



BGGN 213

Course Summary & Exam Preparation

Lecture 19

Barry Grant

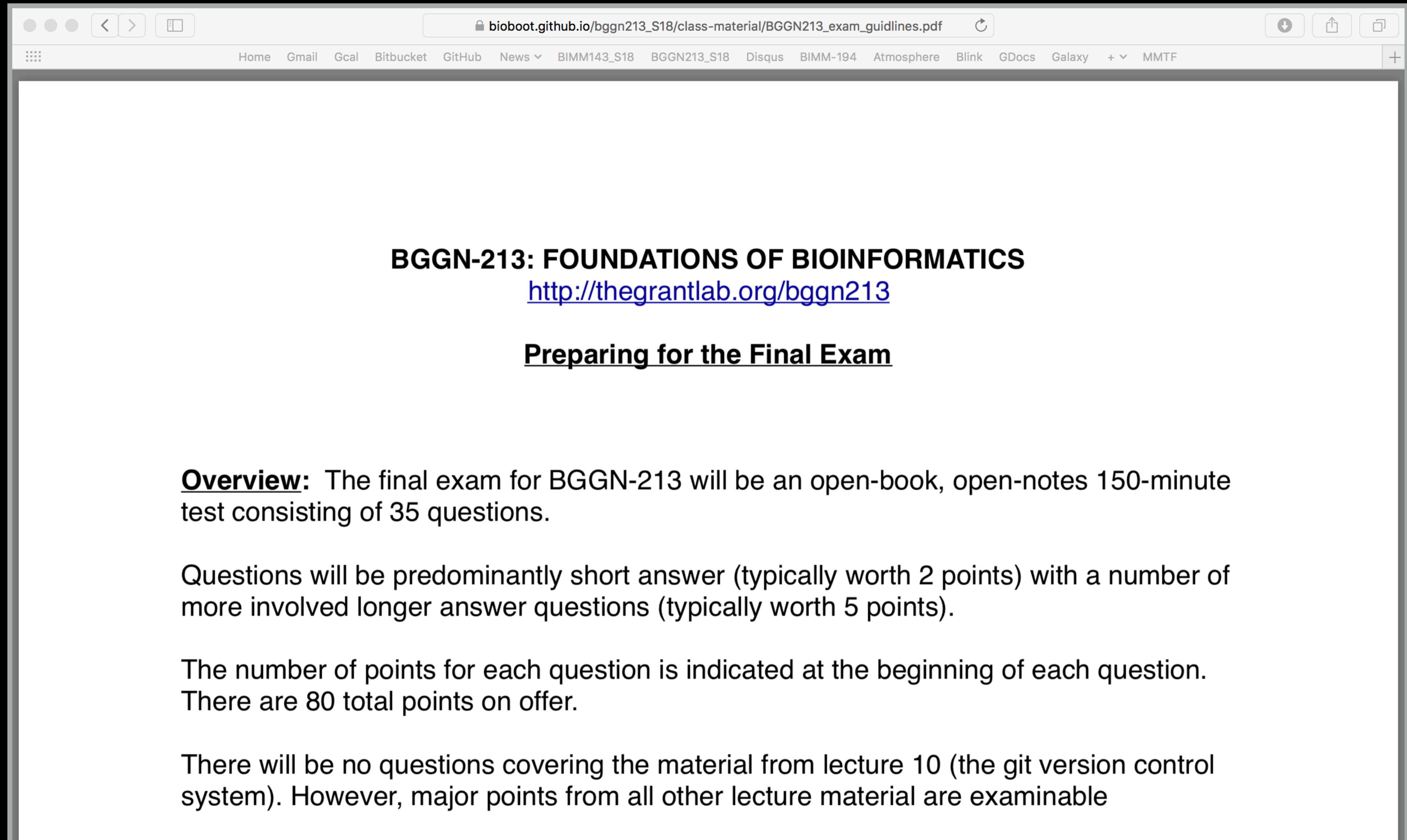
UC San Diego

<http://thegrantlab.org/bggn213>

Today's Menu

- Summary of major learning goals,
- Course discussion and feedback (https://etherpad.net/p/bgggn213_s19)
- CAPs evaluation incentives (<https://cape.ucsd.edu/students>)
- 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

https://bioboot.github.io/bggn213_W19/class-material/BGGN213_exam_guidelines.pdf



The image is a screenshot of a web browser window. The address bar shows the URL: bioboot.github.io/bggn213_S18/class-material/BGGN213_exam_guidelines.pdf. The browser's tab bar contains several 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:

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

- 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 in the future?
- 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://etherpad.net/p/bgggn213_s19


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

Thank you very much!

GitHub Spit & Polish

https://bioboot.github.io/bggn213/

Foundations of Bioinformatics Class S18



A demo site of students cool class work portfolio

[View the Project on GitHub](#)
bioboot/bggn213

BGGN213

This is my classwork from BGGN213 at UC San Diego (S18). The main class homepage is [here](#)

- **Class05:** [Data Visualization in R](#) (for other self contained formats see [HTML](#), [MD](#) and [R](#)).
- [Class06: Why, when and how of writing your own R functions](#)
- [Class07: Bioinformatics R packages from CRAN and BioConductor](#)
- **Class08:** [Machine Learning for Bioinformatics 1](#)
- **Class09:** [Machine learning project](#)
- Etc.

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

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

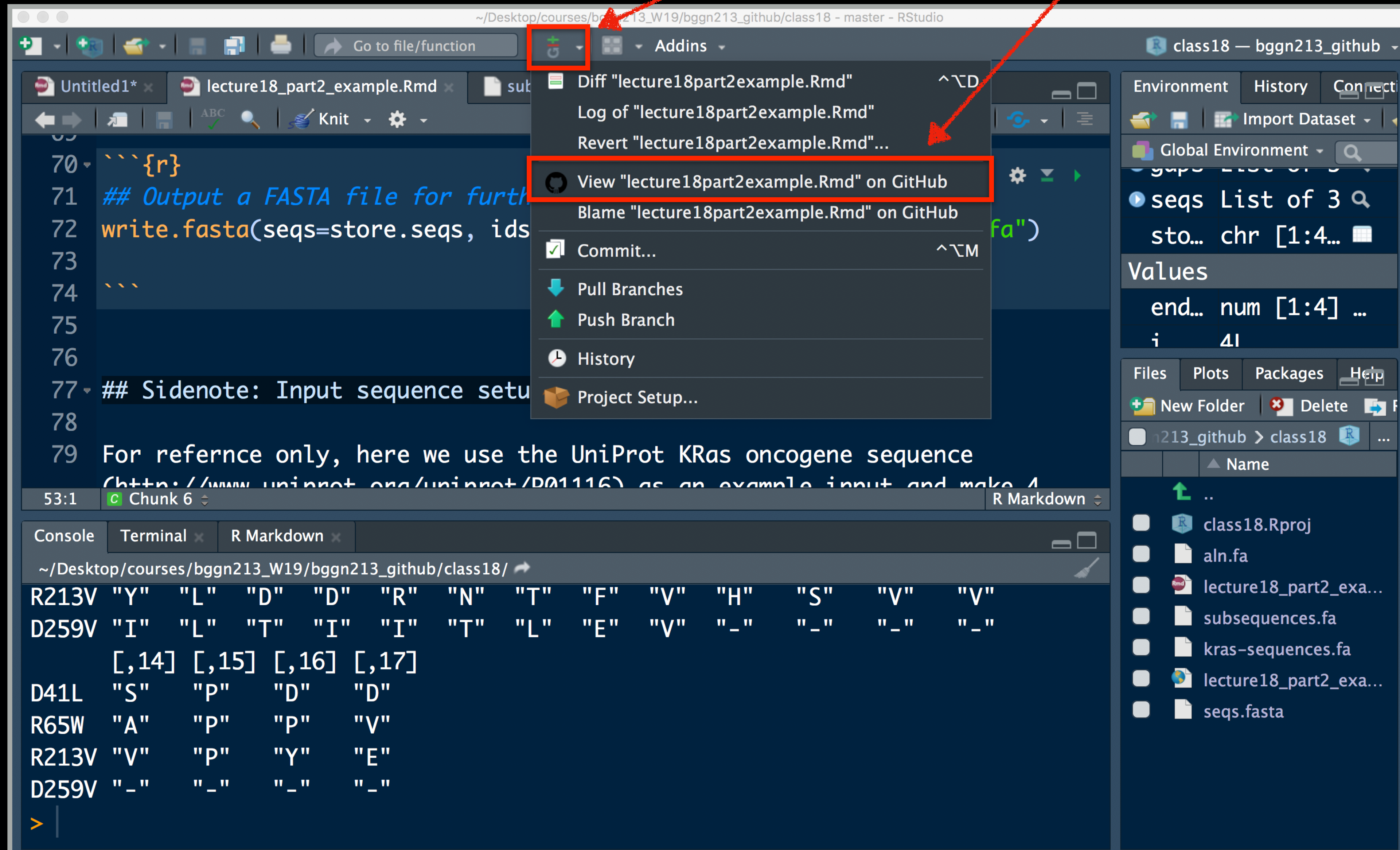
Side-note:

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 current branch is **master**. There are buttons for "New pull request", "Create new file", "Upload files", "Find file", and "Clone or download". The commit history shows a recent commit by **bioboot** titled "Add class18" and two folders: **class05** (Add class 5) and **class08** (add class08).

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



The screenshot shows the RStudio interface with a context menu open for the file 'lecture18part2example.Rmd'. The menu is located in the top right area of the editor. The 'GIT' icon in the top toolbar is highlighted with a red box. A red arrow points from the 'GIT' icon to the 'View "lecture18part2example.Rmd" on GitHub' option in the menu, which is also highlighted with a red box. Another red arrow points from the text 'VIEW on GITHUB' in the top instruction to the same menu option. The background shows the R Markdown editor with code for writing a FASTA file and a console window displaying sequence data.

```
70  ````{r}
71  ## Output a FASTA file for further analysis
72  write.fasta(seqs=store.seqs, ids=seqs$names)
73  ````
74
75
76
77  ## Sidenote: Input sequence setup
78
79  For refernce only, here we use the UniProt KRas oncogene sequence
  (http://www.uniprot.org/uniprot/P01116) as an example input and make 4
  sub-sequences of length 14, 15, 16, and 17.

53:1  Chunk 6  R Markdown
```

```
~/Desktop/courses/bgg213_W19/bgg213_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 "_" "_" "_" "_"
>
```

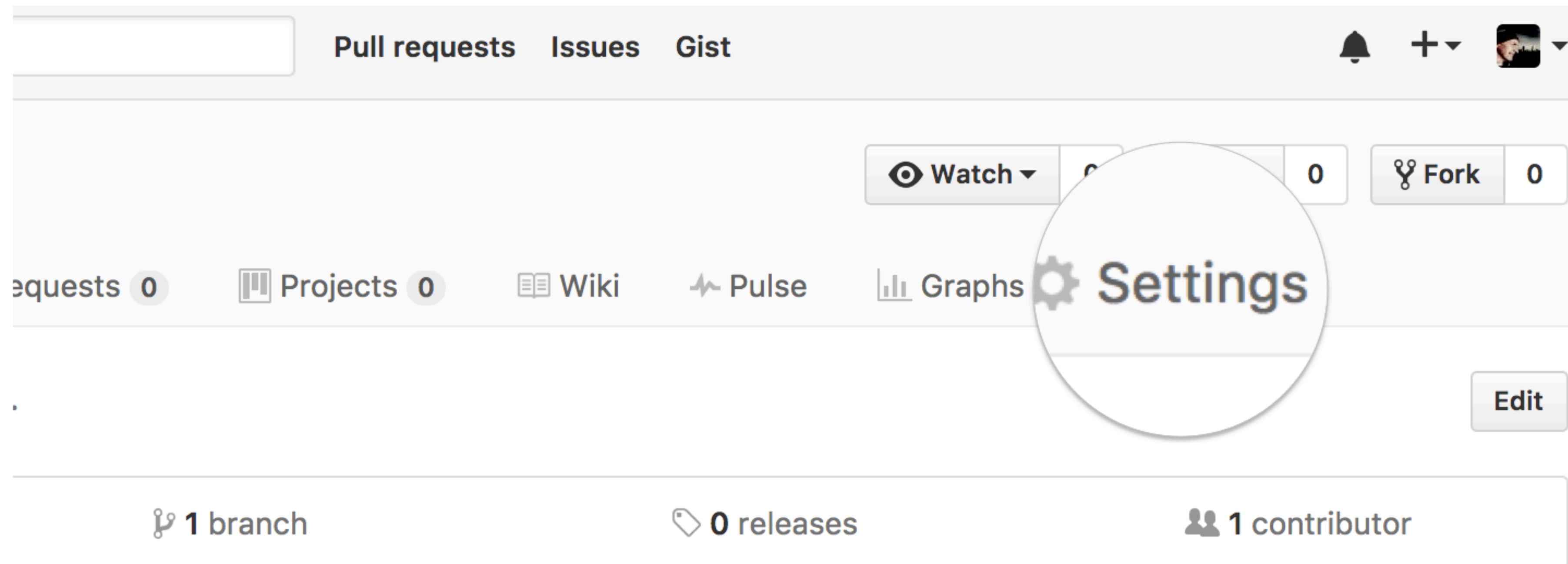
Environment History Connect
Global Environment
seqs List of 3
sto... chr [1:4...
Values
end... num [1:4] ...
i 41
Files Plots Packages Help
New Folder Delete
213_github > class18
Name
..
class18.Rproj
aln.fa
lecture18_part2_exa...
subsequences.fa
kras-sequences.fa
lecture18_part2_exa...
seqs.fasta

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**.

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.

The screenshot shows the GitHub theme selection interface. At the top, there is a navigation bar with the GitHub logo, a search bar, and links for Pull requests, Issues, and Gist. Below this is a carousel of theme thumbnails. The themes shown are Cayman, Slate, MERLOT, Time Machine, MINIMAL (highlighted with a red box), and Leap Day. Below the carousel, there is a button labeled 'Hide thumbnails' and a green button labeled 'Select theme'.

Slate theme

Slate is a theme for GitHub Pages.

[View on GitHub](#)

Edit content

Use the **GitHub** online editor to add content.
In particular, add links to each classes .MD file

The screenshot shows the GitHub online editor interface for the repository `jldec / new-pages-site`. The repository has 0 Watchers, 0 Stars, and 0 Forks. The `Code` tab is selected, showing the `README.md` file. The editor is in `Edit file` mode, with a `Preview changes` tab also visible. The code content 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/gi  
     \(https://github.com/contact\) and we'll help you sort it out.  
38
```



Commit changes

Add content to new pages site|

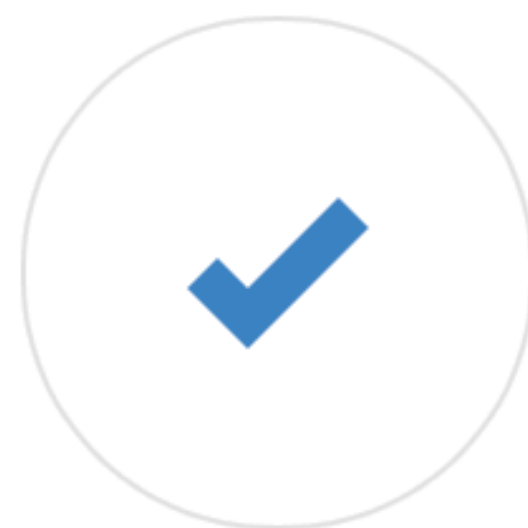
Add an optional extended description...

Commit directly to the `master` branch.

6


...and you're done!

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



<https://bioboot.github.io/bggn213/>

Foundations of Bioinformatics Class S18



A demo site of students cool class work portfolio

[View the Project on GitHub](#)
bioboot/bggn213

BGGN213

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- [Class06: Why, when and how of writing your own R functions](#)
- [Class07: Bioinformatics R packages from CRAN and BioConductor](#)
- **Class08:** [Machine Learning for Bioinformatics 1](#)
- **Class09:** [Machine learning project](#)
- Etc.

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

https://bioboot.github.io/tmp_test/

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

<https://bioboot.github.io/bggn213/>

Foundations of Bioinformatics Class S18



A demo site of students cool class work portfolio

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- Etc.

[View the Project on GitHub](#)
bioboot/bggn213

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

https://bioboot.github.io/tmp_test/

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
```


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 (BIMM143)



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 BIMM-143

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](#)

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

Thank you very much!

**Please do fill out your official course evaluations if you get a chance.
It is important to the courses we offer in the future and how we teach them!**

Going Further With DataCamp

<https://www.datacamp.com/tracks/custom-bioinformatics-extension>

The screenshot shows a web browser window with the URL www.datacamp.com/tracks/custom-bioinformatics-extension. The page features 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 icon with "3,050 XP". Below the header, the page is titled "CUSTOM TRACK Bioinformatics Extension". A paragraph of text 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, there is a square icon depicting a DNA double helix with a magnifying glass over it, containing the binary code "101" and "110". At the bottom of the track description, there is a row of tags: "R Language", "Shell", "Git", "Spreadsheets", "111 hours", and "26 Courses".

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

Thank you very much!

```
2. class-material (bash)
# Remove the "date:" line from our class13.md file
> sed -i.bk '/date:/d' class13/class13.md
# Check if it worked!
> head class13/class13.md
```

This is a comment line

Don't type the ">" bit it is the "shell prompt"!

Q. What do you see after each command?

Q. Does it make sense