



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_s25)
- 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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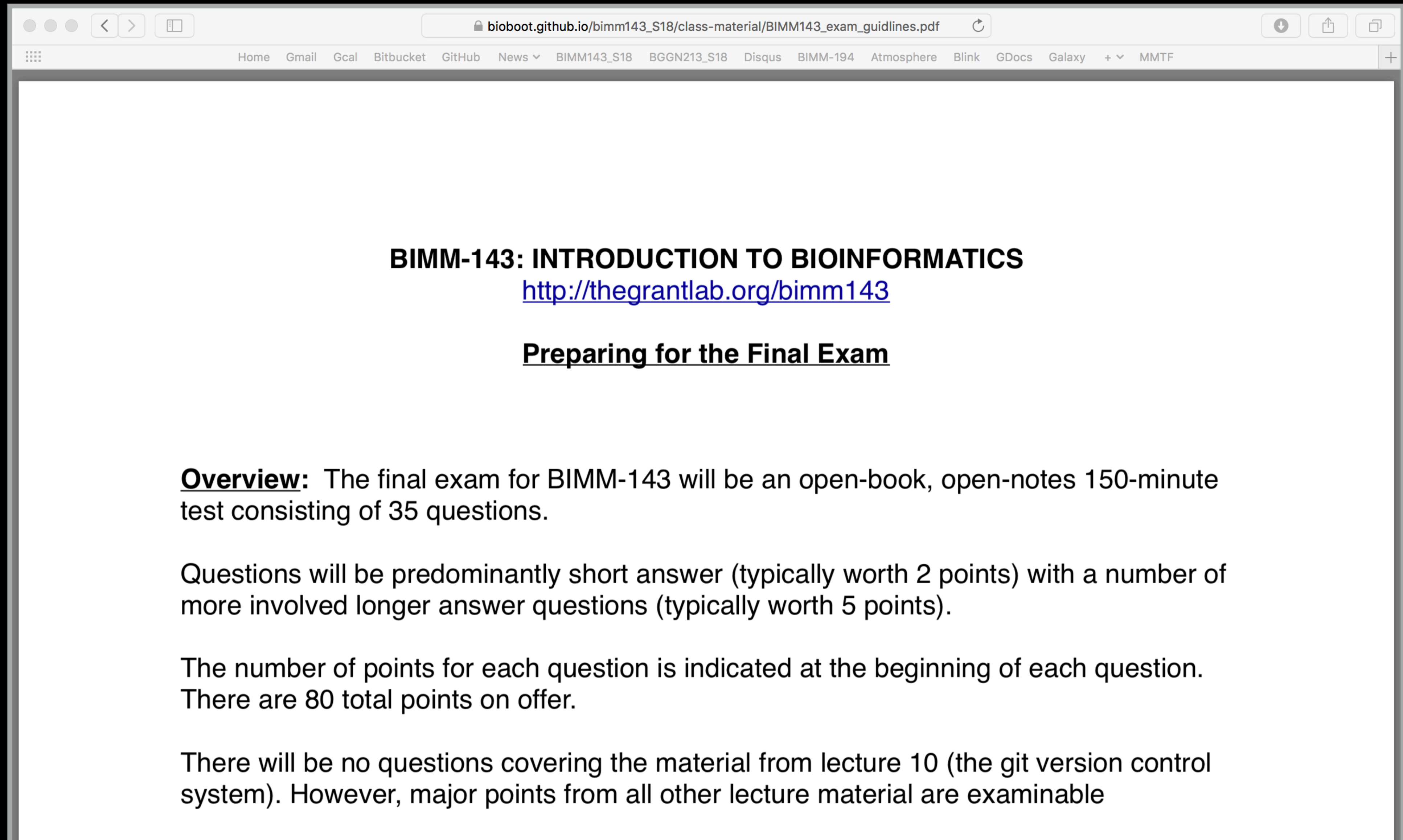


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https://bioboot.github.io/bimm143_F22/class-material/BIMM143_exam_guidelines.pdf



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. 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: https://etherpad.wikimedia.org/p/bimm143_s25

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](#)

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Bioinformatics Class

This is my repository for my Bioinformatics class from UC San Diego in S18.

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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 the GitHub repository page for `bioboot/bggn214`. The browser's address bar shows `github.com`. The repository is public and has 0 stars, 0 forks, and 1 watch. The repository contains a `class10` directory and a `README.md` file. The commit history shows a recent commit by `bioboot` titled "Add class 10" with 4 commits. The repository is currently on the `main` branch.

bioboot / **bggn214** Public

Pin Unwatch 1 Fork 0 Star 0

Code Issues Pull requests Actions Projects Wiki Security Insights Settings

main 1 branch 0 tags

Go to file Add file Code

bioboot Add class 10 16c0acd 13 days ago 4 commits

File	Commit Message	Time
class10	Add class 10	13 days ago
README.md	A change on my laptop.	13 days ago

README.md

About

class work

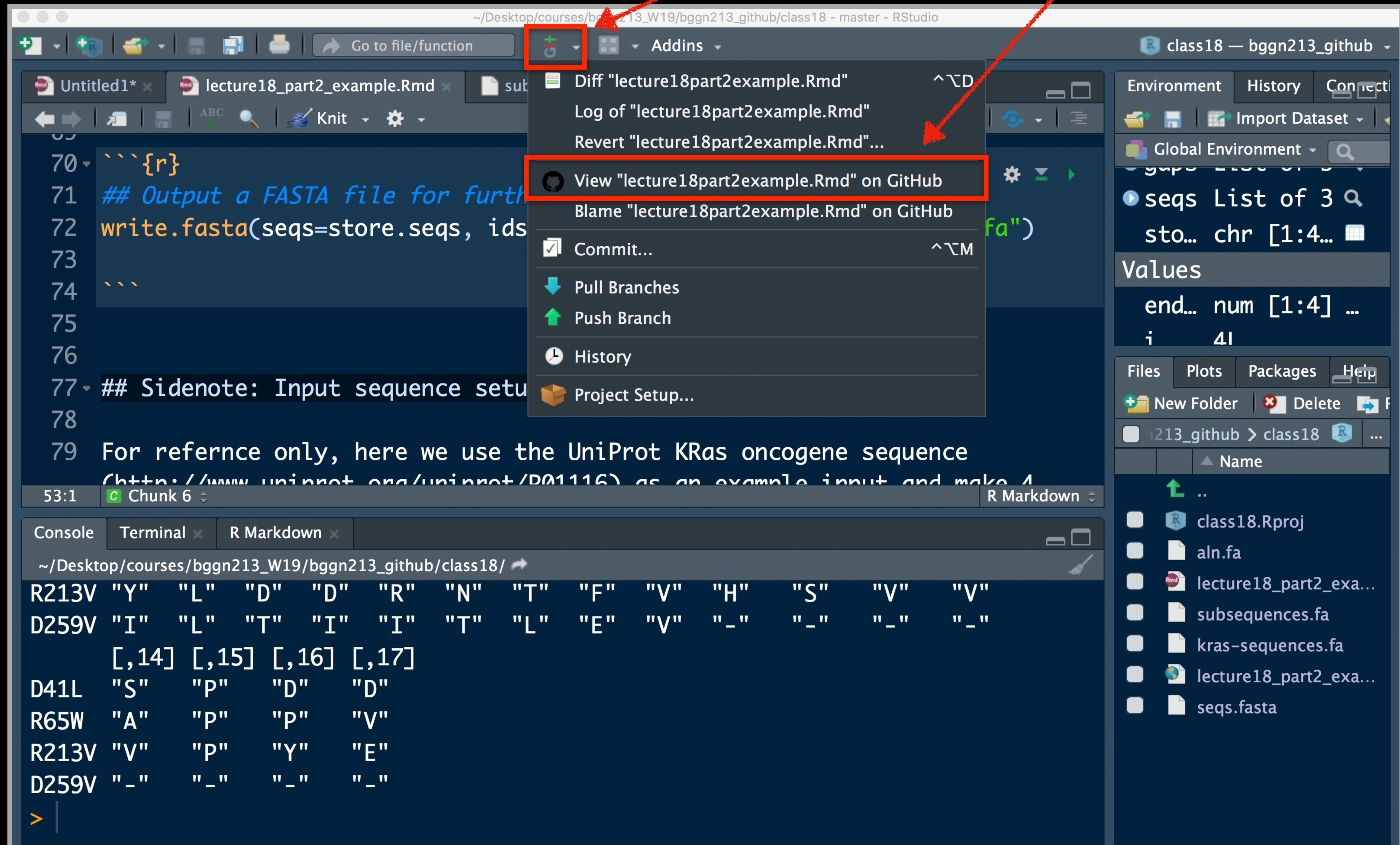
Readme

0 stars

1 watching

0 forks

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



The screenshot shows the RStudio interface with the following components:

- Top Panel:** Displays the file path `~/Desktop/courses/bgg213_W19/bgg213_github/class18 - master - RStudio`. The **Git** icon (a green 'G' with a plus sign) is highlighted with a red box. A red arrow points from the text "GIT icon" in the instruction above to this icon.
- Source Panel:** Shows the file `lecture18_part2_example.Rmd`. The **Git** menu is open, and the option `View "lecture18part2example.Rmd" on GitHub` is highlighted with a red box. A red arrow points from the text "**VIEW on GITHUB**" in the instruction above to this menu item.
- Editor:** Displays R Markdown code. The visible code includes:

```
70 ```{r}
71 ## Output a FASTA file for further analysis
72 write.fasta(seqs=store.seqs, ids=store.ids)
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
```
- Console:** Shows the output of the `write.fasta` function:

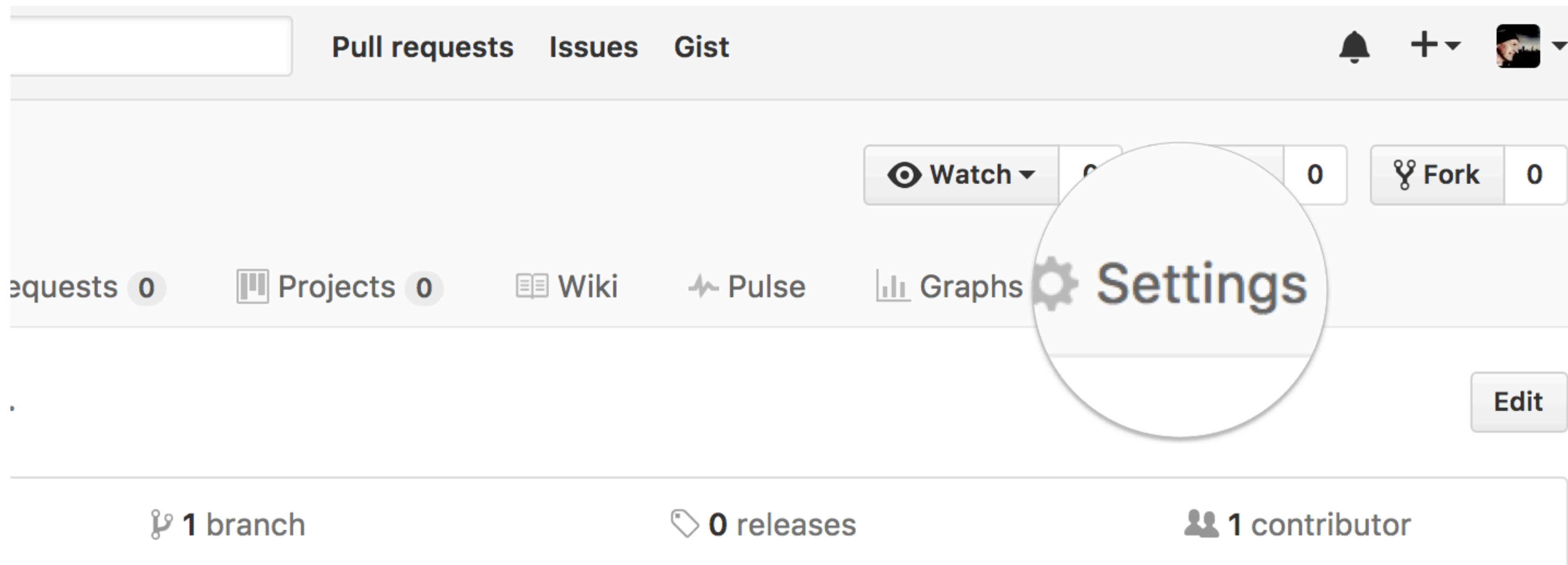
```
~/Desktop/courses/bgg213_W19/bgg213_github/class18/
R213V "Y" "L" "D" "D" "R" "N" "T" "F" "V" "H" "S" "V" "V"
D259V "I" "L" "T" "I" "I" "T" "L" "E" "V" "_" "_" "_" "_"
      [,14] [,15] [,16] [,17]
D41L  "S"  "P"  "D"  "D"
R65W  "A"  "P"  "P"  "V"
R213V "V"  "P"  "Y"  "E"
D259V "_"  "_"  "_"  "_"
>
```
- Environment Panel:** Shows the `Global Environment` with a list of objects:
 - `seqs`: List of 3
 - `sto...`: chr [1:4...]
 - `end...`: num [1:4] ...
 - `i`: 41
- Files Panel:** Shows the project files:
 - `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

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.](#) ×

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 interface for the repository 'jldec / new-pages-site'. At the top, there are buttons for 'Watch', 'Star', and 'Fork', each with a count of 0. Below these are tabs for 'Code', 'Issues', 'Pull requests', 'Projects', 'Wiki', 'Pulse', 'Graphs', and 'Settings'. The 'Code' tab is selected, and the file 'README.md' is shown. The editor interface has two tabs: 'Edit file' and 'Preview changes'. The 'Edit file' tab is active, showing the content of 'README.md' with line numbers 1 through 14. The content includes a welcome message, instructions on how to use the GitHub editor, and a section on Markdown syntax.

jldec / new-pages-site

Watch 0 Star 0 Fork 0

<> Code Issues 0 Pull requests 0 Projects 0 Wiki Pulse Graphs Settings

new-pages-site / README.md or cancel

<> Edit file Preview changes Spaces 2 Soft wrap

```
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/github-pages-faq)(<https://help.github.com/categories/github-pages-faq>)
(<https://github.com/contact>) and we'll help you sort it out.

38



Commit changes

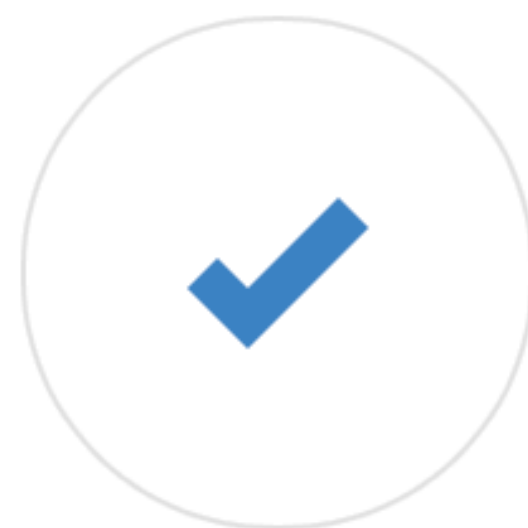
Add content to new pages site|

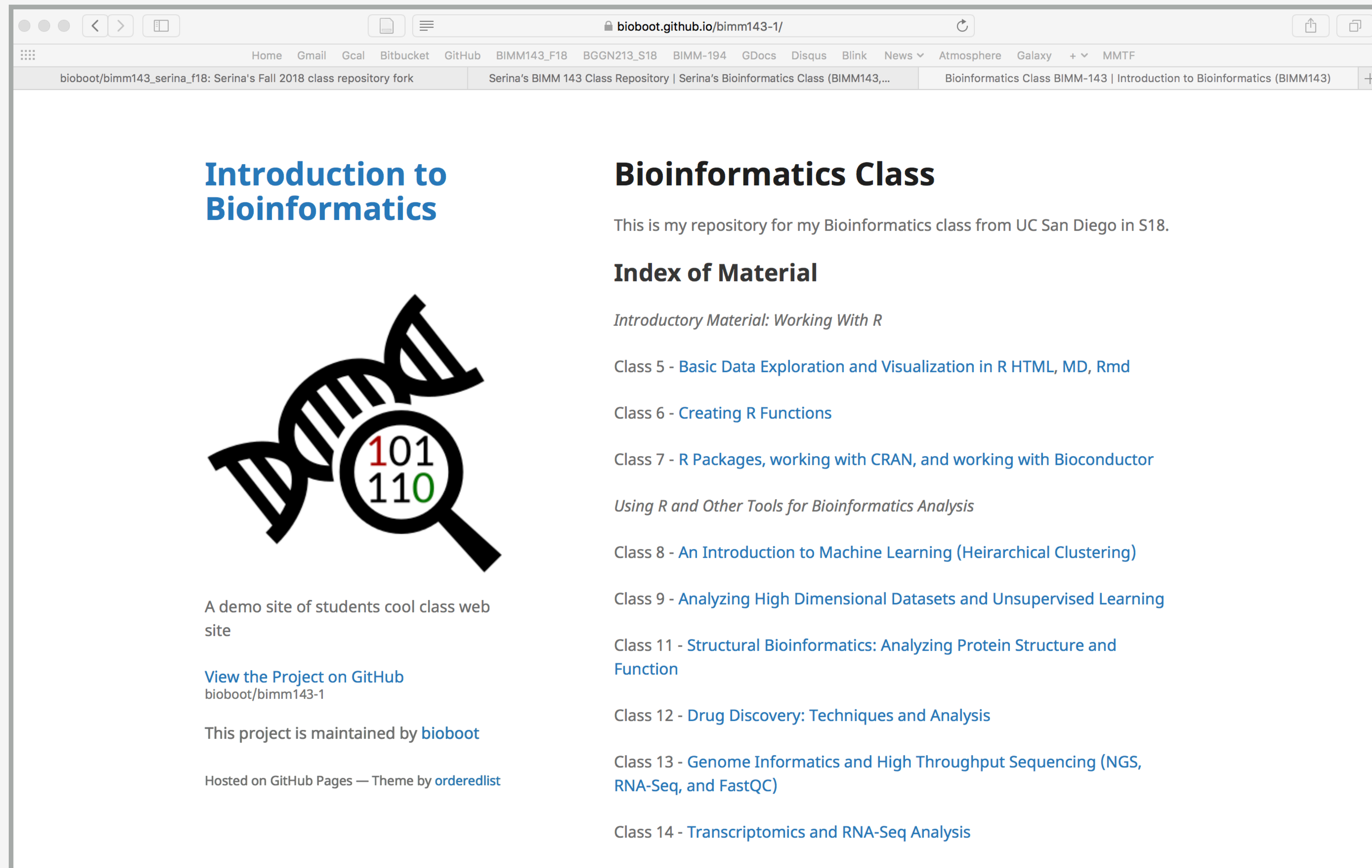
Add an optional extended description...

☒ Commit directly to the `master` branch.

...and you're done!

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





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

◂ ◃ 📄

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 forkSerina'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

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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.github.io/bimm143-1/

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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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bioboot.github.io/bimm143-1/

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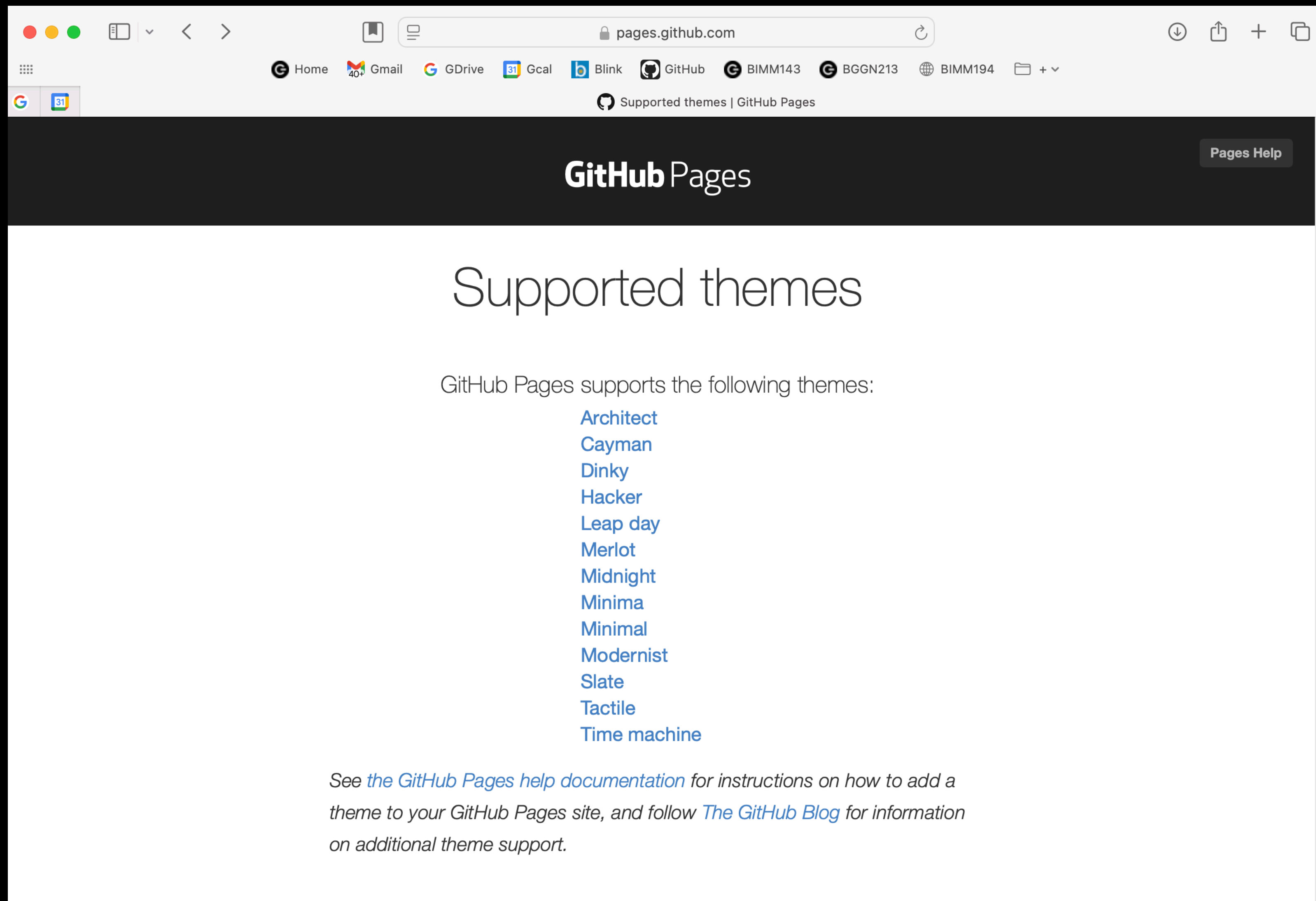
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Formats: **HTML**, **GFM** or **htmlpreview**

- 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...

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



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!

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!

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 corner. A search bar contains the text "What would you like to learn t". Navigation links include "Learn", "Practice", "Projects", "Pricing", "My Classes", and a user profile with "3,050 XP". The main content area features the heading "CUSTOM TRACK Bioinformatics Extension" and 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!". A yellow "Enroll" button is present. To the right is a square icon with a DNA helix and binary code. At the bottom, a list of topics includes "R Language", "Shell", "Git", and "Spreadsheets", along with "111 hours" and "26 Courses". Below this, a section titled "Introduction to Shell for Data Science" is partially visible, featuring a terminal icon and a description of the Unix command line. To the right, an "INSTRUCTORS" section lists "Greg Wilson" (Co-founder of Software Carpentry) and "Jonathan Cornelissen".

www.datacamp.com/tracks/custom-bioinformatics-extension

Home Gmail Gcal GitHub BIMM143 BGGN213 Atmosphere BIMM194 Blink News +

What would you like to learn t Learn Practice Projects Pricing My Classes 3,050 XP

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

Announcement!

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The background of the slide is an abstract composition of numerous overlapping, semi-transparent spheres in shades of purple, pink, orange, and blue. These spheres are arranged in a way that creates a sense of depth and movement, resembling a molecular structure or a cluster of cells. The overall color palette is vibrant and modern.

GitHub Copilot

Hands-on Lab Session

Barry Grant
UC San Diego

<http://thegrantlab.org>

GitHub Copilot

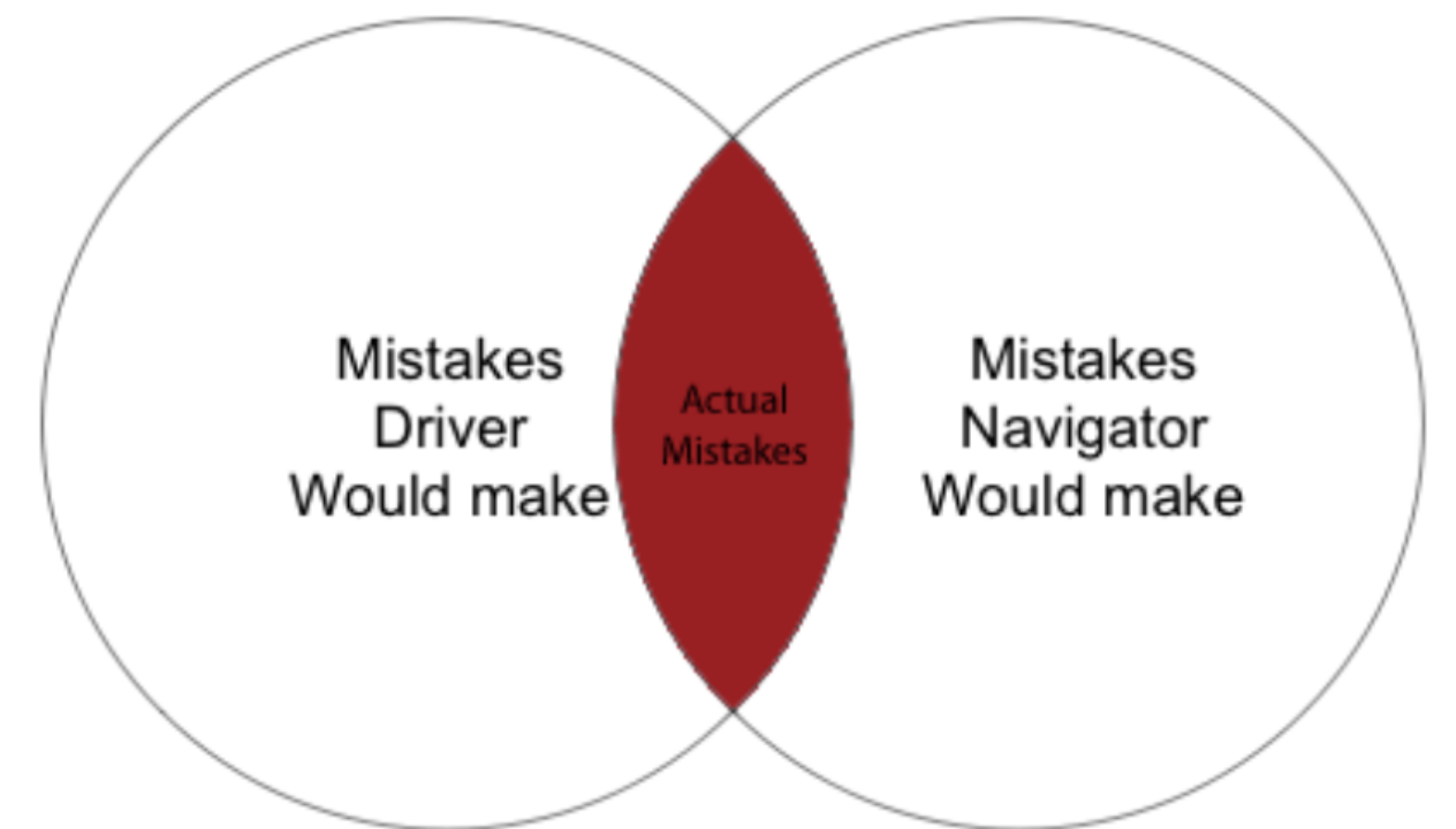
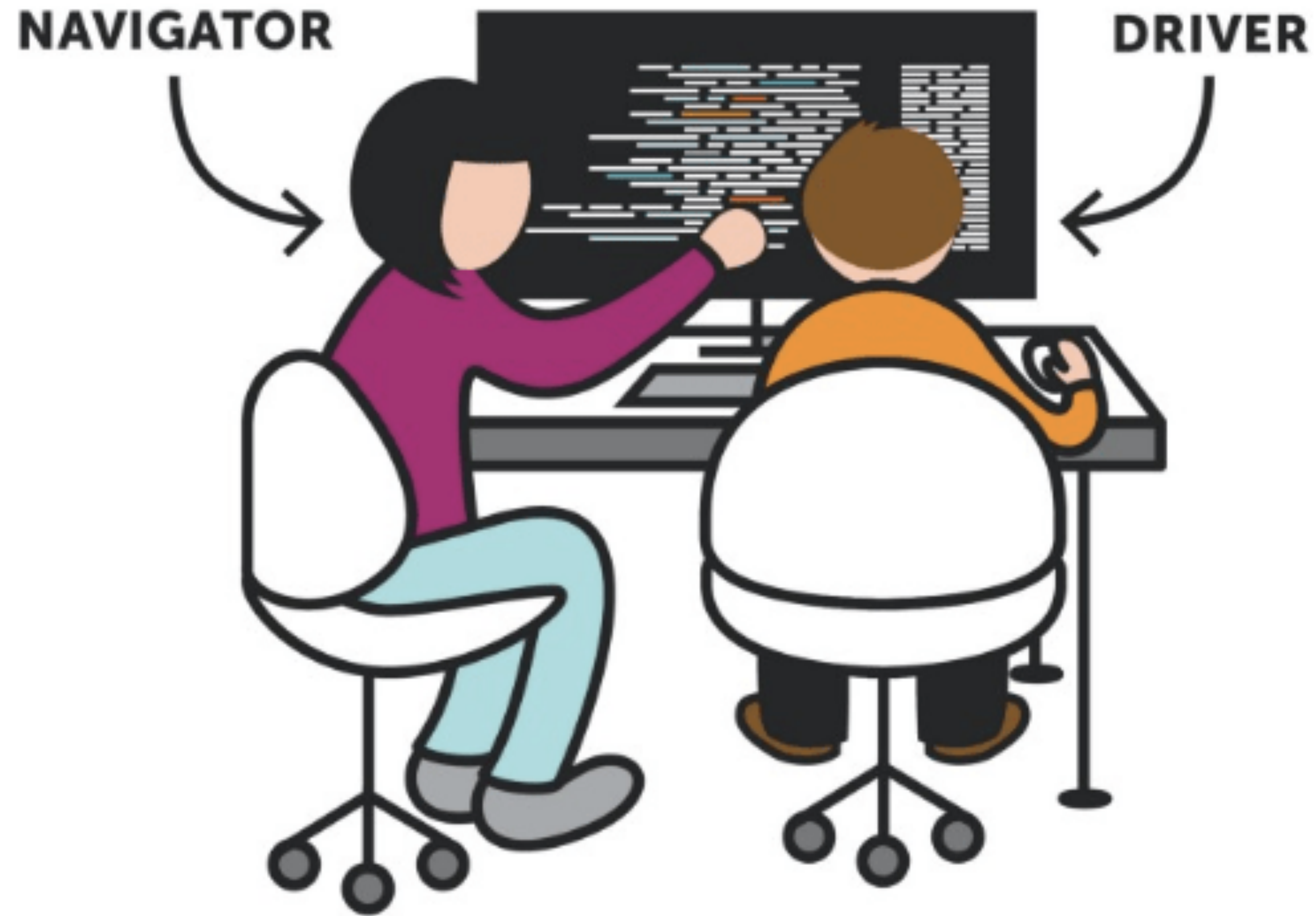


GitHub Copilot



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?

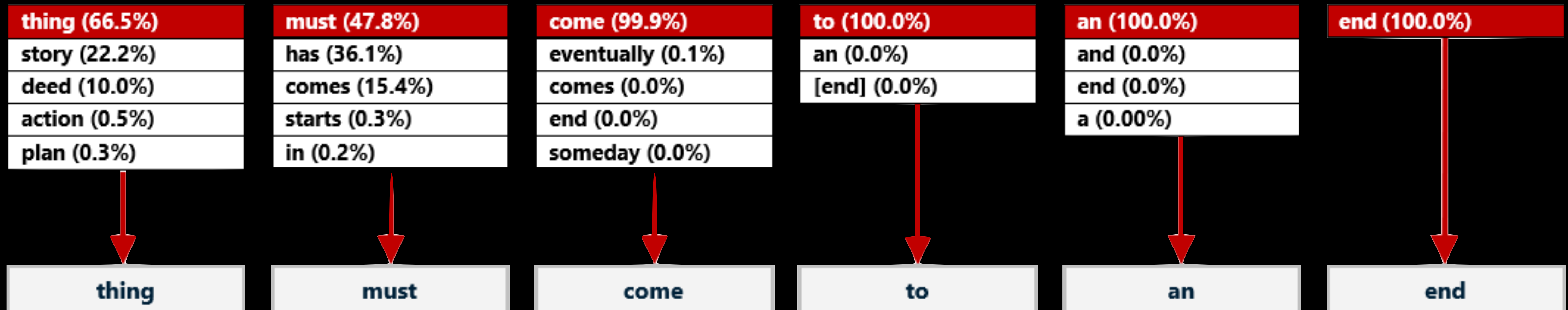
- It provides autocomplete suggestions while you code.
- You can get suggestions by typing code or describing it in natural language (i.e. code comments or markdown text).
- Copilot analyzes your file (and related files), offering suggestions in your editor.
- It uses [OpenAI Codex](#) to derive context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



OpenAI

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'
```

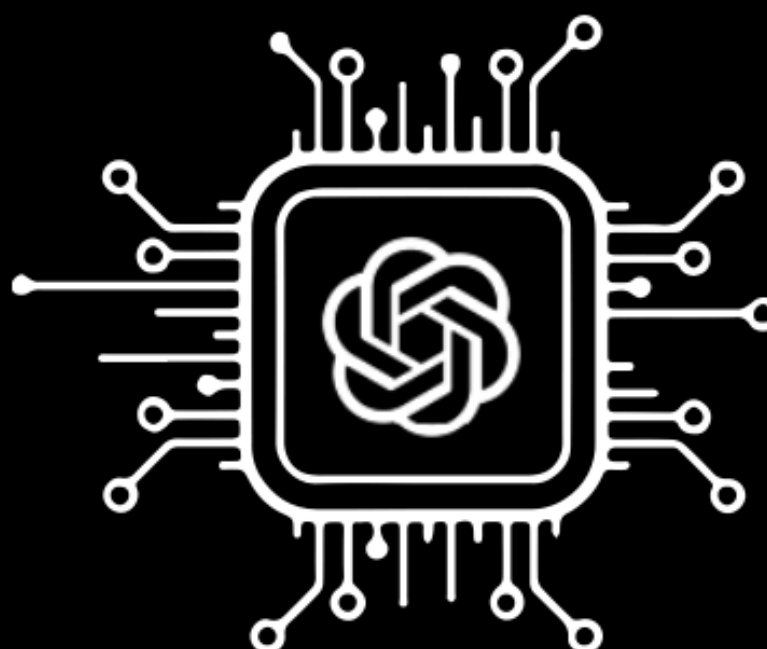
DALL·E

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.

GitHub Student Developer Pack

https://education.github.com/pack





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

Request a discount - GitHub EduXVirtual Event Kit - GitHub EducaXIntro to GitHub Flow - GitHub EdXData Science & Machine LearninXPrimer: Copilot - GitHub EducatiX+

https://education.github.com/discount_requests/application

GitHub.com

Education

StudentsTeachersSchoolsBenefitsEventsGlobal Campus

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

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

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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