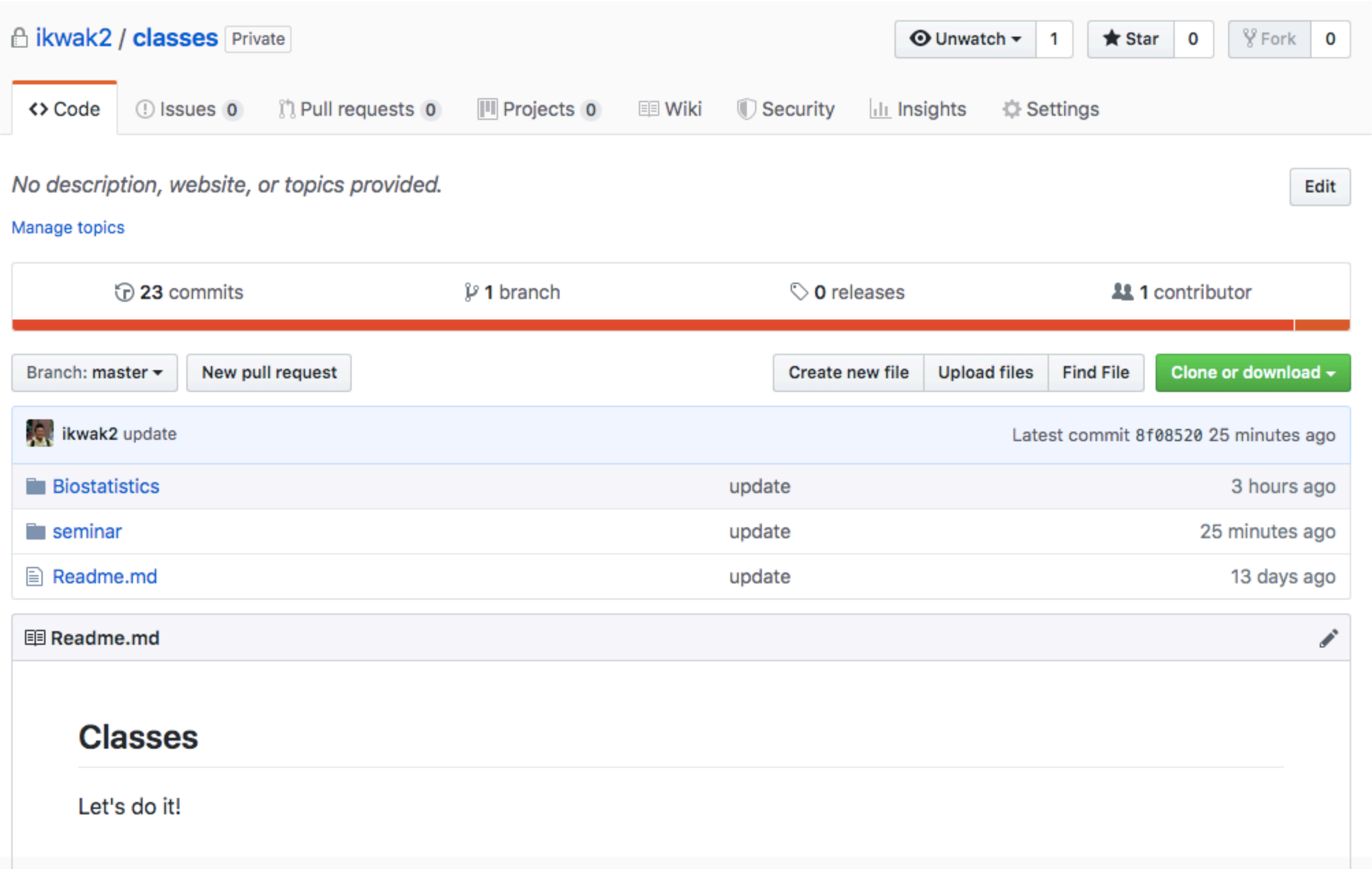
Why use formal version control

1. Save history of changes of your codes

2. Able to go back

3. Merging Changes from multiple people

Example repository



No description, website, or topics provided.

ikwak2 update — Latest commit 8f08520 25 minutes ago

Biostatistics	update	3 hours ago
seminar	update	25 minutes ago
Readme.md	update	13 days ago

Readme.md

Classes

Let's do it!

What is Git?

1. **Formal version control system**

2. **Developed by Linus Torvalds**
   - used to manage the source code for Linux

3. **Tracks any content (mostly plain text files)**

Why use Git?

1. Fast

2. Amazingly good at merging simultaneous changes

3. Everyone’s using it

What is Github?

1. Interface for exploring git repositories

2. Like facebook for programmers

3. Free 2-year account for students
   (https://education.github.com/)

Basic use

- **Change some files**
- **See what you’ve changed:** git status, git diff, git log
- **Indicate what changes to save:** git add
- **Commit to those changes:** git commit
- **Push the changes to GitHub:** git push
- **Pull changes from your collaborator:** git pull
- **Removing/moving:** git rm, git mv

First use of git

```
> git config –global user.name “ikwak2”
> git config –global user.email “ilyoup.kwak@gmail.com”
```

Initialize Repository

```
> mkdir test
> cd test
> git init
```

Create a Readme.md

```
## Test Repository

Author: My name

Blah blah
```

Git commit

```
> git commit –m “readme update (any comment)”
```

- **Use .gitignore file to indicate files to be ignored**

```
*~
Figs/*.pdf
*.log
*.Rout
```

Set up GitHub repository

- Click “Create New repo”
- Provide info and click “Create repository”
- Back at the command line:

```
> cd test
> git init
> git add Readme.md
> git remote add origin https://github.com/username/repo
> git push -u origin master
```

Using git on existing project

```
> git status   (did you miss any?)
> git add .  (or filenames)
> git status (did you miss any?)
> git commit -m “message”
> git push
```

GitHub Practice

Thank you!
Q & A