



# BIMM 143

## Course Summary & GitHub Portfolio

Class 19

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\\_f22](https://board.net/p/bimm143_f22) )
- 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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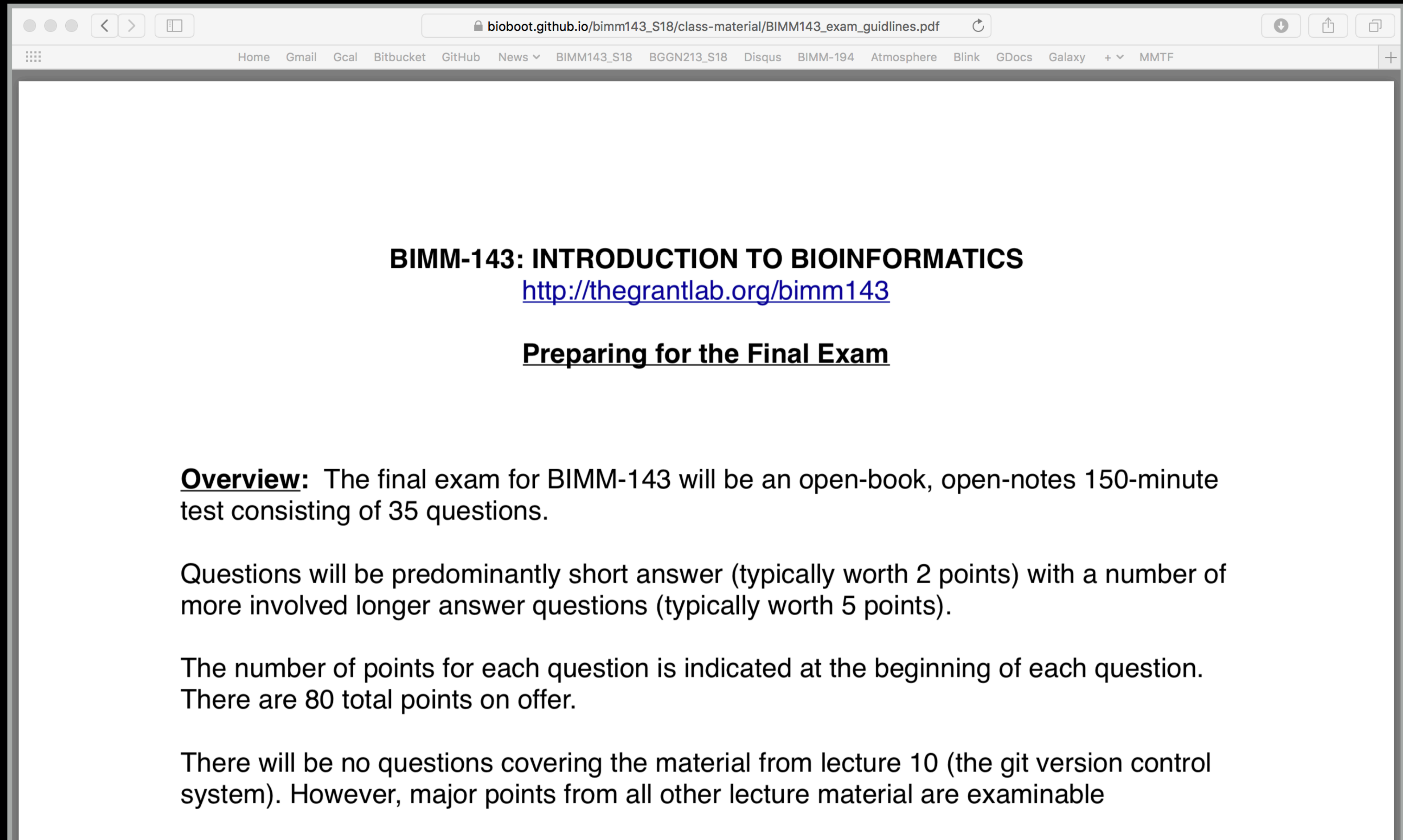
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- Summary of major learning goals,
- Course discussion and feedback ( [https://board.net/p/bimm143\\_f21](https://board.net/p/bimm143_f21) )
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[https://bioboot.github.io/bimm143\\_F22/class-material/BIMM143\\_exam\\_guidelines.pdf](https://bioboot.github.io/bimm143_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](https://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\\_f22](https://board.net/p/bimm143_f22)

**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

# 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



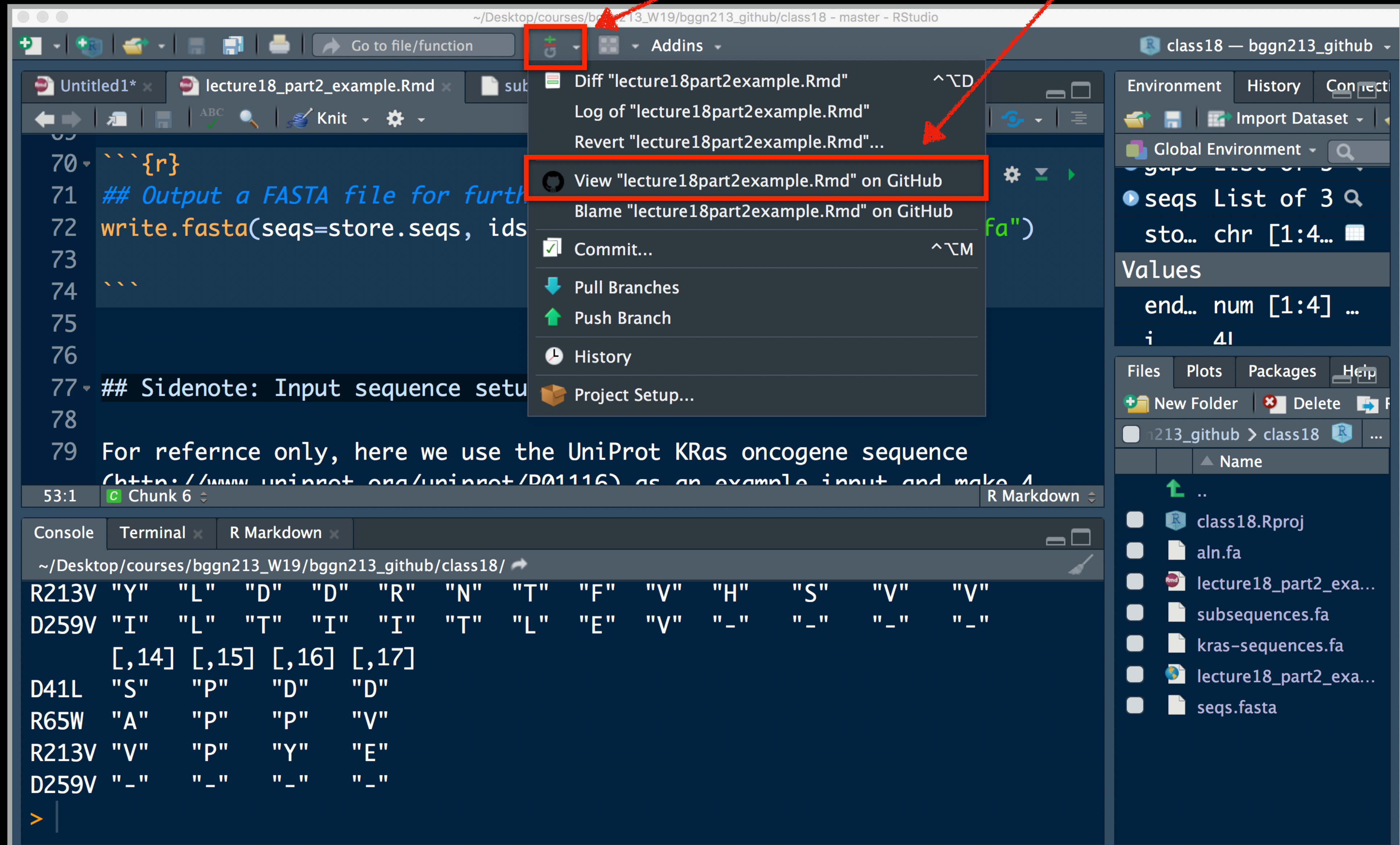
In your web browser navigate to your GitHub class repository < <https://github.com/> >

**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 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 a file named `lecture18_part2_example.Rmd` open in the editor. The Git icon (a green 'G' with a plus sign) in the top toolbar 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, which is also highlighted with a red box. The menu options include: Diff "lecture18part2example.Rmd", Log of "lecture18part2example.Rmd", Revert "lecture18part2example.Rmd...", View "lecture18part2example.Rmd" on GitHub, Blame "lecture18part2example.Rmd" on GitHub, Commit..., Pull Branches, Push Branch, History, and Project Setup... The editor shows R Markdown code with a chunk of R code and a text block. The console at the bottom displays 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 [C] Chunk 6
70 ````{r}
71 ## Output a FASTA file for further analysis
72 write.fasta(seqs=store.seqs, ids=store.ids, file="aln.fa")
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
81 sub-sequences of length 14, 15, 16, and 17.

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

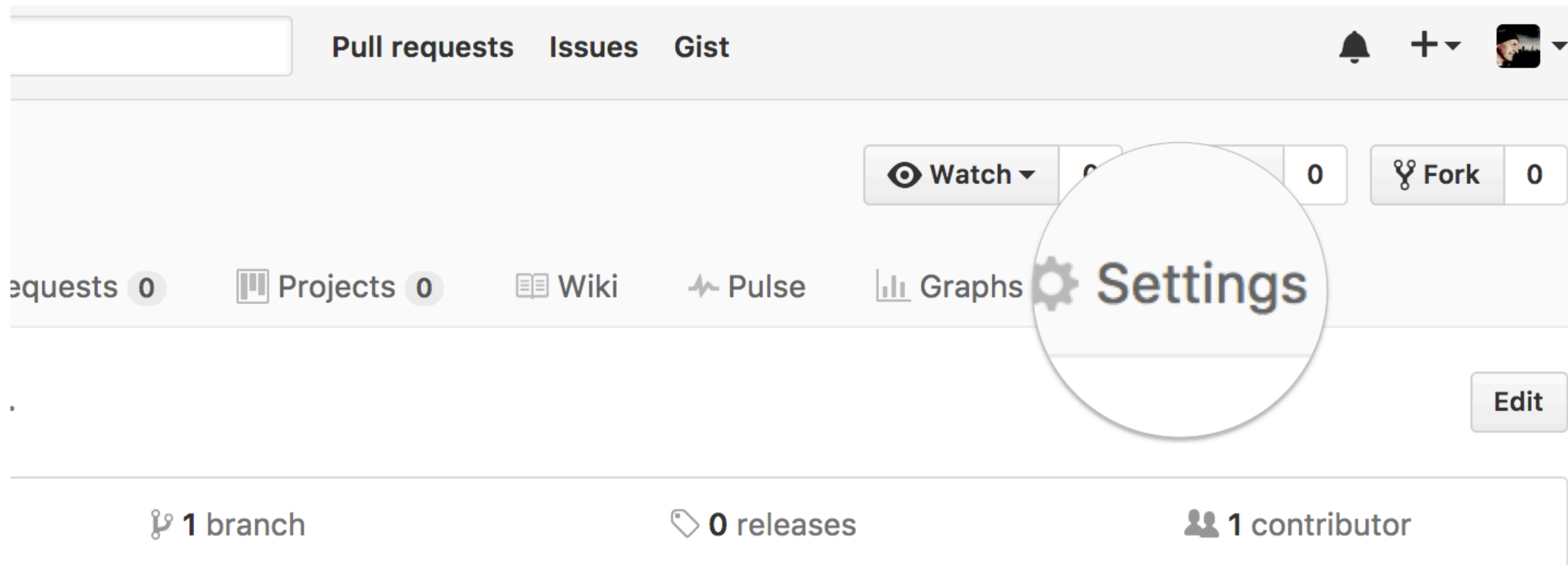


1

# 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



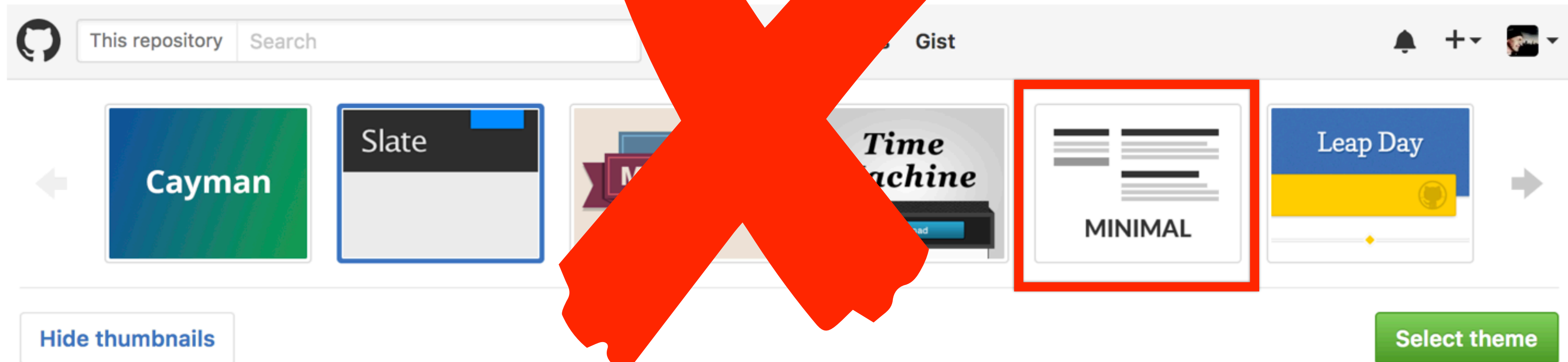
**Publish privately to people with read access to this repository**

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/](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

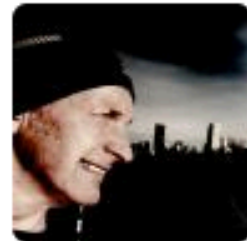
The screenshot shows the GitHub interface for the repository 'jldec / new-pages-site'. At the top, there are buttons for 'Watch' (0), 'Star' (0), and 'Fork' (0). Below these are tabs for 'Code', 'Issues' (0), 'Pull requests' (0), 'Projects' (0), 'Wiki', 'Pulse', 'Graphs', and 'Settings'. The 'Code' tab 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 line numbers on the left. The content of the README.md file is as follows:

```
1  ## Welcome to GitHub Pages
2
3  You can use the \[editor on GitHub\] to maintain and preview the content
4  for your website in Markdown files.
5
6  Whenever you commit to this repository, GitHub Pages will run \[Jekyll\] to rebuild the pages in your site, from
7  the content in your Markdown files.
8
9  ### Markdown
10
11  Markdown is a lightweight and easy-to-use syntax for styling your writing. It includes conventions for
12  ````markdown
13  Syntax highlighted code block
14
15  # 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|

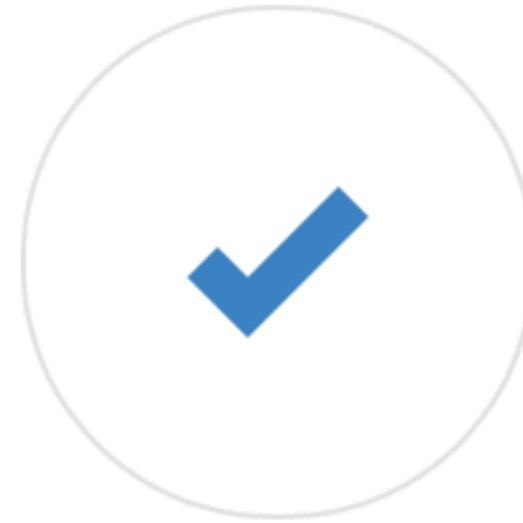
Add an optional extended description...

☒ Commit directly to the `master` branch.



...and you're done!

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



◂◃

📄

☰

bioboot.github.io/bimm143-1/

↺


📄

📄

HomeGmailGcalBitbucketGitHubBIMM143\_F18BGGN213\_S18BIMM-194GDocDisqusBlinkNewsAtmosphereGalaxy+MMTF

bioboot/bimm143\_serina\_f18: Serina's Fall 2018 class repository forkSerina's BIMM 143 Class Repository | Serina's Bioinformatics Class (BIMM143,...Bioinformatics Class BIMM-143 | Introduction to Bioinformatics (BIMM143)

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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)

 **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)
```

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)

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bioboot / tmp\_test

Unwatch 1 Star 0 Fork 0

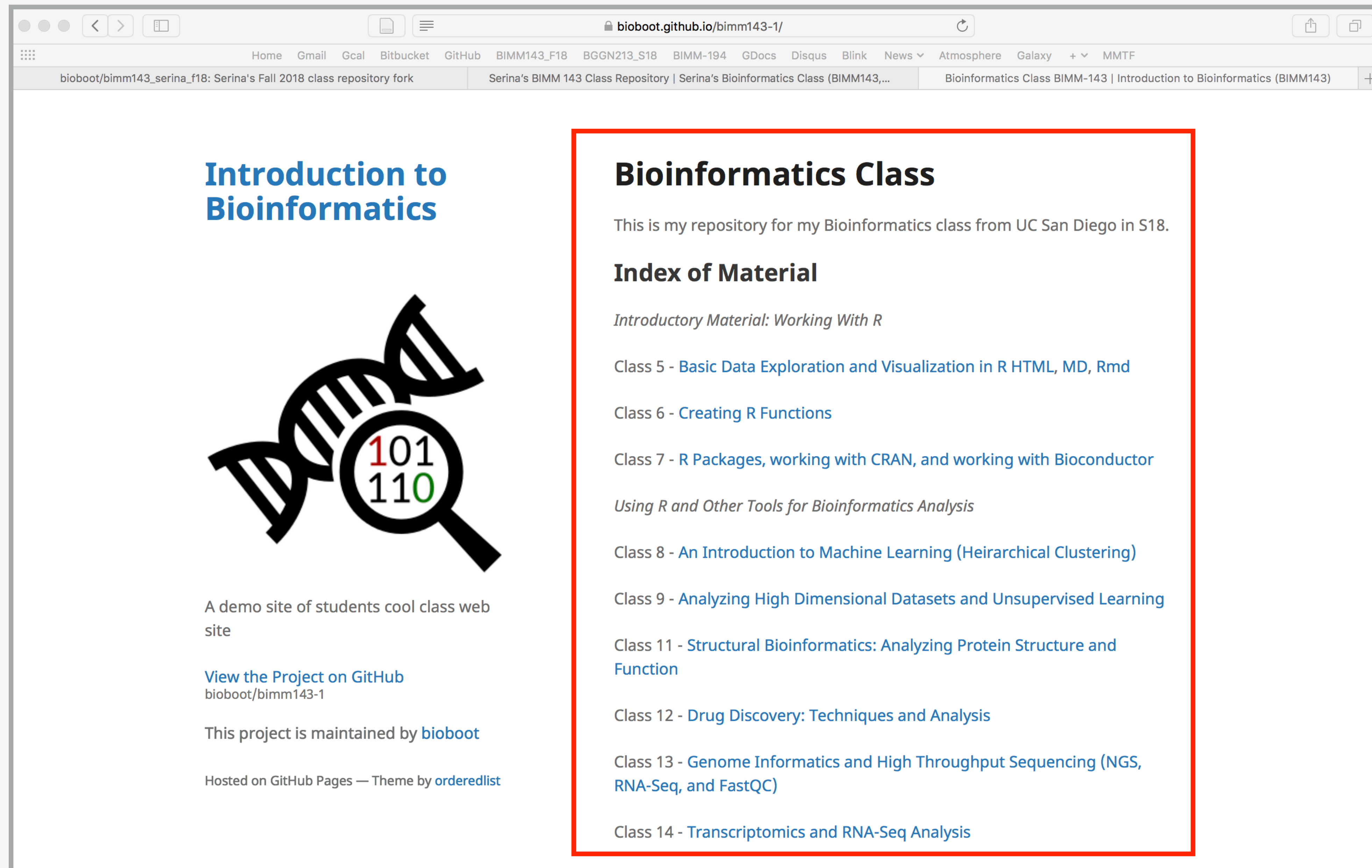
<> Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

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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# 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](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 website has 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 section 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 yellow "Enroll" button is positioned to the left of a square graphic on the right. The graphic depicts a DNA double helix with a magnifying glass over it, containing the binary code "101" and "110".

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 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!

EMBL-EBI

Services

Research

Training

About us

EMBL-EBI

AlphaFold Protein Structure Database

HomeAboutFAQsDownloads

# 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