



# BGGN 213

## Course Summary & GitHub Portfolio

Class 20

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\\_f23](https://board.net/p/bggn213_f23) )
- 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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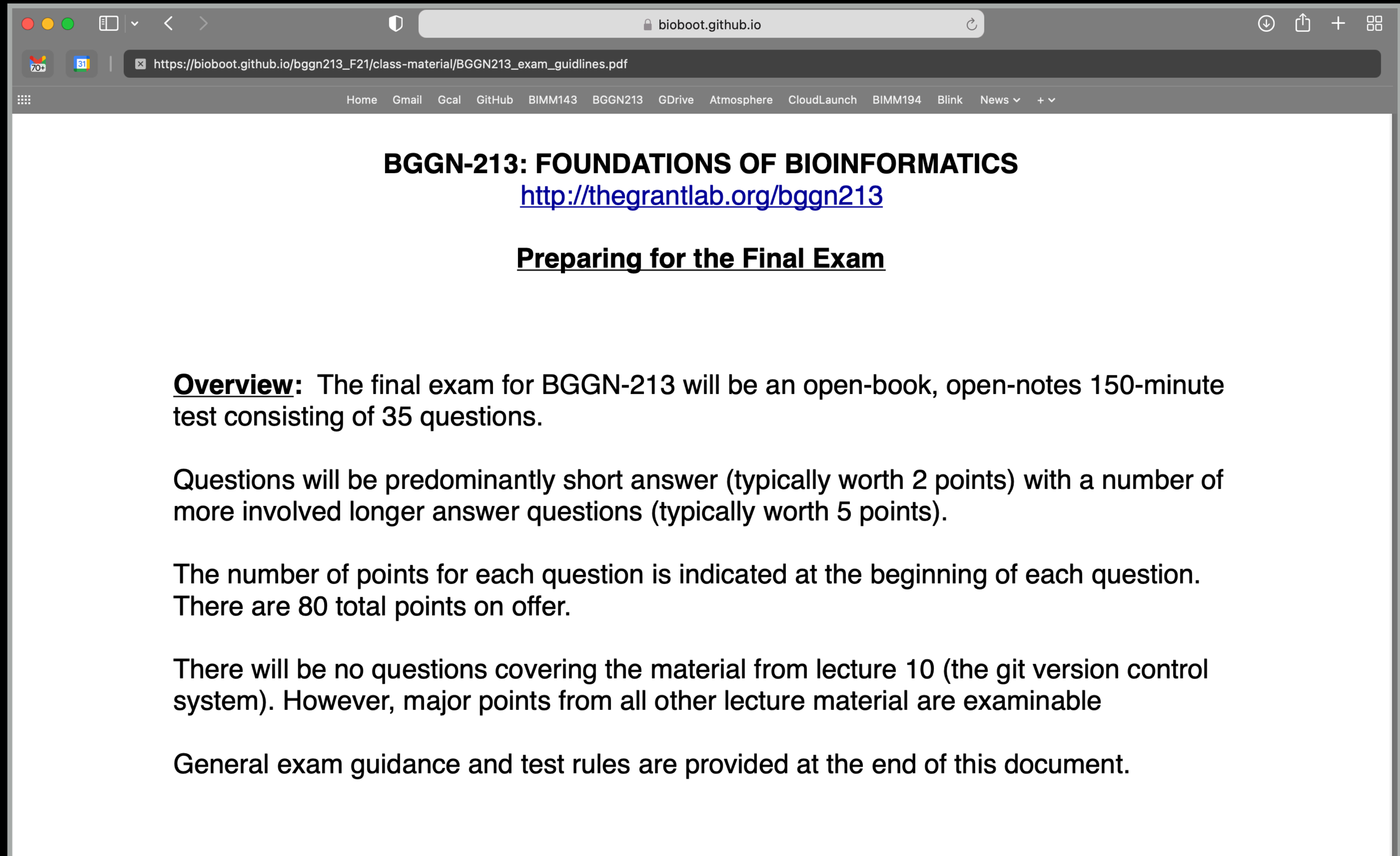


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[https://bioboot.github.io/bggn213\\_F22/class-material/BGGN213\\_exam\\_guidelines.pdf](https://bioboot.github.io/bggn213_F22/class-material/BGGN213_exam_guidelines.pdf)



The image shows a browser window with the URL [https://bioboot.github.io/bggn213\\_F22/class-material/BGGN213\\_exam\\_guidelines.pdf](https://bioboot.github.io/bggn213_F22/class-material/BGGN213_exam_guidelines.pdf). 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/bgggn213\\_f23](https://board.net/p/bgggn213_f23)

**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

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](#)

Hosted on GitHub Pages — Theme by [orderedlist](#)

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Class 13 - [Genome Informatics and High Throughput Sequencing \(NGS, RNA-Seq, and FastQC\)](#)

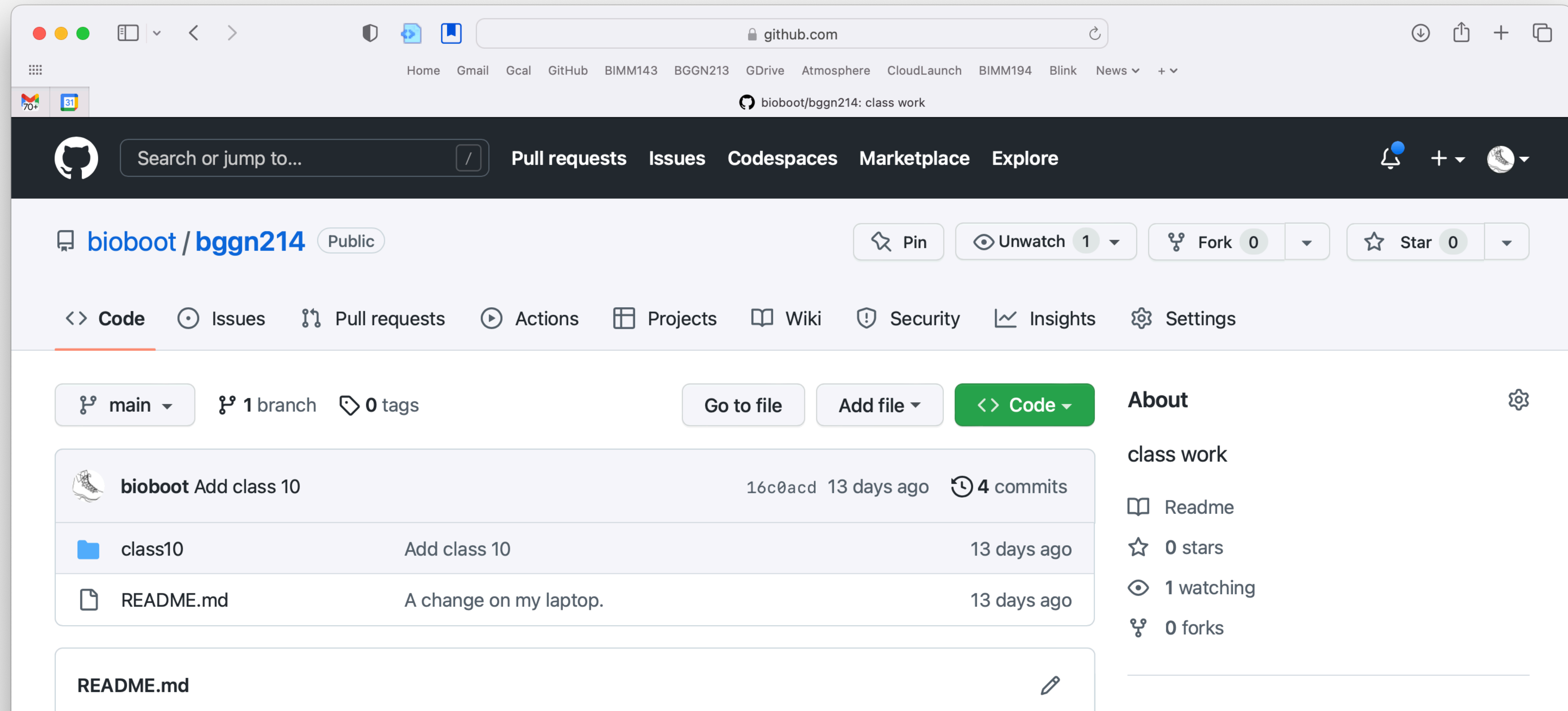
Class 14 - [Transcriptomics and RNA-Seq Analysis](#)

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
```



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

The screenshot shows the RStudio interface with a file named "lecture18part2example.Rmd" open. The Git icon in the top toolbar is highlighted with a red box. A red arrow points from the text "GIT icon" in the top instruction 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 main editor shows R Markdown code with a code chunk containing a FASTA file. The console at the bottom displays the output of the FASTA file, showing sequence alignments for R213V, D259V, D41L, R65W, and another R213V and D259V. The right-hand pane shows the Environment and Files sections, with the Files section listing the project files including "class18.Rproj", "aln.fa", "lecture18\_part2\_exa...", "subsequences.fa", "kras-sequences.fa", "lecture18\_part2\_exa...", and "seqs.fasta".

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

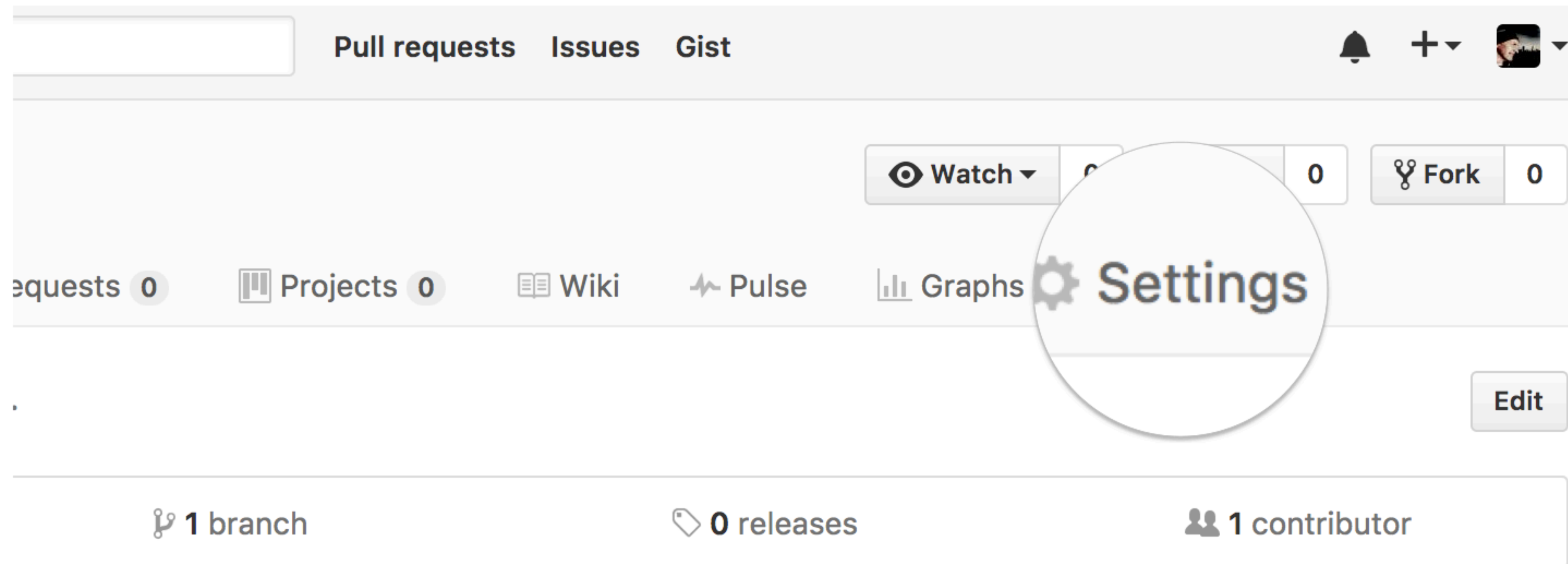
```
~/Desktop/courses/bgg213_W19/bgg213_github/class18/
R213V "Y" "L" "D" "D" "R" "N" "T" "F" "V" "H" "S" "V" "V"
D259V "I" "L" "T" "I" "I" "T" "L" "E" "V" "-" "-" "-" "-"
      [,14] [,15] [,16] [,17]
D41L  "S" "P" "D" "D"
R65W  "A" "P" "P" "V"
R213V "V" "P" "Y" "E"
D259V "-" "-" "-" "-"
>
```

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**

**GitHub Pages**

**Access**

GitHub Pages is designed to host your personal, organization, or project pages from a GitHub repository.

**Collaborators**

**Moderation options**

**Code and automation**

**Branches**

**Tags**

**Actions**

**Webhooks**

**Environments**

**Codespaces**

**Pages**

**Security**

**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

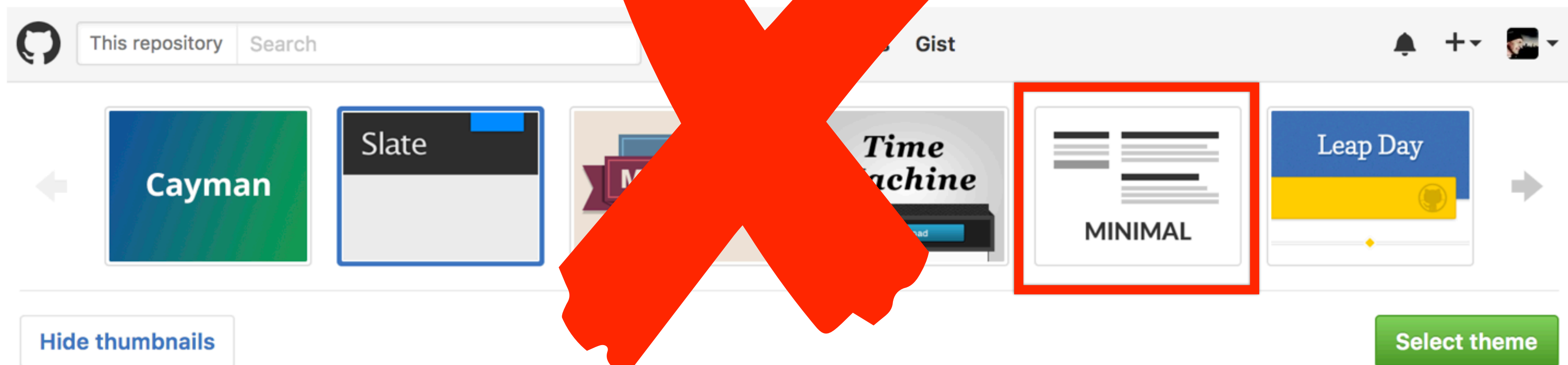
**Publish privately to people with read access to this repository**

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.



The screenshot shows the GitHub theme selection interface. At the top, there is a search bar with the text "This repository" and "Search". Below the search bar, there is a carousel of theme cards. The cards are: "Cayman" (green), "Slate" (blue border), "Time Machine" (purple), "MINIMAL" (red border), and "Leap Day" (blue). A large red "X" is drawn over the "MINIMAL" theme card. Below the carousel, there is a "Hide thumbnails" button on the left and a "Select theme" button 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 repository editor interface for the file `README.md` in the repository `jldec / new-pages-site`. The repository has 0 Watchers, 0 Stars, and 0 Forks. The editor is currently in the "Edit file" mode, with a "Preview changes" tab also visible. The code in the editor 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  
38   https://github.com/contact) and we'll help you sort it out.
```

```
38
```



## Commit changes

Add content to new pages site|

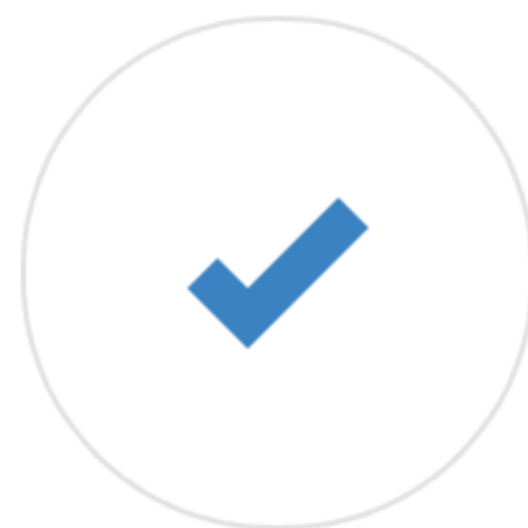
Add an optional extended description...

Commit directly to the `master` branch.

6

...and you're done!

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




bioboot.github.io/bimm143-1/

Home Gmail Gcal Bitbucket GitHub BIMM143\_F18 BGGN213\_S18 BIMM-194 GDocs Disqus Blink News Atmosphere Galaxy + MMTF

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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

bioboot.github.io/bimm143-1/

Home Gmail Gcal Bitbucket GitHub BIMM143\_F18 BGGN213\_S18 BIMM-194 GDocs Disqus Blink News Atmosphere Galaxy + MMTF

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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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The screenshot shows a web browser displaying a GitHub repository page. The browser's address bar shows the URL `bioboot.github.io/bimm143-1/`. The page title is "Introduction to Bioinformatics". On the left side, there is a logo featuring a DNA double helix and a magnifying glass over the binary code "101" and "110". Below the logo, the text reads: "A demo site of students cool class web site", "View the Project on GitHub" with the link `bioboot/bimm143-1`, "This project is maintained by bioboot", and "Hosted on GitHub Pages — Theme by orderedlist". On the right side, there is a red-bordered box containing the following content: "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)", and "Class 14 - Transcriptomics and RNA-Seq Analysis".

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# Thank you very much!

Please do fill out your CAPs evaluation ( [Link!](#) ) if you get a change.  
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](https://www.datacamp.com/tracks/custom-bioinformatics-extension). The page features a dark blue header with a search bar, navigation links (Learn, Practice, Projects, Pricing, My Classes), and a user profile with 3,050 XP. The main content area is titled 'CUSTOM TRACK Bioinformatics Extension' and includes a description: '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!' and an 'Enroll' button. A graphic of a DNA helix with binary code is also present. At the bottom, a progress bar shows 'R Language | Shell | Git | Spreadsheets | 111 hours | 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**

Announcement!

# Bonus:

# Bioinformatics & Genomics in Industry

## Live Stream Video

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# GitHub Copilot

## Hands-on Lab Session

Barry Grant  
UC San Diego

<http://thegrantlab.org>

# GitHub Copilot



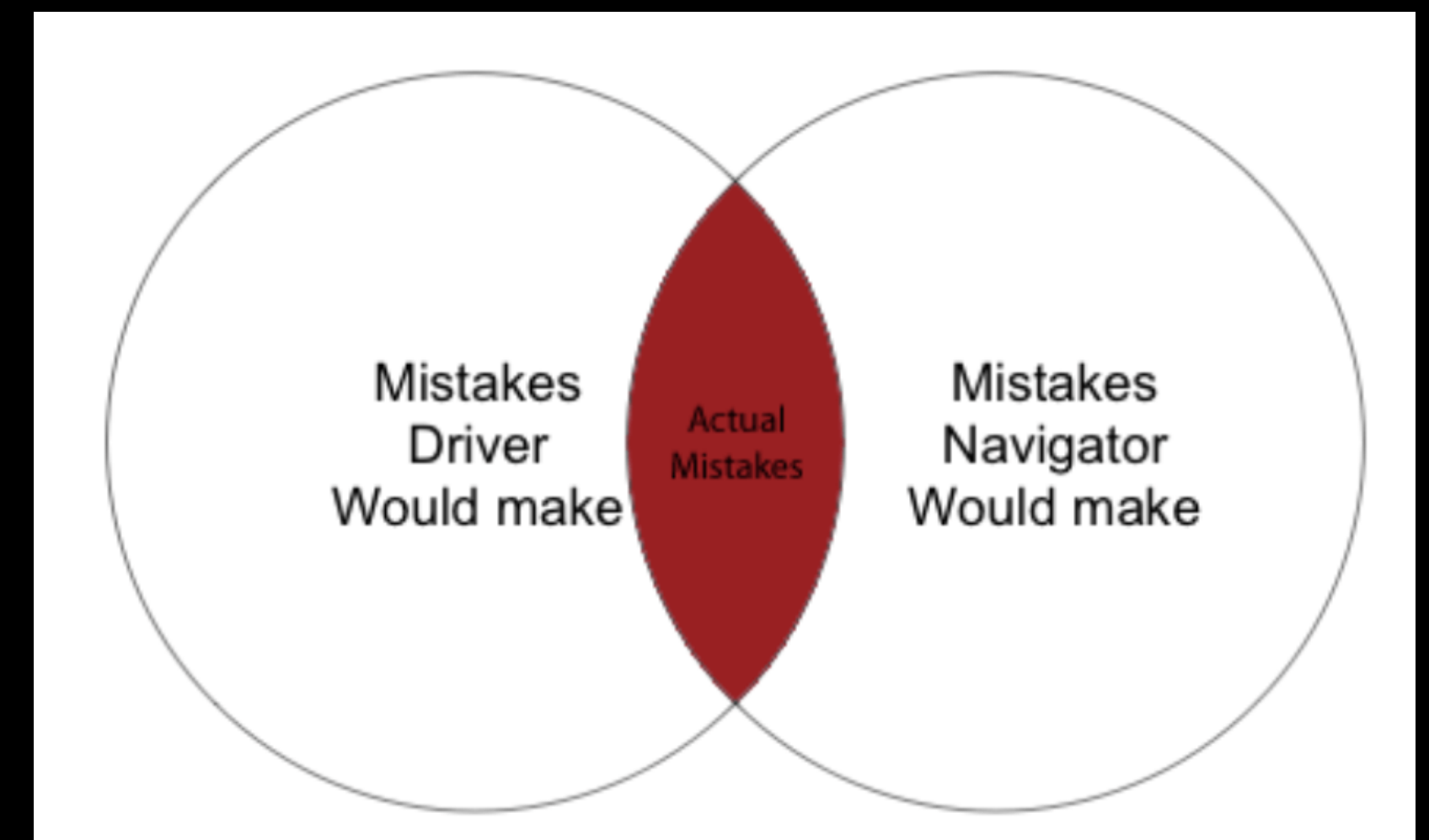
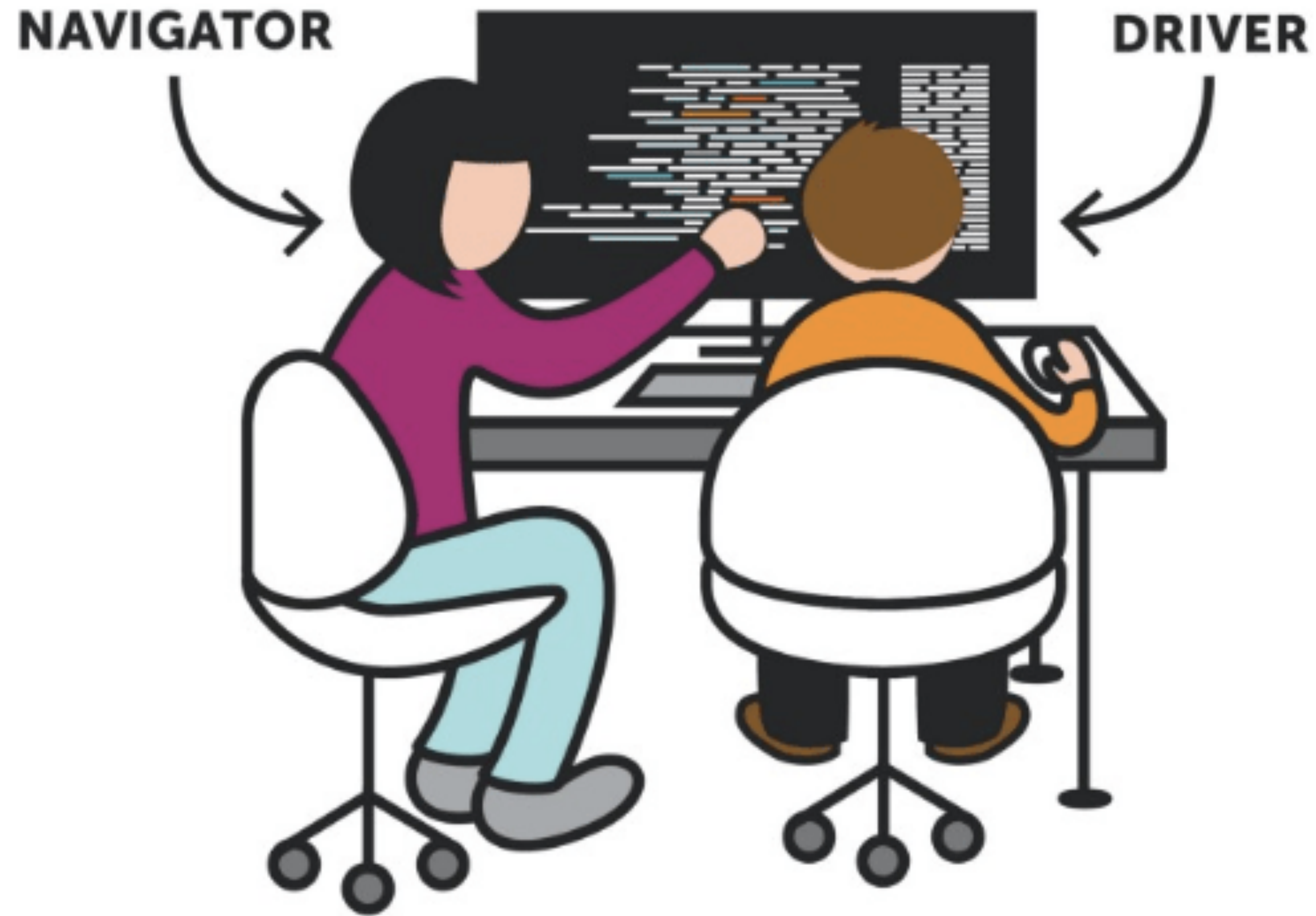
# GitHub Copilot



Your AI “pair programmer”



# PAIR PROGRAMMING



# GitHub Copilot



**AI powered add-on that aims to give helpful suggestions when writing code or documentation**

**AI pair programmer**

**GitHub Copilot** is an **AI pair programmer** that offers autocomplete-style suggestions and real-time hints for the code you are writing by providing suggestions as “**ghost text**” based on the context of the surrounding code

# What can GitHub Copilot do?

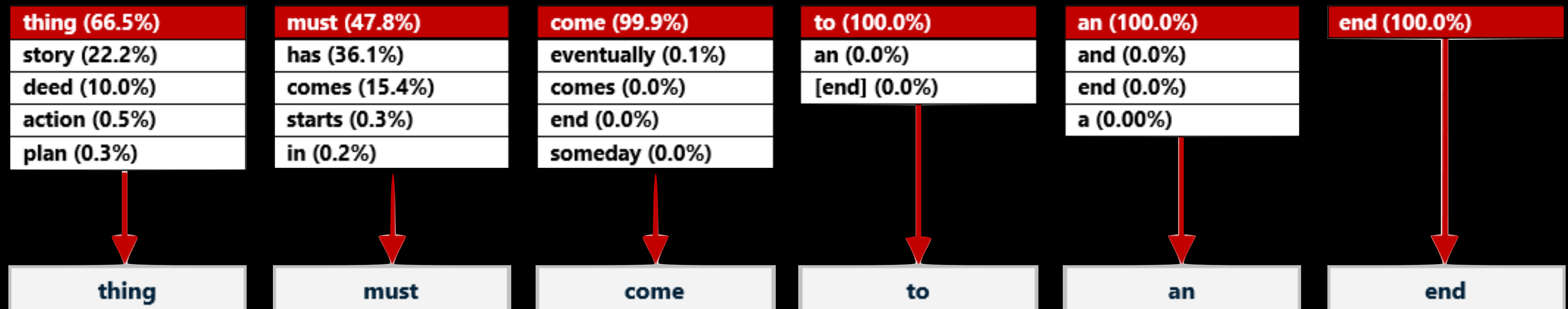
- It provides autocomplete suggestions while you code.
- You can get suggestions by typing code or describing it in natural language (i.e. code comments or markdown text).
- Copilot analyzes your file (and related files), offering suggestions in your editor.
- It uses [OpenAI Codex](#) to derive context from your code and comments, and then suggests new lines or entire functions.



# Generative AI Models

# Generative AI

- For text generation, Generative AI just wants to predict the next word/token/string!
- I might ask **ChatGPT**: > “Complete the sentence every good...”





## Generative AI

### GPT-3

Prompt:

Write a tagline for an ice cream shop.

Response:

We serve up smiles with every scoop!

### Codex

Prompt:

Table customers, columns = [CustomerId, FirstName, LastName, Company, Address, City, State, Country, PostalCode]

Create a SQL query for all customers in Texas named Jane  
query =

Response:

```
SELECT *  
FROM customers  
WHERE State = 'TX' AND FirstName = 'Jane'
```

### DALL·E

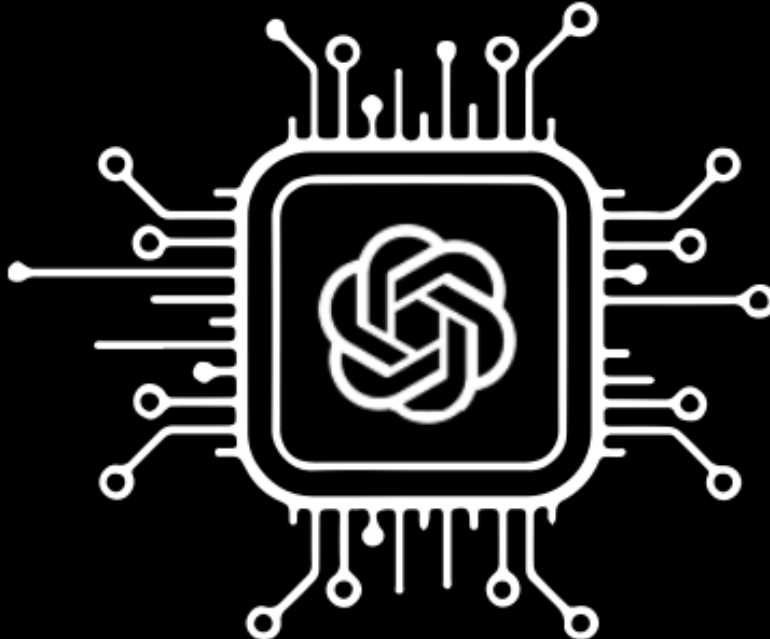
Prompt: A white Siamese cat

Response:





# Training Data



**Prompt**

**Model**

**Completion**



# Generative AI can:



## Generate text, images and code

Different models are trained on different corpuses, depending on the application.



## Generate “humanlike” output

What is a likely continuation of the prompt, given the training data?



## Extract information

The continuation is likely to be similar to text frequently represented in the training data.



## Create novel content

Text, images and code not contained in its training set. Translations. “Creative” works.



# Generative AI is not:



## Intelligent

It's just a predictive system, designed to give a likely continuation of the prompt given the training data.



## Deterministic

Run the same prompt. Get back a different response (probably).



## Trustworthy

It can "hallucinate" facts and confidently assert them to be true.

TODO



# Generative AI does not:



## Learn

The model is fixed at the time of its training.



## Contain all of the information of its training set

Think: a [blurry jpeg](#) of its training data.



## Include verbatim copies of its training data

But it can generate stuff that looks like it.

# GitHub Student Developer Pack

Learn to ship software like a pro. There's no substitute for hands-on experience. But for most students, real world tools can be cost-prohibitive. That's why we created the GitHub Student Developer Pack with some of our partners and friends.

[Sign up for Student Developer Pack](#)

Love the pack? Spread the word

[Tweet](#)

[Like 77K](#)

## Experiences

Discover the best ways to use pack offers with Experiences. Experiences are curated bundles of pack partner products, GitHub tools, and other resources that are designed for you learn new skills and make the most out of the Student Developer Pack and your journey in Global Campus.



Tools

### Security and Monitoring

Explore industry standard tools that keep your code safe, your permissions secure and your infrastructure monitored so that you can confidently scale your brilliant ideas.

Offers in this bundle

- GitHub
- Blackfire
- Honeybadger
- AstraSecurity
- +3

[Learn more about Security and Monitoring >](#)



Primer

### Primer: Copilot

What is Copilot and how do you get started using it? Use this Experience as a Primer on Copilot. We share tutorials, guides and templates to learn how to use AI in your development process.

Offers in this bundle

- Github Copilot
- GitHub Codespaces
- Visual Studio Code

[Learn more about Primer: Copilot >](#)



Tools

### Career Readiness

Whether you're approaching graduation or just want to get a head start, it's never too early to prepare for your future in the industry.

Offers in this bundle

- Educative
- InterviewCake
- DailyBot
- GitHub Pages
- +2

[Learn more about Career Readiness >](#)



Tools

### Intro to Web Dev

Everything you need to build your next website.



Tools

### Hackathon in the Cloud

Learn how to organize, promote, and communicate



Tools

### Aspiring Creatives

Working on a creative project? Develop your design

Home / Benefits / Benefits application

# Get your GitHub benefits

Learn and teach using real-world developer tools

Select your academic status \*

Teacher  Student

## Benefits for Students

<p><b>STUDENT</b></p> <p>FREE <a href="#">GitHub Pro</a> while you are a student</p>	<p><b>STUDENT</b></p> <p>Valuable <a href="#">GitHub Student Developer Pack</a> partner offers</p>	<p><b>STUDENT</b></p> <p><a href="#">GitHub Campus Expert</a> training for qualified applicants</p>
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### To qualify for student benefits, you must:

- Have a GitHub account.
- Be at least 13 years old.

# Quick Start Guide

<https://docs.github.com/en/copilot/quickstart>



# Additional Learning Resources

- **Video series from GitHub:**
  - <https://learn.microsoft.com/en-us/shows/introduction-to-github-copilot/>
- **Blog post series:**
  - <https://github.blog/2023-06-20-how-to-write-better-prompts-for-github-copilot/>
- **RStudio Docs:**
  - <https://docs.posit.co/ide/user/ide/guide/tools/copilot.html>