



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_f21)
- 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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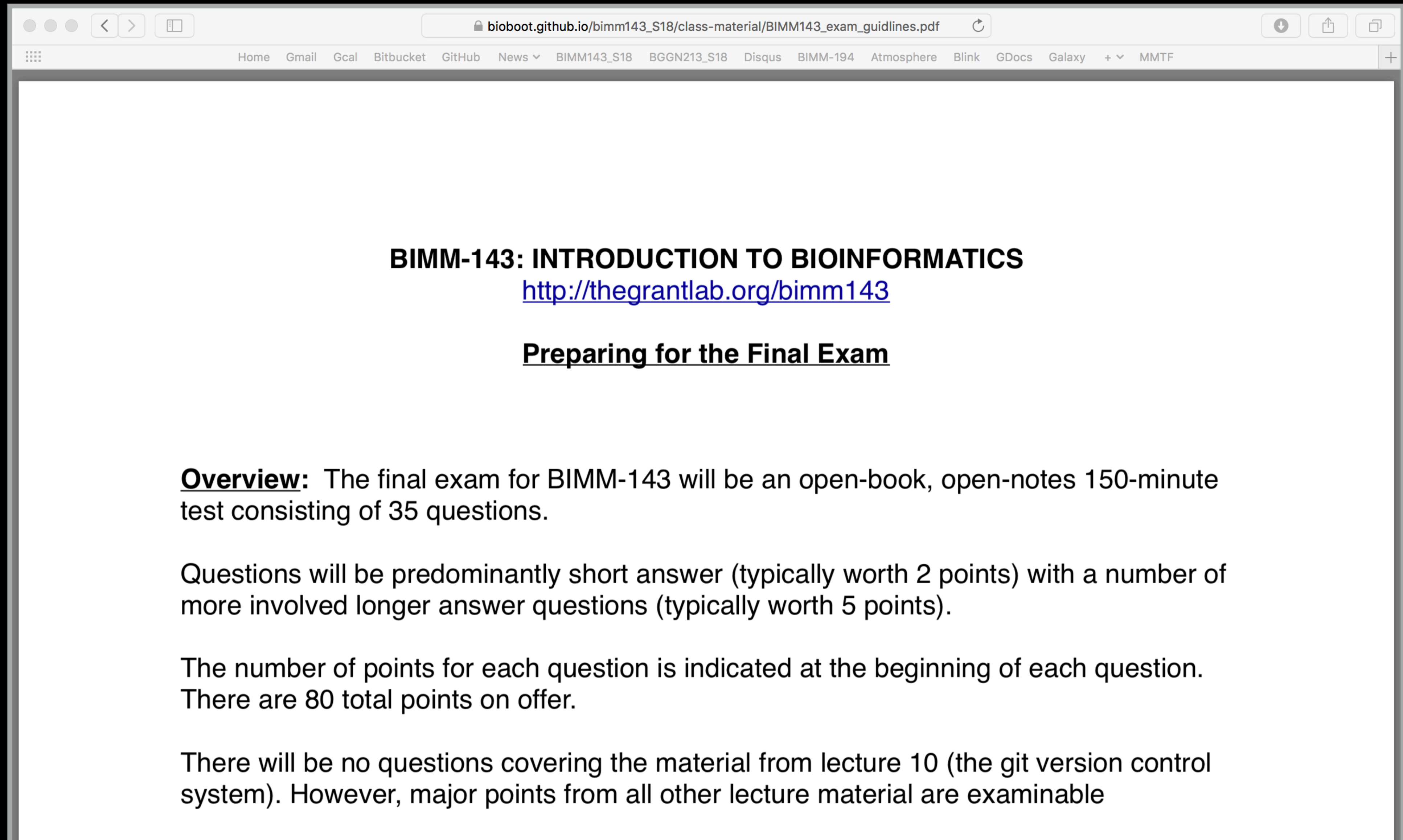


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https://bioboot.github.io/bimm143_F21/class-material/BIMM143_exam_guidelines.pdf



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 shows several open tabs: 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://board.net/p/bimm143_f21

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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bioboot.github.io/bimm143-1/

HomeGmailGcalBitbucketGitHubBIMM143_F18BGGN213_S18BIMM-194GDocsDisqusBlinkNewsAtmosphereGalaxy+MMTF

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Introduction to Bioinformatics (BIMM143)



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This is my repository for my Bioinformatics class from UC San Diego in S18.

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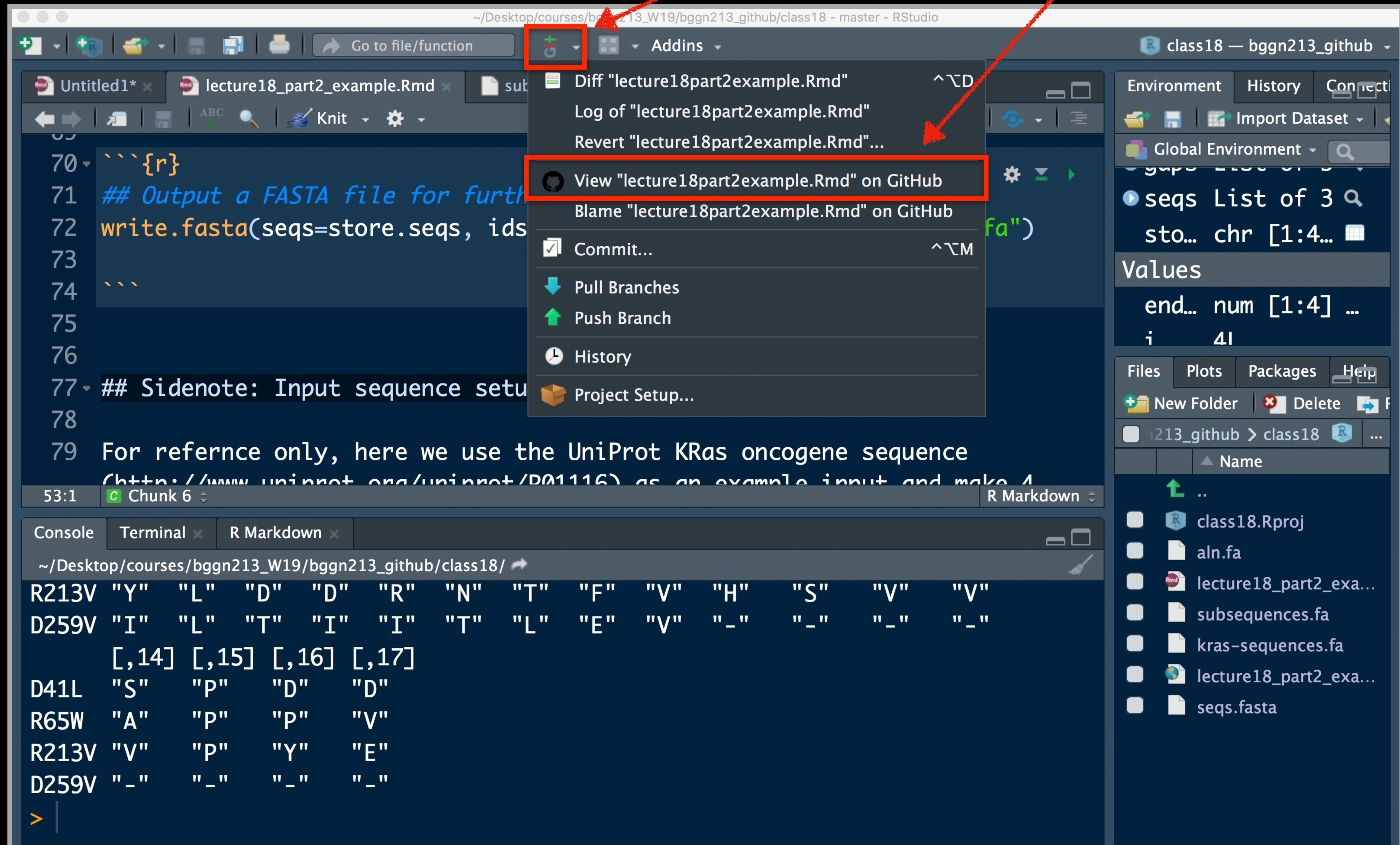
In your web browser navigate to your GitHub class repository < <https://github.com/> >

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 like 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`. It shows 1 watch, 0 stars, and 0 forks. The repository description is "My class repo for bimm143 at UCSD". It has 22 commits, 1 branch, 0 releases, and 1 contributor. The latest commit is by `bioboot` with the message "Add class18" 7 minutes ago. The repository contains two folders: `class05` (Add class 5, a month ago) and `class08` (add class08, a month ago).

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



The screenshot shows the RStudio interface with the Git menu open for the file "lecture18part2example.Rmd". The menu options are:

- 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... (^⌘M)
- Pull Branches
- Push Branch
- History
- Project Setup...

The background shows the R Markdown editor with the following content:

```
70 ```{r}
71 ## Output a FASTA file for further analysis
72 write.fasta(seqs=store.seqs, ids=store.ids)
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 make 4
```

The console output shows the following sequence data:

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

The file explorer on the right shows the following files:

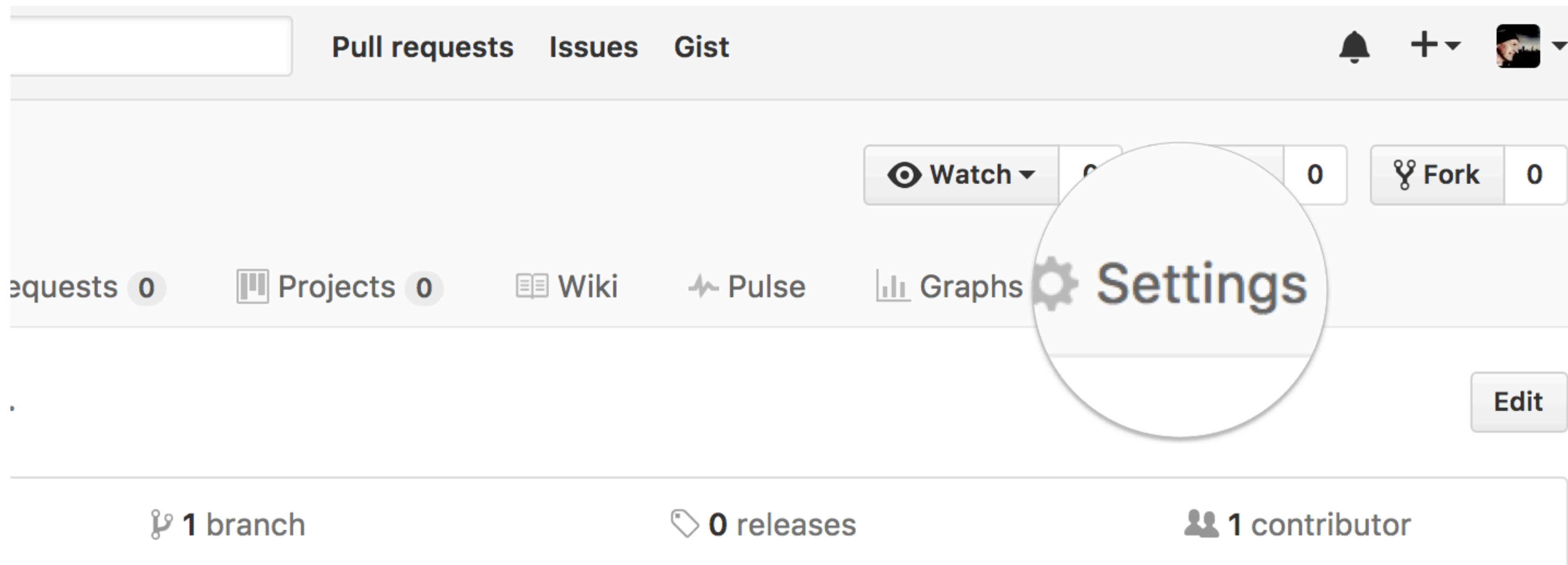
- class18.Rproj
- aln.fa
- lecture18_part2_example.Rmd
- subsequences.fa
- kras-sequences.fa
- lecture18_part2_example.Rmd
- seqs.fasta

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 “main 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

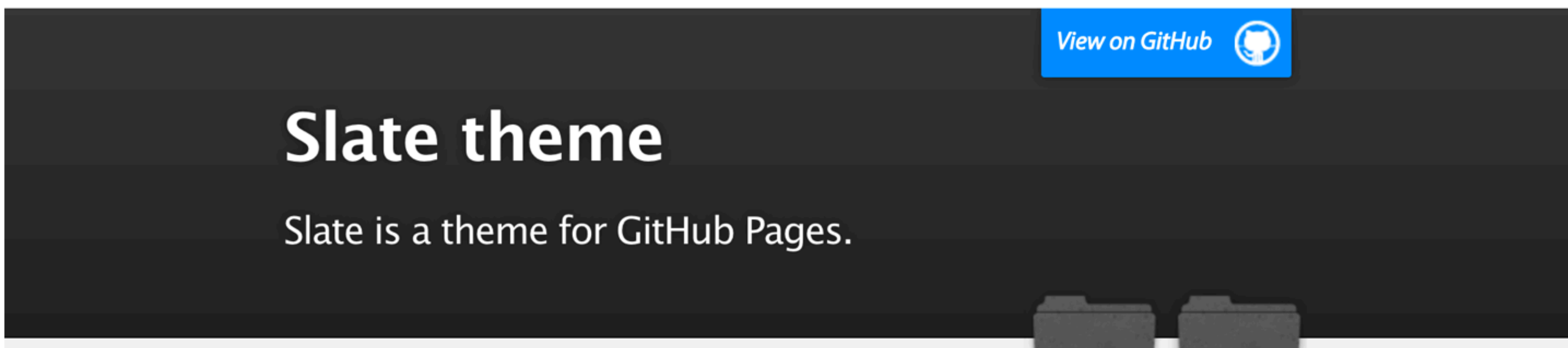
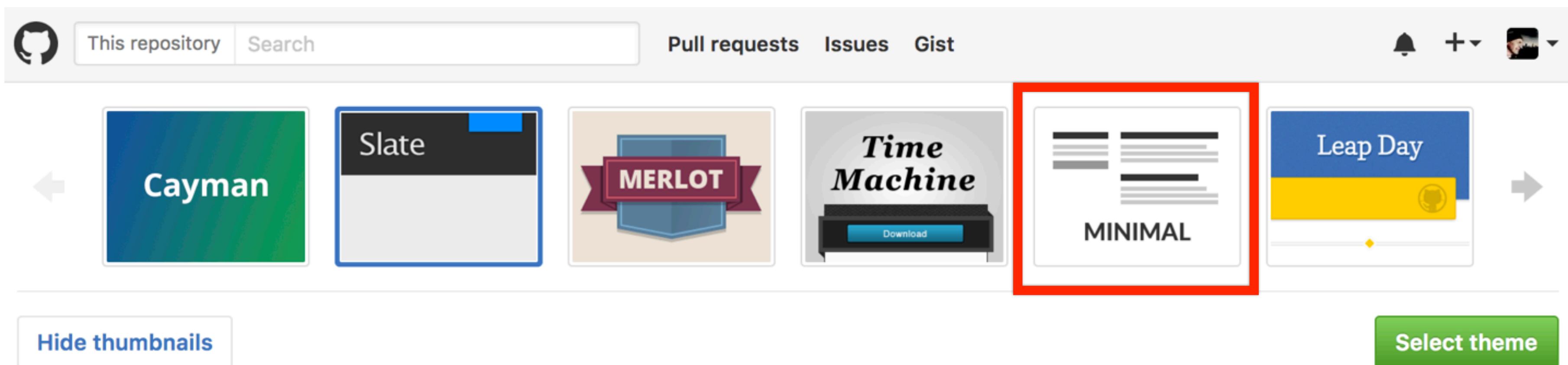
Select a theme to build your site with a Jekyll theme using the `master branch`. [Learn more.](#)

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 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 has tabs for 'Edit file' and 'Preview changes', with 'Edit file' being active. The code is displayed in a monospaced font with syntax highlighting. The content of the README.md file 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/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

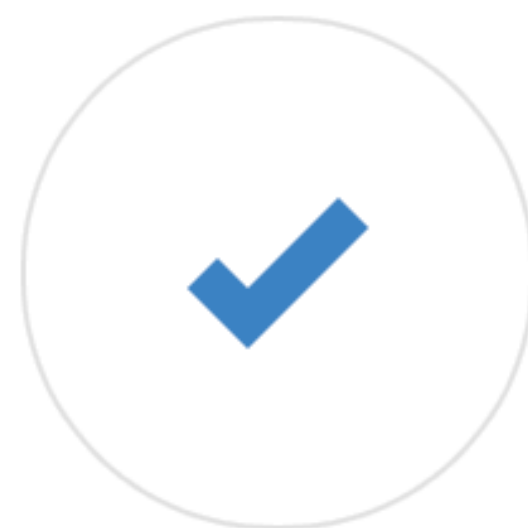
Add content to new pages site|

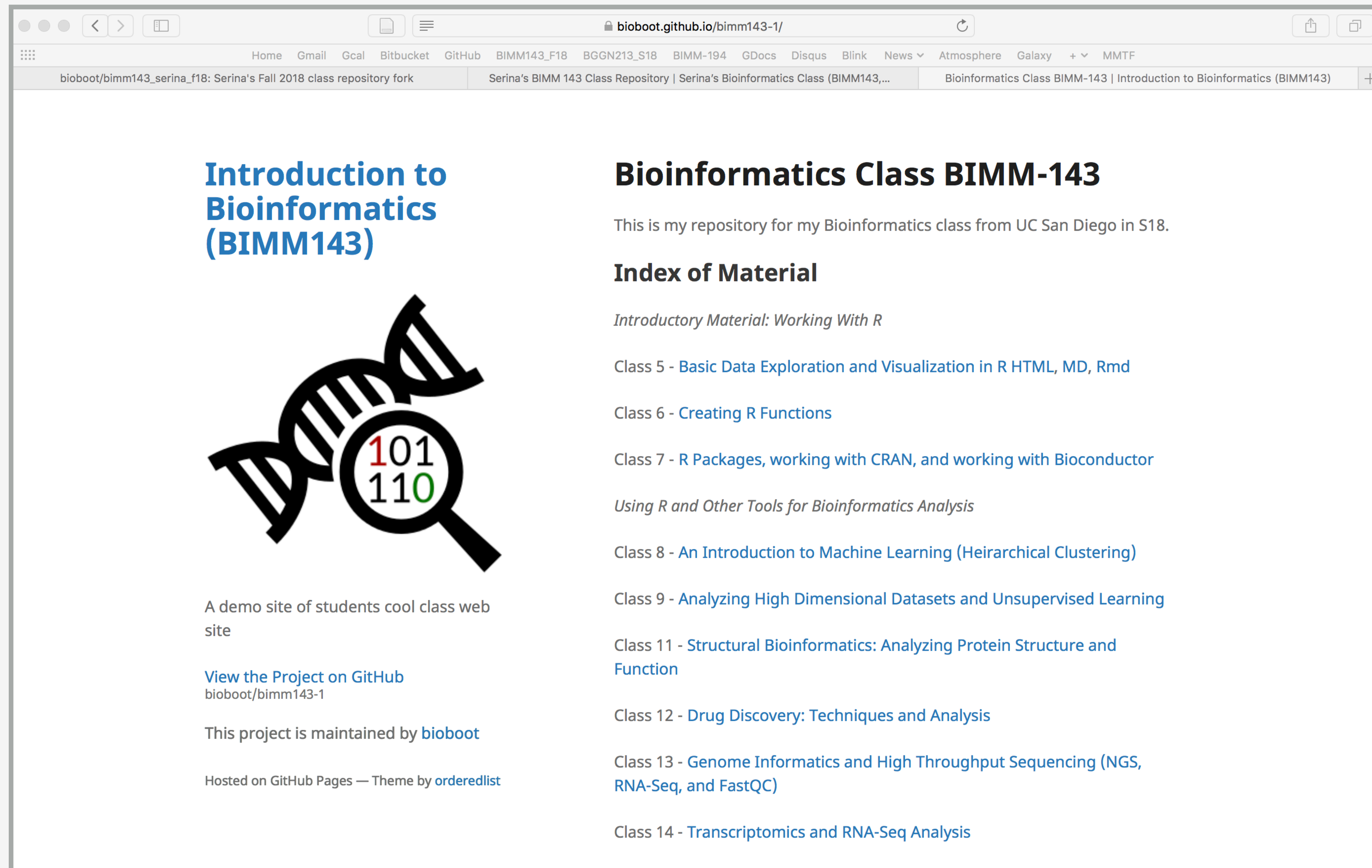
Add an optional extended description...

☒ 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)

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

Unwatch ▾1

★ Star0

🍴 Fork1

<> Code

🔗 Pull requests0

📁 Projects0


📖 Wiki

📊 Insights

⚙️ Settings

Branch: master ▾ **bimm143_serina_f18** / **_config.yml**

Find fileCopy path

 **bioboot** Update _config.yml3b72493 just now

1 contributor

4 lines (3 sloc) | 151 Bytes

RawBlameHistory🖨️✎️🗑️

```
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)
```


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bioboot.github.io/bimm143-1/

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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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bioboot.github.io/bimm143-1/

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

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this Friday and receive another 5pts credit!**

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 with ">_" and the title "Introduction to Shell for Data Science". The second box is titled "INSTRUCTORS" and lists two people: "Greg Wilson" (Co-founder of Software Carpentry) and "Jonathan Cornelissen".

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