



BIMM 143

Course Summary & Exam Preparation

Lecture 19

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UC San Diego

<http://thegrantlab.org/bimm143>

Today's Menu

- Summary of major learning goals,
- Course discussion and feedback (https://etherpad.net/p/bimm143_s19)
- 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/bimm143_S19/class-material/BIMM143_exam_guidlines.pdf

The screenshot shows a web browser window with the URL https://bioboot.github.io/bimm143_S18/class-material/BIMM143_exam_guidlines.pdf in the address bar. The page content is a PDF document titled "BIMM-143: INTRODUCTION TO BIOINFORMATICS" with the URL <http://thegrantlab.org/bimm143>. Below the title, there is a section titled "Preparing for the Final Exam". The text discusses the final exam format, which is open-book and open-notes, lasting 150 minutes and consisting of 35 questions. It specifies that most questions are short answer (worth 2 points) and includes some longer answer questions (worth 5 points). The number of points for each question is indicated at the beginning of each question. A total of 80 points are available. The document notes that no questions from lecture 10 (git version control system) will be asked, but major points from all other lecture material are examinable.

BIMM-143: INTRODUCTION TO BIOINFORMATICS
<http://thegrantlab.org/bimm143>

Preparing for the Final Exam

Overview: The final exam for BIMM-143 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? (e.g. more/less DataCamp & Projects)

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/bimm143_s19

Form Version: <https://tinyurl.com/bimm143-end>

Thank you very much!

Bonus:
GitHub Spit & Polish

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

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Class 11 - [Structural Bioinformatics: Analyzing Protein Structure and Function](#)

Class 12 - [Drug Discovery: Techniques and Analysis](#)

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

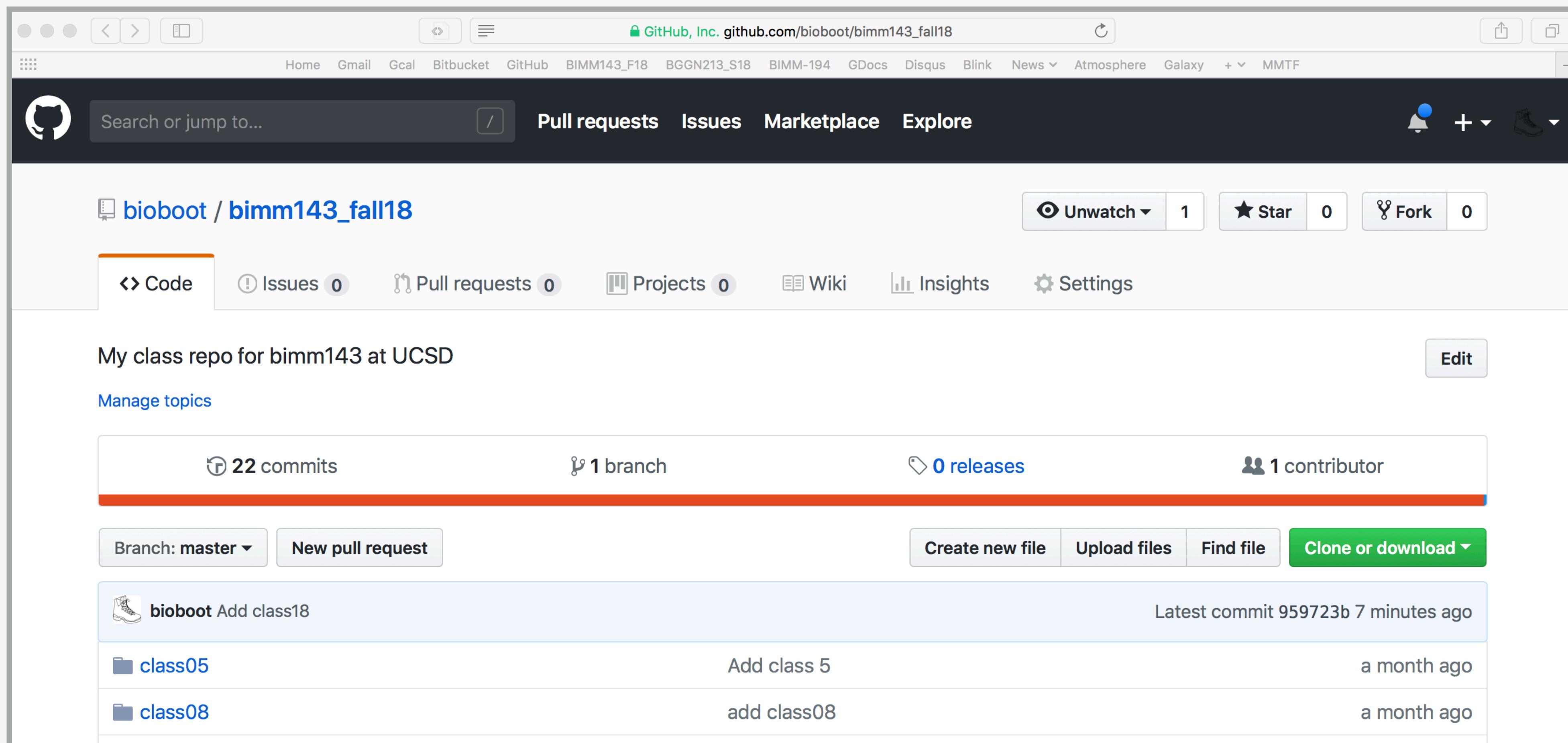
Class 14 - [Transcriptomics and RNA-Seq Analysis](#)

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

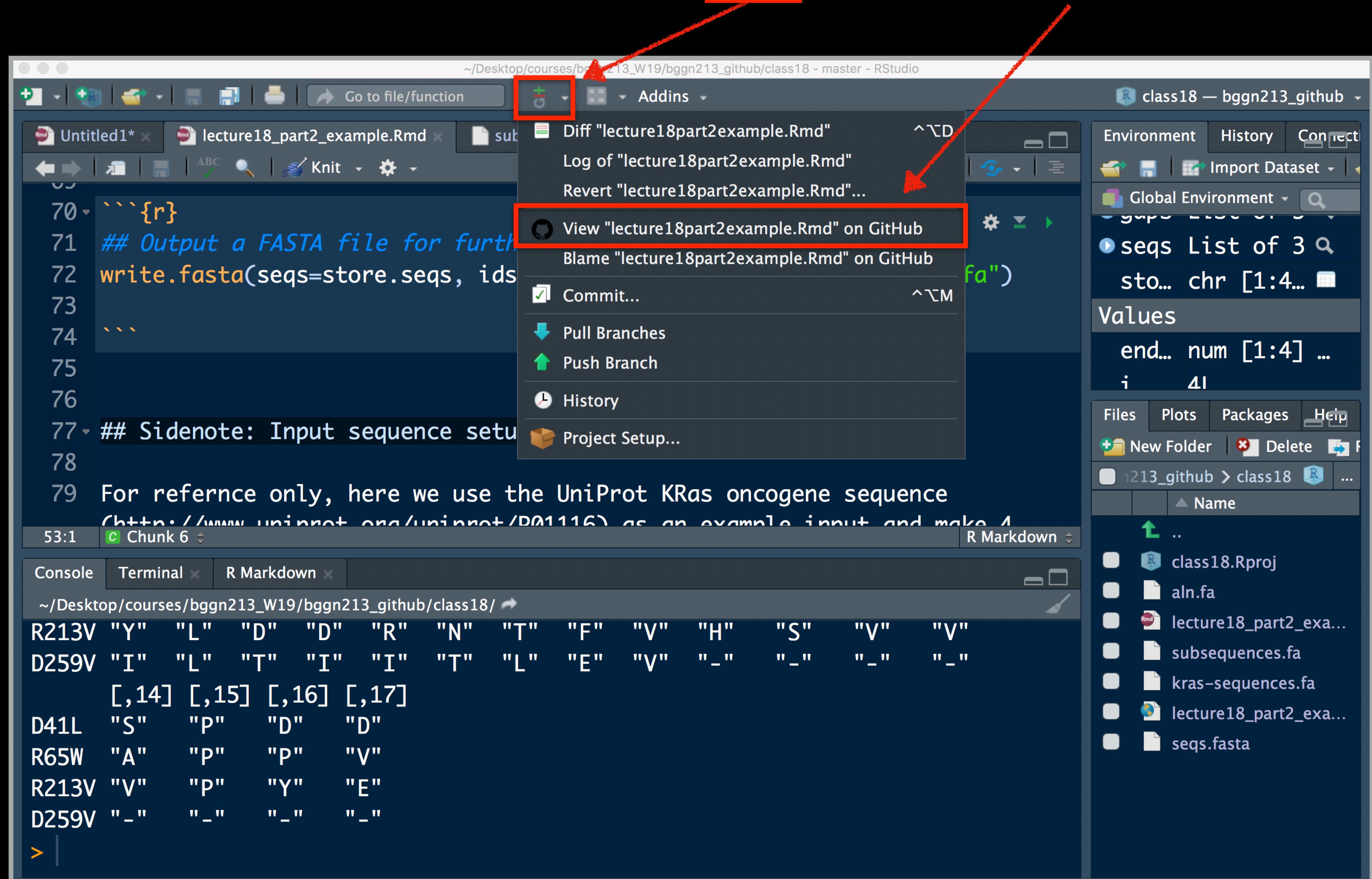
Side-note:

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"

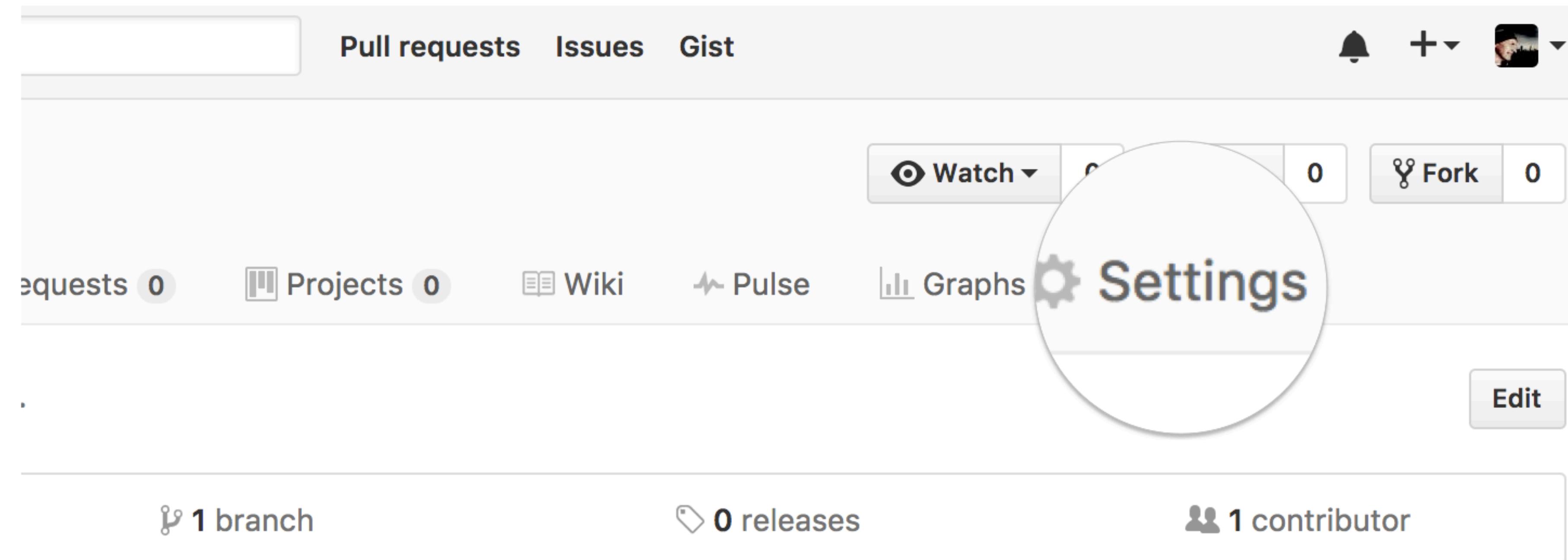


1

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**.
And set the **Source** to "master branch"

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

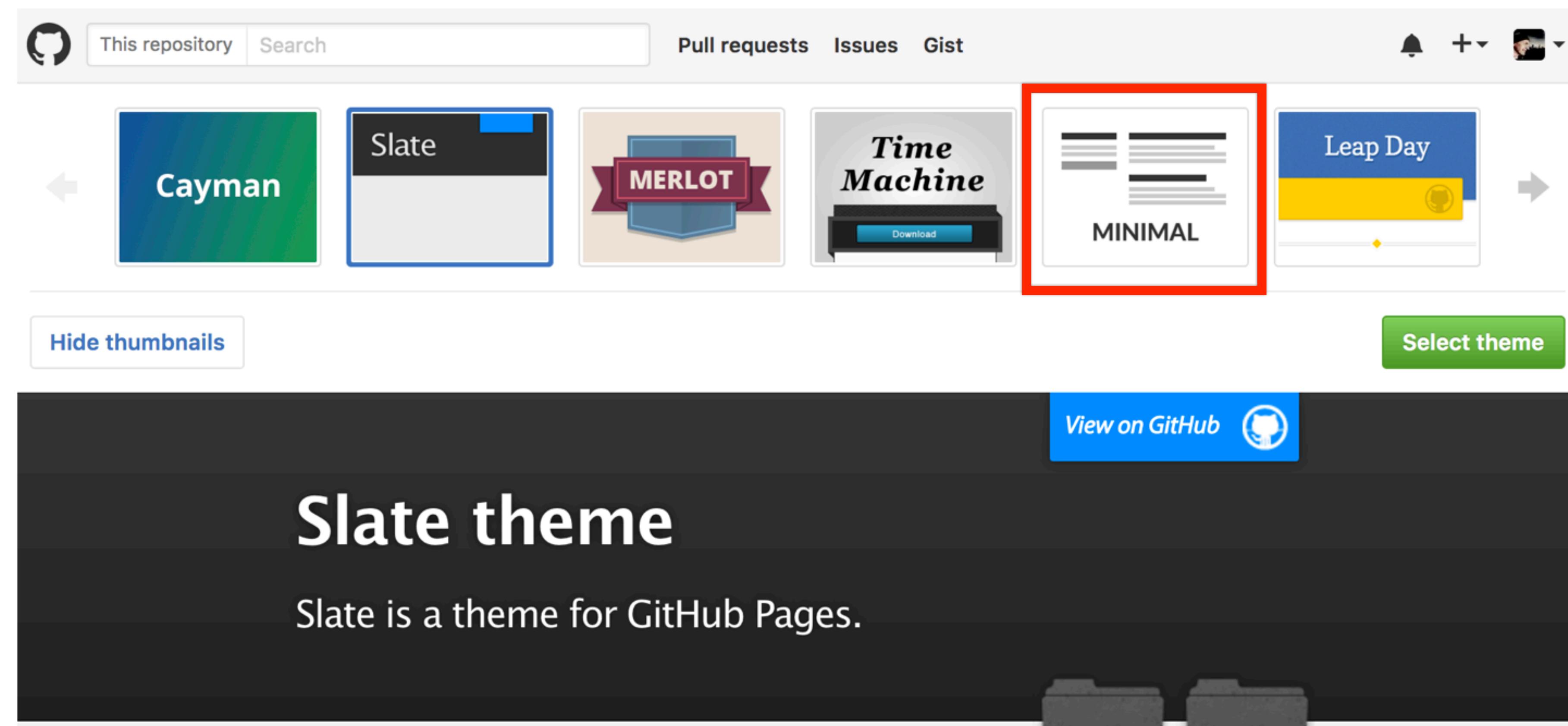
Select a theme to build your site with a Jekyll theme using the `master` branch. [Learn more](#).

[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.



Side-note:

**Scroll down again to the [GitHub Pages](#) section to find the link to your new website.
Open this link in a [New Tab](#) of your browser:**

GitHub Pages

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

Your site is ready to be published at https://bioboot.github.io/bimm143_serina_f18/.

Source

Your GitHub Pages site is currently being built from the `master` branch. [Learn more.](#)

`master branch` ▾

Save

Theme Chooser

Select a theme to publish your site with a Jekyll theme. [Learn more.](#)

Your site is currently using the Minimal theme.

Change theme

Edit content

**Back on the repository main page use the [GitHub](#) online editor to add content.
In particular, add links to each classes .MD file**

The screenshot shows a GitHub repository page 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 navigation are links for 'Issues 0', 'Pull requests 0', 'Projects 0', 'Wiki', 'Pulse', 'Graphs', and 'Settings'. The main content area shows the 'new-pages-site / README.md' file being edited. The file contains the following Markdown content:

```
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

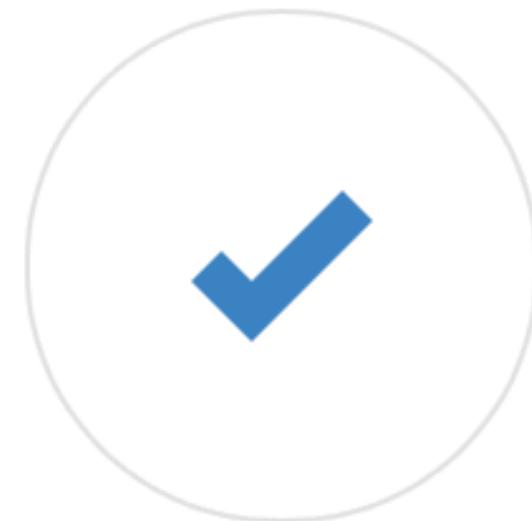
Add an optional extended description...

Commit directly to the `master` branch.

6

...and you're done!

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



Introduction to Bioinformatics (BIMM143)



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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)

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

Code Pull requests 0 Projects 0 Wiki Insights Settings

Branch: master **bimm143_serina_f18 / _config.yml** Find file Copy path

bioboot Update _config.yml 3b72493 just now

1 contributor

4 lines (3 sloc) | 151 Bytes Raw Blame History

```
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

<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 unwatcher, 0 stars, and 0 forks. The 'Code' tab is selected. Below it, there's a search bar for 'tmp_test / README.md' with a 'Search' button and a 'cancel' link. The main area shows the content of the README.md file:

```
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

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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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Incentive...

> 80% response rate we will remove your worst 5pt final exam question!

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Send me and the IAs your [GitHub Pages](#) portfolio with all classes by this Friday and receive another 5pts final exam boost!

Going Further With DataCamp

<https://www.datacamp.com/tracks/custom-bioinformatics-extension>

The screenshot shows a web browser displaying the DataCamp website at the URL <https://www.datacamp.com/tracks/custom-bioinformatics-extension>. The page title is "Bioinformatics Extension". The main content area features a blue header with the text "CUSTOM TRACK" and "Bioinformatics Extension". Below this, a description reads: "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 visible. To the right, there is a graphic of a DNA double helix being examined through a magnifying glass, with binary code "101 110" visible inside the helix. At the bottom, course details are listed: "R Language | Shell | Git | Spreadsheets | 111 hours | 26 Courses". The footer section displays the first course in the track, "Introduction to Shell for Data Science", with a brief description: "The Unix command line helps users combine existing programs in new ways, automate repetitive tasks, and run programs ...". It also lists two instructors: Greg Wilson and Jonathan Cornelissen.

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!

[Enroll](#)

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!

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