



BIMM 143

Course Summary & Exam Preparation

Lecture 19

Barry Grant

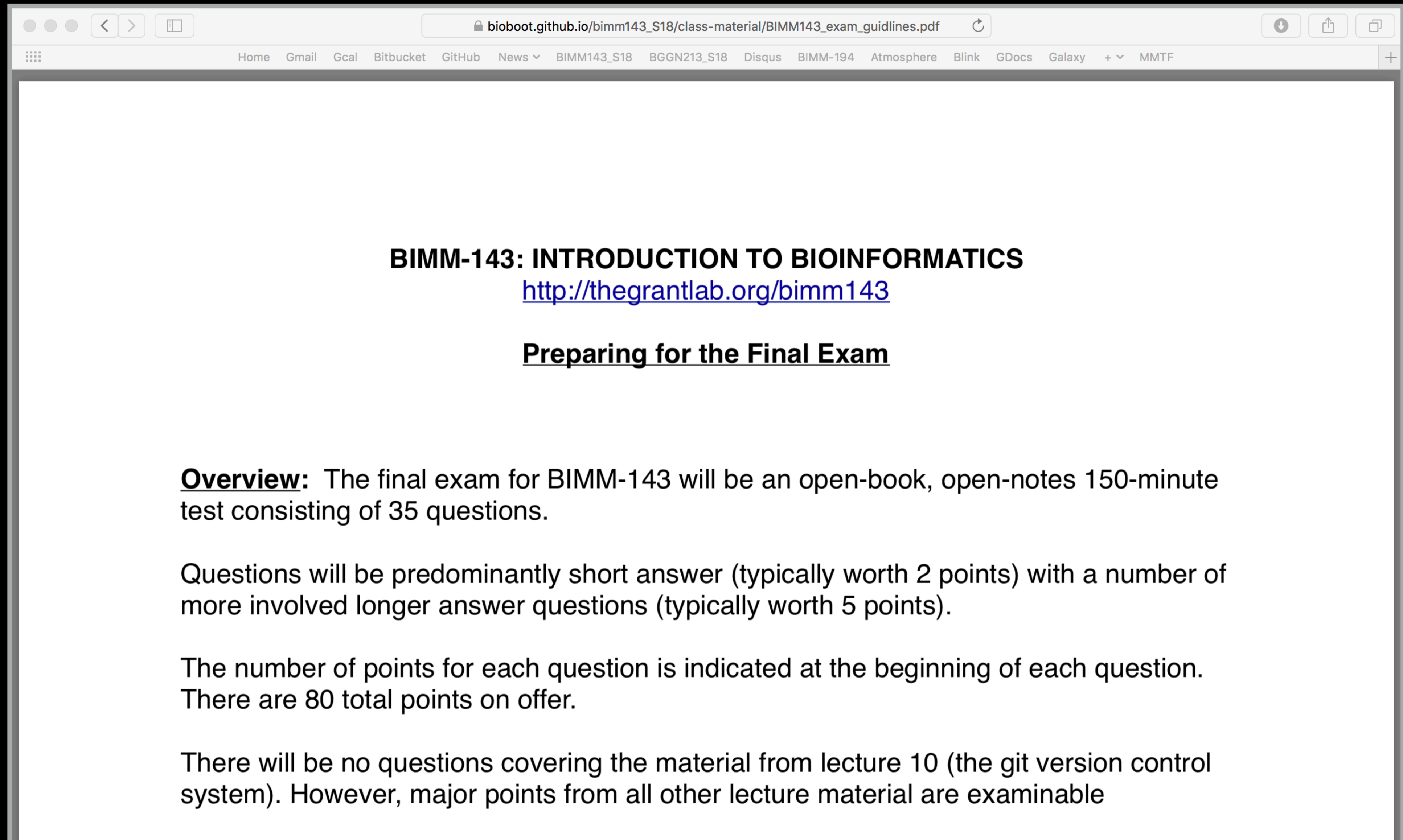
UC San Diego

<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 ([Link](#))
- 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_guidelines.pdf



The image shows a screenshot of a web browser window. The address bar contains the URL bioboot.github.io/bimm143_S19/class-material/BIMM143_exam_guidelines.pdf. The browser's tab bar shows several open tabs, including 'Home', 'Gmail', 'Gcal', 'Bitbucket', 'GitHub', 'News', 'BIMM143_S18', 'BGGN213_S18', 'Disqus', 'BIMM-194', 'Atmosphere', 'Blink', 'GDocs', 'Galaxy', and 'MMTF'. The main content area of the browser displays the following text:

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

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)



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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.

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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
```

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 for 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**. The page shows 1 watch, 0 stars, and 0 forks. The repository description is "My class repo for bimm143 at UCSD". The repository statistics show 22 commits, 1 branch, 0 releases, and 1 contributor. The current branch is **master**. There are buttons for "New pull request", "Create new file", "Upload files", "Find file", and "Clone or download". The commit history shows the latest commit by **bioboot** with the message "Add class18" 7 minutes ago, and two previous commits: "Add class 5" and "add class08", both from a month ago.

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

The screenshot shows the RStudio interface with a file named "lecture18part2example.Rmd" open. The Git icon in the top toolbar is highlighted with a red box. A context menu is open over the file, with the "View 'lecture18part2example.Rmd' on GitHub" option highlighted by a red box. A red arrow points from the text "VIEW on GITHUB" in the top instruction to this menu option. The menu also includes options like "Diff", "Log of", "Revert", "Commit...", "Pull Branches", "Push Branch", "History", and "Project Setup...".

```
70  ````{r}
71  ## Output a FASTA file for further analysis
72  write.fasta(seqs=store.seqs, ids=seqs$names)
73  ````
74
75
76
77  ## Sidenote: Input sequence setup
78
79  For refernce only, here we use the UniProt KRas oncogene sequence
  (http://www.uniprot.org/uniprot/P01116) as an example input and make 4
  sub-sequences of length 14, 15, 16, and 17.
53:1  [C] Chunk 6  R Markdown
```

Console Terminal R Markdown
~/Desktop/courses/bgg213_W19/bgg213_github/class18/

```
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 "_" "_" "_" "_"
>
```

Environment History Connect
Global Environment
seqs List of 3
sto... chr [1:4...
Values
end... num [1:4] ...
i 41

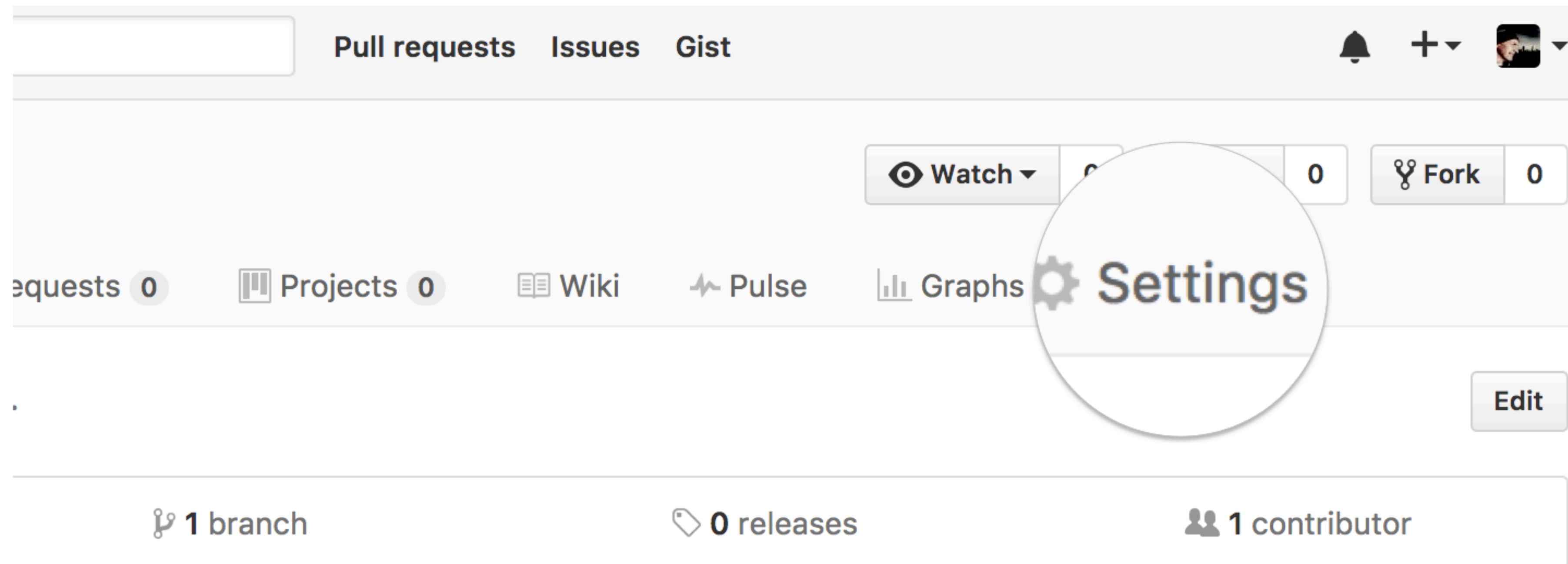
Files Plots Packages Help
New Folder Delete
213_github > class18
Name
..
class18.Rproj
aln.fa
lecture18_part2_exa...
subsequences.fa
kras-sequences.fa
lecture18_part2_exa...
seqs.fasta

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

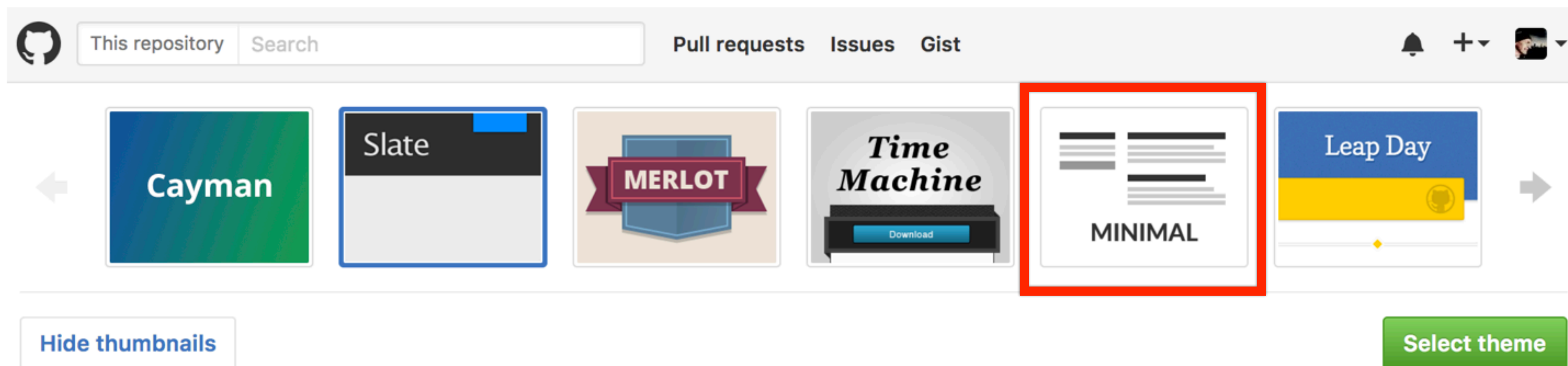
Select a theme to build your site with a Jekyll theme using the `master branch`. [Learn more](#).

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.



The screenshot shows the GitHub theme selection interface. At the top, there is a navigation bar with the GitHub logo, a search bar labeled "This repository", and links for "Pull requests", "Issues", and "Gist". On the right side of the navigation bar, there are icons for notifications, a plus sign, and a user profile. Below the navigation bar is a carousel of theme thumbnails. The thumbnails are: "Cayman" (blue and green gradient), "Slate" (black and white), "MERLOT" (blue and red), "Time Machine" (grey with a printer icon), "MINIMAL" (white with black text, highlighted with a red border), and "Leap Day" (blue and yellow). Below the carousel, there is a "Hide thumbnails" button on the left and a "Select theme" button on the right.

Slate theme

Slate is a theme for GitHub Pages.

[View on GitHub](#)

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

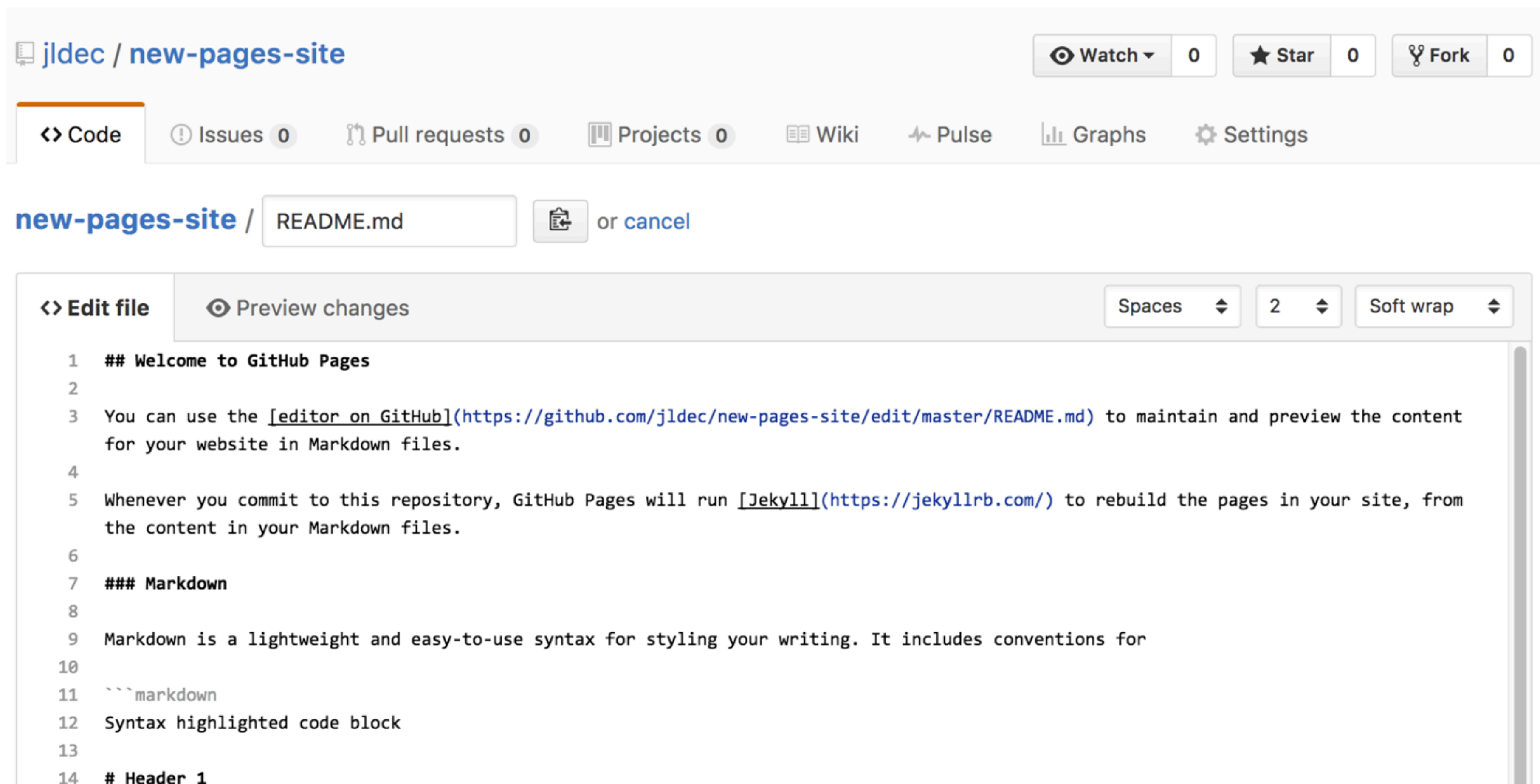
Select a theme to publish your site with a Jekyll theme. [Learn more.](#)

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 the GitHub repository editor interface for the file `README.md` in the repository `jldec / new-pages-site`. The repository has 0 Watchers, 0 Stars, and 0 Forks. The editor is currently in the "Edit file" mode, with a "Preview changes" tab also visible. The code content 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  
38   https://github.com/contact) and we'll help you sort it out.
```

```
38
```



Commit changes

Add content to new pages site|

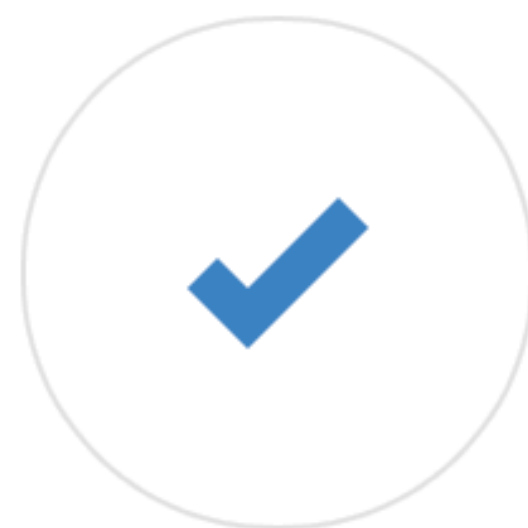
Add an optional extended description...

Commit directly to the `master` branch.

6

...and you're done!

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




bioboot.github.io/bimm143-1/

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

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Hosted on GitHub Pages — Theme by [orderedlist](#)

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

bioboot / **bimm143_serina_f18**
forked from serinahuang/bimm143




Unwatch 1 Star 0 Fork 1

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

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.

[View the Project on GitHub](#)
bioboot/bggn213

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 1 Star 0 Fork 0

<> Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

tmp_test / README.md or cancel

<> Edit file Preview changes Spaces 2 Soft 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/

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Thank you very much!

Please do fill out your CAPs evaluation ([Link!](#)) if you get a change.
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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Incentive...

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

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 window with the URL www.datacamp.com/tracks/custom-bioinformatics-extension. The page features a dark blue header with a search bar containing the text "What would you like to learn t", navigation links for "Learn", "Practice", "Projects", "Pricing", and "My Classes", and a user profile icon with "3,050 XP". Below the header, the page is titled "CUSTOM TRACK Bioinformatics Extension". A paragraph of text 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 positioned below the text. To the right, there is a square icon depicting a DNA double helix with a magnifying glass over it, containing the binary code "101" and "110". At the bottom of the track description, there is a row of tags: "R Language", "Shell", "Git", "Spreadsheets", "111 hours", and "26 Courses".

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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