

Bonus: Bioinformatics & Genomics in Industry Friday @ 1PM

TATA Hall, Kavi Auditorium (i.e. Upstairs!)

Come and enjoy a set of short open ended guest lectures from leading genomic scientists at **Illumina Inc.**, **Synthetic Genomics Inc.**, and **Samumed, LCC**. Come prepared for networking and to have your questions about industry careers in Genomics & Bioinformatics answered.



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://etherpad.net/p/bggn213_w19)
- CAPs evaluation incentives (<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_W19/class-material/BGGN213_exam_guidlines.pdf

The screenshot shows a web browser window with the URL https://bioboot.github.io/bggn213_S18/class-material/BGGN213_exam_guidlines.pdf in the address bar. The page content is a PDF document titled "BGGN-213: FOUNDATIONS OF BIOINFORMATICS" with the subtext "<http://thegrantlab.org/bggn213>". Below this, the section "Preparing for the Final Exam" is highlighted with a blue underline. The text discusses the exam format, point distribution, and excluded material.

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://etherpad.net/p/bggn213_w19

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

Thank you very much!

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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

BGPN213

This is my classwork from BGPN213 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.

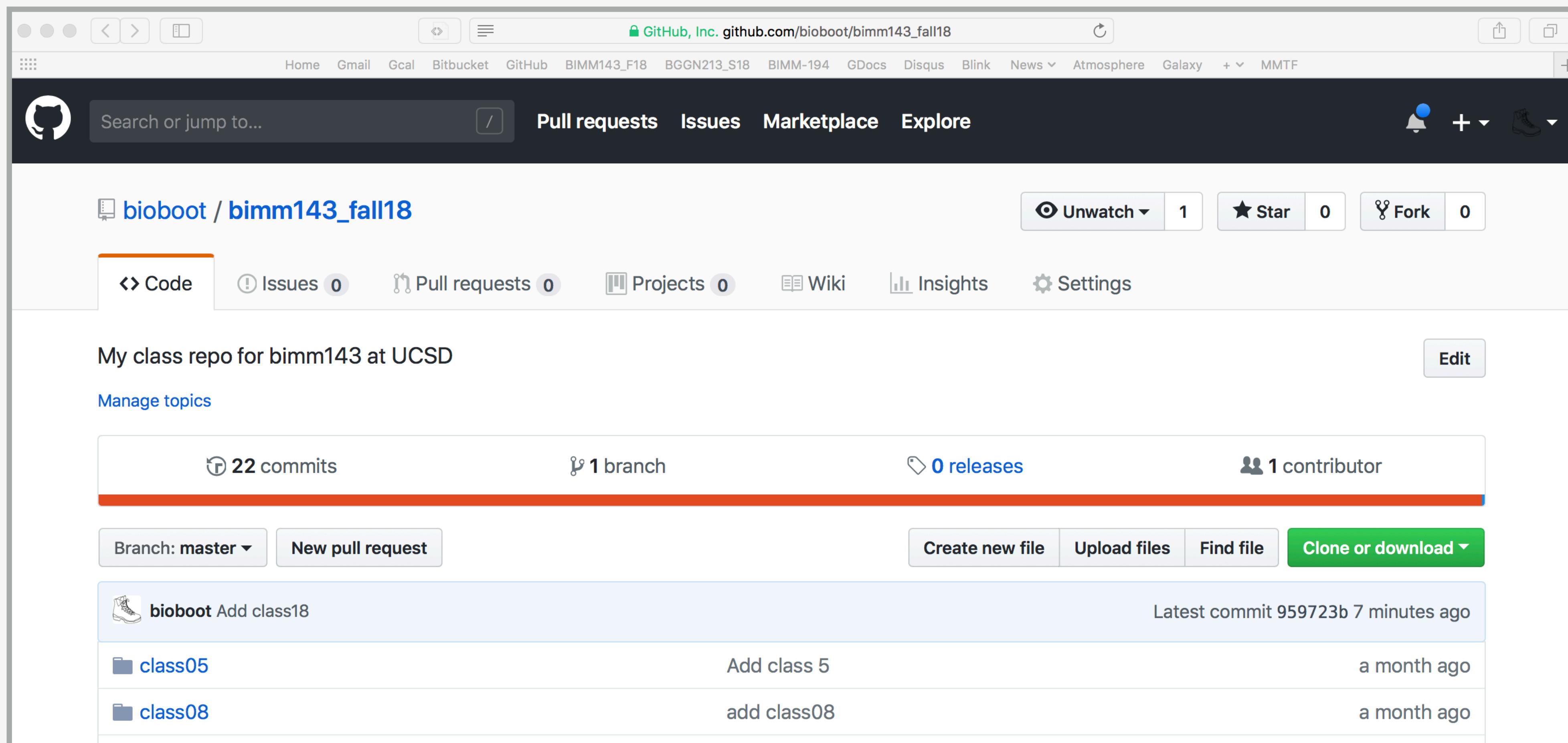
Here I: (1) Chose the “minimal” theme, (3) Edited `_config.yml` (adding logo and title), (4) Fixed a “date:” .md problem

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

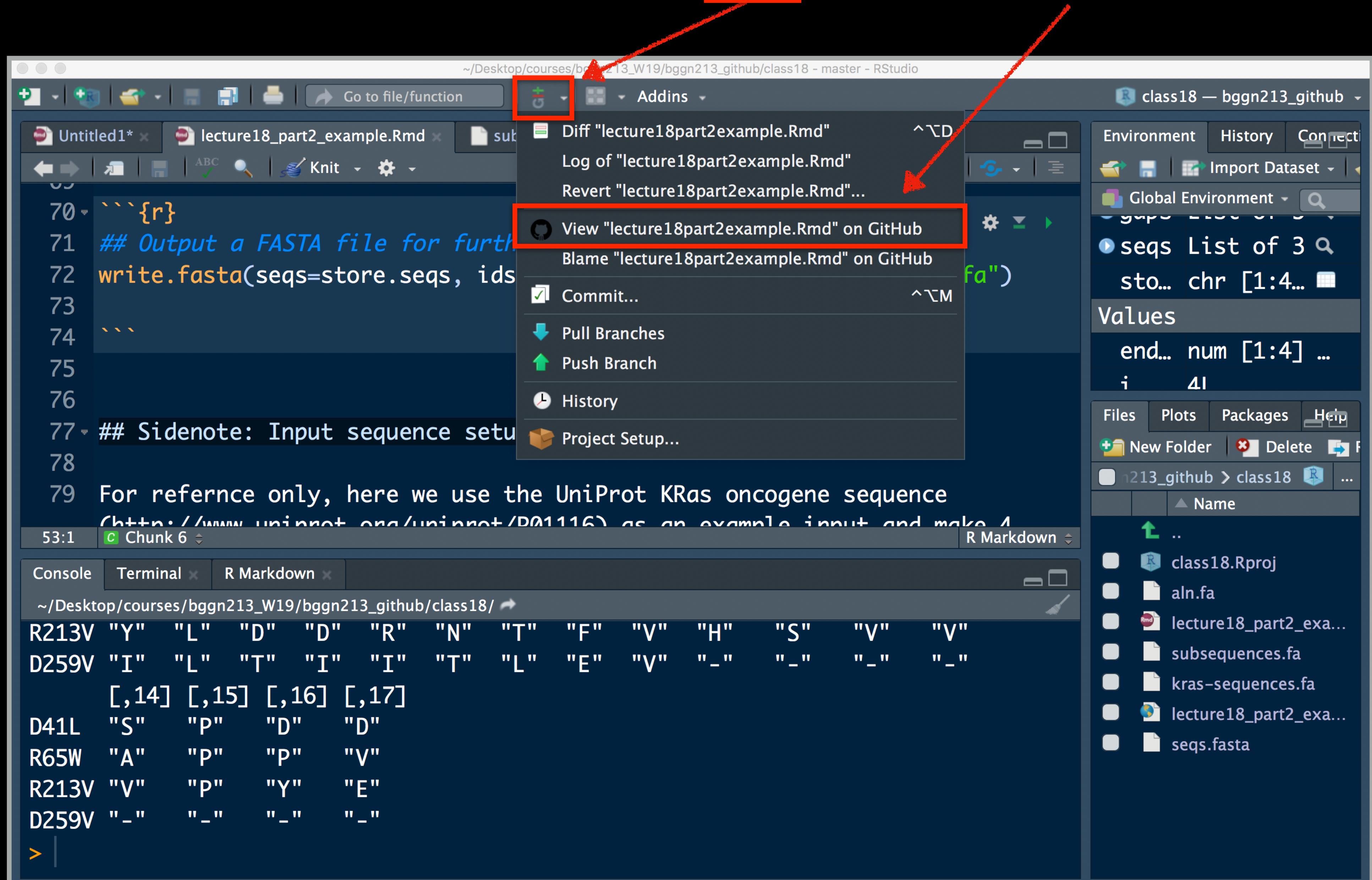
Side-note:

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



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

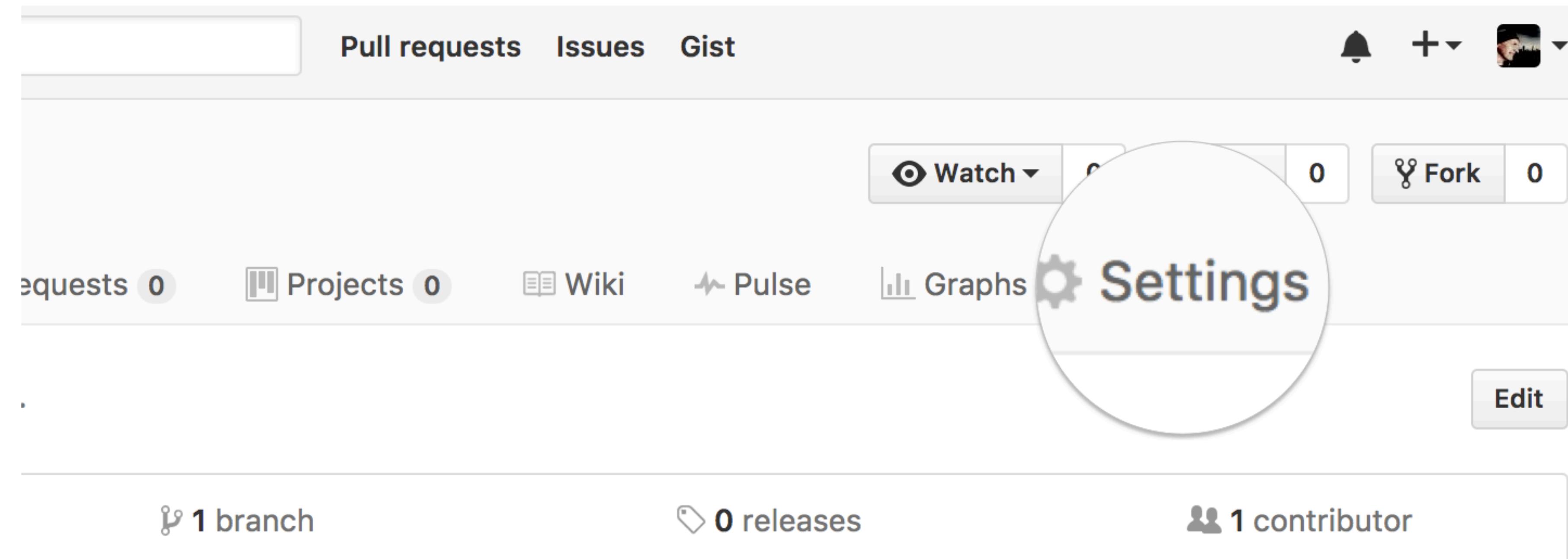


1

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

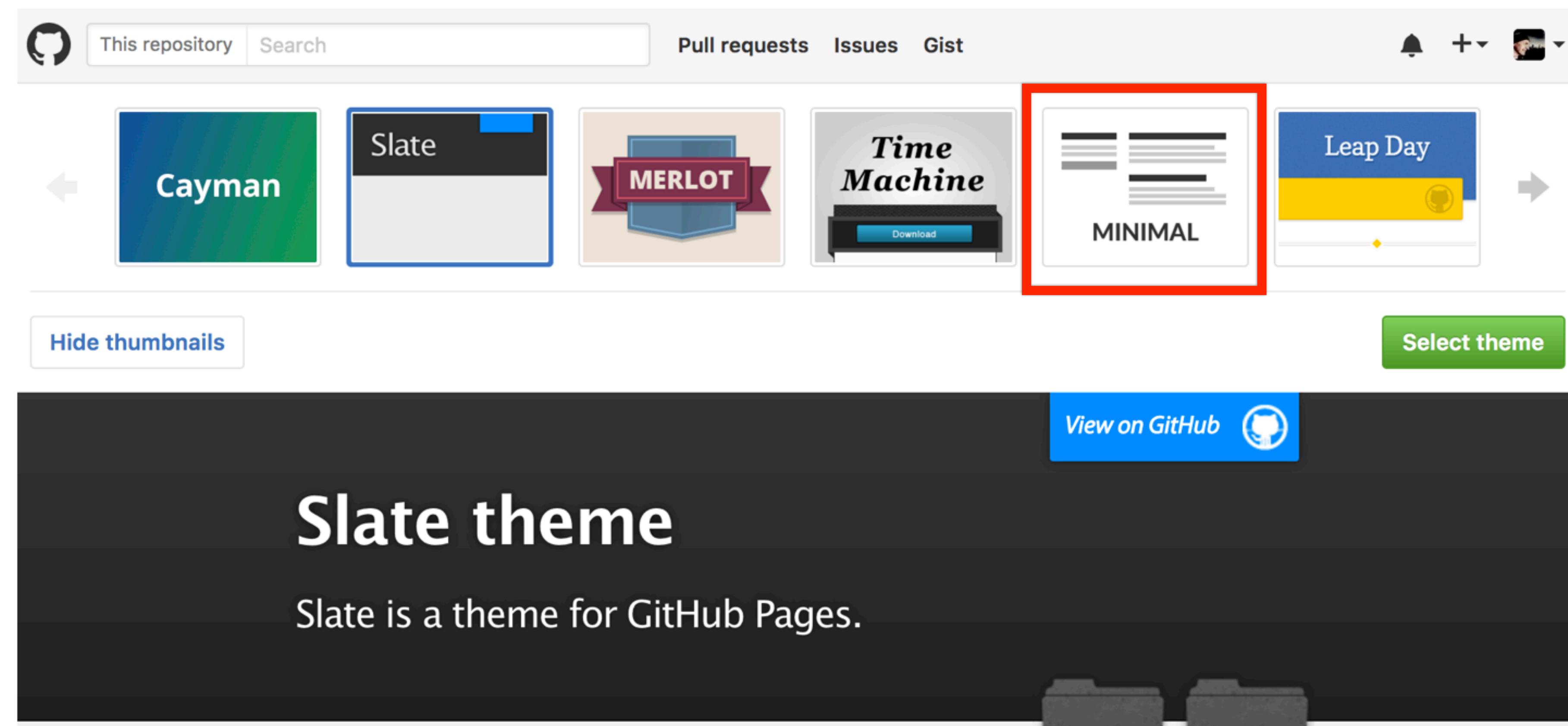
Select a theme to build your site with a Jekyll theme using the `master` branch. [Learn more](#).

[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.



Edit content

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

The screenshot shows the GitHub repository interface for 'jldec / new-pages-site'. The top navigation bar includes the repository name, a 'Watch' button (0), a 'Star' button (0), and a 'Fork' button (0). Below the bar are links for 'Issues 0', 'Pull requests 0', 'Projects 0', 'Wiki', 'Pulse', 'Graphs', and 'Settings'. A search bar at the top right contains the text 'new-pages-site / README.md'. The main area is a code editor titled 'Edit file' with a preview of changes. The code in the editor is:

```
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 \[documentation\]\(https://help.github.com/categories/gi\)  
\(\) and we'll help you sort it out.  
38
```



Commit changes

Add content to new pages site

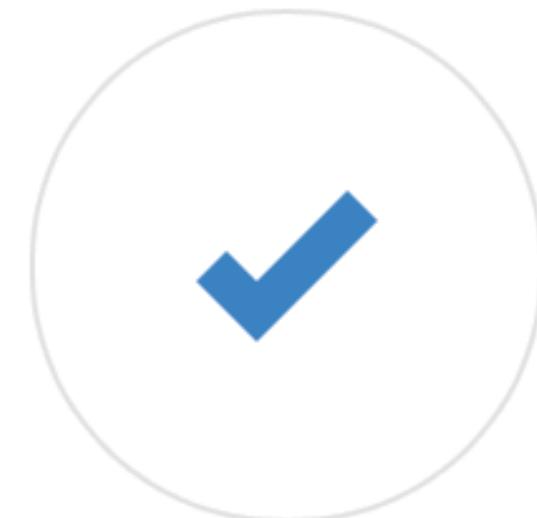
Add an optional extended description...

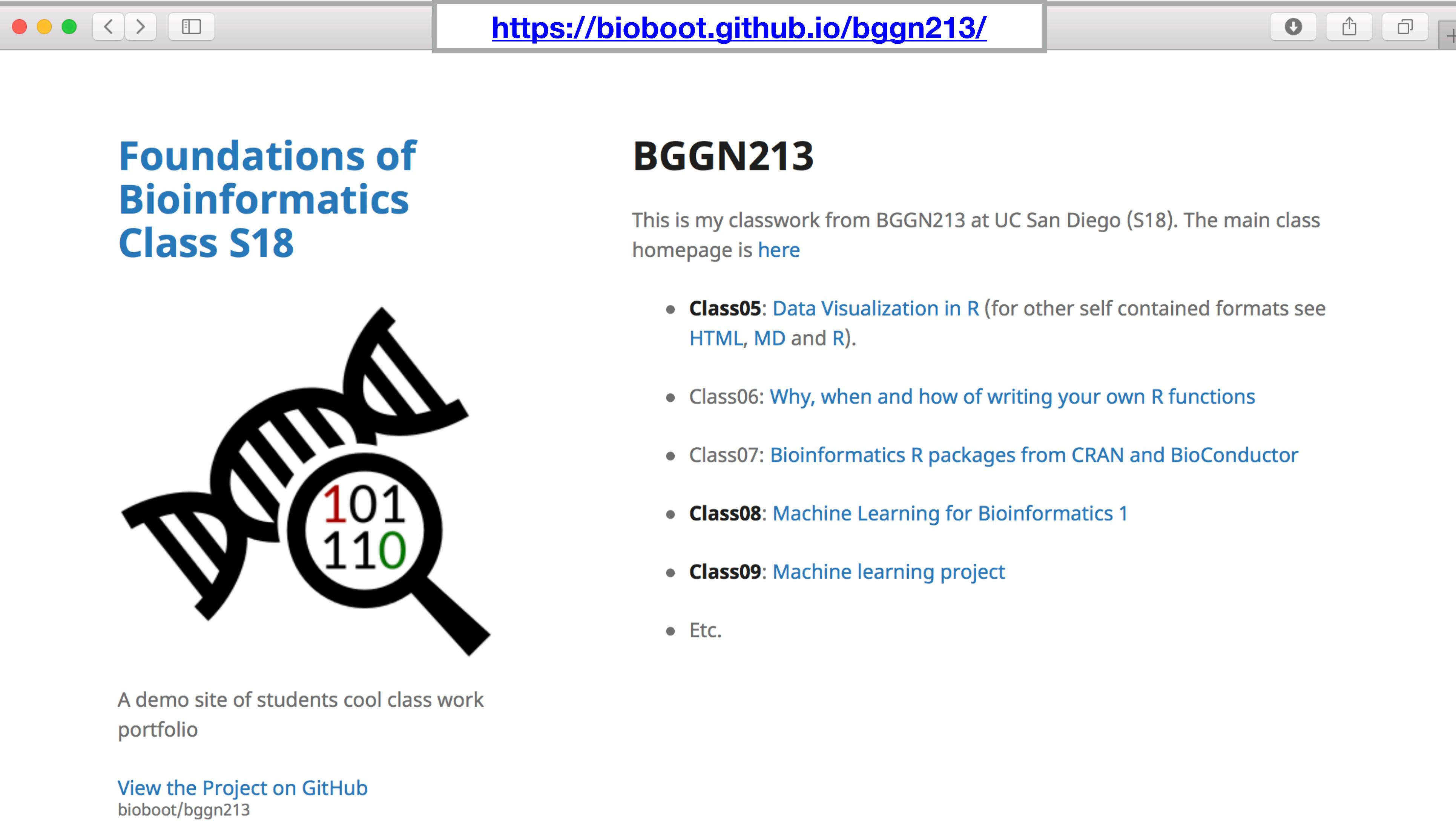
Commit directly to the `master` branch.

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/

A screenshot of a GitHub repository page. At the top, the repository name is 'bioboot / bimm143_serina_f18' with a note 'forked from serinahuang/bimm143'. To the right are buttons for 'Unwatch' (1), 'Star' (0), and 'Fork' (1). Below the header are navigation links: 'Code' (highlighted in orange), 'Pull requests' (0), 'Projects' (0), 'Wiki', 'Insights', and 'Settings'. A dropdown shows the branch is 'master'. The main content area shows a single commit by 'bioboot' titled 'Update _config.yml' made 'just now' with commit hash '3b72493'. Below the commit, it says '1 contributor'. The file details show '4 lines (3 sloc)' and '151 Bytes'. The file content is displayed in a code block:

```
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)
```

At the bottom right of the code block are buttons for 'Raw', 'Blame', 'History', and icons for viewing, editing, or deleting the file.

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

BGNN213

This is my classwork from BGNN213 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/

The screenshot shows a GitHub repository page for 'bioboot / tmp_test'. The repository has 1 unwatched star and 0 forks. The 'Code' tab is selected. The README.md file contains the following content:

```
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

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)

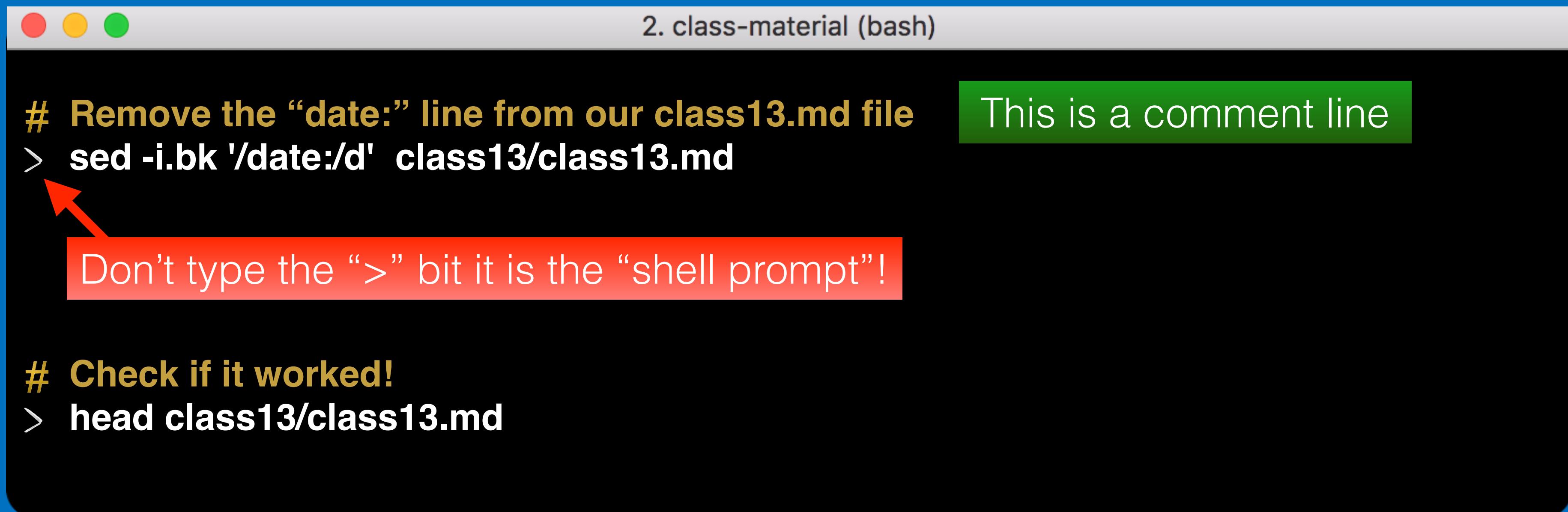
Thank you very much!

Please do fill out your CAPs evaluation (<https://cape.ucsd.edu/students>) if you get a chance.
It is important to the courses we offer in the future and how we teach them!

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Thank you very much!



The screenshot shows a terminal window with the title "2. class-material (bash)". The window contains the following text:

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

A red arrow points from the text "Don't type the ‘>’ bit it is the ‘shell prompt’!" to the first command line starting with ">".

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

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

Q. What do you see after each command?

Q. Does it make sense