



BGGN 213

Course Summary & Exam Preparation

Lecture 19

Barry Grant

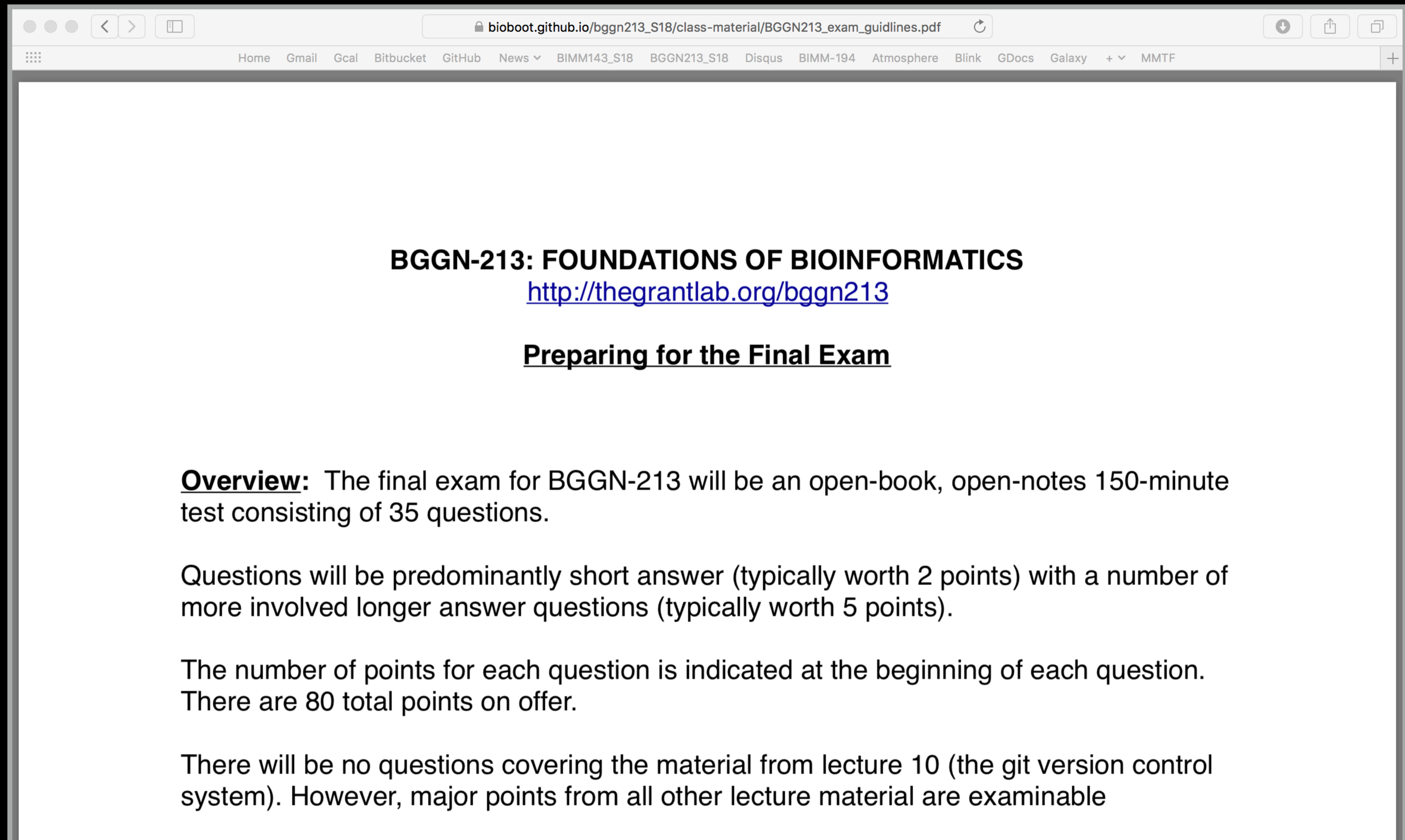
UC San Diego

<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_guidelines.pdf



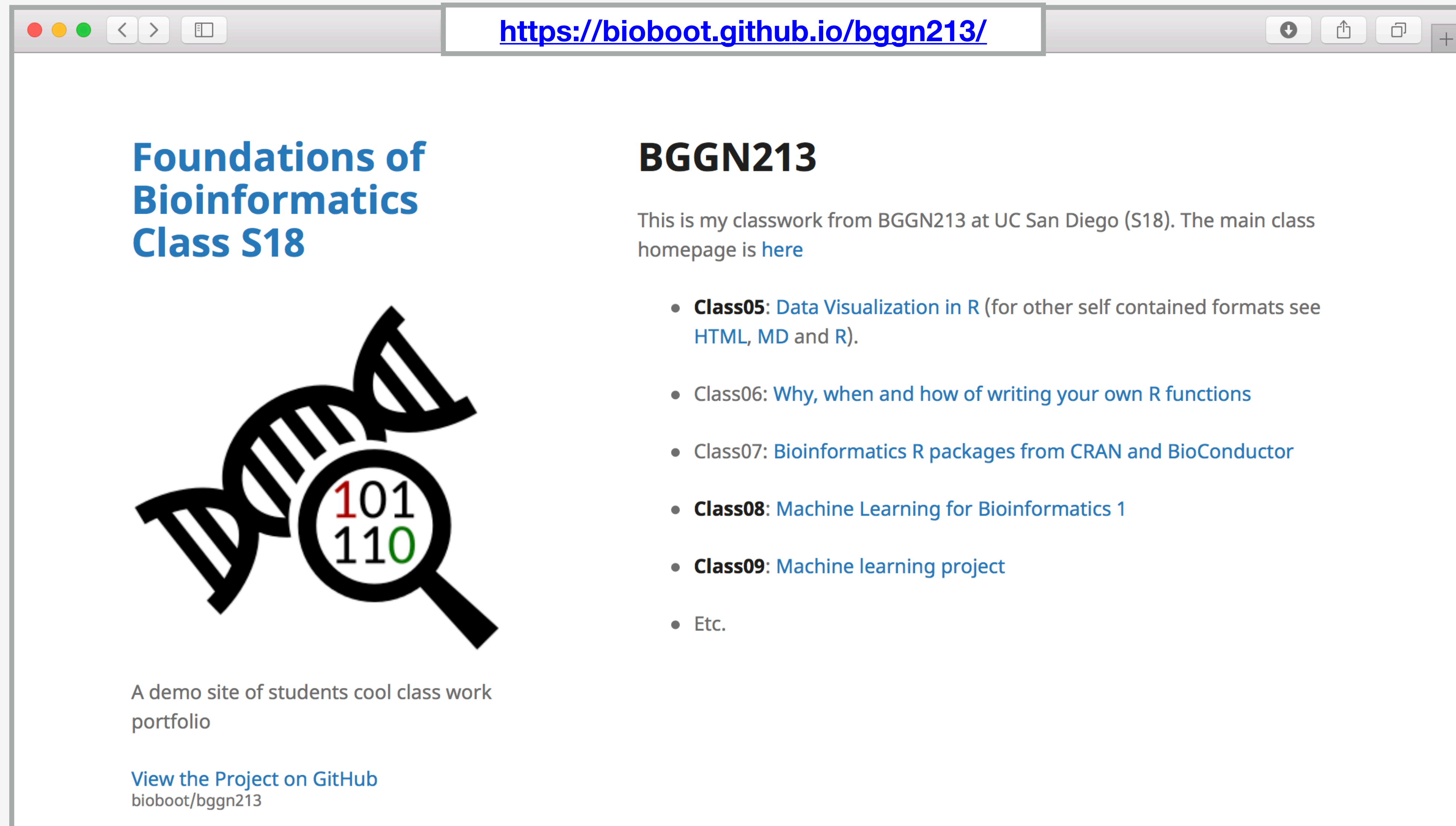
- Q1.** Did you enjoy this course? (Rank in relation to others you have experienced at UCSD)?
- Q2.** Should this course be offered again?
- Q3.** If so what changes would you recommend for this course in the future?
- Q4.** Was the course effectively organized (lecture and lab material online vs handout 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



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

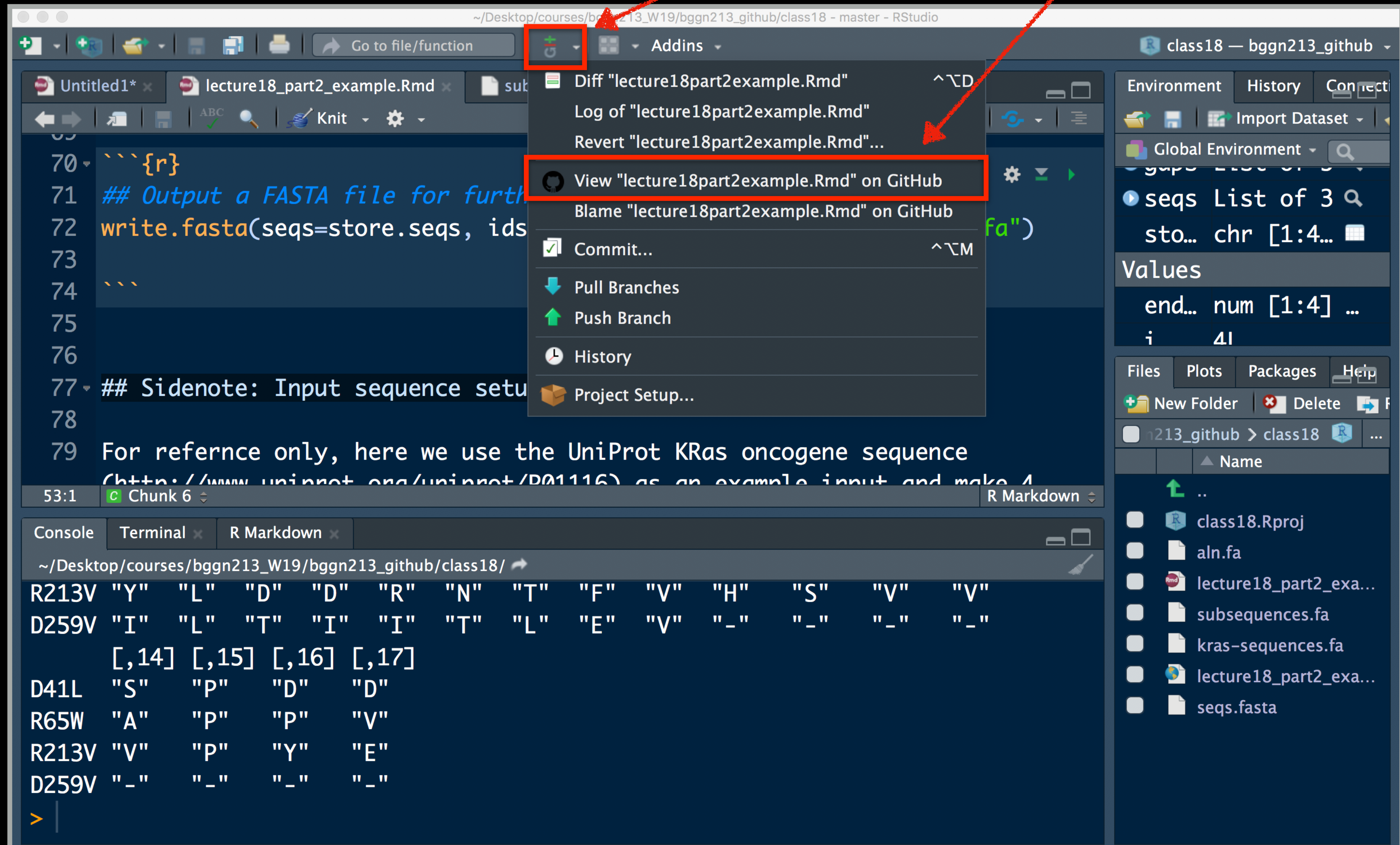
In your web browser navigate to your GitHub class repository < <https://github.com/> >

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

The screenshot shows a web browser window displaying a GitHub repository page. The address bar shows the URL `github.com/bioboot/bimm143_fall18`. The page header includes navigation links like Home, Gmail, Gcal, Bitbucket, GitHub, BIMM143_F18, BGGN213_S18, BIMM-194, GDocs, Disqus, Blink, News, Atmosphere, Galaxy, and MMTF. The repository name is `bioboot / bimm143_fall18`. It shows 1 watch, 0 stars, and 0 forks. The repository description is "My class repo for bimm143 at UCSD". It has 22 commits, 1 branch, 0 releases, and 1 contributor. The latest commit is by `bioboot` with the message "Add class18" 7 minutes ago. The repository contains two folders: `class05` (Add class 5, a month ago) and `class08` (add class08, a month ago).

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



The screenshot shows the RStudio interface with the following components:

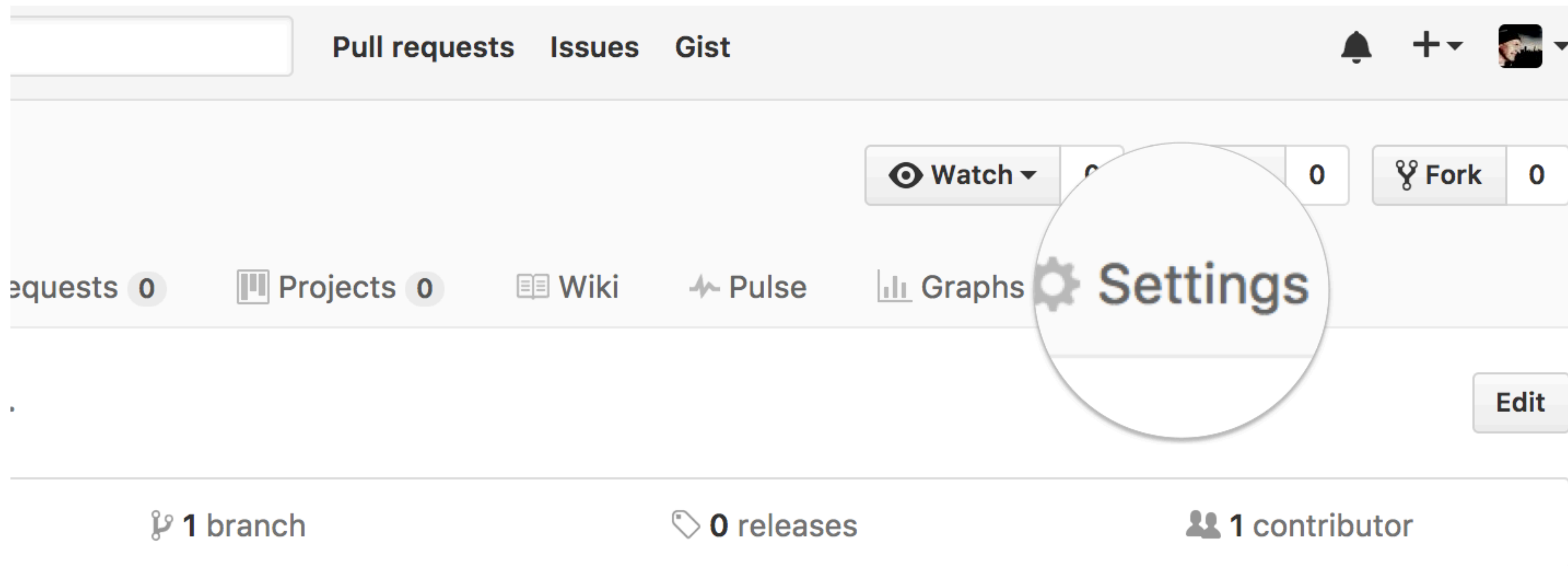
- Top Bar:** The title bar indicates the current project is `class18` within the `bggn213_github` repository. The toolbar includes a **GIT** icon (highlighted with a red box) and an **Addins** dropdown menu.
- Source Editor:** The main editor window displays an R Markdown file named `lecture18_part2_example.Rmd`. The code includes R chunks and text comments, such as `write.fasta` and a reference to the UniProt KRas oncogene sequence.
- Git Menu:** A context menu is open over the source editor, listing various Git actions. The option **View "lecture18part2example.Rmd" on GitHub** is highlighted with a red box. Other options include `Diff`, `Log`, `Revert`, `Blame`, `Commit`, `Pull Branches`, `Push Branch`, `History`, and `Project Setup`.
- Environment Panel:** Located on the right, it shows the `Global Environment` with a list of objects including `seqs` (a list of 3) and `sto...` (a character vector of length 4).
- Files Panel:** Also on the right, it displays the project file structure, including `class18.Rproj`, `aln.fa`, `lecture18_part2_exa...`, `subsequences.fa`, `kras-sequences.fa`, `lecture18_part2_exa...`, and `seqs.fasta`.
- Console:** The bottom panel shows the R console output, displaying a sequence alignment in FASTA format with headers like `R213V`, `D259V`, `D41L`, `R65W`, and `R213V`.

1

Repository Settings

Head over to your [GitHub](#) class repository (where you are “pushing” all your class work)

Click on the **Settings** tab.



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

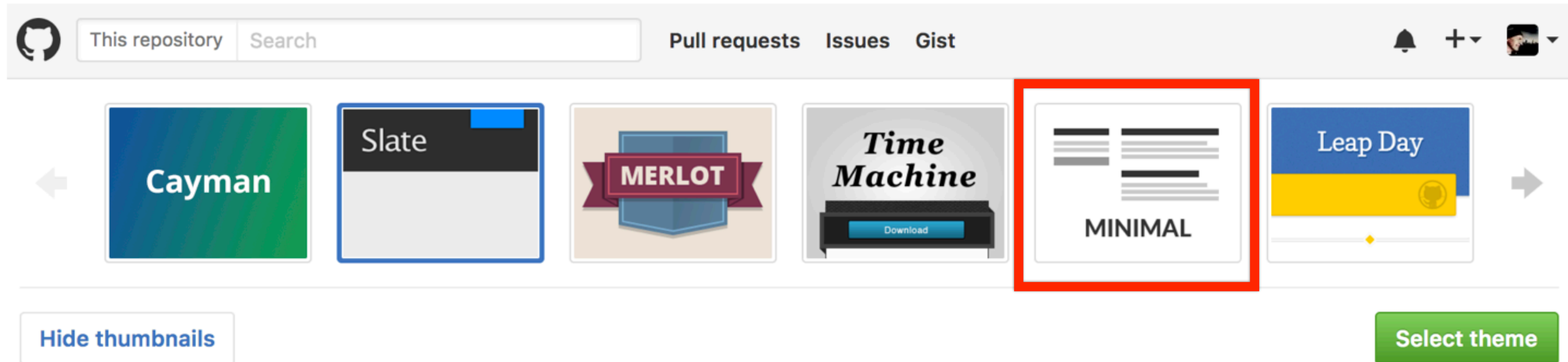
Select a theme to build your site with a Jekyll theme using the `master branch`. [Learn more](#).

Choose a theme

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.

[View on GitHub](#)



Edit content

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

The screenshot shows the GitHub web interface for editing a file. At the top, the repository path is `jldec / new-pages-site`. To the right are buttons for `Watch` (0), `Star` (0), and `Fork` (0). Below this is a navigation bar with tabs for `Code` (selected), `Issues` (0), `Pull requests` (0), `Projects` (0), `Wiki`, `Pulse`, `Graphs`, and `Settings`.

Below the navigation bar, the file path `new-pages-site / README.md` is shown, followed by a `Cancel` button and the text `or cancel`.

The main editor area has a tab for `Edit file` and a `Preview changes` button. On the right side of the editor, there are settings for `Spaces` (set to 2) and `Soft wrap`.

The code in the editor is as follows:

```
1  ## Welcome to GitHub Pages
2
3  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.
4
5  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.
6
7  ### Markdown
8
9  Markdown is a lightweight and easy-to-use syntax for styling your writing. It includes conventions for
10
11  ```markdown
12  Syntax highlighted code block
13
14  # Header 1
```

Commit

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

35 **### Support or Contact**

36

37 Having trouble with Pages? Check out our [\[documentation\]\(https://help.github.com/categories/gi](https://help.github.com/categories/github-pages-faq)
(<https://github.com/contact>) and we'll help you sort it out.

38



Commit changes

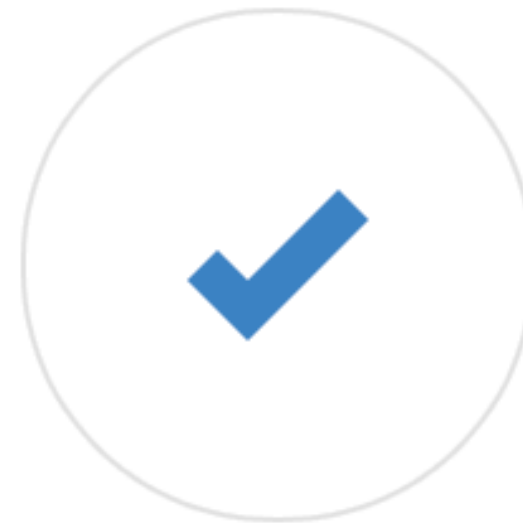
Add content to new pages site|

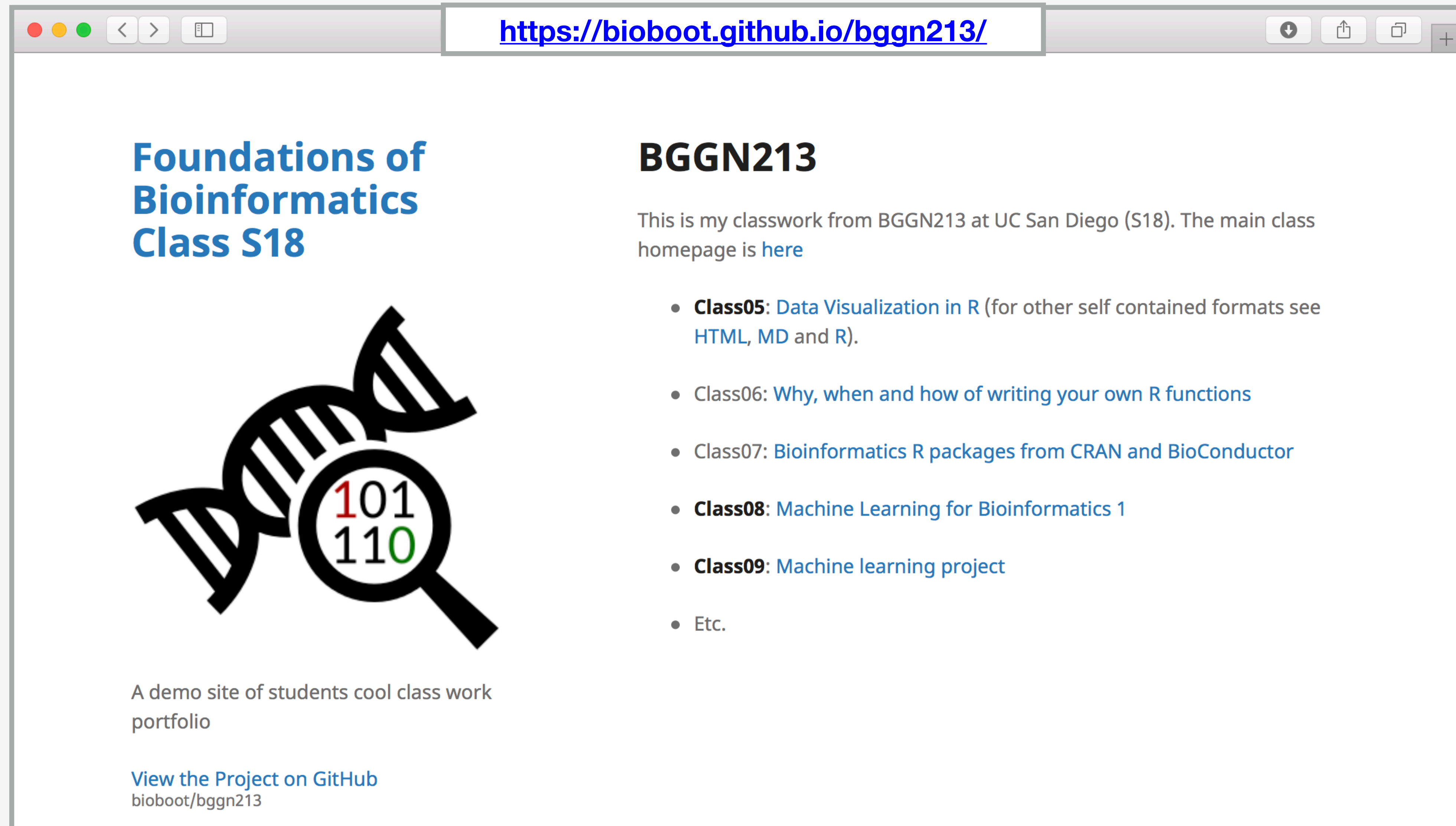
Add an optional extended description...

☒ Commit directly to the `master` branch.

...and you're done!


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





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/


 **bioboot** / **bimm143_serina_f18**
forked from [serinahuang/bimm143](#)


Unwatch ▾1


★ Star0


🍴 Fork1


<> Code

 Pull requests 0

 Projects 0


 Wiki

 Insights

 Settings

Branch: master ▾ **bimm143_serina_f18** / **_config.yml**




Find fileCopy path

 **bioboot** Update _config.yml3b72493 just now

1 contributor

4 lines (3 sloc) | 151 Bytes

RawBlameHistory



1

theme: jekyll-theme-minimal

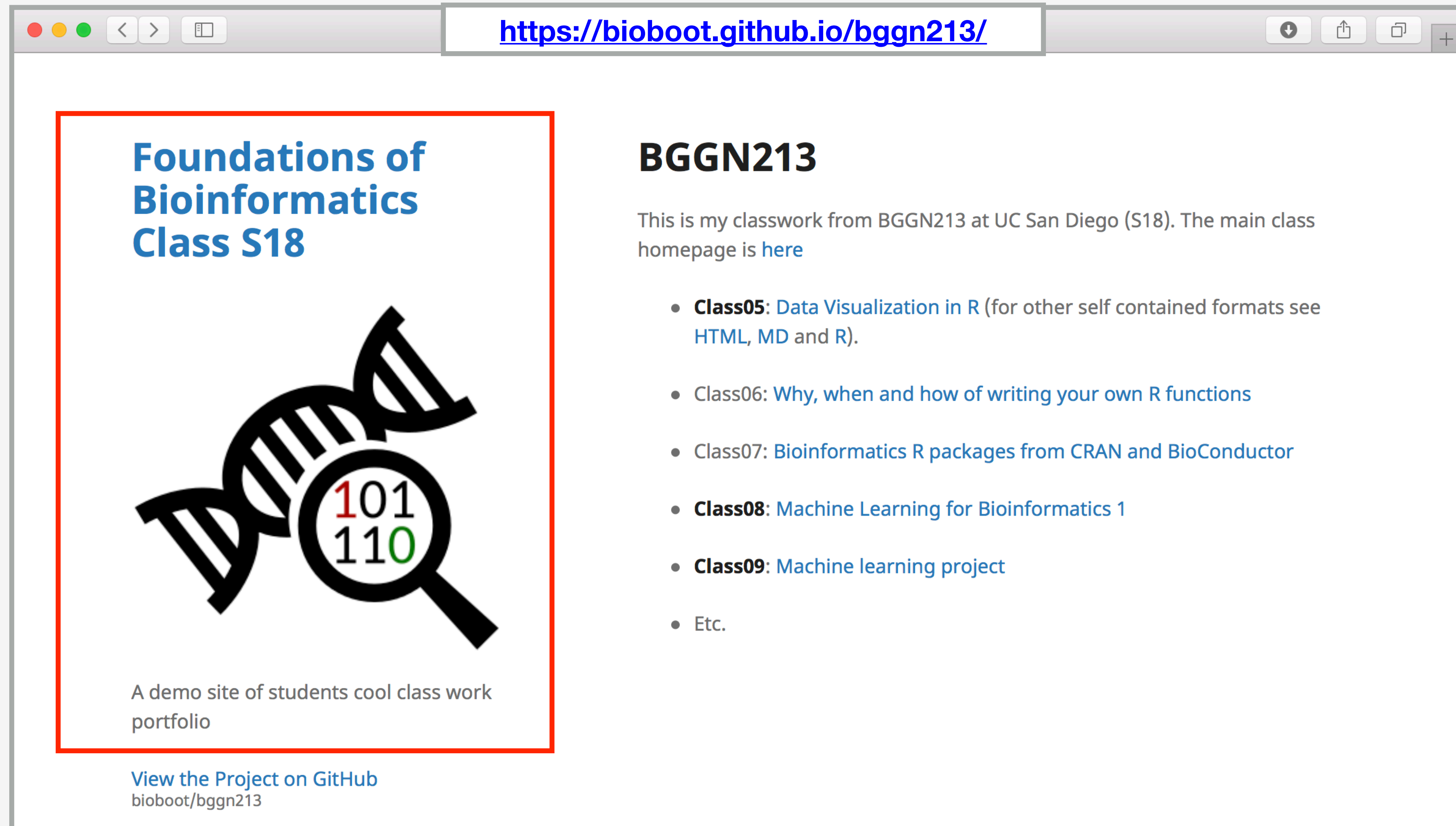
2

logo: https://bioboot.github.io/bimm143_F18/assets/img/logo.png

3

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



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/

bioboot / tmp_test

Unwatch 1Star 0Fork 0

<> CodeIssues 0Pull requests 0Projects 0WikiInsightsSettings

tmp_test / README.md or cancel

<> Edit filePreview changesSpaces 2Soft wrap

```
1  # BIMM143 Classwork
2
3  This is a store of my class-work for [BIMM143 Winter 2019](https://bioboot.github.io/bimm143_W19/) at UC San Diego.
4
5  ## Content
6  - Class05: [R fundamentals](https://github.com/bioboot/tmp_test/blob/master/class05/class05.md)
7  - Class06: [R graphics]()
8  - Class07: R Functions
9  - Class08: R packages from CRAN, Bioconductor and GitHub
10 - Class09: Introduction to machine learning
11 - Class10: Some thing else
12 - Class11: (Structural Bioinformatics)(https://github.com/bioboot/tmp_test/blob/master/class11/class11.md)
13 - Class12: etc. etc.
14
```


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

bioboot.github.io/bimm143-1/

Home Gmail Gcal Bitbucket GitHub BIMM143_F18 BGGN213_S18 BIMM-194 GDocs Disqus Blink News Atmosphere Galaxy + MMTF

bioboot/bimm143_serina_f18: Serina's Fall 2018 class repository fork Serina's BIMM 143 Class Repository | Serina's Bioinformatics Class (BIMM143,... Bioinformatics Class BIMM-143 | Introduction to Bioinformatics (BIMM143)

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](#)

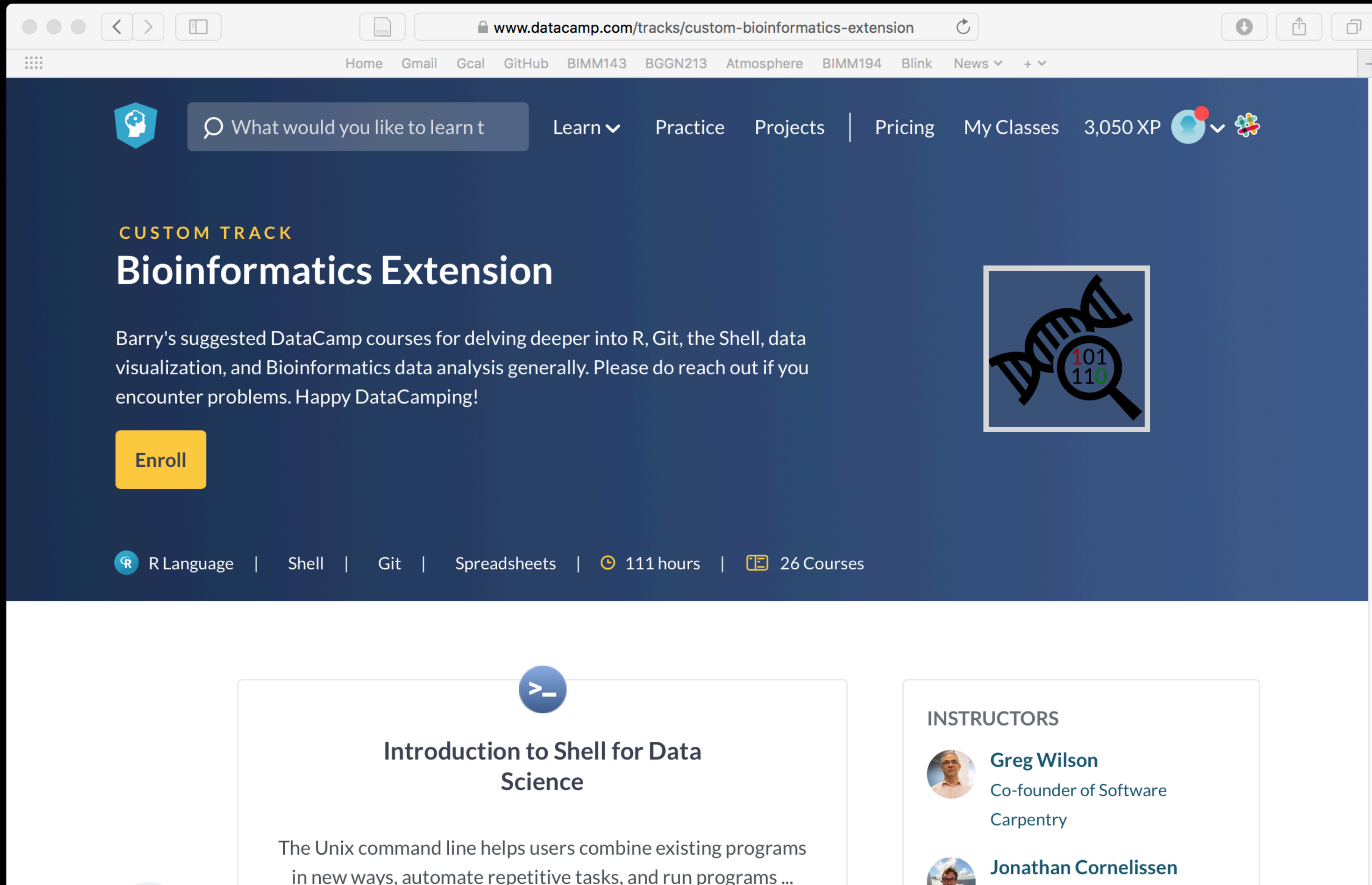
Here I: (1) forked Serina's Repo, (2) Chose the "minimal" theme, (3) Edited _config.yml (adding logo and title)

Thank you very much!

**Please do fill out your official course evaluations if you get a chance.
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



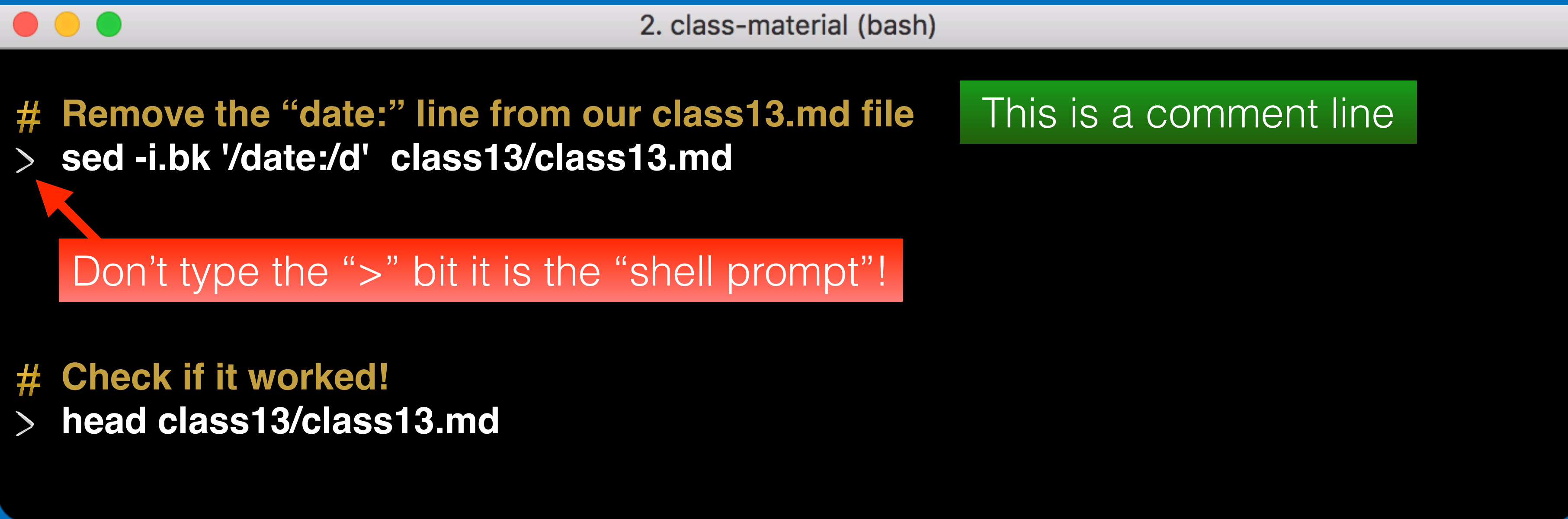
The screenshot shows a web browser window with the URL `www.datacamp.com/tracks/custom-bioinformatics-extension`. The browser's address bar and tabs are visible at the top. The DataCamp logo is in the top left, followed by a search bar containing the text "What would you like to learn t". Navigation links for "Learn", "Practice", "Projects", "Pricing", and "My Classes" are present, along with a user profile icon showing "3,050 XP".

The main content area features the heading "CUSTOM TRACK" in orange, followed by "Bioinformatics Extension" in large white text. Below this, a paragraph states: "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!". A yellow "Enroll" button is positioned to the left of a square icon depicting a DNA double helix and binary code.

A horizontal list of course topics is shown below the main text: "R Language", "Shell", "Git", "Spreadsheets", "111 hours", and "26 Courses".

The bottom section of the page is divided into two columns. The left column is titled "Introduction to Shell for Data Science" and includes a terminal icon. The right column is titled "INSTRUCTORS" and lists two individuals: Greg Wilson (Co-founder of Software Carpentry) and Jonathan Cornelissen.

Thank you very much!



```
2. class-material (bash)

# 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