



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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- Summary of major learning goals,
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- Project troubleshooting
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https://bioboot.github.io/bggn213_F22/class-material/BGGN213_exam_guidlines.pdf

The screenshot shows a web browser window with the URL https://bioboot.github.io/bggn213_F21/class-material/BGGN213_exam_guidlines.pdf in the address bar. The page content is as follows:

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/bggn213_f22

Form Version: <https://tinyurl.com/bggn213-summary>

Thank you very much!

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

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

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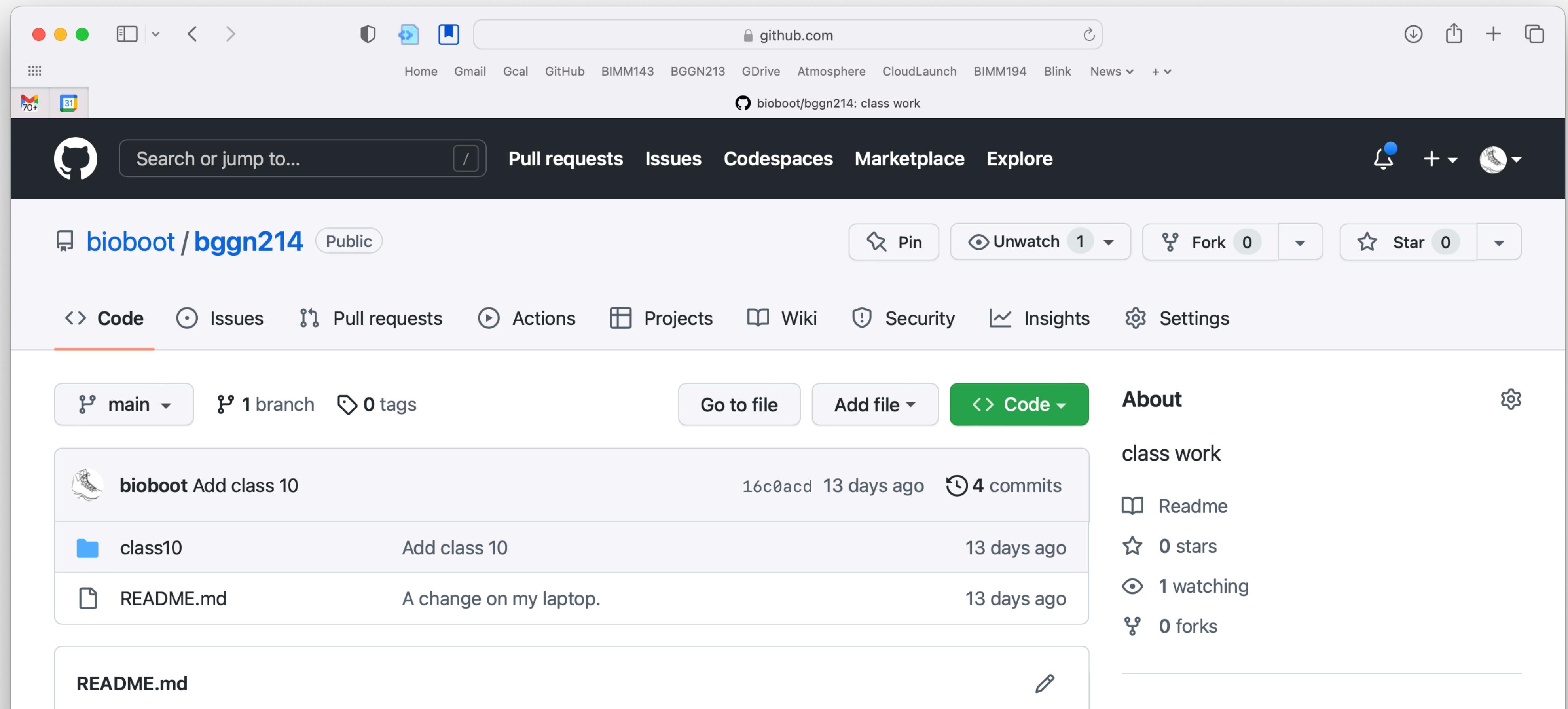
Class 14 - [Transcriptomics and RNA-Seq Analysis](#)

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

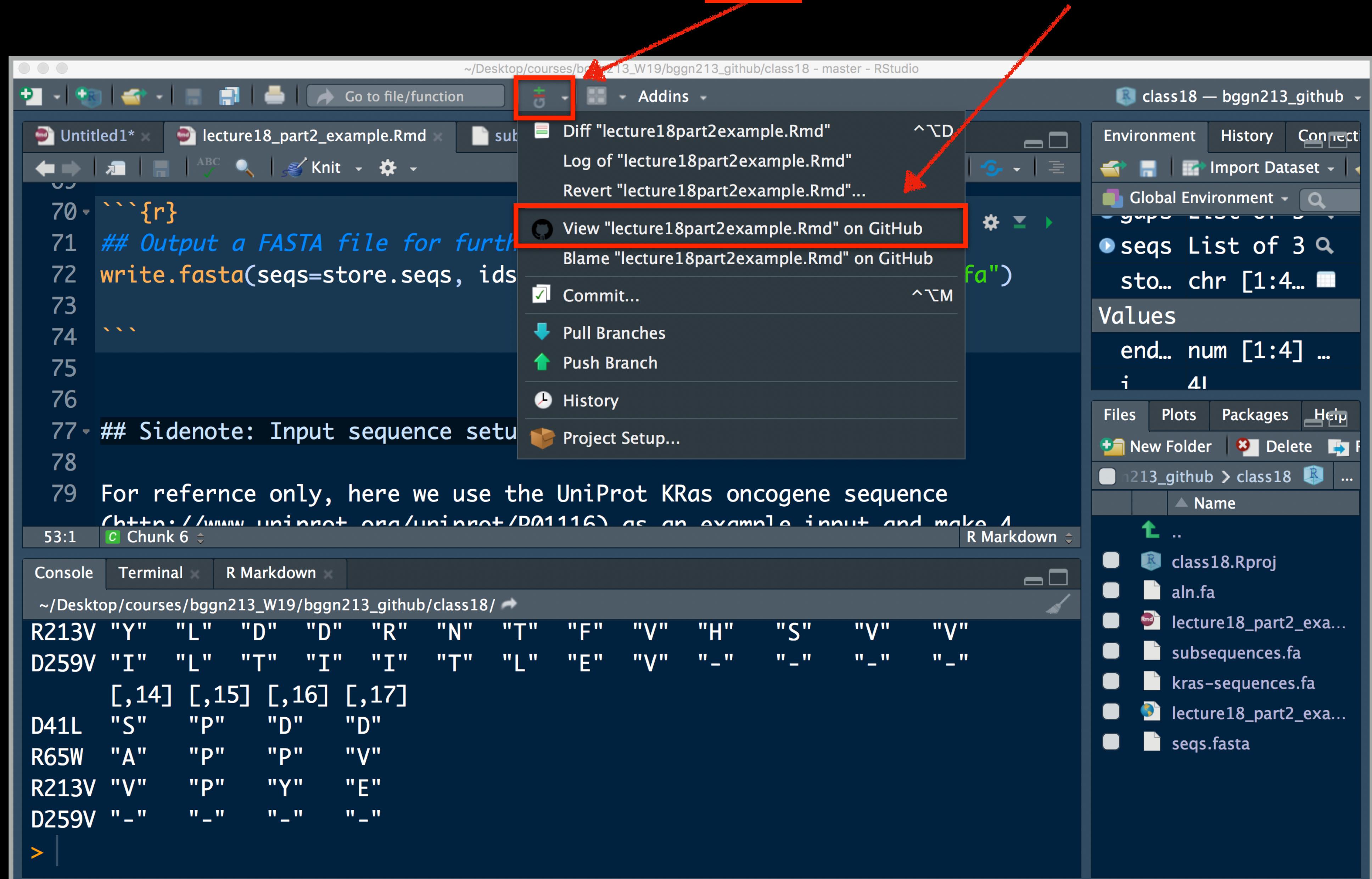
Side-note:

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



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

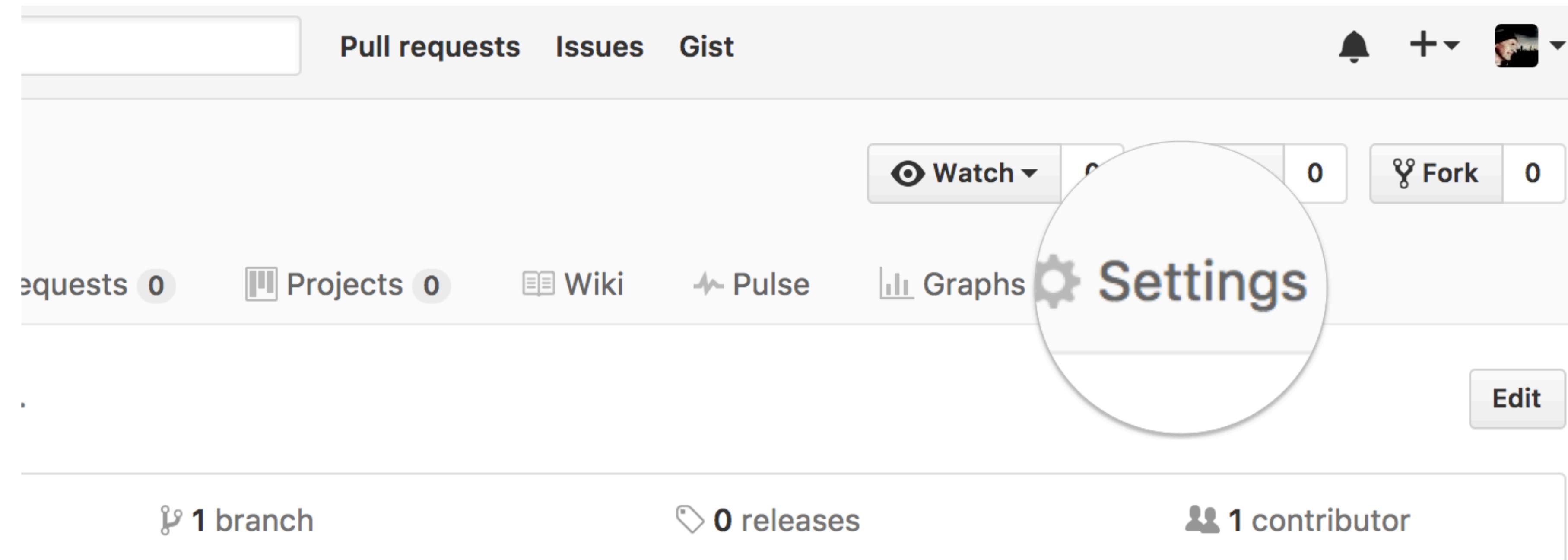


1

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 “main branch”

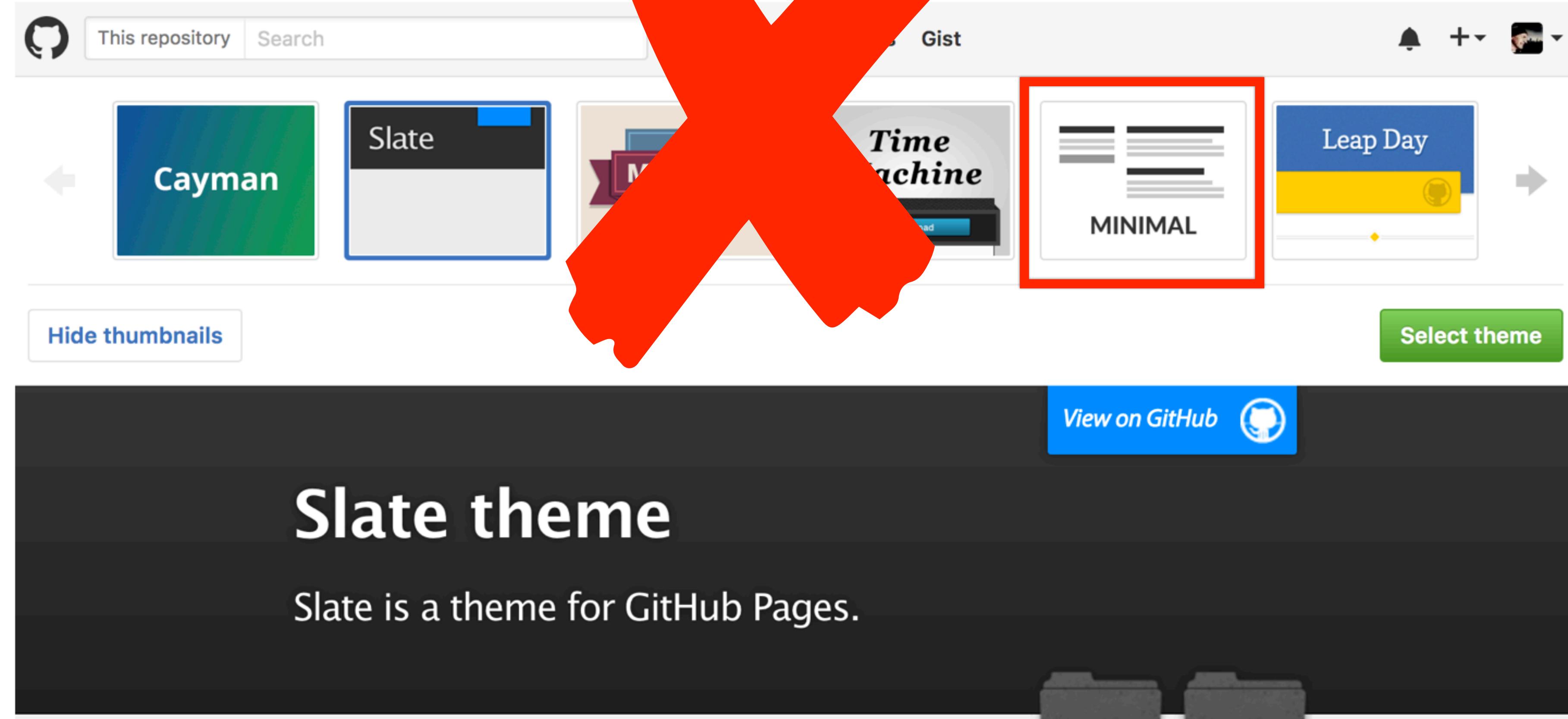
The screenshot shows the GitHub repository settings page for a repository named "luisabreu/Portfolio". The left sidebar lists various settings categories: General, Access, Collaborators, Moderation options, Code and automation, Branches, Tags, Actions, Webhooks, Environments, Codespaces, and Pages. The "Pages" option is highlighted with a red box. The main content area is titled "GitHub Pages" and contains the following information:

- GitHub Pages**: A brief description stating "GitHub Pages is designed to host your personal, organization, or project pages from a GitHub repository."
- Build and deployment**: A section under "Code and automation" with a "Source" dropdown menu set to "Deploy from a branch".
- Branch**: A note stating "GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository." with a "Learn more" link.
- Source selection buttons**: Buttons for "main" (with a red box around it), "/ (root)", and "Save".
- Private publishing option**: A callout box with an icon showing a document and lock, stating "Publish privately to people with read access to this repository" and "Try risk-free for 30 days using a GitHub Enterprise organization, or learn more about changing the visibility of your GitHub Pages site." with a close button.

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 repository interface 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 bar 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

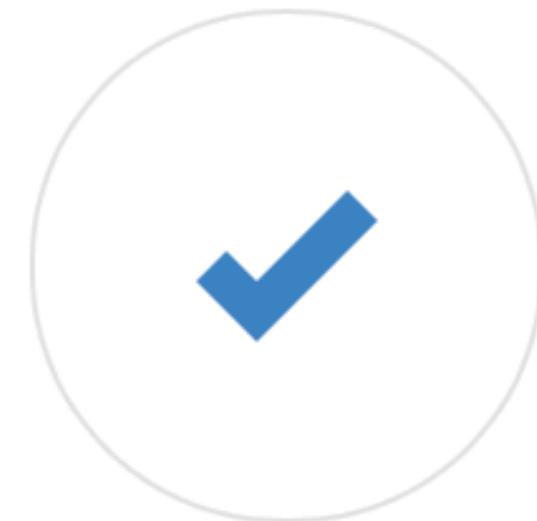
Add an optional extended description...

Commit directly to the `master` branch.

6

...and you're done!

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



The screenshot shows a web browser window with the URL bioboot.github.io/bimm143-1/ in the address bar. The page content is as follows:

Introduction to Bioinformatics



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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) forked Serina's Repo, (2) Chose the “minimal” theme, (3) Edited `_config.yml` (adding logo and title)

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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

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bioboot/bimm143_serina_f18: Serina's Fall 2018 class repository fork

bioboot.github.io/bimm143-1/

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

Serina's BIMM 143 Class Repository | Serina's Bioinformatics Class (BIMM143,...)

Bioinformatics Class BIMM-143 | Introduction to Bioinformatics (BIMM143)

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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 is a code editor for 'README.md' with the following content:

```
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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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 for the DataCamp website (www.datacamp.com/tracks/custom-bioinformatics-extension). The page title is "CUSTOM TRACK Bioinformatics Extension". The main content area describes Barry's suggested DataCamp courses for delving deeper into R, Git, the Shell, data visualization, and Bioinformatics data analysis generally. It includes a yellow "Enroll" button, a DNA helix icon with a magnifying glass over binary code (101 110), and a summary of 111 hours and 26 Courses across R Language, Shell, Git, and Spreadsheets.

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**

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!

The screenshot shows the homepage of the AlphaFold Protein Structure Database. At the top, there is a dark grey header with the EMBL-EBI logo and links for Services, Research, Training, About us, and a green EMBL-EBI logo. Below this is a blue header with the text "AlphaFold Protein Structure Database" on the left and "Home", "About", "FAQs", and "Downloads" on the right. The main title "AlphaFold Protein Structure Database" is prominently displayed in large white text against a blue background featuring a faint protein structure model. Below the title, it says "Developed by DeepMind and EMBL-EBI". A search bar at the bottom left contains the placeholder "Search for protein, gene, UniProt accession or organism" and includes a "BETA" button and a "Search" button. Below the search bar, there is a row of example queries: "Free fatty acid receptor 2", "At1g58602", "Q5VSL9", "E. coli", and "Help: AlphaFold DB search help". At the bottom of the page, a light blue footer bar contains the text "AlphaFold DB provides open access to protein structure".

Option: New lecture on AlphaFold or project trouble shooting