BGGN 213

Course Summary & Exam Preparation

Lecture 19

Barry Grant

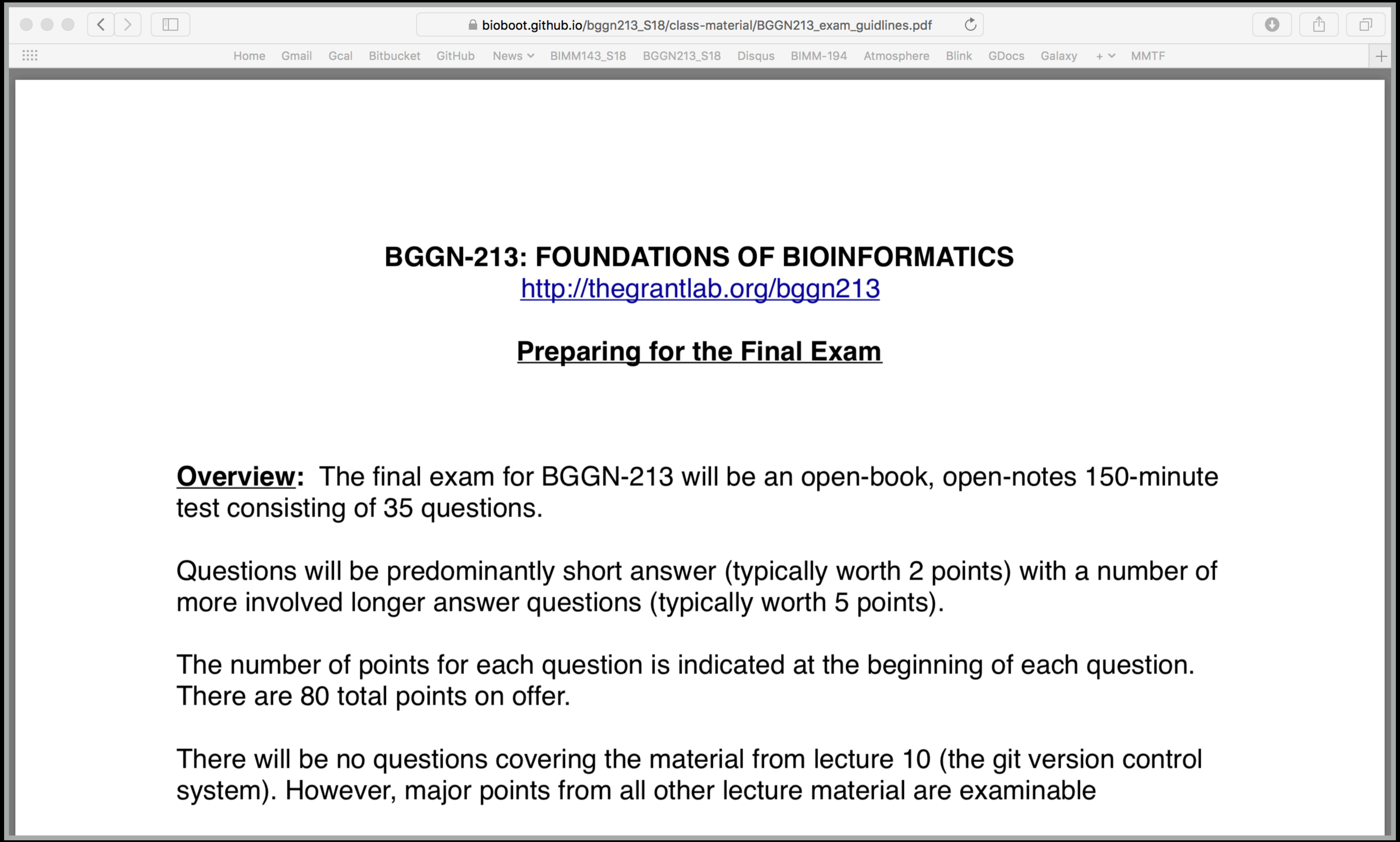
UC San Diego

http://thegrantlab.org/bggn213

Today’s Menu

- Summary of major learning goals,
- Course discussion and feedback (https://board.net/p/bggn213_w20)
- CAPs evaluation (https://cape.ucsd.edu/students)
- Final exam
  - Test structure, guidelines and rules
  - Topics and example questions
  - Exam preparation, discussion and open study
- Polish our GitHub content and publish your own website portfolios

https://bioboot.github.io/bggn213_W20/class-material/BGGN213_exam_guidlines.pdf



BGGN-213: FOUNDATIONS OF BIOINFORMATICS
http://thegrantlab.org/bggn213

Preparing for the Final Exam

Overview: The final exam for BGGN-213 will be an open-book, open-notes 150-minute test consisting of 35 questions.

Questions will be predominantly short answer (typically worth 2 points) with a number of more involved longer answer questions (typically worth 5 points).

The number of points for each question is indicated at the beginning of each question. There are 80 total points on offer.

There will be no questions covering the material from lecture 10 (the git version control system). However, major points from all other lecture material are examinable

Q1. Did you enjoy this course? (Rank in relation to others you have experienced at UCSD)?

Q2. Should this course be offered again?

Q3. If so what changes would you recommend for this course in the future?

Q4. Was the course effectively organized (lecture and lab material online vs handout or TritonEd site)?

Q5. What advice would you give to another student who is considering taking this course?

Q6. Considering both the limitations and possibilities of the subject matter and the course, how would you rate the overall effectiveness of this course and instructor?

Q7. Do you agree or disagree - The course developed my abilities and skills for the subject?

Q8. On average, how many hours per week have you spent on this course, including attending classes, doing homework's and assignments?

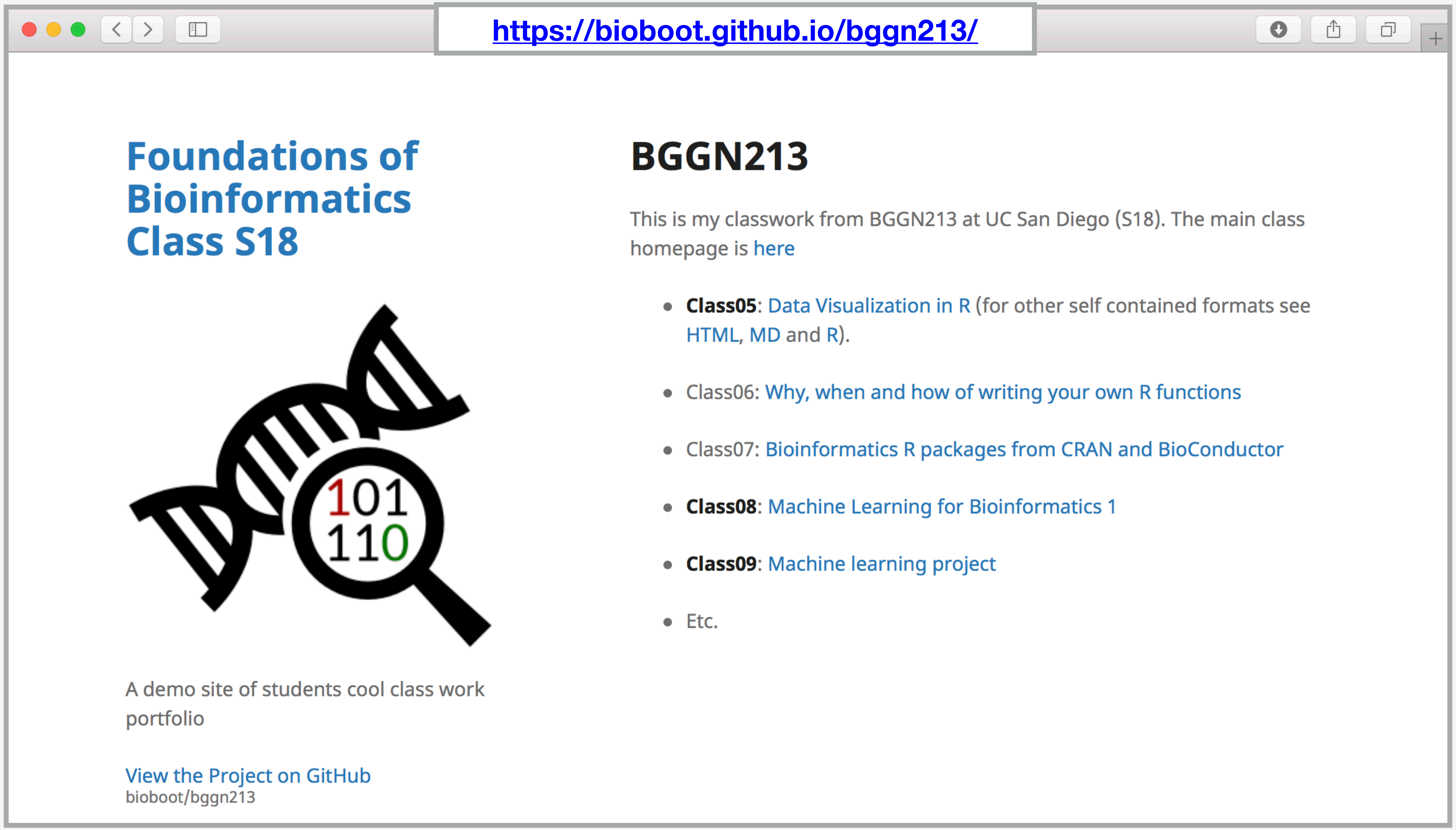
Q9. Any other comments you would like to share?

EtherPad Version: https://board.net/p/bggn213_w20

Form Version: https://tinyurl.com/bggn213-end

Thank you very much!

GitHub Spit & Polish



https://bioboot.github.io/bggn213/

Foundations of Bioinformatics Class S18

A demo site of students cool class work portfolio

View the Project on GitHub
bioboot/bggn213

BGGN213

This is my classwork from BGGN213 at UC San Diego (S18). The main class homepage is here

- **Class05**: Data Visualization in R (for other self contained formats see HTML, MD and R).
- Class06: Why, when and how of writing your own R functions
- Class07: Bioinformatics R packages from CRAN and BioConductor
- **Class08**: Machine Learning for Bioinformatics 1
- **Class09**: Machine learning project
- Etc.

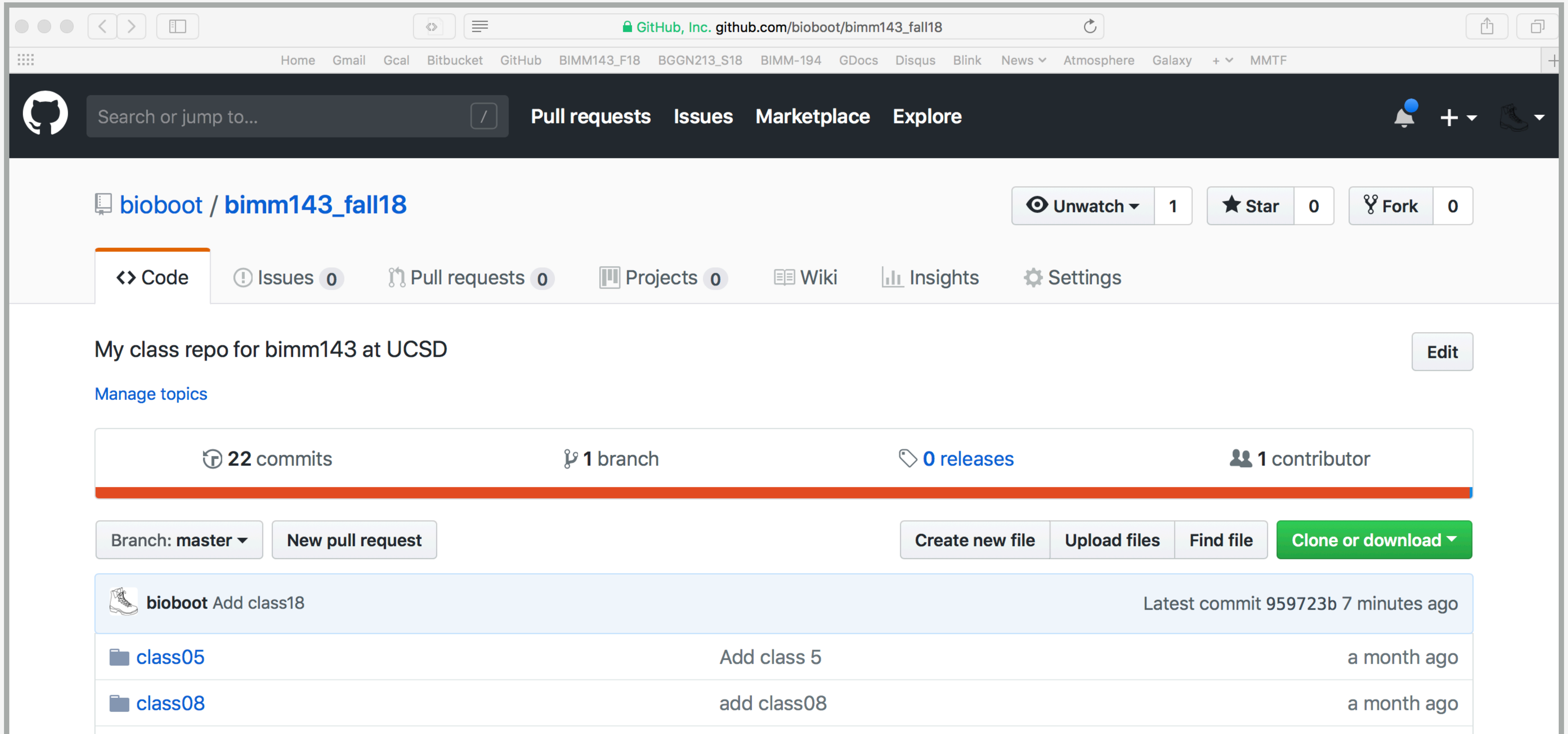
Here I: (1) Chose the “minimal” theme, (3) Edited _config.yml (adding logo and title), (4) Fixed a “date:” .md problem

In your web browser navigate to your GitHub class repository < https://github.com/ >

Side-note:

To find the link to your GitHub repository from RStudio, open one of your past class projects and in the terminal type:

```
git remote -v
```

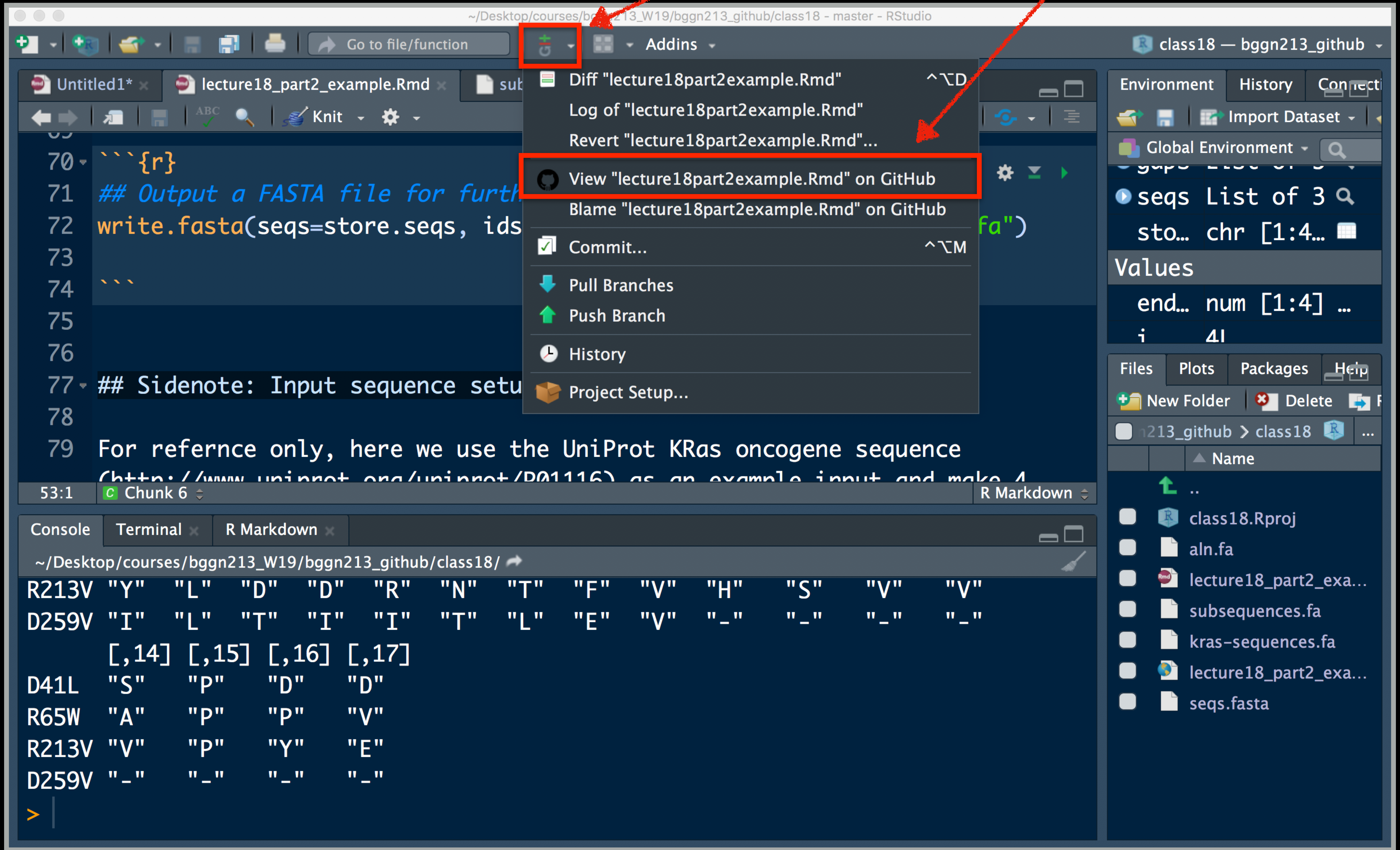


My class repo for bimm143 at UCSD

bioboot Add class18 — Latest commit 959723b 7 minutes ago

class05	Add class 5	a month ago
class08	add class08	a month ago

Or for a given GitHub tracked file click GIT icon and "VIEW on GITHUB"



~~~
```{r}
## Output a FASTA file for furth
write.fasta(seqs=store.seqs, ids                                fa")

~~~

Sidenote: Input sequence setu

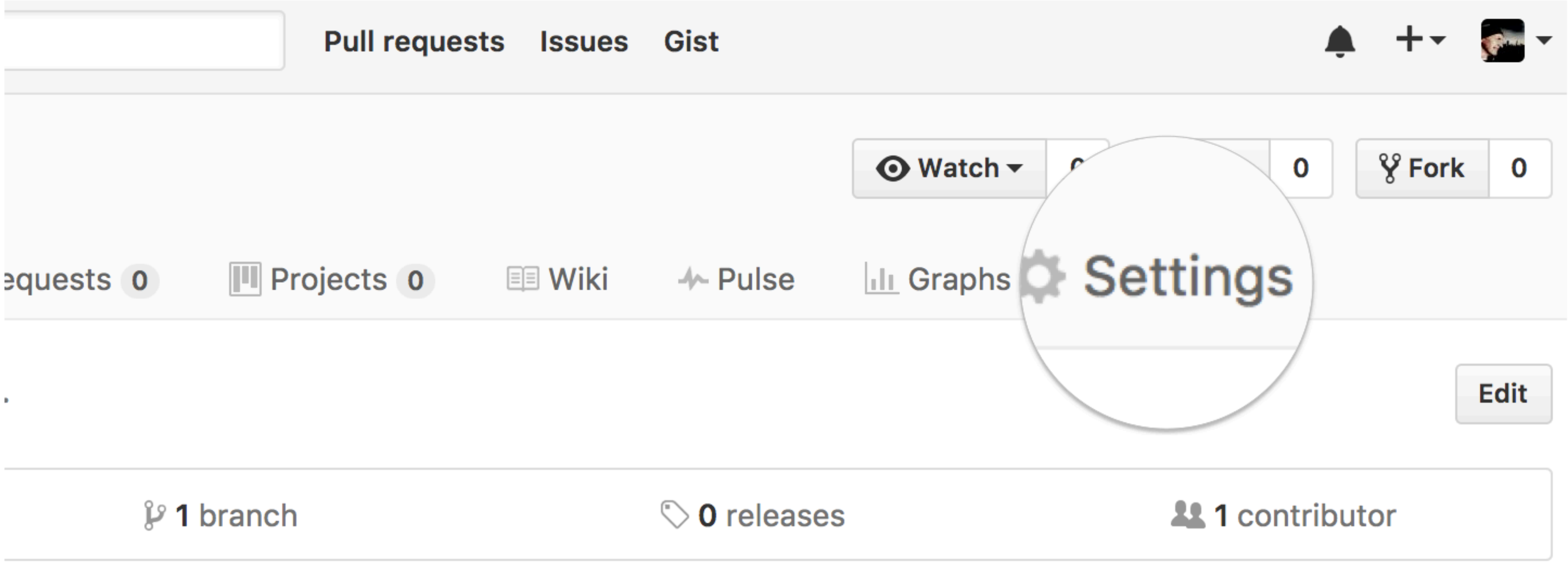
For refernce only, here we use the UniProt KRas oncogene sequence
(http://www.uniprot.org/uniprot/P01116) as an example input and make 4
```

```
R213V "Y"   "L"   "D"   "D"   "R"   "N"   "T"   "F"   "V"   "H"    "S"    "V"    "V"
D259V "I"   "L"   "T"   "I"   "I"   "T"   "L"   "E"   "V"   "-"    "-"    "-"    "-"
      [,14] [,15] [,16] [,17]
D41L  "S"   "P"   "D"   "D"
R65W  "A"   "P"   "P"   "V"
R213V "V"   "P"   "Y"   "E"
D259V "-"   "-"   "-"   "-"
>
```
```

1

# Repository Settings

**Head over to your GitHub class repository (where you are "pushing" all your class work)**

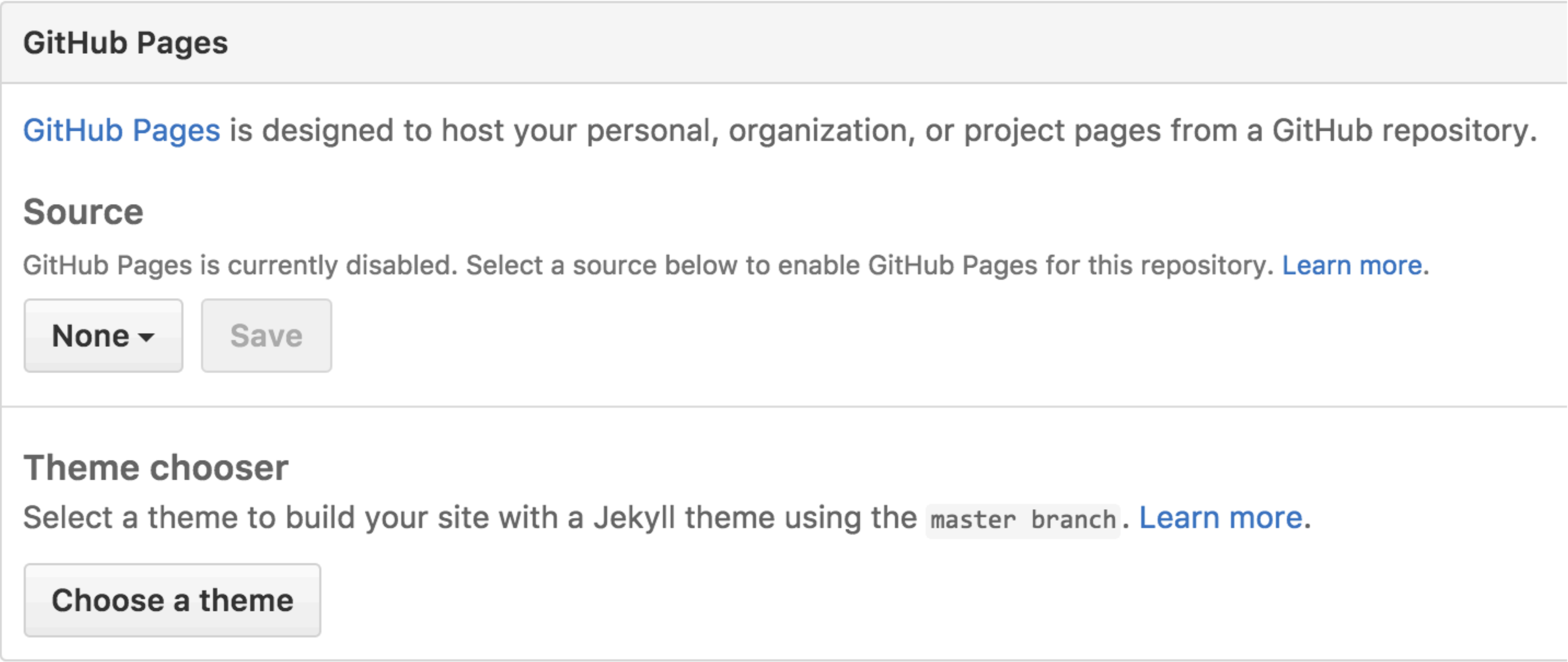
**Click on the Settings tab.**



2

# Theme chooser

Scroll down to the **GitHub Pages** section. Press **Choose a theme**.



**GitHub Pages**

GitHub Pages is designed to host your personal, organization, or project pages from a GitHub repository.

**Source**

GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository. Learn more.

None ▾ Save

**Theme chooser**

Select a theme to build your site with a Jekyll theme using the `master branch`. Learn more.

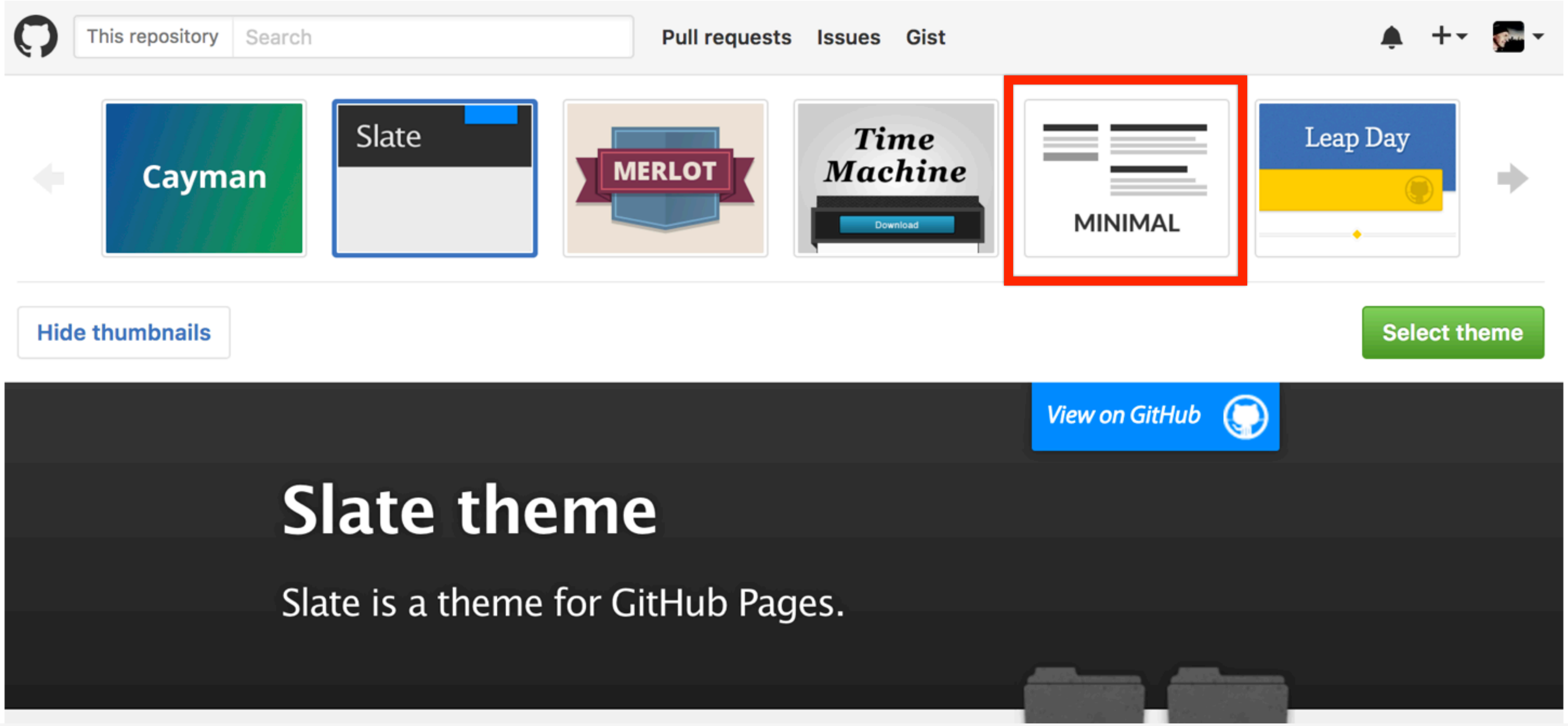
Choose a theme

3

# Pick a theme

Choose one of the themes from the carousel at the top.

When you're done, click **Select theme** on the right.



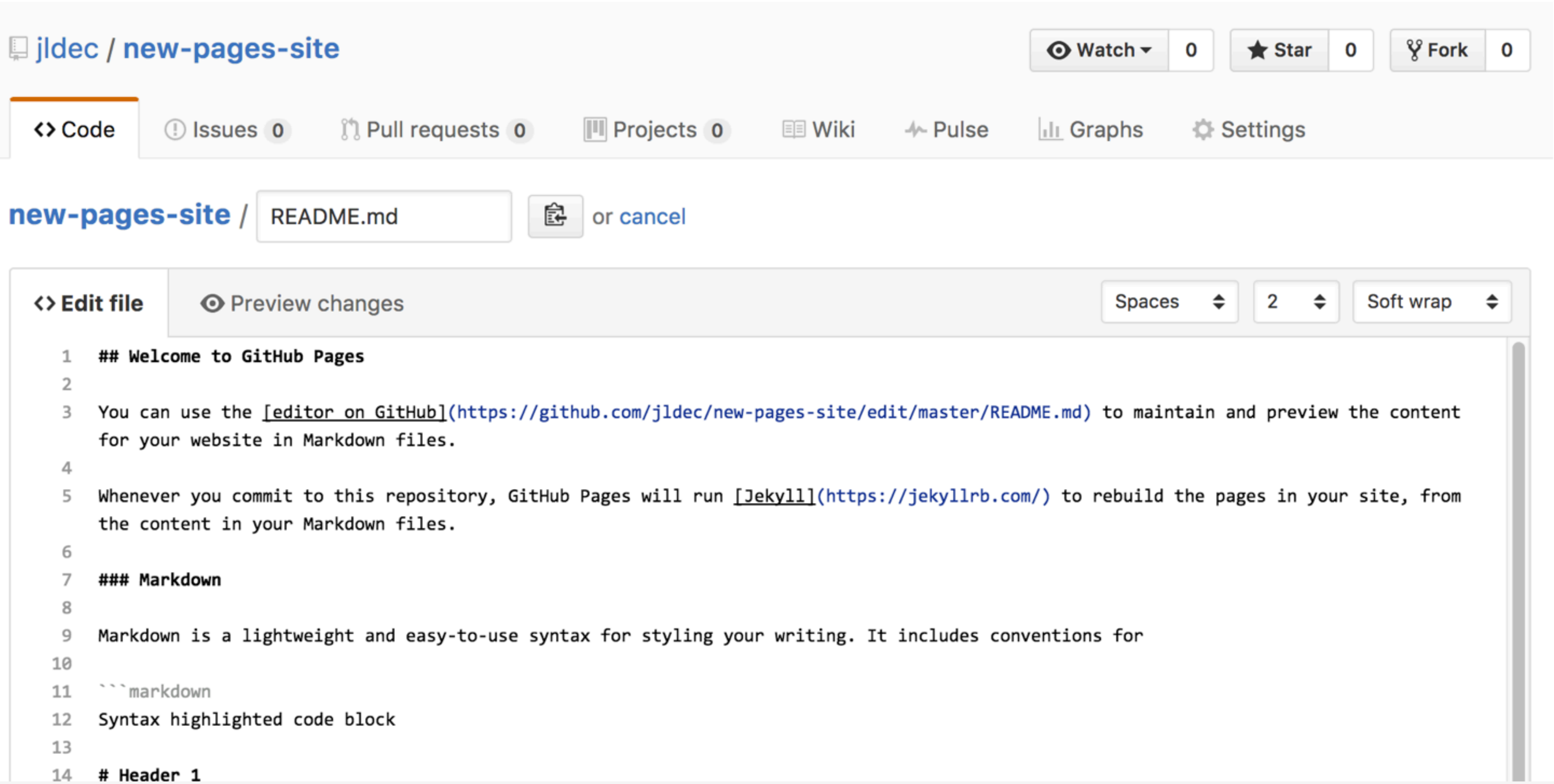
Slate theme

Slate is a theme for GitHub Pages.

4

# Edit content

**Use the GitHub online editor to add content.**
**In particular, add links to each classes .MD file**

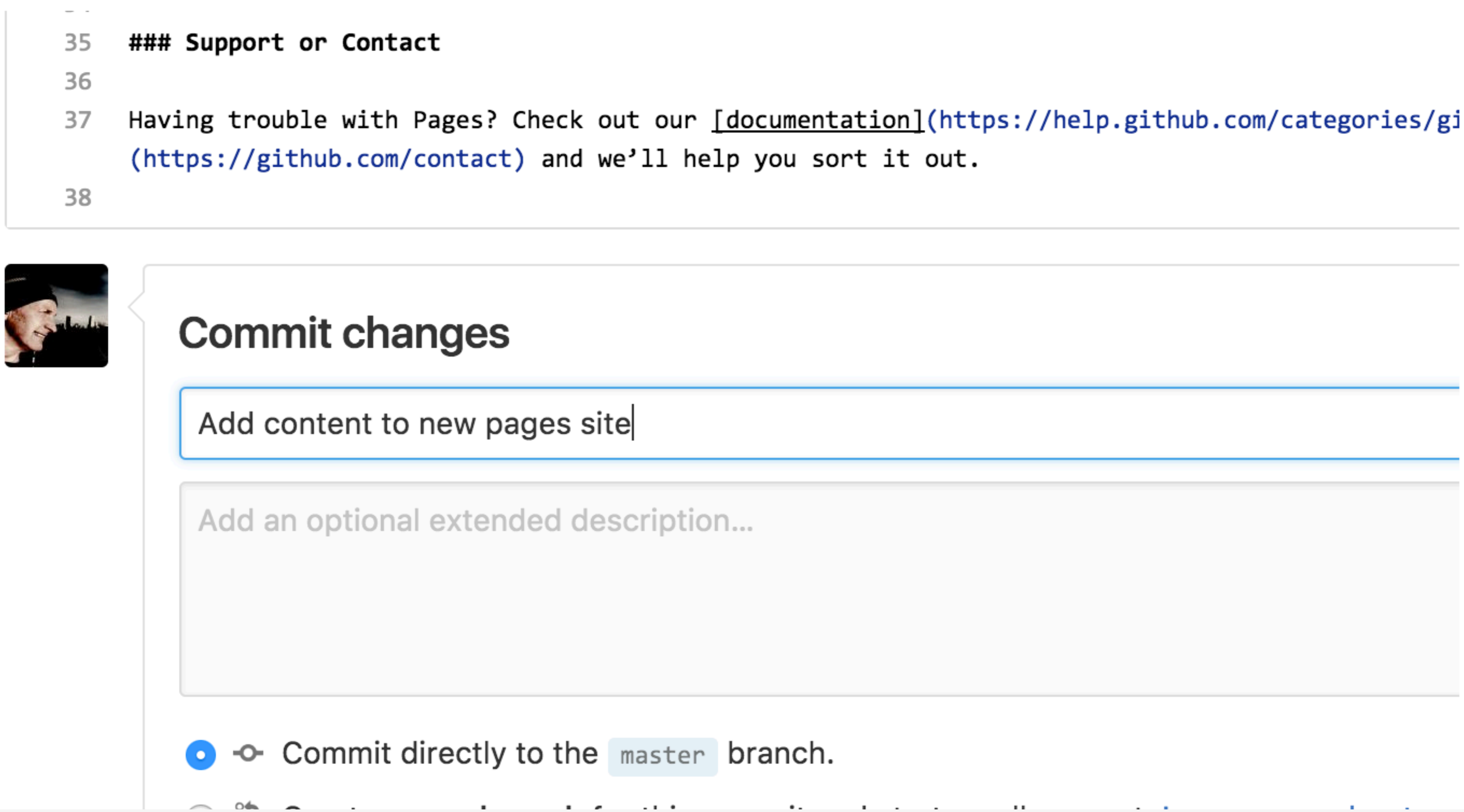


~~~
## Welcome to GitHub Pages

You can use the [editor on GitHub](https://github.com/jldec/new-pages-site/edit/master/README.md) to maintain and preview the content for your website in Markdown files.

Whenever you commit to this repository, GitHub Pages will run [Jekyll](https://jekyllrb.com/) to rebuild the pages in your site, from the content in your Markdown files.

### Markdown

Markdown is a lightweight and easy-to-use syntax for styling your writing. It includes conventions for

```markdown
Syntax highlighted code block

# Header 1
~~~

5

# Commit

Enter a commit comment and click on **Commit changes** below the editor.



```
Support or Contact

Having trouble with Pages? Check out our [documentation](https://help.github.com/categories/gi
(https://github.com/contact) and we’ll help you sort it out.

```

**Commit changes**

Add content to new pages site

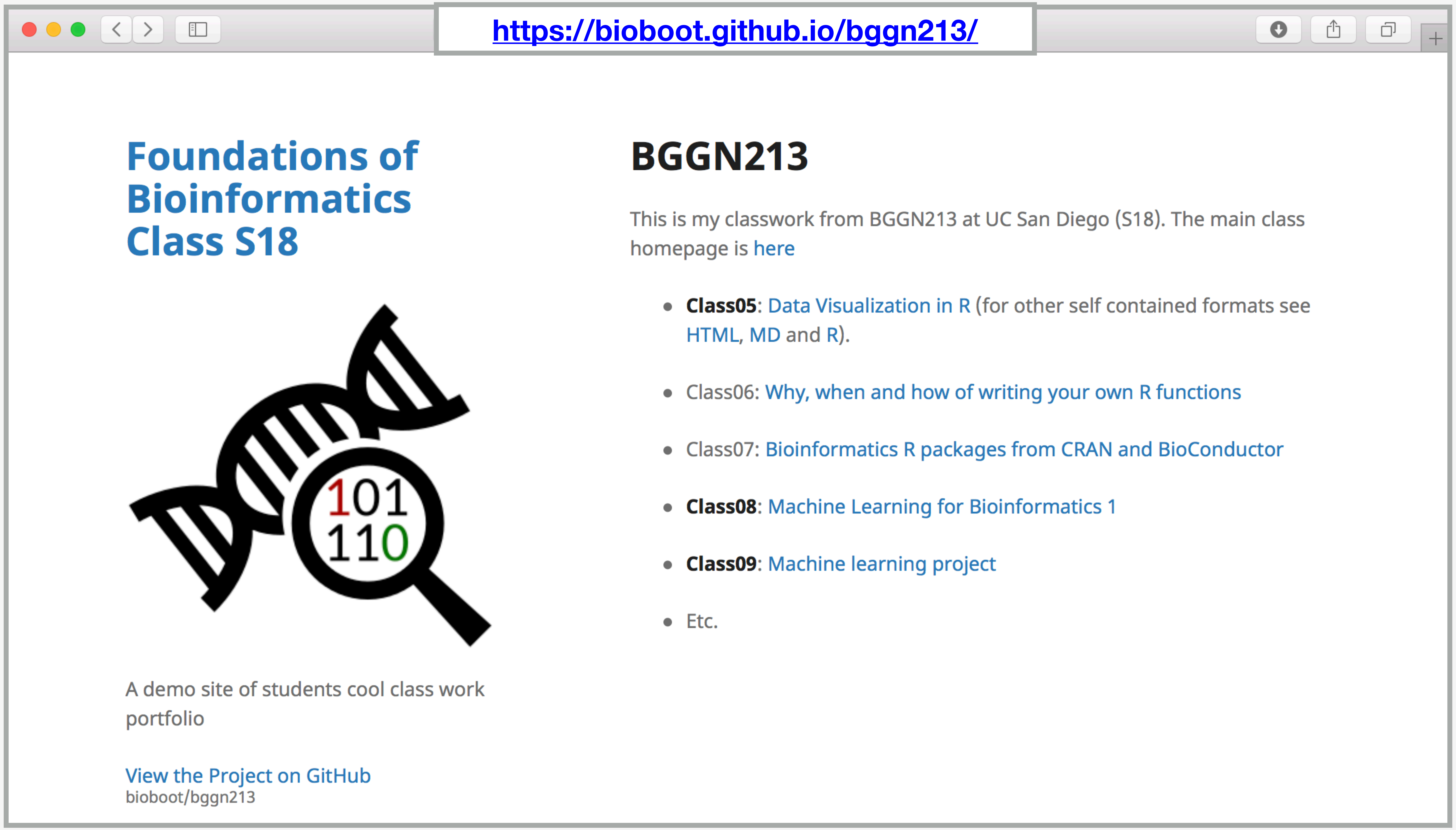
Add an optional extended description...

● Commit directly to the `master` branch.

6

# …and you're done!

Fire up a browser and go to **http://*username*.github.io/*repository***.



https://bioboot.github.io/bggn213/

## Foundations of Bioinformatics Class S18

A demo site of students cool class work portfolio

View the Project on GitHub
bioboot/bggn213

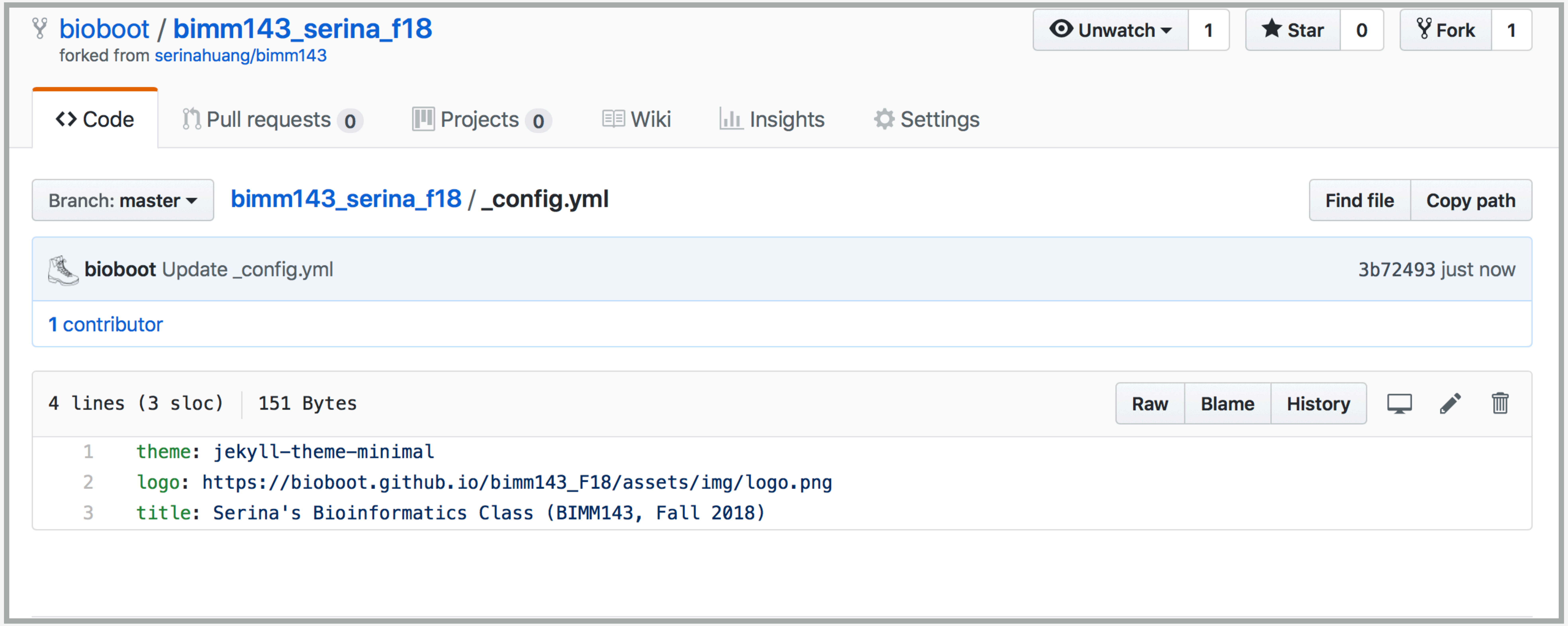
# BGGN213

This is my classwork from BGGN213 at UC San Diego (S18). The main class homepage is here

- **Class05**: Data Visualization in R (for other self contained formats see HTML, MD and R).
- Class06: Why, when and how of writing your own R functions
- Class07: Bioinformatics R packages from CRAN and BioConductor
- **Class08**: Machine Learning for Bioinformatics 1
- **Class09**: Machine learning project
- Etc.

**Here I: (1) Chose the “minimal” theme, (3) Edited _config.yml (adding logo and title), (4) Edited README.md**

https://bioboot.github.io/tmp_test/



bimm143_serina_f18 / _config.yml

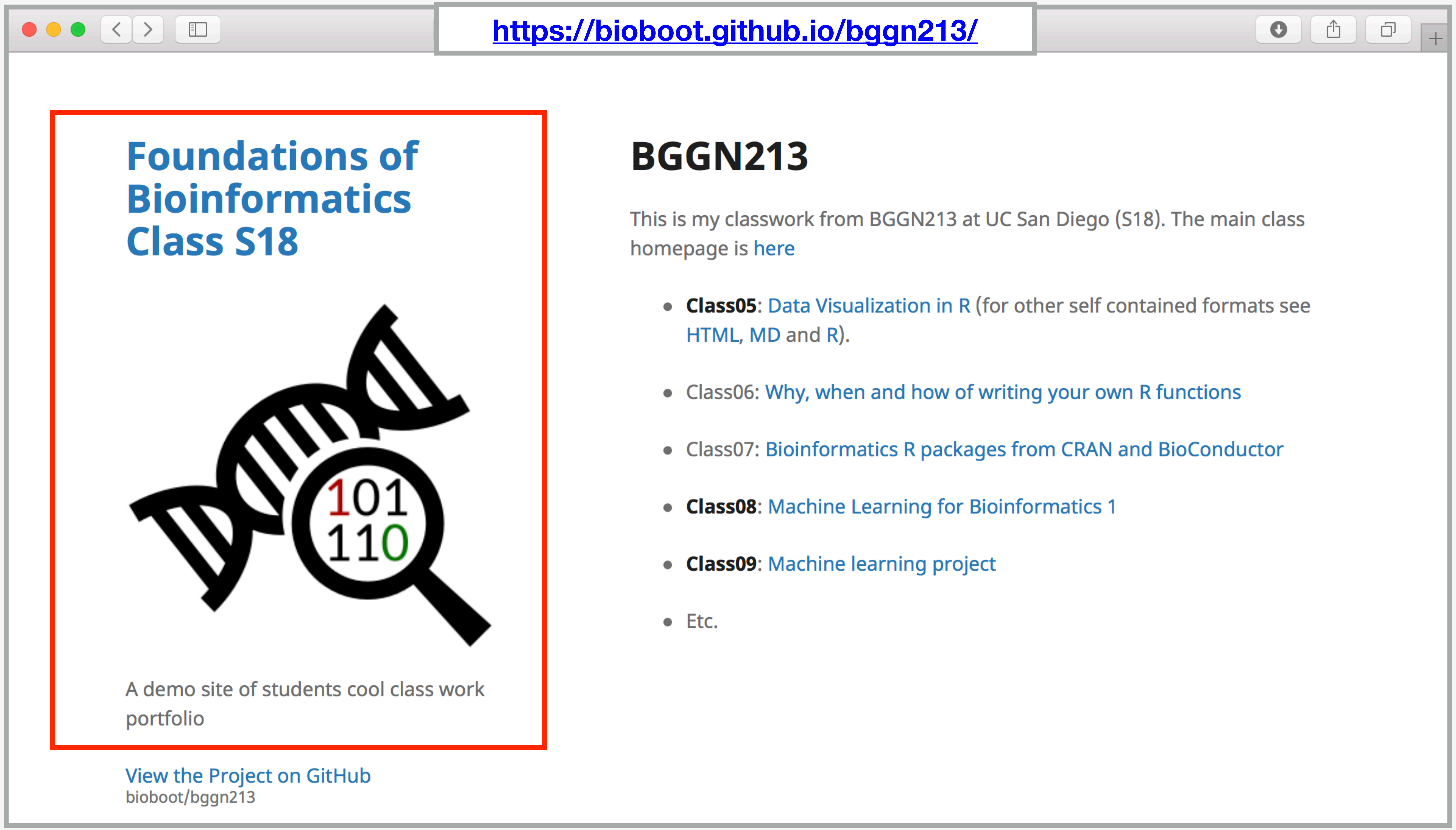
bioboot Update _config.yml 3b72493 just now

1 contributor

4 lines (3 sloc) | 151 Bytes

```yaml
theme: jekyll-theme-minimal
logo: https://bioboot.github.io/bimm143_F18/assets/img/logo.png
title: Serina's Bioinformatics Class (BIMM143, Fall 2018)
```

Here I: (1) Chose the “minimal” theme, (3) Edited _config.yml (adding logo and title), (4) Edited README.md



https://bioboot.github.io/bggn213/

Foundations of Bioinformatics Class S18

A demo site of students cool class work portfolio

View the Project on GitHub
bioboot/bggn213

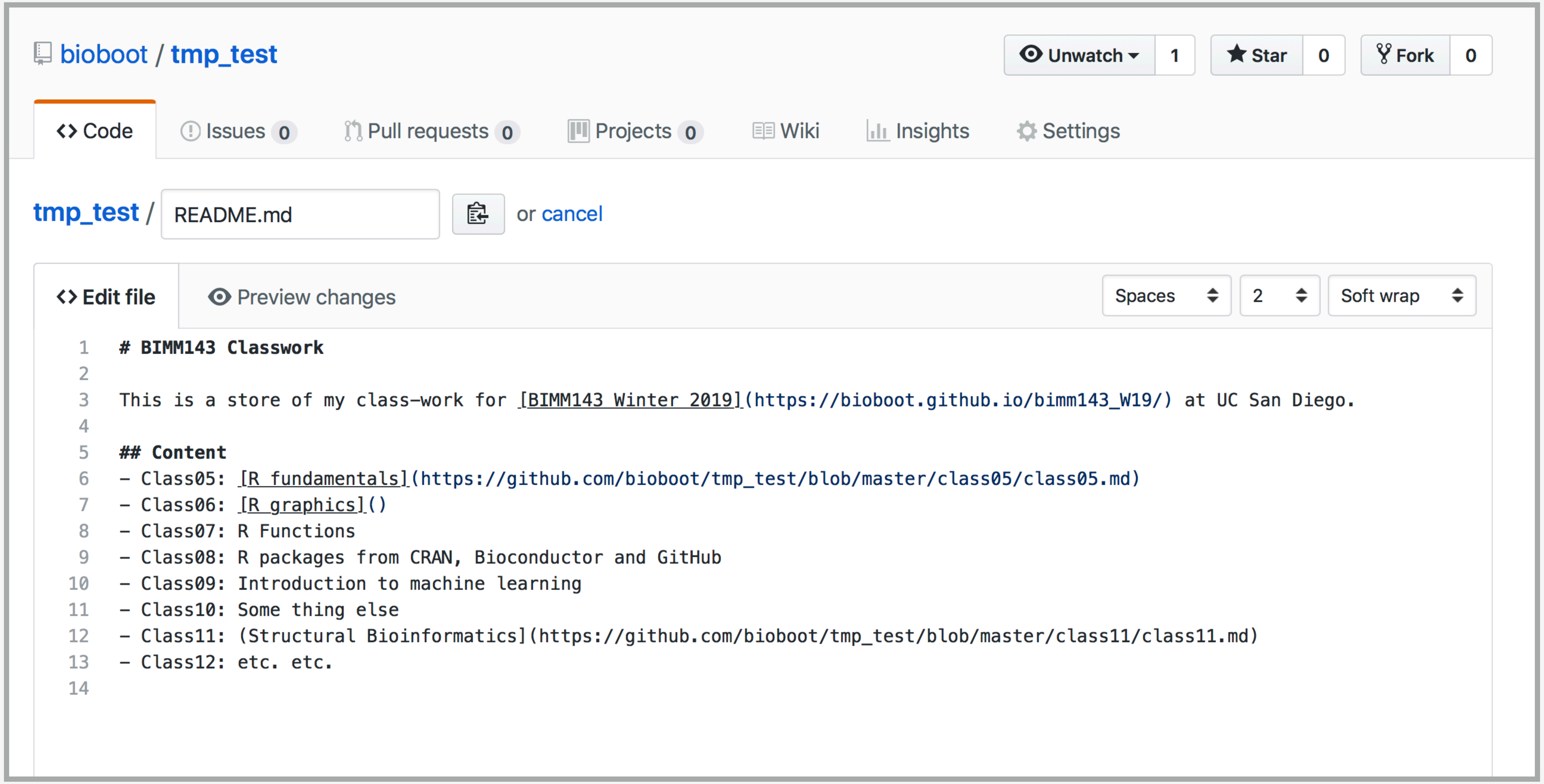
BGGN213

This is my classwork from BGGN213 at UC San Diego (S18). The main class homepage is here

- **Class05**: Data Visualization in R (for other self contained formats see HTML, MD and R).
- Class06: Why, when and how of writing your own R functions
- Class07: Bioinformatics R packages from CRAN and BioConductor
- **Class08**: Machine Learning for Bioinformatics 1
- **Class09**: Machine learning project
- Etc.

Here I: (1) Chose the "minimal" theme, (3) Edited _config.yml (adding logo and title), (4) Edited README.md

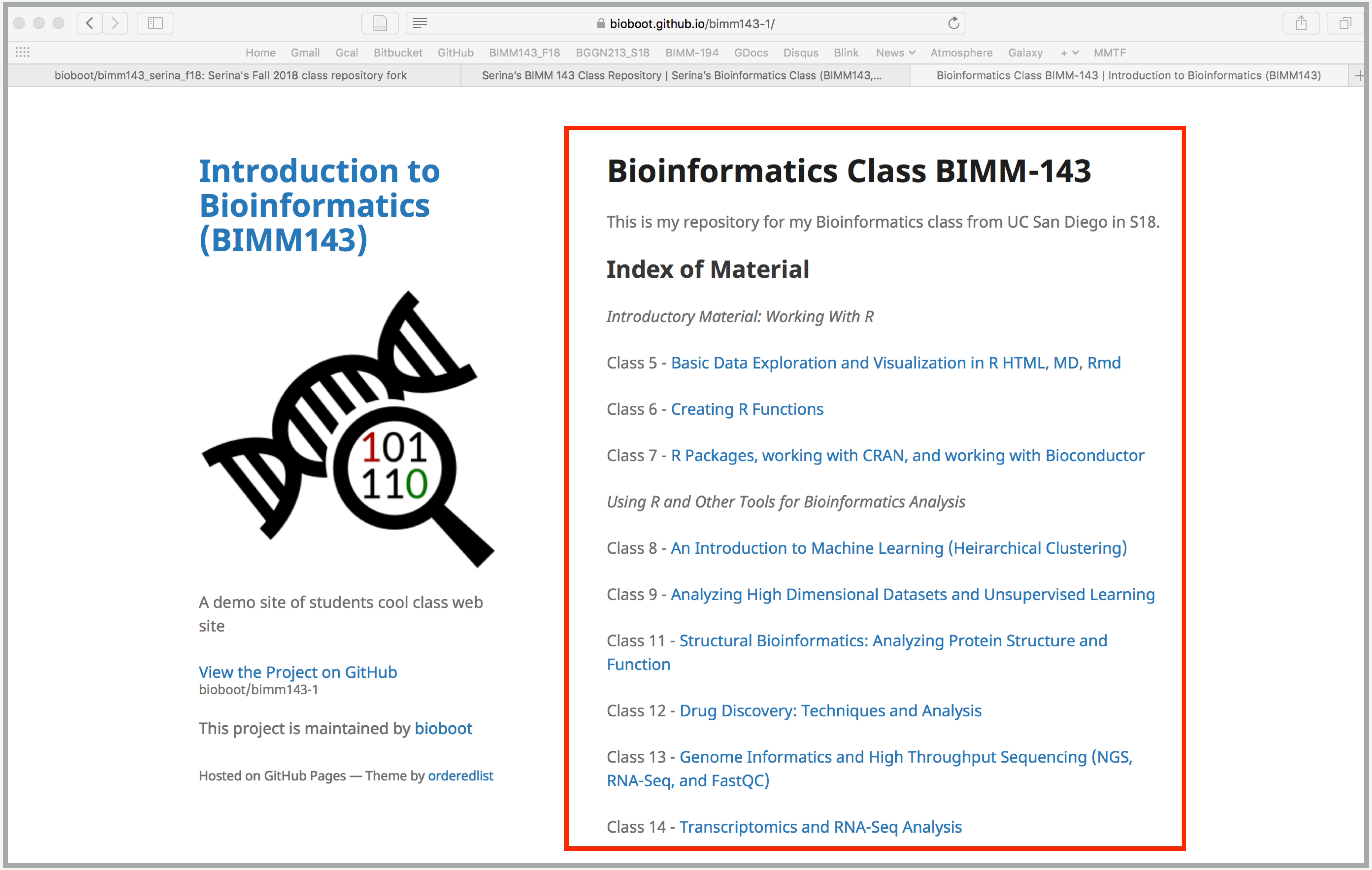
https://bioboot.github.io/tmp_test/



README.md

```
# BIMM143 Classwork

This is a store of my class-work for [BIMM143 Winter 2019](https://bioboot.github.io/bimm143_W19/) at UC San Diego.

## Content
- Class05: [R fundamentals](https://github.com/bioboot/tmp_test/blob/master/class05/class05.md)
- Class06: [R graphics]()
- Class07: R Functions
- Class08: R packages from CRAN, Bioconductor and GitHub
- Class09: Introduction to machine learning
- Class10: Some thing else
- Class11: (Structural Bioinformatics](https://github.com/bioboot/tmp_test/blob/master/class11/class11.md)
- Class12: etc. etc.

```

Here I: (1) Chose the “minimal” theme, (3) Edited _config.yml (adding logo and title), (4) Edited README.md



Introduction to Bioinformatics (BIMM143)

A demo site of students cool class web site

View the Project on GitHub
bioboot/bimm143-1

This project is maintained by bioboot

Hosted on GitHub Pages — Theme by orderedlist

Bioinformatics Class BIMM-143

This is my repository for my Bioinformatics class from UC San Diego in S18.

Index of Material

Introductory Material: Working With R

Class 5 - Basic Data Exploration and Visualization in R HTML, MD, Rmd

Class 6 - Creating R Functions

Class 7 - R Packages, working with CRAN, and working with Bioconductor

Using R and Other Tools for Bioinformatics Analysis

Class 8 - An Introduction to Machine Learning (Heirarchical Clustering)

Class 9 - Analyzing High Dimensional Datasets and Unsupervised Learning

Class 11 - Structural Bioinformatics: Analyzing Protein Structure and Function

Class 12 - Drug Discovery: Techniques and Analysis

Class 13 - Genome Informatics and High Throughput Sequencing (NGS, RNA-Seq, and FastQC)

Class 14 - Transcriptomics and RNA-Seq Analysis

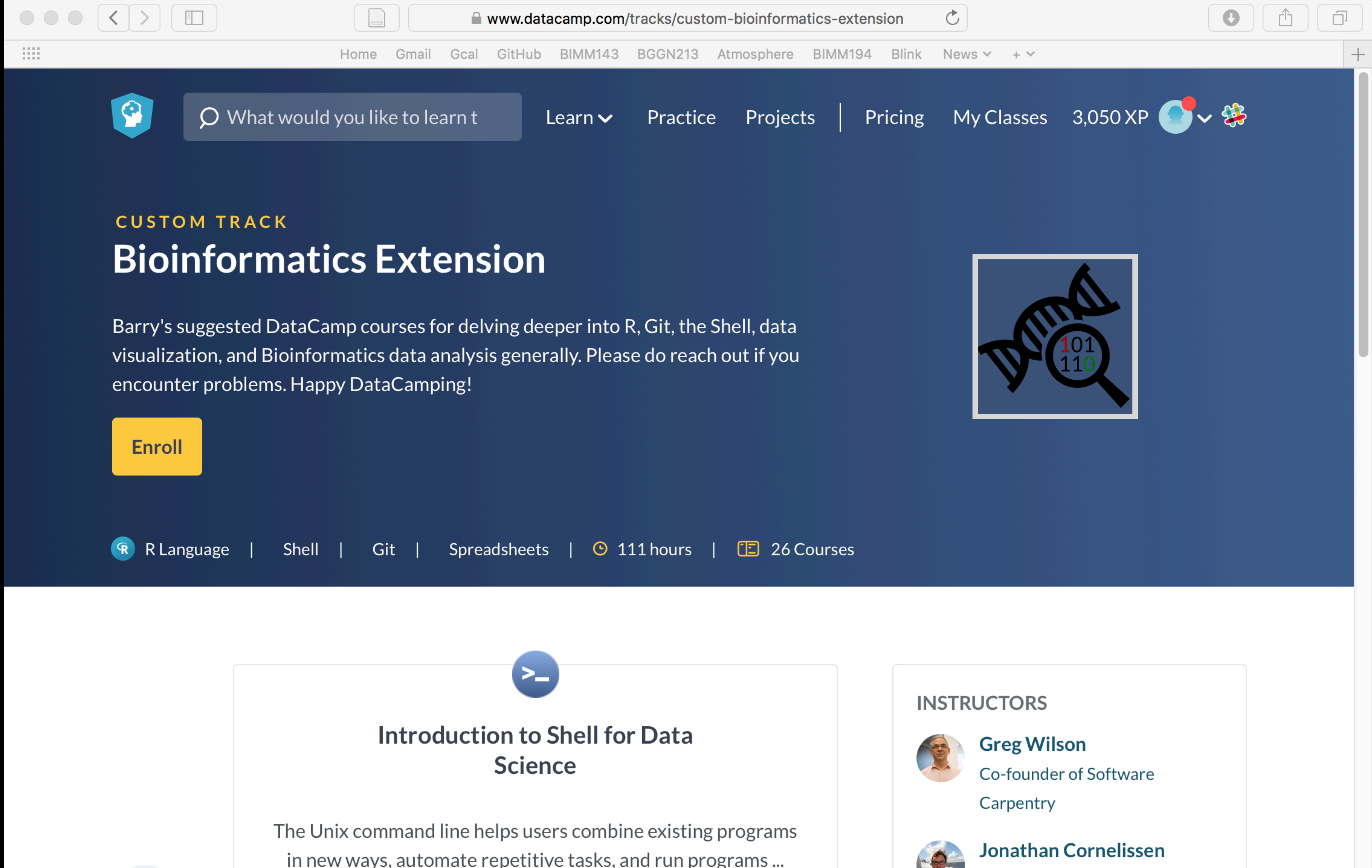
Here I: (1) forked Serina's Repo, (2) Chose the "minimal" theme, (3) Edited _config.yml (adding logo and title)

Thank you very much!

Please do fill out your official course evaluations if you get a change.
It is important to the courses we offer in the future and how we teach them!

Going Further With DataCamp

https://bioboot.github.io/bggn213_W19/class-material/datacamp_extras.pdf



CUSTOM TRACK

Bioinformatics Extension

Barry's suggested DataCamp courses for delving deeper into R, Git, the Shell, data visualization, and Bioinformatics data analysis generally. Please do reach out if you encounter problems. Happy DataCamping!

R Language | Shell | Git | Spreadsheets | 111 hours | 26 Courses

Introduction to Shell for Data Science

The Unix command line helps users combine existing programs in new ways, automate repetitive tasks, and run programs ...

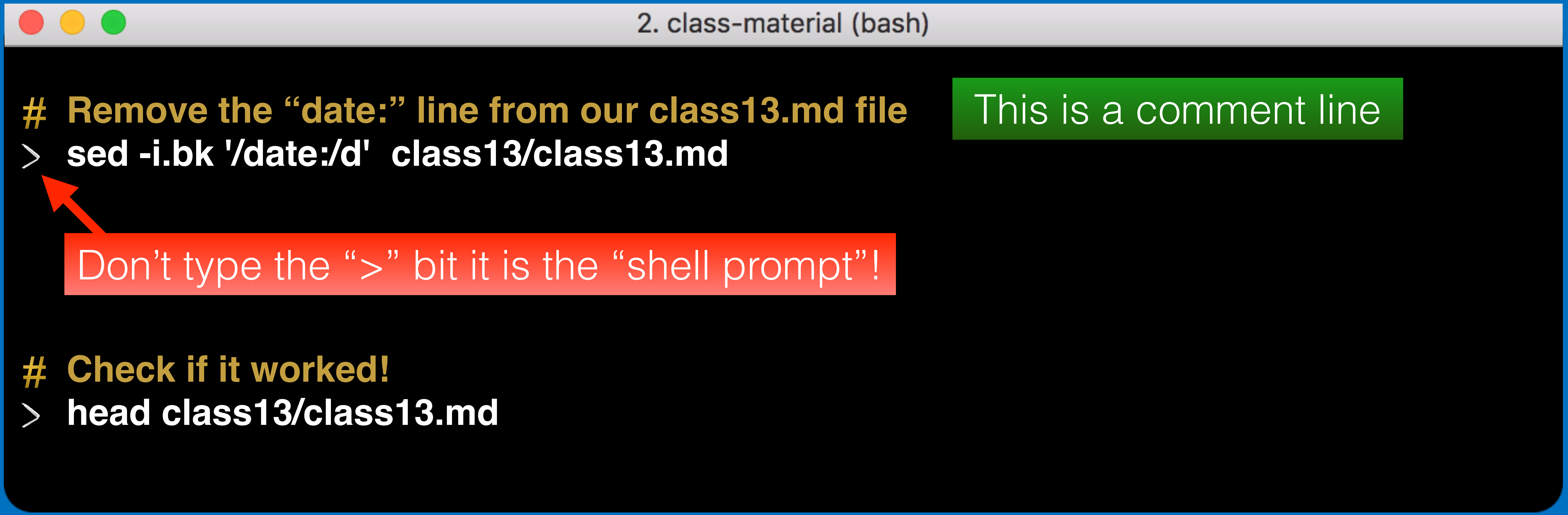
INSTRUCTORS

Greg Wilson
Co-founder of Software Carpentry

Jonathan Cornelissen

Thank you very much!

Optional



```
#  Remove the “date:” line from our class13.md file
>  sed -i.bk '/date:/d'  class13/class13.md

#  Check if it worked!
>  head class13/class13.md
```

This is a comment line

Don’t type the “>” bit it is the “shell prompt”!

Q. What do you see after each command?

Q. Does it make sense