



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://etherpad.wikimedia.org/p/bimm143_w26)
- SET/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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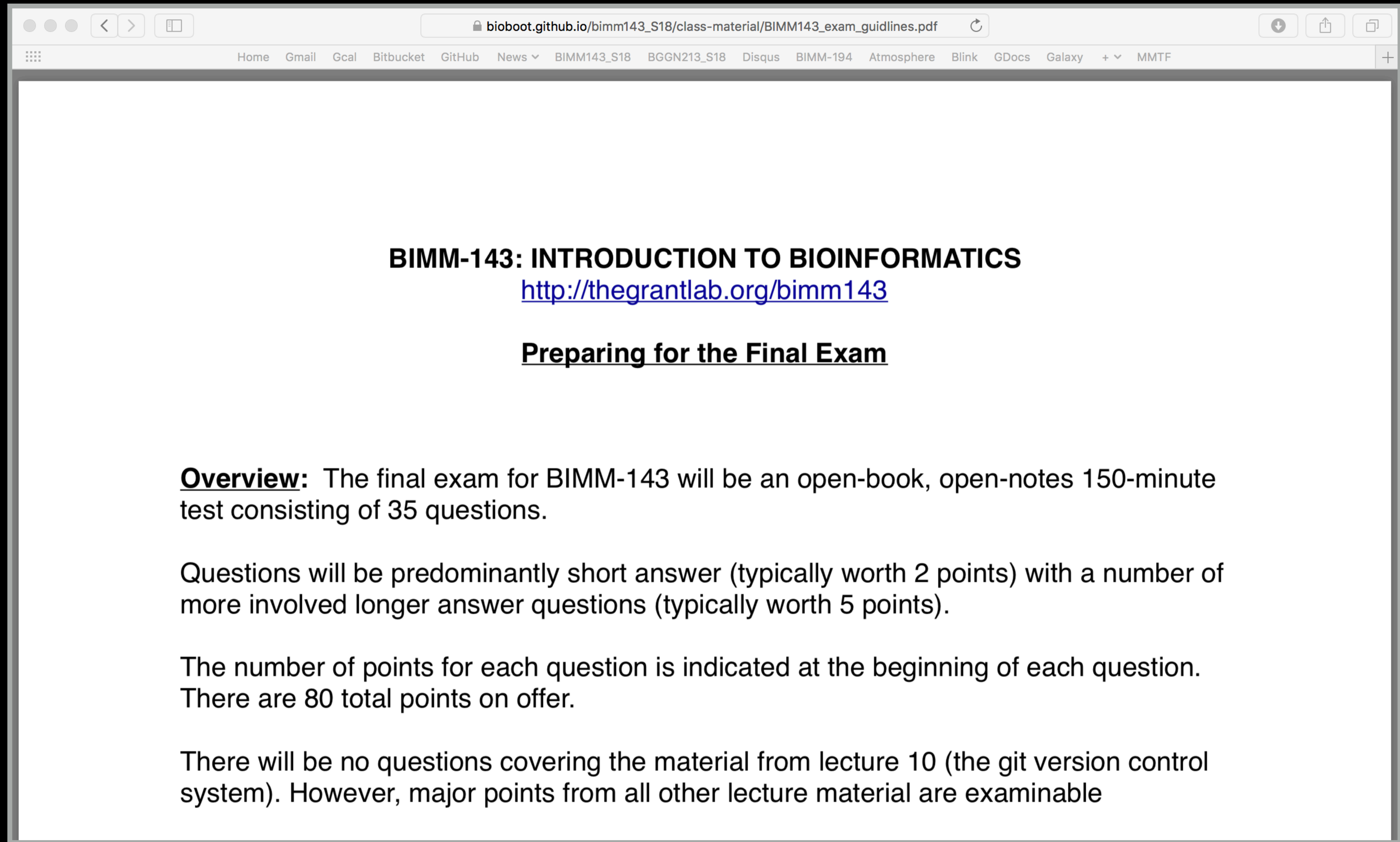


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- Summary of major learning goals,
- Course discussion and feedback (https://etherpad.wikimedia.org/p/bimm143_w26)
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- Project troubleshooting
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https://bioboot.github.io/bimm143_F22/class-material/BIMM143_exam_guidelines.pdf



- 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: https://etherpad.wikimedia.org/p/bimm143_w26

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

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



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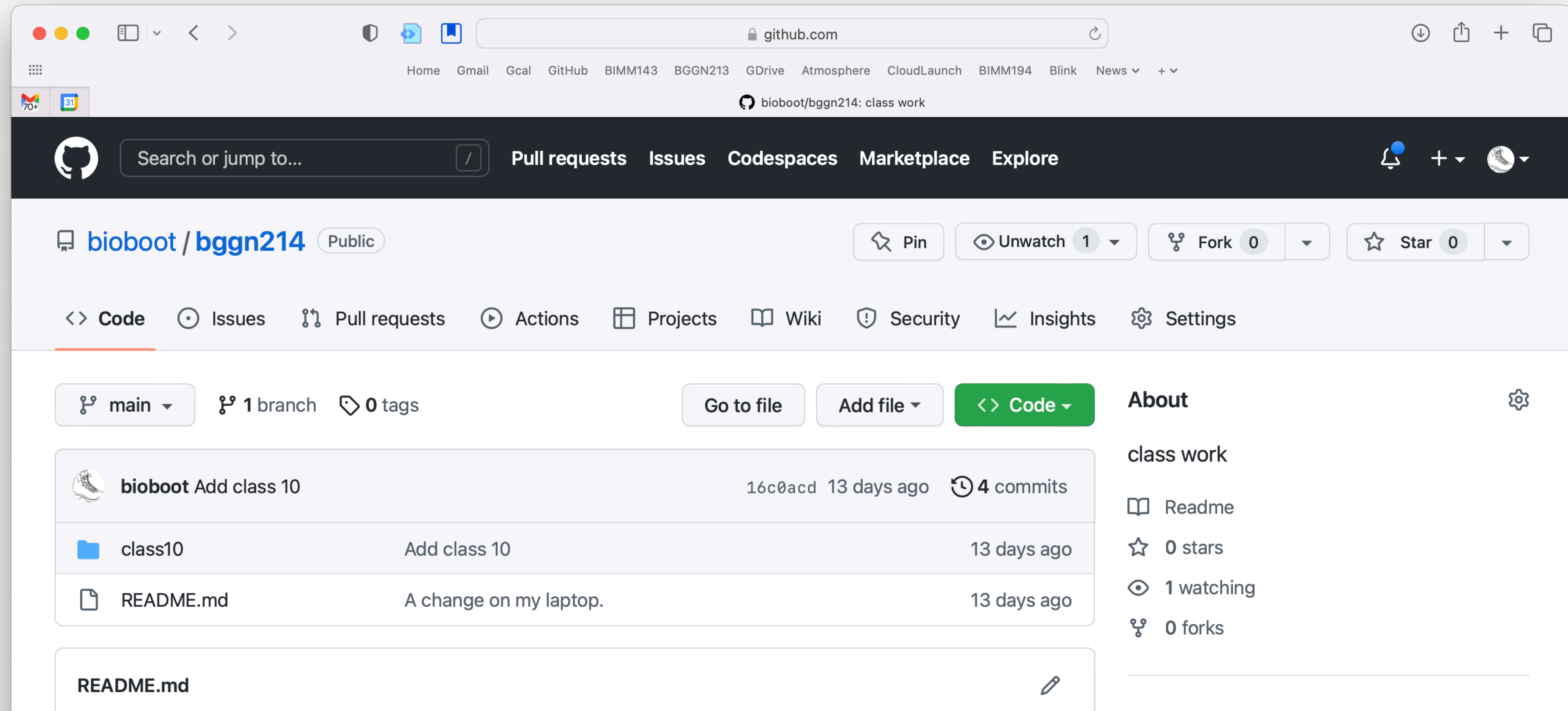
Class 14 - [Transcriptomics and RNA-Seq Analysis](#)

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"**

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 context menu is open over the file, with the "View 'lecture18part2example.Rmd' on GitHub" option highlighted by a red box. A red arrow points from the text "VIEW on GITHUB" in the top instruction to this menu item. The menu also includes options like "Diff", "Log", "Revert", "Commit...", "Pull Branches", "Push Branch", "History", and "Project Setup...".

```
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
```

53:1 | C Chunk 6 | R Markdown

Console | Terminal | 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

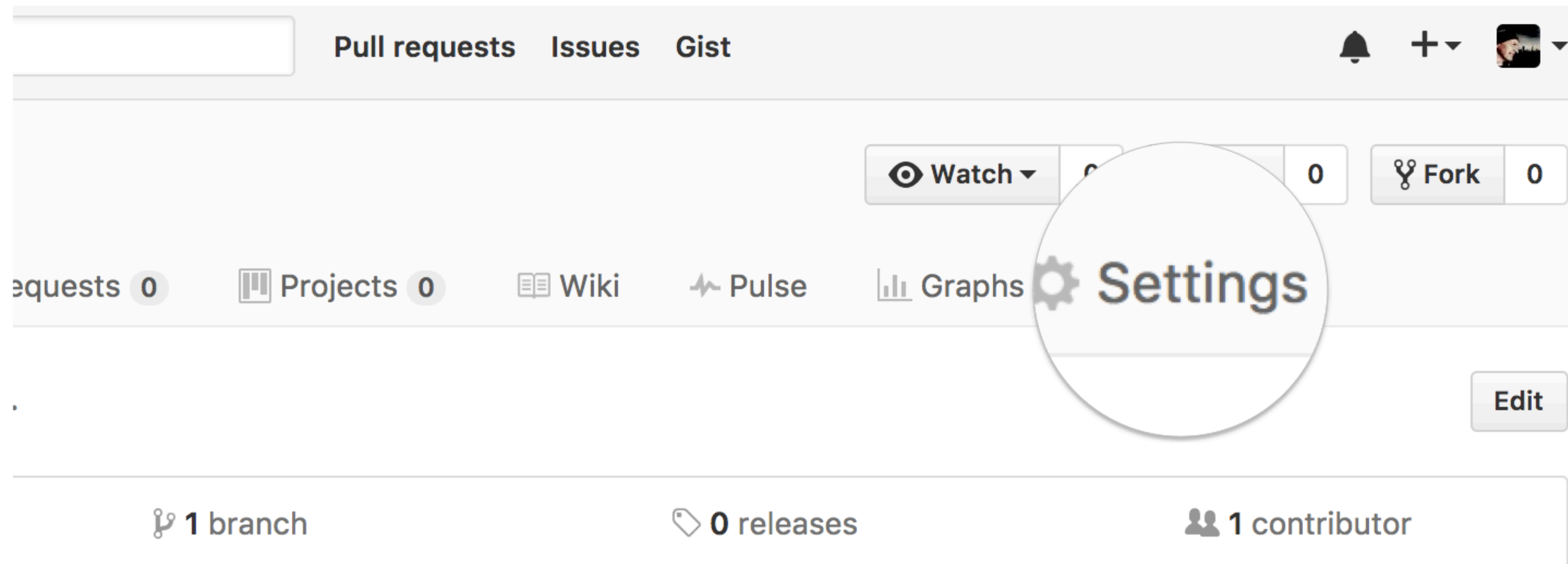
- ..
- class18.Rproj
- aln.fa
- lecture18_part2_exa...
- subsequences.fa
- kras-sequences.fa
- lecture18_part2_exa...
- seqs.fasta

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.**~~
And set the **Source** to "main branch"

General

GitHub Pages

Access

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.](#) ✕

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 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 \[documentation\]
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.

6

...and you're done!

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




bioboot.github.io/bimm143-1/

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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)
```


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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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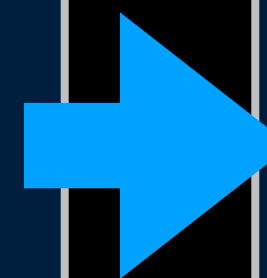
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Formats for Portfolio Lab Reports

- Your Quarto lab reports (input for `quarto render`) likely produced pdf format outputs:
- Ideally we want something nicer for online viewing. Enter the `gfm` format (short for GitHub Flavored Markdown).
- We can edit our YAML header and `quarto render`, `git add`, `git commit` and `git push` to test this out on GitHub... <demo>

```
1 ---
2 title: "Class 5: Data Viz with ggplot"
3 author: "Barry (PID: 911)"
4 format: pdf
5 ---
6
7 Today we are exploring the ggplot package and how to
8 make nice figures in R.
```



```
1 ---
2 title: "Class 5: Data Viz with ggplot"
3 author: "Barry (PID: 911)"
4 format: gfm
5 ---
6
7 Today we are exploring the ggplot package and how to
8 make nice figures in R.
```

Formats: **HTML**, **GFM** or **htmlpreview**

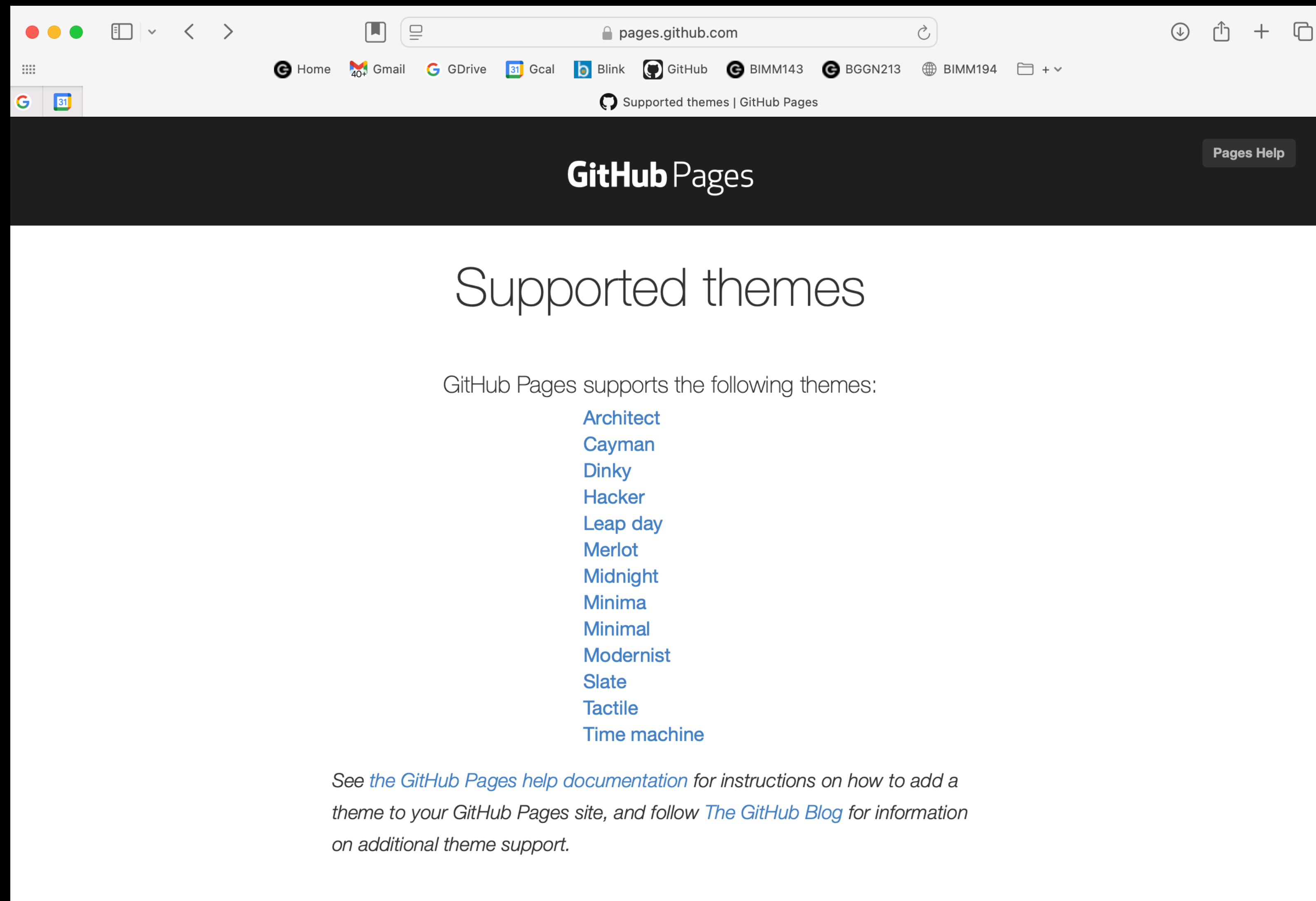
- There are three options to get “nice” lab reports on GitHub Pages
 1. Link to a HTML file e.g. `[class05](class05/class05.html)`
 2. Create and link to a special “gfm” format (GitHub Flavored Markdown):

```
quarto render class05.qmd --to gfm
```
 3. Or you can prepend <https://htmlpreview.github.io/?>:
 - Go to the HTML file in the GitHub repository
 - Click on the "Raw" button to get the raw file URL
 - Construct your link like so: [https://htmlpreview.github.io/?\[raw-file-url\]](https://htmlpreview.github.io/?[raw-file-url])
 - This will work on both the repo README and the GitHub website...

Why Vim Opens During `git pull`

- You edited a file locally and also on GitHub.com.
- Git detects the two versions don't match, so it needs to **merge** them.
- Git opens **Vim** to confirm the merge with a commit message.
- To finish the merge: type `:wq` and press Enter.
- To avoid this: Always run `git pull` before editing locally.

<https://pages.github.com/themes/>



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

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, followed by a search bar containing the text "What would you like to learn t". Navigation links for "Learn", "Practice", "Projects", "Pricing", and "My Classes" are present, along with 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 is a paragraph: "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 to the left of a square image showing a DNA double helix with a magnifying glass over the binary code "101110".

At the bottom of the track description, there is a list of skills: "R Language", "Shell", "Git", and "Spreadsheets", followed by a clock icon for "111 hours" and a document icon for "26 Courses".

The course card has a blue icon with a terminal prompt `>_` at the top. The title is "Introduction to Shell for Data Science". The description reads: "The Unix command line helps users combine existing programs in new ways, automate repetitive tasks, and run programs ...".

The "INSTRUCTORS" section lists two individuals:

- Greg Wilson**: Co-founder of Software Carpentry
- Jonathan Cornelissen**

Announcement!

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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

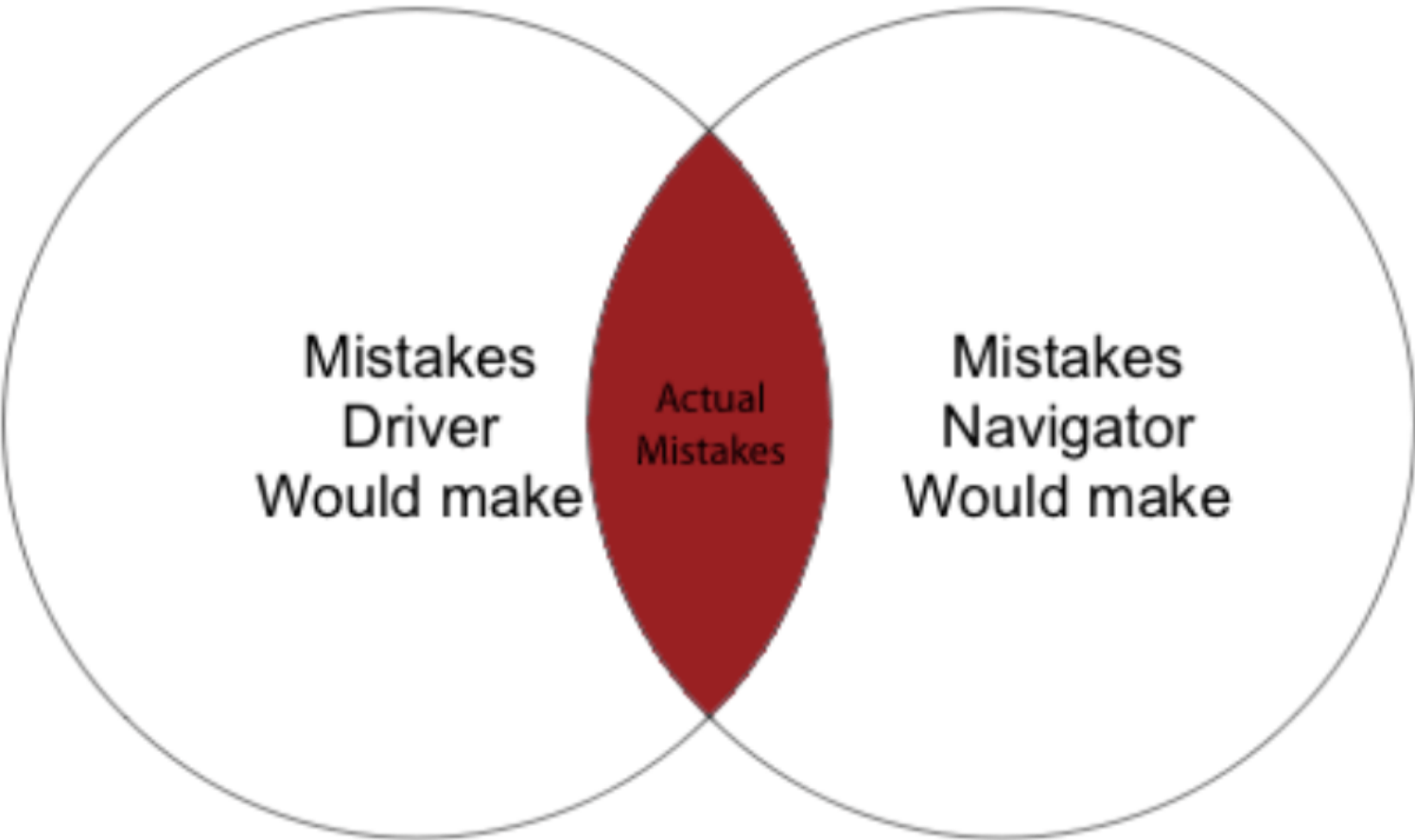
NAVIGATOR



DRIVER

Turn left
in 1 block.

Ok, that's a
good route.



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?

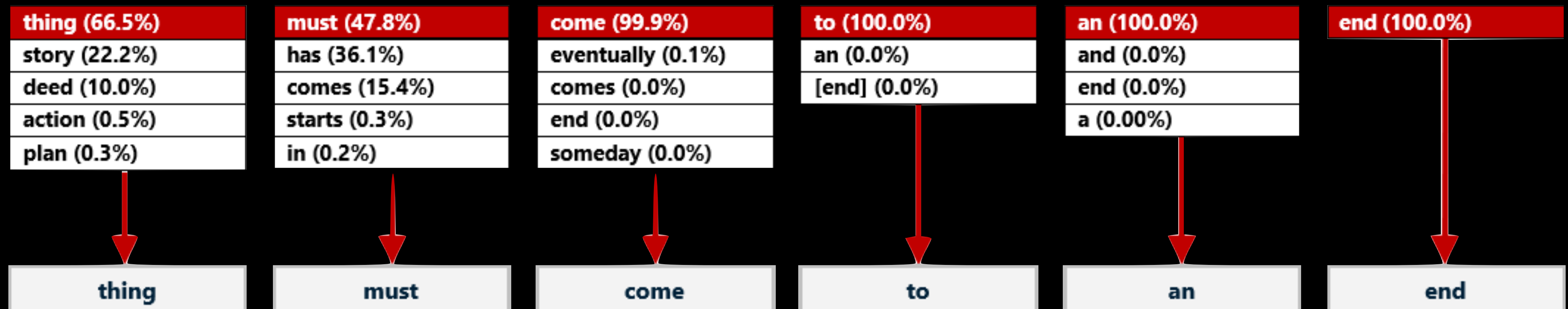
- It provides autocomplete suggestions while you code.
- You can get suggestions by typing code or describing it in natural language (i.e. code comments or markdown text).
- Copilot analyzes your file (and related files), offering suggestions in your editor.
- It uses [OpenAI Codex](#) to derive context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

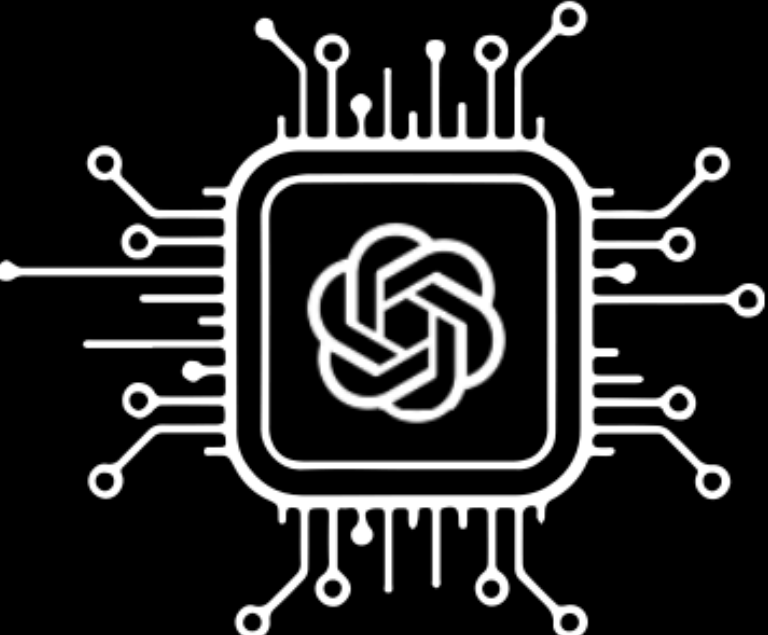
DALL·E

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 × +

← → ↻ <https://education.github.com/pack> ☆ 📌 ☰

GitHub.com

 Education Students ▾ Teachers ▾ Schools Benefits Events [Sign in](#)

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

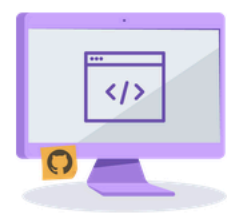
Career Readiness

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

Get your GitHub benefits

Learn and teach using real-world developer tools

Select your academic status *

Teacher Student

Benefits for Students

STUDENT FREE GitHub Pro while you are a student	STUDENT Valuable GitHub Student Developer Pack partner offers	STUDENT GitHub Campus Expert training for qualified applicants
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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>



The End!

<http://thegrantlab.org>



Thank You!

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