



BGGN 213

Course Summary & GitHub Portfolio

Class 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_f22)
- Course evaluation (**official**)
- 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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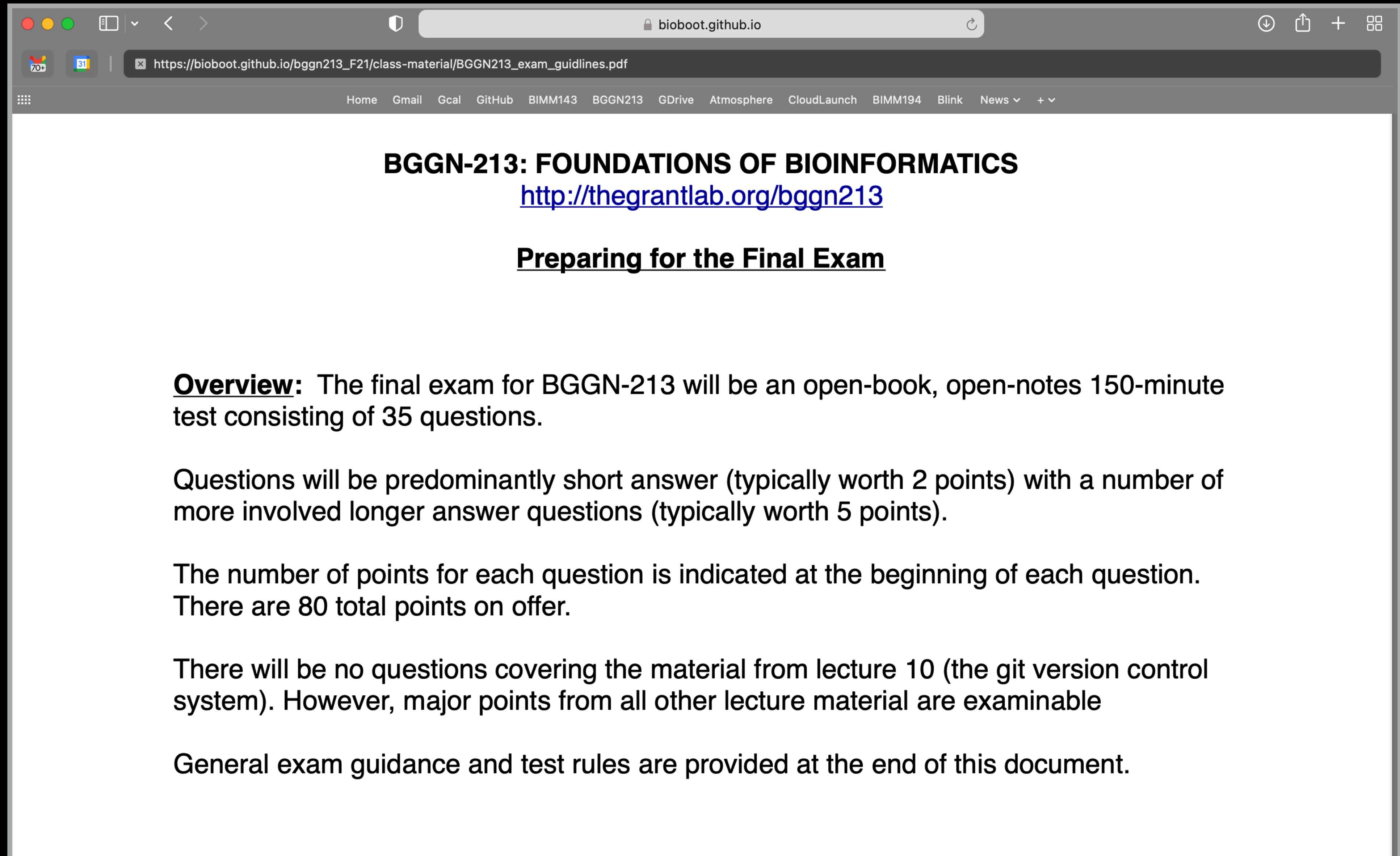


Today's Menu

- Summary of major learning goals,
- Course discussion and feedback (https://board.net/p/bggn213_f22)
- Course evaluation (**official**)
- Project troubleshooting
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 - Exam preparation, discussion and open study
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https://bioboot.github.io/bggn213_F22/class-material/BGGN213_exam_guidelines.pdf



The screenshot shows a web browser window with the address bar displaying the URL `https://bioboot.github.io/bggn213_F21/class-material/BGGN213_exam_guidelines.pdf`. The browser's address bar also shows the domain `bioboot.github.io`. The page content is centered and includes the following text:

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

General exam guidance and test rules are provided at the end of this document.

- 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/bgggn213_f22

Form Version: <https://tinyurl.com/bgggn213-summary>

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

Introduction to Bioinformatics



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

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

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 tabs for Code, Issues, Pull requests, Actions, Projects, Wiki, Security, Insights, and Settings. The main content area shows the repository's file structure with a commit history table. The table lists the following commits:

Commit Hash	Commit Message	Time Ago	Commits
16c0acd	13 days ago	4	commits
class10	Add class 10	13 days ago	
README.md	A change on my laptop.	13 days ago	

On the right side of the repository page, there is an 'About' section for the repository `class work`, which includes a README link, 0 stars, 1 watching, and 0 forks.

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

The screenshot shows the RStudio IDE interface. The top toolbar has a 'Go to file/function' button and a 'GIT' icon (a green 'G' with a plus sign) which is highlighted with a red box. A red arrow points from the text 'GIT icon' in the instruction above to this icon. Another red arrow points from the text '"VIEW on GITHUB"' to the 'View "lecture18part2example.Rmd" on GitHub' option in the Git menu. The Git menu is open, showing options: 'Diff "lecture18part2example.Rmd"', 'Log of "lecture18part2example.Rmd"', 'Revert "lecture18part2example.Rmd"...', 'View "lecture18part2example.Rmd" on GitHub' (highlighted with a red box), 'Blame "lecture18part2example.Rmd" on GitHub', 'Commit...', 'Pull Branches', 'Push Branch', 'History', and 'Project Setup...'. The main editor shows an R Markdown file 'lecture18_part2_example.Rmd' with R code and text. The console at the bottom shows the output of the R code, which is a FASTA file format. The file explorer on the right shows the project structure, including 'class18.Rproj', 'aln.fa', 'lecture18_part2_example.Rmd', 'subsequences.fa', 'kras-sequences.fa', 'lecture18_part2_example.Rmd', and 'seqs.fasta'.

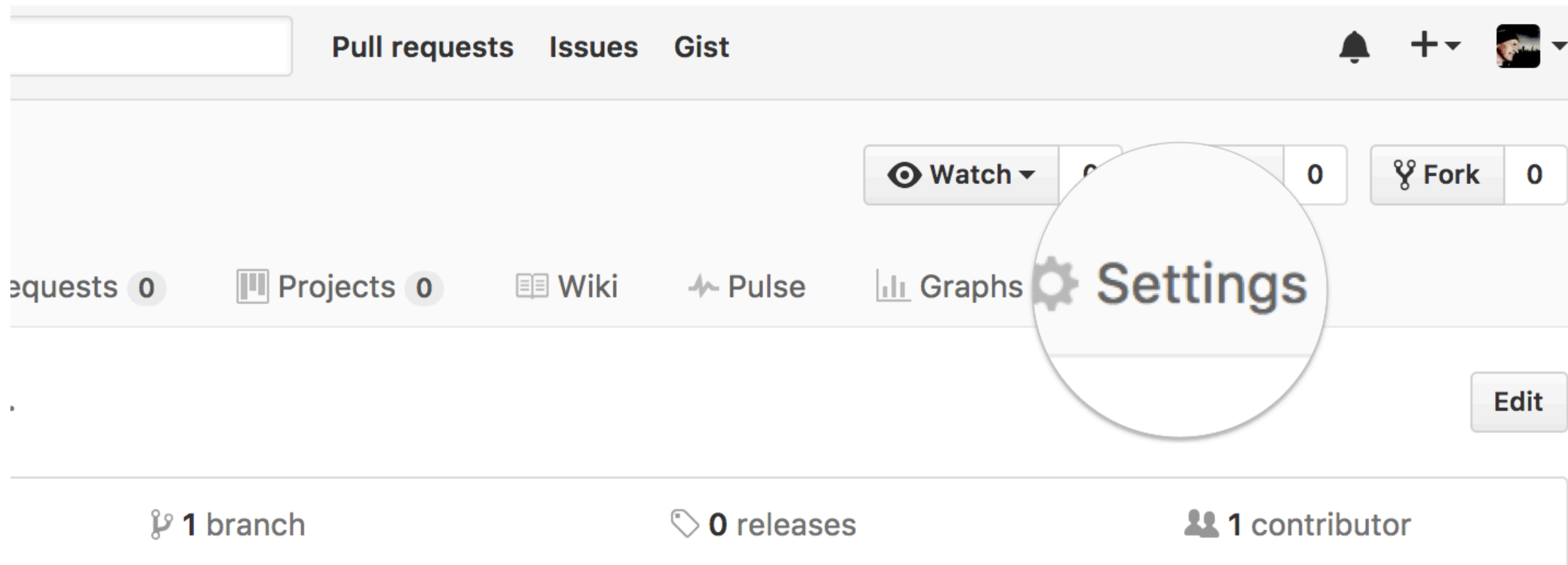
```
53:1 53:15 53:16 53:17 53:18 53:19 53:20 53:21 53:22 53:23 53:24 53:25 53:26 53:27 53:28 53:29 53:30 53:31 53:32 53:33 53:34 53:35 53:36 53:37 53:38 53:39 53:40 53:41 53:42 53:43 53:44 53:45 53:46 53:47 53:48 53:49 53:50 53:51 53:52 53:53 53:54 53:55 53:56 53:57 53:58 53:59 53:60 53:61 53:62 53:63 53:64 53:65 53:66 53:67 53:68 53:69 53:70 53:71 53:72 53:73 53:74 53:75 53:76 53:77 53:78 53:79 53:80 53:81 53:82 53:83 53:84 53:85 53:86 53:87 53:88 53:89 53:90 53:91 53:92 53:93 53:94 53:95 53:96 53:97 53:98 53:99 53:100 53:101 53:102 53:103 53:104 53:105 53:106 53:107 53:108 53:109 53:110 53:111 53:112 53:113 53:114 53:115 53:116 53:117 53:118 53:119 53:120 53:121 53:122 53:123 53:124 53:125 53:126 53:127 53:128 53:129 53:130 53:131 53:132 53:133 53:134 53:135 53:136 53:137 53:138 53:139 53:140 53:141 53:142 53:143 53:144 53:145 53:146 53:147 53:148 53:149 53:150 53:151 53:152 53:153 53:154 53:155 53:156 53:157 53:158 53:159 53:160 53:161 53:162 53:163 53:164 53:165 53:166 53:167 53:168 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```

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



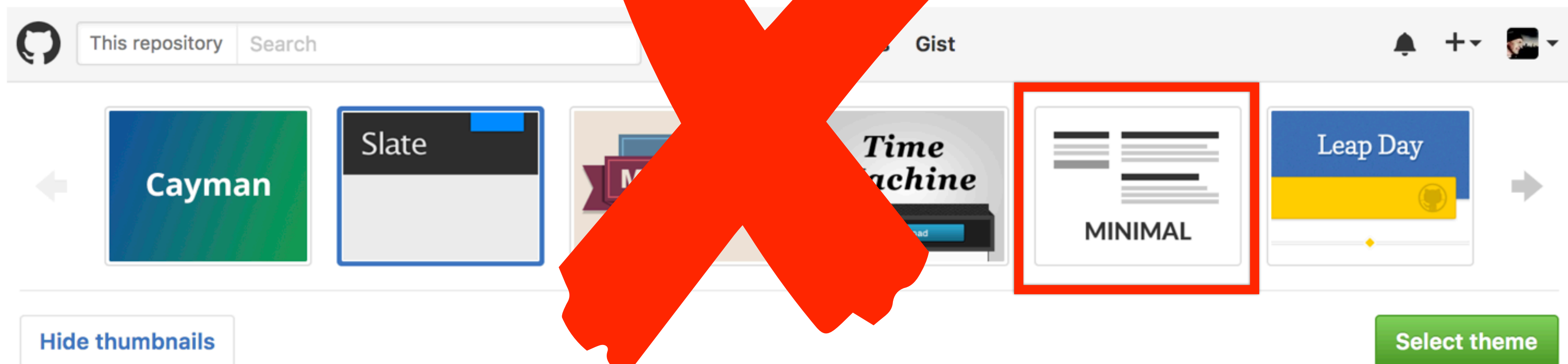
Publish privately to people with read access to this repository

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 toolbar with 'Edit file' and 'Preview changes' tabs, and settings for 'Spaces' (2) and 'Soft wrap'. The main content area displays the README.md file with the following text:

```
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.
```



Commit changes

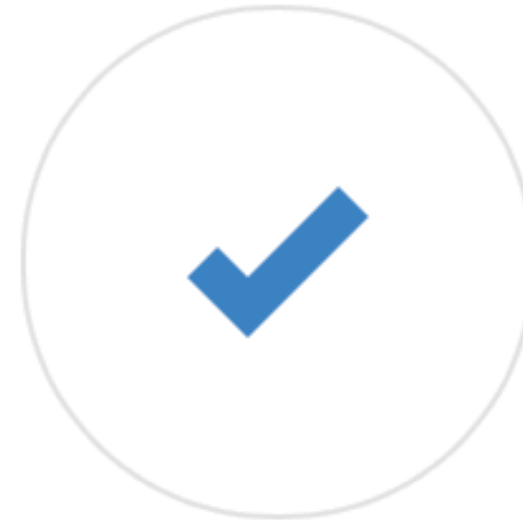
Add content to new pages site|

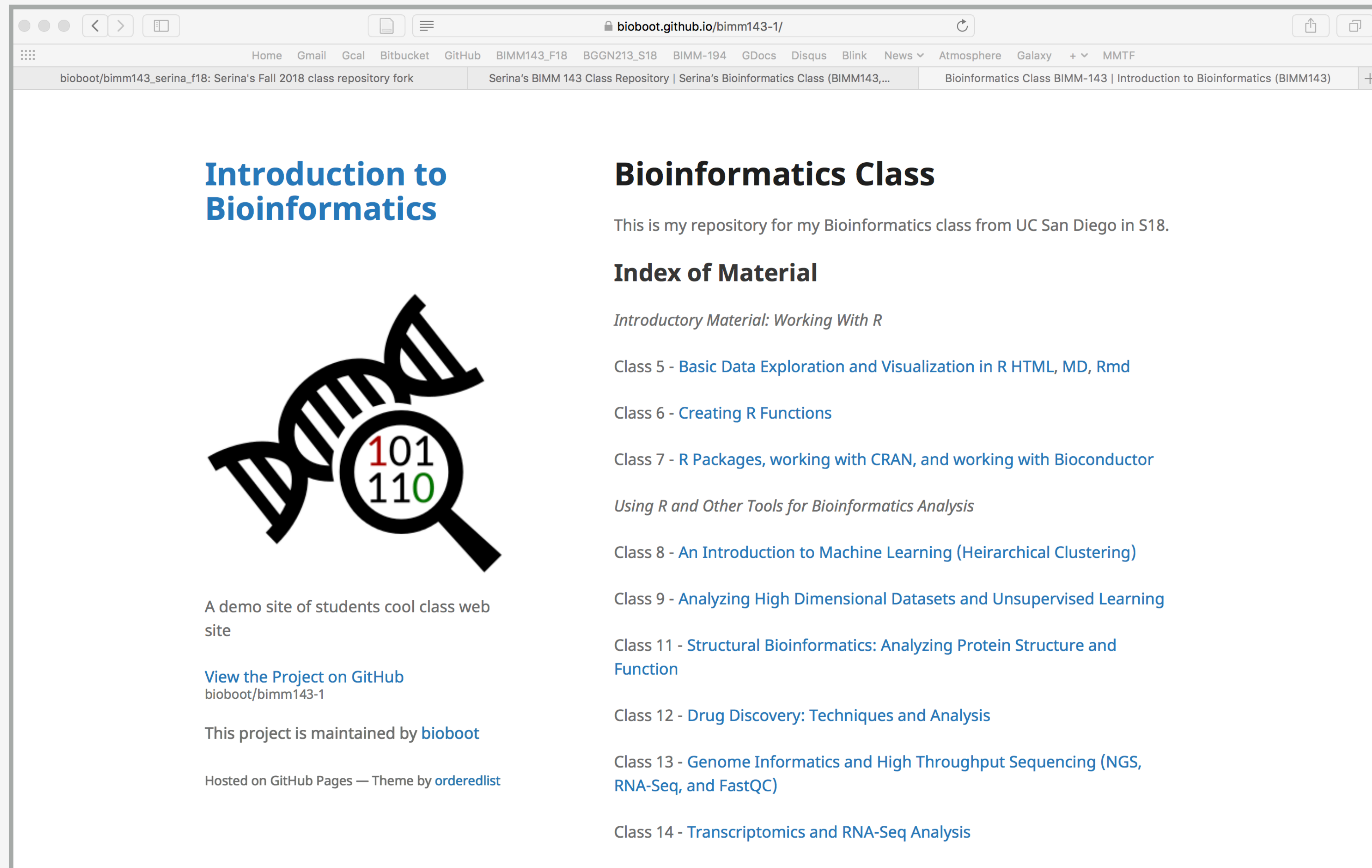
Add an optional extended description...

☒ Commit directly to the `master` branch.

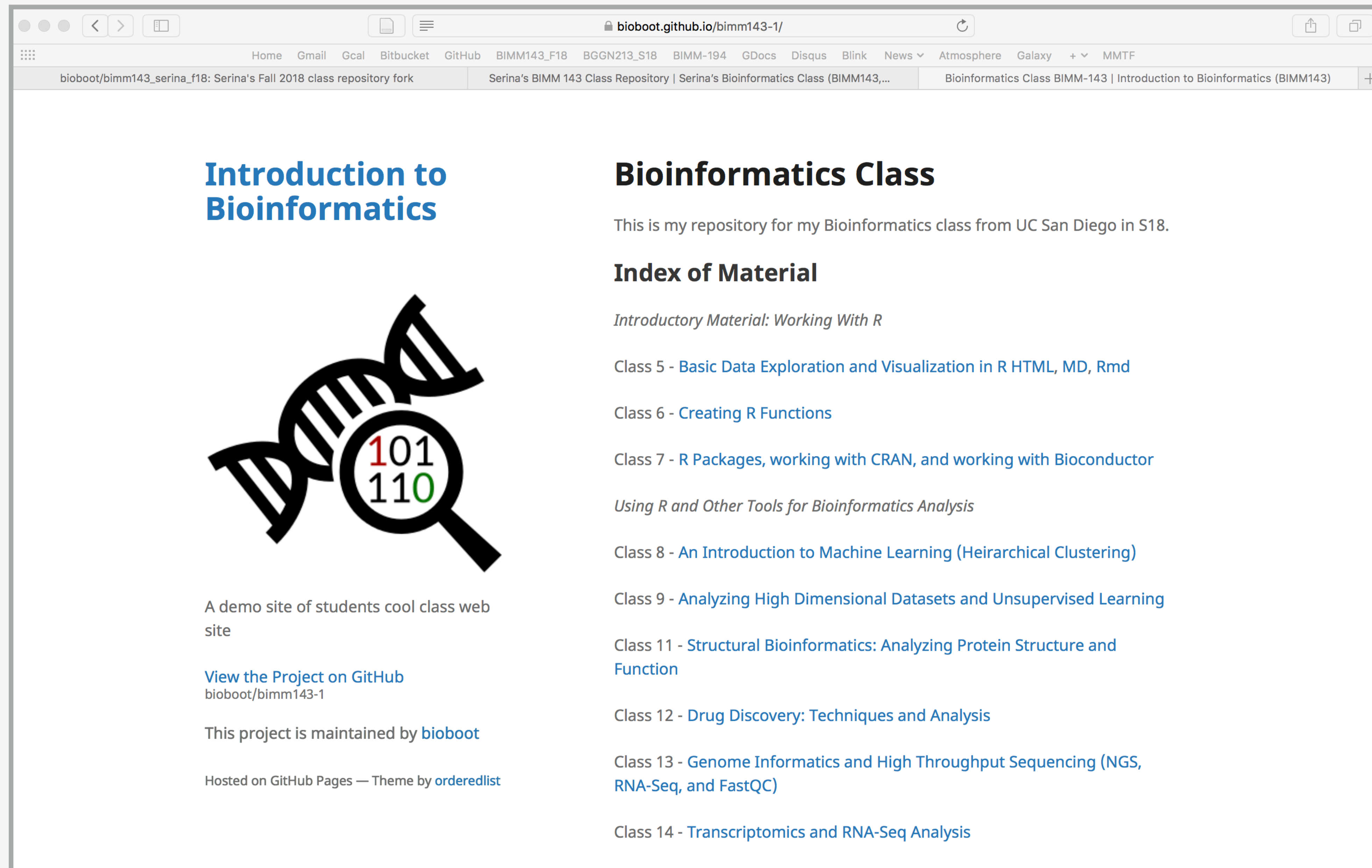
...and you're done!

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)



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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



A demo site of students cool class web site

[View the Project on GitHub](#)
bioboot/bimm143-1

This project is maintained by [bioboot](#)

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Bioinformatics Class

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Introductory Material: Working With R

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

bioboot / tmp_test

Unwatch 1 Star 0 Fork 0

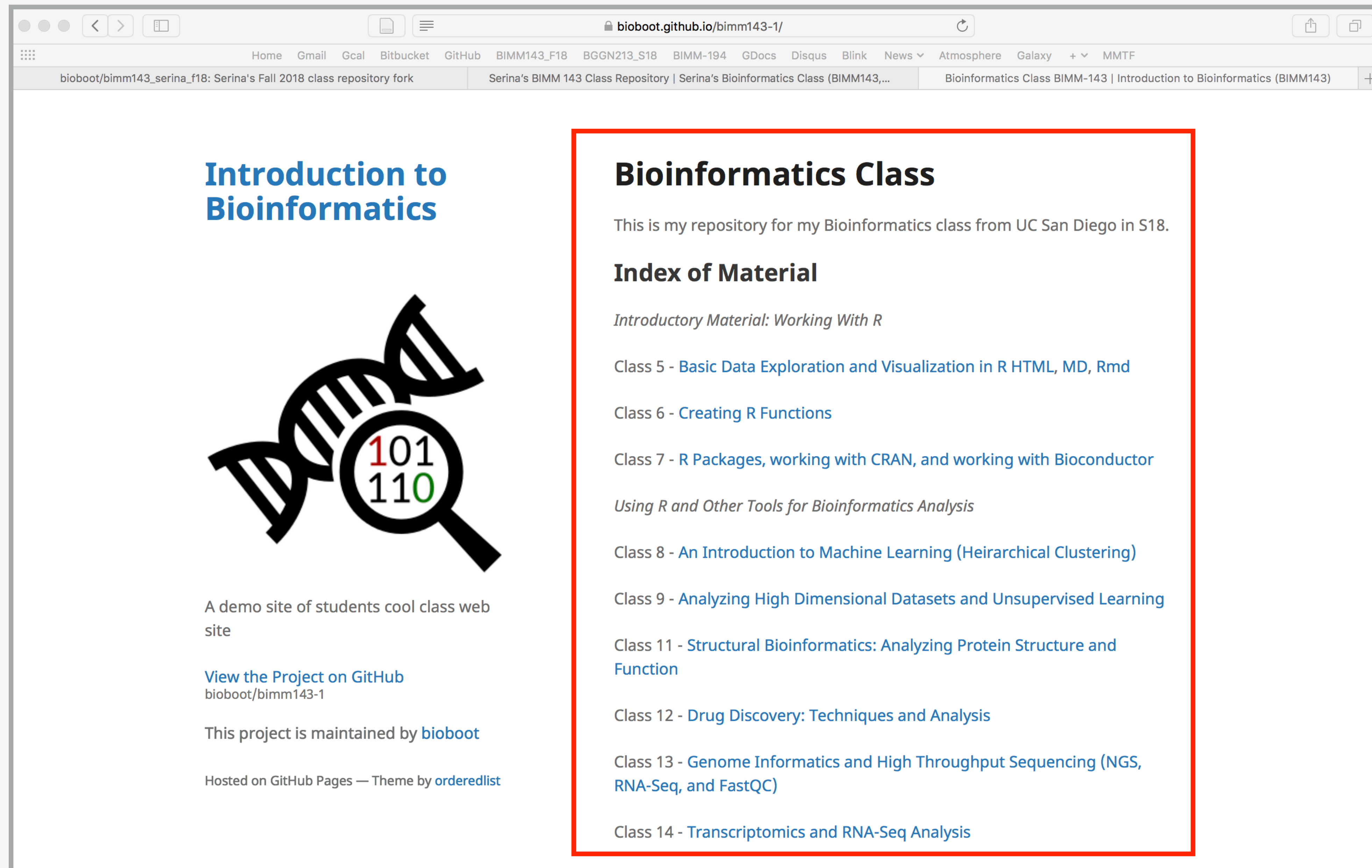
<> Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

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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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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It is important to the courses we offer in the future and how we teach them!

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 corner. A search bar contains the text "What would you like to learn t". Navigation links include "Learn", "Practice", "Projects", "Pricing", "My Classes", and 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 yellow "Enroll" button is positioned below the text.

To the right of the text is a square icon with a black background, featuring a white DNA double helix and a magnifying glass with the binary code "101110" inside it.

At the bottom of the main section, a horizontal list of tags includes: "R Language", "Shell", "Git", "Spreadsheets", "111 hours", and "26 Courses".

Below the main section, two white boxes are visible. The first box has a blue terminal icon at the top, followed by the title "Introduction to Shell for Data Science". Below the title, it says: "The Unix command line helps users combine existing programs in new ways, automate repetitive tasks, and run programs ...". The second box is titled "INSTRUCTORS" and lists two people: "Greg Wilson" (Co-founder of Software Carpentry) and "Jonathan Cornelissen".

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.

The future? Combining AI and Physics based approaches

Missing class!

AlphaFold Protein Structure Database

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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