



BIMM 143

Course Summary & GitHub Portfolio

Class 20

Barry Grant

UC San Diego

<http://thegrantlab.org/bimm143>

Today's Menu

- Summary of major learning goals,
- Course discussion and feedback (https://board.net/p/bimm143_w23)
- CAPs evaluation ([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

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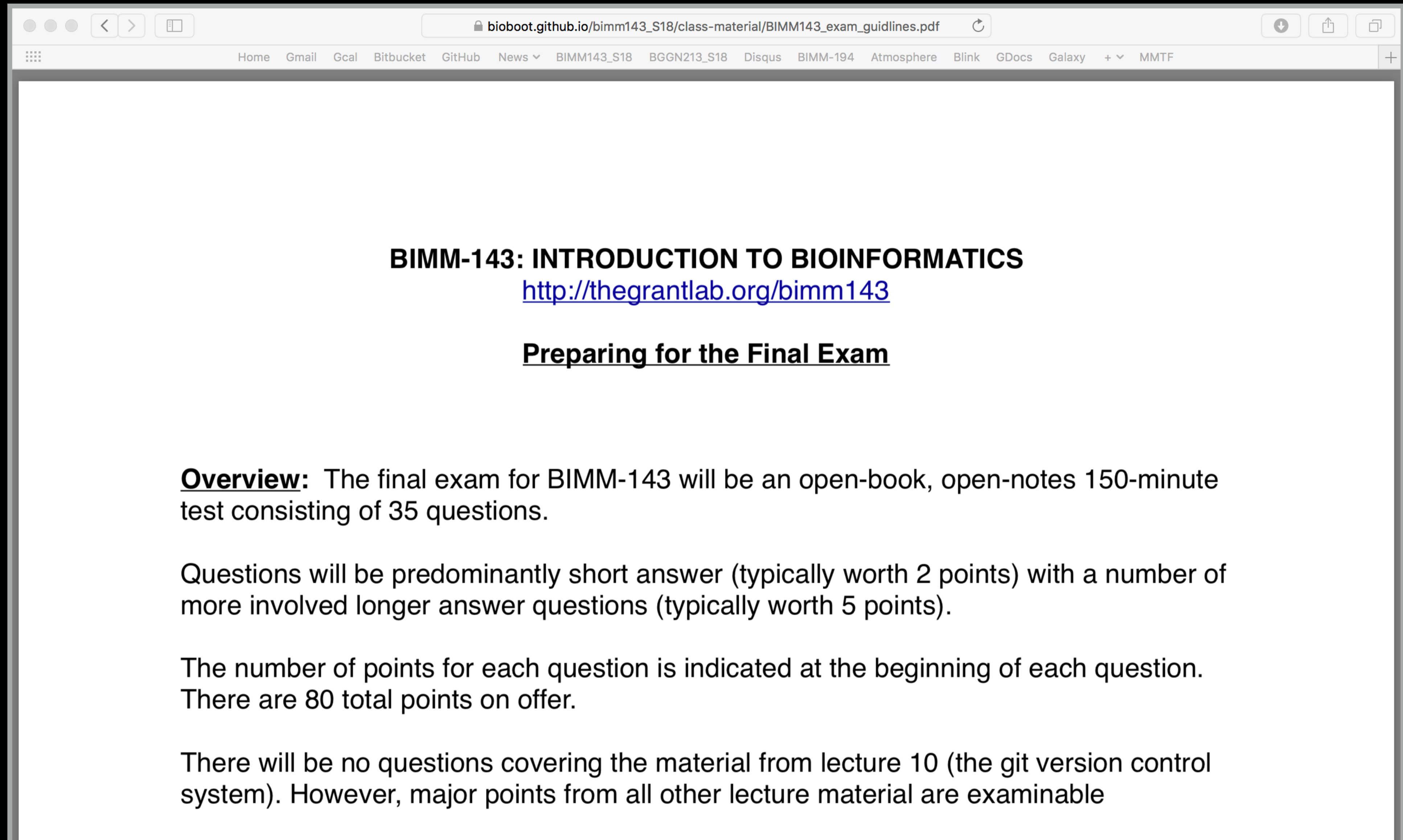


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- Summary of major learning goals,
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- Project troubleshooting
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https://bioboot.github.io/bimm143_F22/class-material/BIMM143_exam_guidelines.pdf



The screenshot shows a web browser window with the address bar displaying the URL `bioboot.github.io/bimm143_S18/class-material/BIMM143_exam_guidelines.pdf`. The browser's tab bar includes links for 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 page features 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://board.net/p/bimm143_w23

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

Thank you very much!

Announcement!

Bonus:

Bioinformatics & Genomics in Industry

Live Stream Video

Enjoy a set of short open ended guest lectures from leading genomic scientists at **Illumina Inc.**, **Synthetic Genomics Inc.**, and the **La Jolla Institute for Allergy and Immunology**. Feel free to contact these scientists for networking and to have your questions about industry careers in Bioinformatics and Genomics answered.

Bonus:

GitHub Spit & Polish

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A demo site of students cool class web site

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bioboot/bimm143-1

This project is maintained by [bioboot](#)

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Bioinformatics Class

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
```

The screenshot shows a web browser window displaying the GitHub repository page for `bioboot/bggn214`. The browser's address bar shows `github.com`. The repository page includes a search bar, navigation links for Pull requests, Issues, Codespaces, Marketplace, and Explore, and a header for the repository `bioboot / bggn214` (Public). Below the header, there are buttons for Pin, Unwatch (1), Fork (0), and Star (0). The main content area shows the repository's file structure with a table of commits. The first commit is by `bioboot` titled "Add class 10" with commit hash `16c0acd` and 4 commits. The file list includes `class10` (Add class 10, 13 days ago) and `README.md` (A change on my laptop, 13 days ago). The right sidebar shows the repository's "About" section with details like "class work", "Readme", "0 stars", "1 watching", and "0 forks".

Commit Hash	Author	Message	Time
16c0acd	bioboot	Add class 10	13 days ago

File	Message	Time
class10	Add class 10	13 days ago
README.md	A change on my laptop.	13 days ago

The logo for Git, featuring the word "GIT" in a bold, sans-serif font. The "G" is white, the "I" is red, and the "T" is green, all set against a black background with a red border.

View "lecture18part2example.Rmd" on GitHub

Blame "lecture18part2example.Rmd" on GitHub

 Commit...

↓ Pull Branches

↑ Push Branch

History

 Project Setup...

```
70 ~~~{r}
71 ## Output a FASTA file for further analysis
72 write.fasta(seqs=store.seqs, ids=store.ids, file="sequences.fasta")
73 ~~~
74
75
76
77 ## Sidenote: Input sequence setup
78
79 For reference only, here we use the UniProt KRas oncogene sequence
80 (http://www.uniprot.org/uniprot/P01116) as an example input and m
```

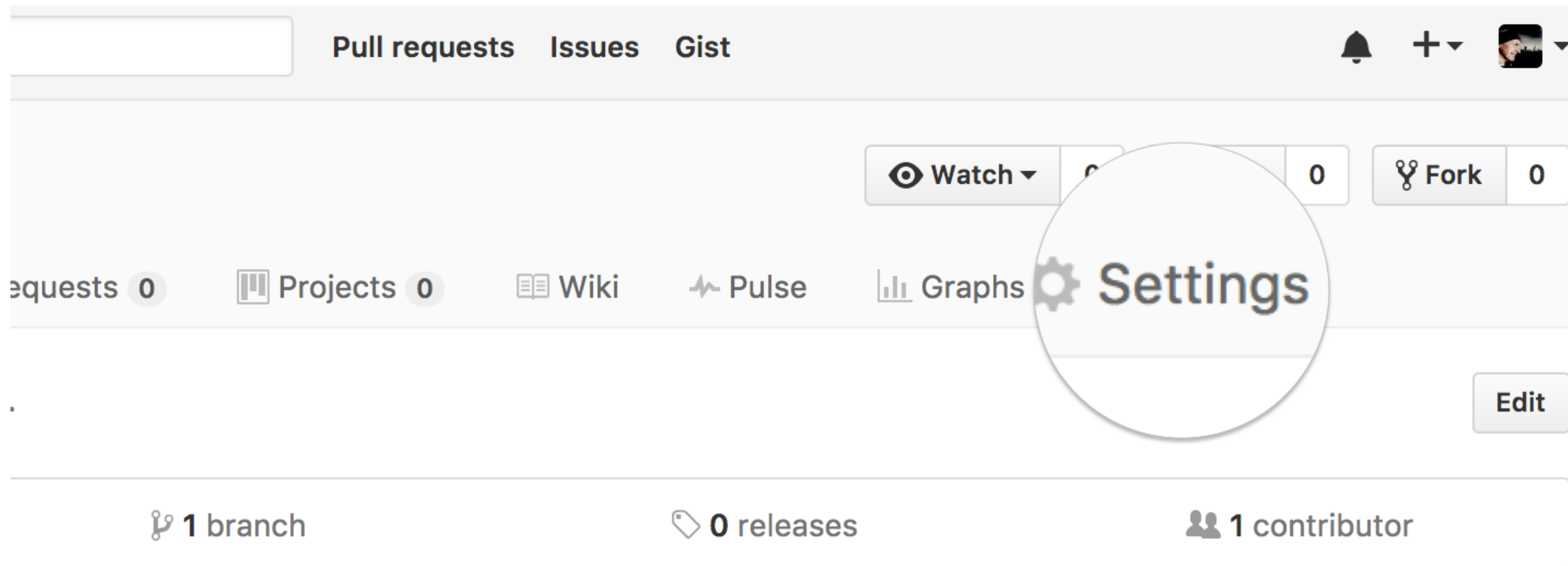
```
~/Desktop/courses/bggg213_W19/bggg213_github/class18/ ➜  
R213V "Y" "L" "D" "D" "R" "N" "T" "F" "V" "H" "S" "V" "V"  
D259V "I" "L" "T" "I" "I" "T" "L" "E" "V" "_" "_" "_" "  
      [,14] [,15] [,16] [,17]  
D41L  "S"   "P"   "D"   "D"  
R65W  "A"   "P"   "P"   "V"  
R213V "V"   "P"   "Y"   "E"  
D259V "_"   "_"   "_"   "  
>
```

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 "main branch"

General

Access

Collaborators

Moderation options

Code and automation

Branches

Tags

Actions

Webhooks

Environments

Codespaces

Pages

Security

GitHub Pages

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

Build and deployment

Source

Deploy from a branch

Branch

GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository. [Learn more.](#)

main

/ (root)

Save

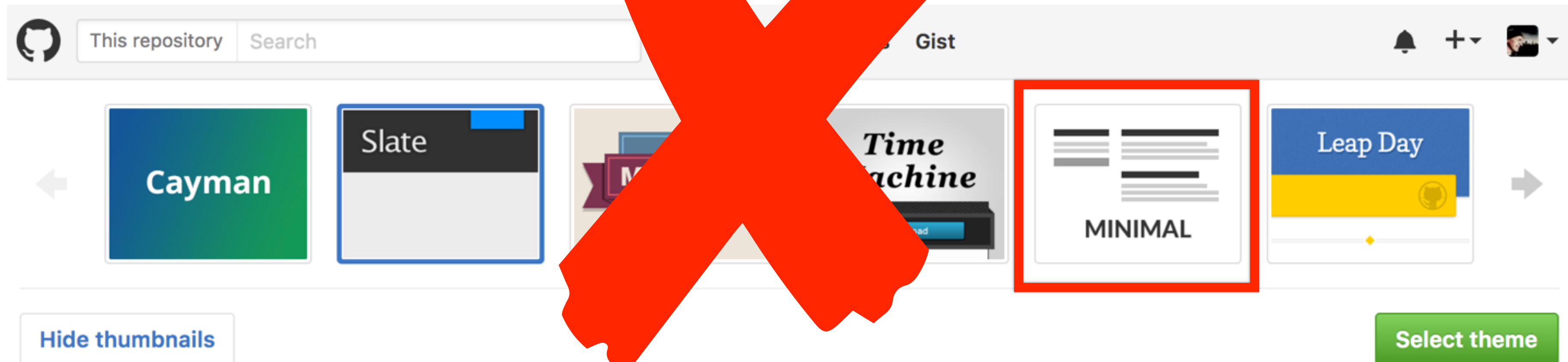


Publish privately to people with read access to this repository
Try risk-free for 30 days using a GitHub Enterprise organization, or [learn more about changing the visibility of your GitHub Pages site.](#) ×

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](#)



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 interface for the repository 'jldec / new-pages-site'. At the top, there are buttons for 'Watch', 'Star', and 'Fork', each with a count of 0. Below these are tabs for 'Code', 'Issues', 'Pull requests', 'Projects', 'Wiki', 'Pulse', 'Graphs', and 'Settings'. The 'Code' tab is selected, and the file 'README.md' is shown. The editor interface includes a 'Preview changes' button and settings for 'Spaces' (set to 2) and 'Soft wrap'. The content of the README.md file is displayed in a code editor with line numbers 1 through 14.

```
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/github-pages-faq)(<https://help.github.com/categories/github-pages-faq>)
(<https://github.com/contact>) and we'll help you sort it out.

38



Commit changes

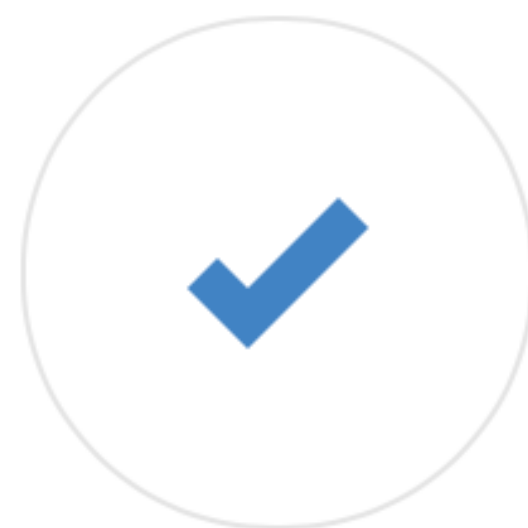
Add content to new pages site|

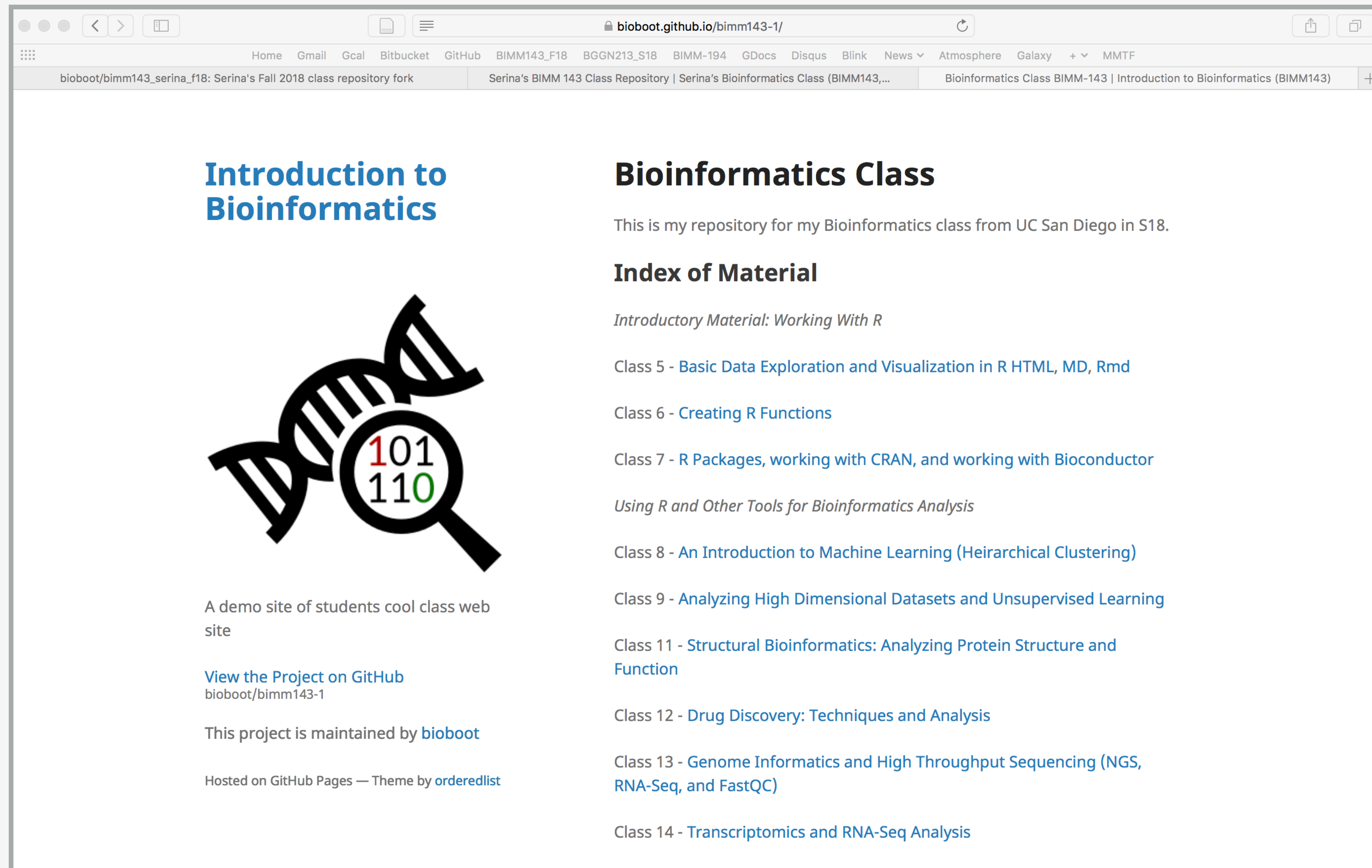
Add an optional extended description...

☒ Commit directly to the `master` branch.

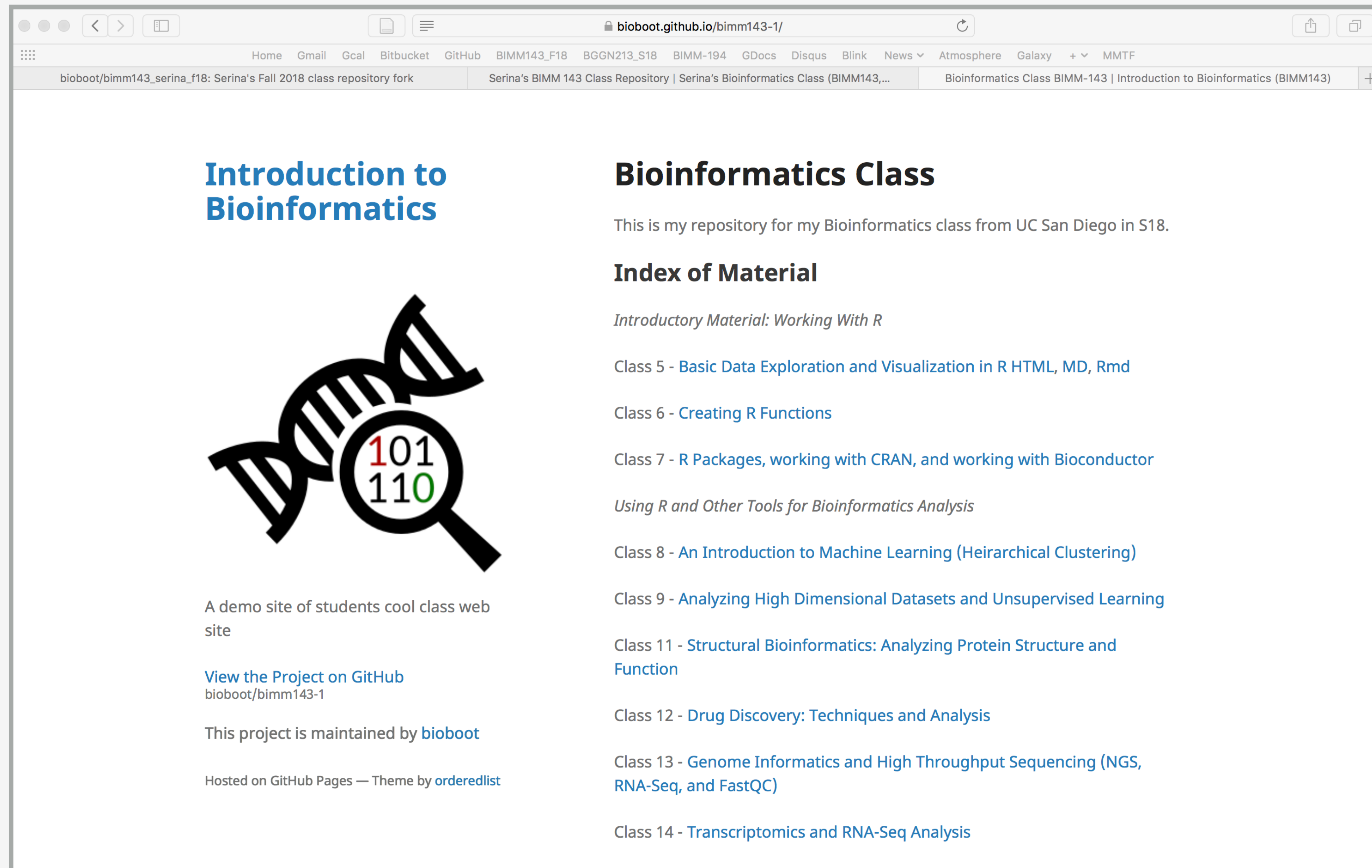
...and you're done!

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





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



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

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

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



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bioboot / tmp_test

Unwatch 1 Star 0 Fork 0

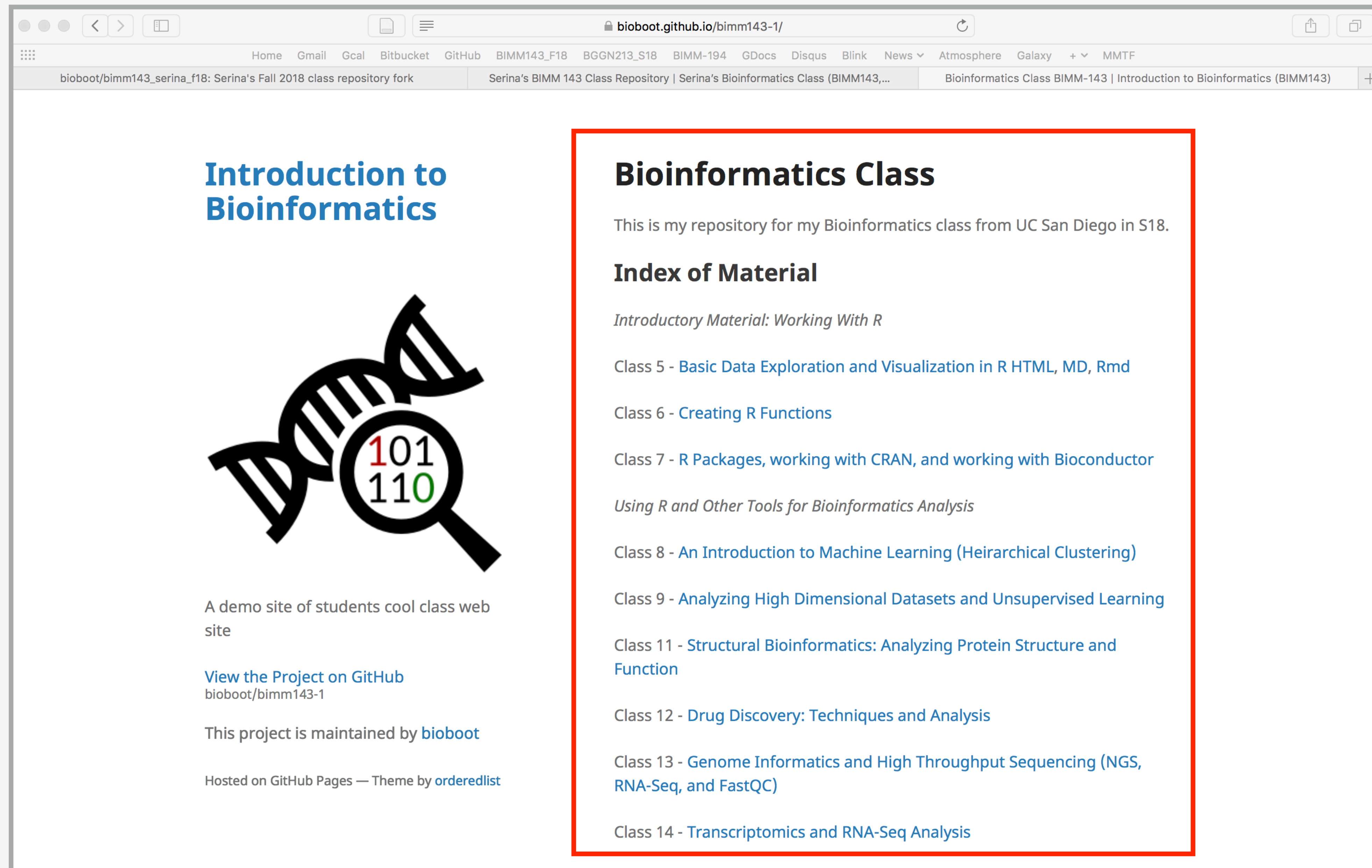
<> Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

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
```

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

Thank you very much!

Please do fill out your CAPs evaluation ([Link!](#)) 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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Post to GradeScope your [GitHub Pages](#) portfolio [URL](#) to GradeScope!

Going Further With DataCamp

https://bioboot.github.io/bimm143_F19/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 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 prominent orange "Enroll" button is located below the text.

To the right of the text is a square icon depicting a DNA double helix with a magnifying glass over it, containing the binary code "101" and "110".

A horizontal bar at the bottom of the main section lists the track's components: "R Language", "Shell", "Git", "Spreadsheets", "111 hours", and "26 Courses", each with a corresponding icon.

Below the main section, two white boxes are visible. The first box is titled "Introduction to Shell for Data Science" with a terminal icon in a blue circle above the title. The second box is titled "INSTRUCTORS" and lists two individuals: "Greg Wilson" (Co-founder of Software Carpentry) and "Jonathan Cornelissen".

Announcement!

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The future? Combining AI and Physics based approaches

Missing class!

AlphaFold Protein Structure Database

Home About FAQs Downloads

AlphaFold Protein Structure Database

Developed by DeepMind and EMBL-EBI

Search for protein, gene, UniProt accession or organism **BETA** **Search**

Examples: [Free fatty acid receptor 2](#) [At1g58602](#) [Q5VSL9](#) [E. coli](#) Help: [AlphaFold DB search help](#)

AlphaFold DB provides open access to protein structure

Option: New lecture on AlphaFold or project trouble shooting