

Class 16

Course Summary

Git & GitHub

Barry Grant
UC San Diego

<http://thegrantlab.org>

Today's Menu

- Summary of major learning goals,
- Course discussion and feedback
(https://etherpad.wikimedia.org/p/bggn213_W22)
- Final exam
 - ➔ Test structure, guidelines and rules
 - ➔ Topics and example questions
 - ➔ Exam preparation, discussion and open study
- Introduction to Git & GitHub (+ website portfolios)

Today's Menu

- Summary of major learning goals,
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 - Exam preparation, discussion and open study
- Introduction to Git & GitHub (+ website portfolios)



https://bioboot.github.io/bggn213_F21/class-material/BGGN213_exam_guidlines.pdf

The screenshot shows a web browser window with the URL https://bioboot.github.io/bggn213_F21/class-material/BGGN213_exam_guidlines.pdf in the address bar. 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 Canvas 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 Link:
https://etherpad.wikimedia.org/p/bggn213_W22

Thank you very much!

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:
Introduction to Git & GitHub



What is Git?

(1) An unpleasant or contemptible person. Often incompetent, annoying, senile, elderly or childish in character.



(2) A modern distributed version control system with an emphasis on speed and data integrity.



What is Git?

(1) An unpleasant or contemptible person. Often incompetent, annoying, senile, elderly or childish in character.



(2) A modern distributed version control system with an emphasis on speed and data integrity.



Version Control

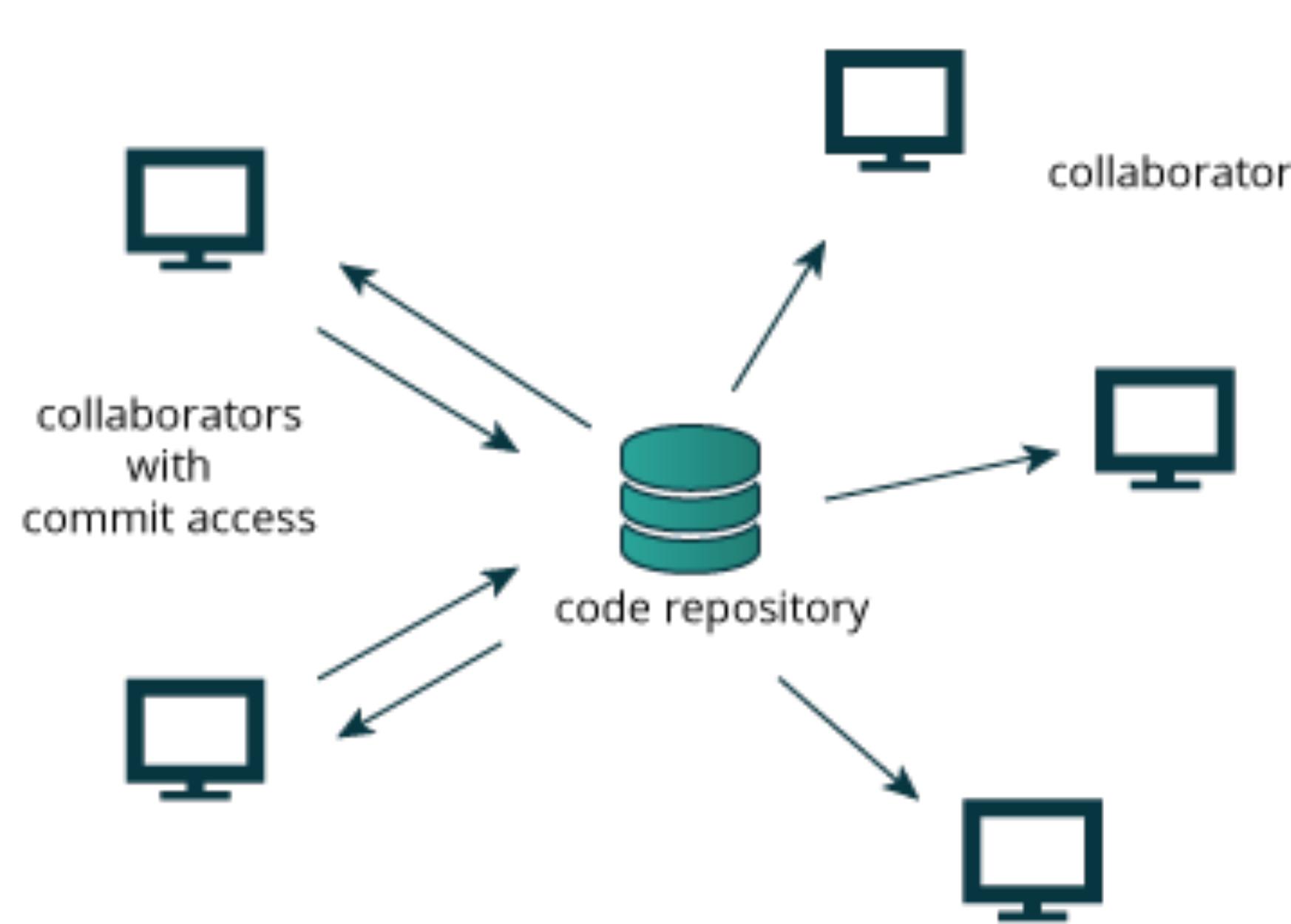
Version control systems (VCS) record changes to a file or set of files over time so that you can recall specific versions later.

	Free/open-source	CVS (1986, 1990 in C) · CVSNT (1998) · QVCS Enterprise (1998) · Subversion (2000)
	Proprietary	Software Change Manager (1970s) · Panvalet (1970s) · Endevor (1980s) · Dimensions CM (1980s) · DSEE (1984) · Synergy (1990) · ClearCase (1992) · CMVC (1994) · Visual SourceSafe (1994) · Perforce (1995) · StarTeam (1995) · Integrity (2001) · Surround SCM (2002) · AccuRev SCM (2002) · SourceAnywhere (2003) · Vault (2003) · Team Foundation Server (2005) · Team Concert (2008)
Client–server	Free/open-source	GNU arch (2001) · Darcs (2002) · DCVS (2002) · ArX (2003) · Monotone (2003) · SVK (2003) · Codeville (2005) · Bazaar (2005) · Git (2005) · Mercurial (2005) · Fossil (2007) · Veracity (2010)
	Proprietary	TeamWare (1990s?) · Code Co-op (1997) · BitKeeper (1998) · Plastic SCM (2006)

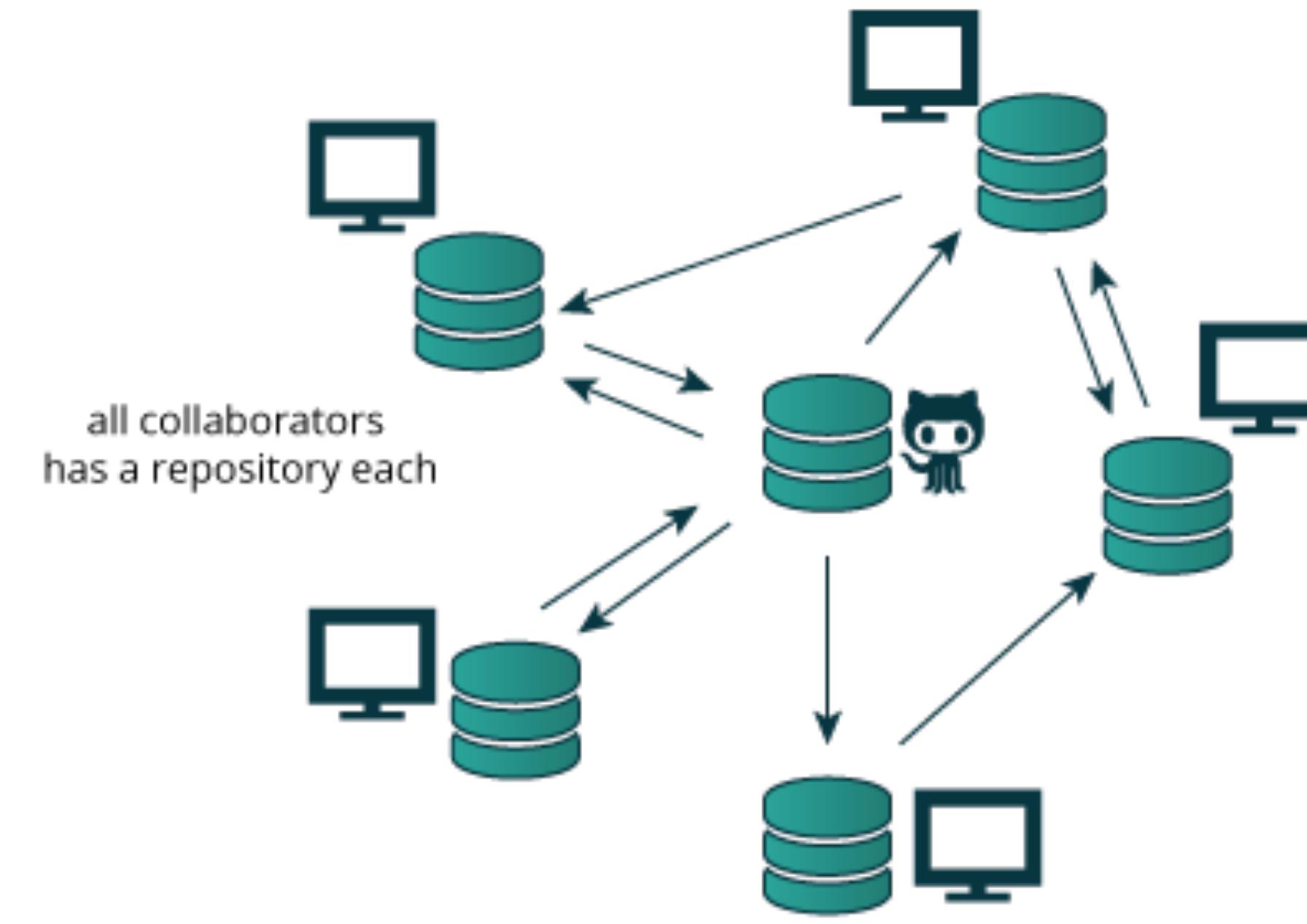
There are many VCS available, see:

https://en.wikipedia.org/wiki/Revision_control

Client-Server vs Distributed VCS



Client-server approach



Distributed approach

Distributed version control systems (DCVS) allows multiple people to work on a given project without requiring them to share a common network.

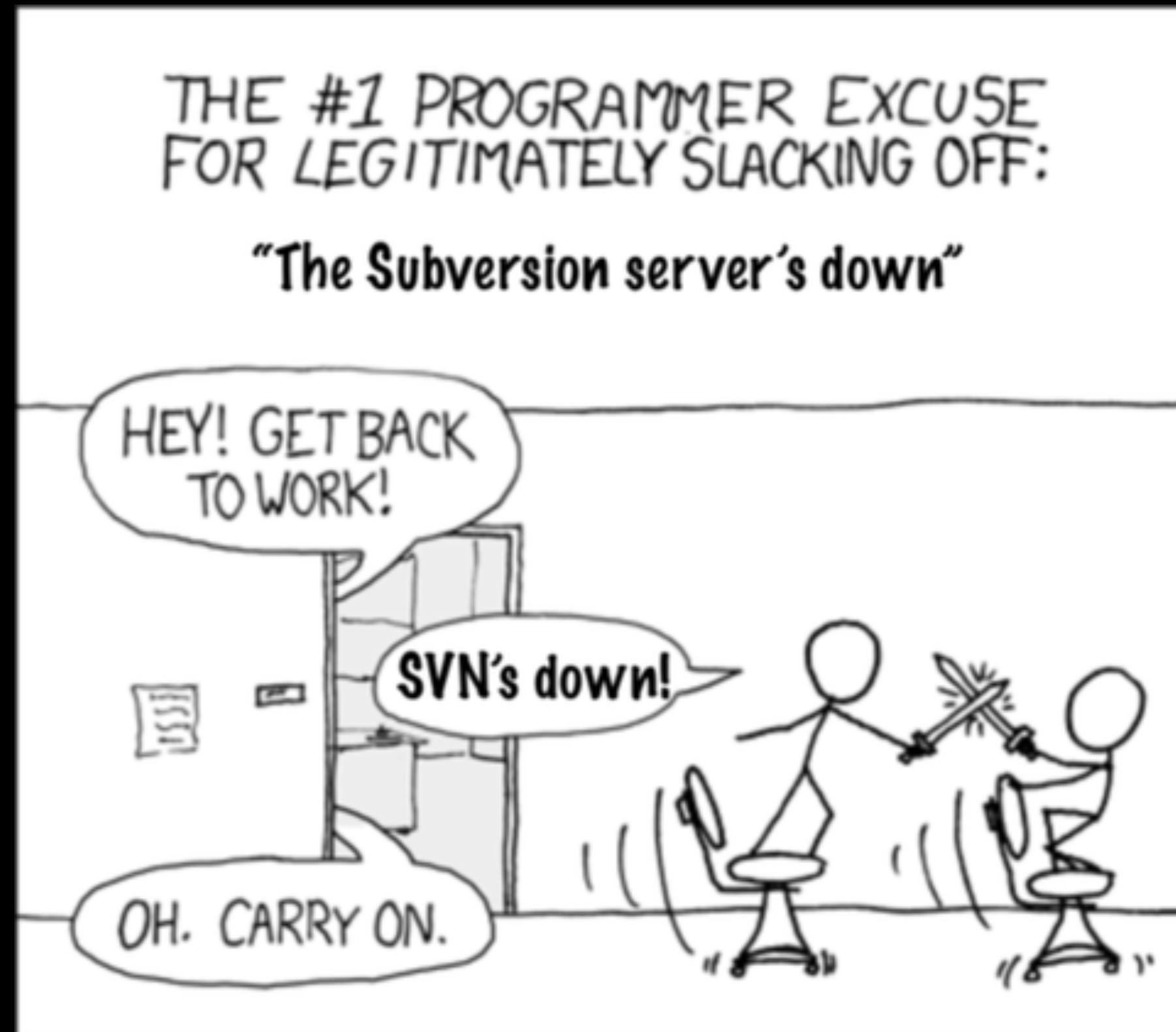
THE #1 PROGRAMMER EXCUSE
FOR LEGITIMATELY SLACKING OFF:

"The Subversion server's down"



<http://tinyurl.com/distributed-advantages>

Git is now the most popular free VCS!



Git offers:

- Speed
- Backups
- Off-line access
- Small footprint
- Simplicity*
- Social coding

<http://tinyurl.com/distributed-advantages>

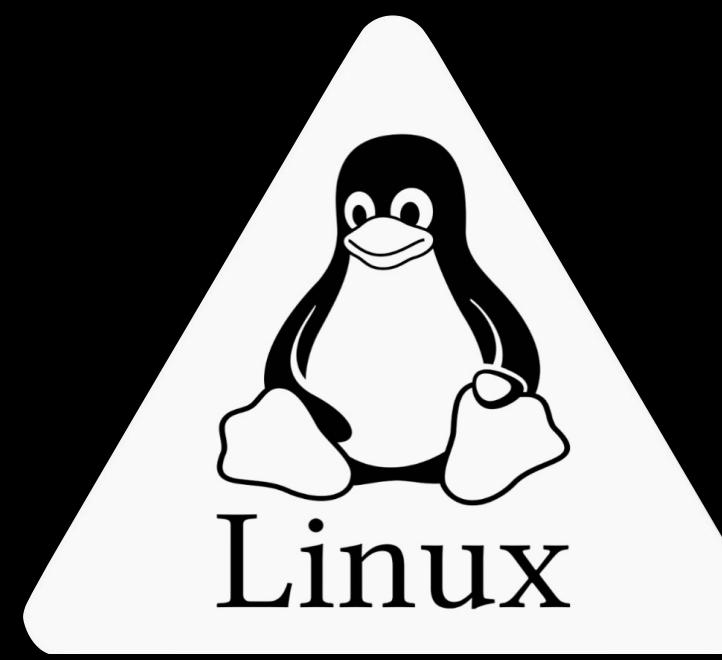
Where did Git come from?

Written initially by Linus Torvalds to support Linux kernel and OS development.

Meant to be distributed, fast and more natural.

Capable of handling large projects.

Now the most popular free VCS!





Why use Git?

Q. Would you write your lab book in pencil, then erase and overwrite it every day with new content?

Q. Would you write your lab book in pencil, then erase and overwrite it every day with new content?

Version control is the lab notebook of the digital world: it's what professionals use to keep track of what they've done and to collaborate with others.

Why use Git?

- Provides ‘snapshots’ of your project during development and provides a full record of project history.
- Allows you to easily reproduce and rollback to past versions of analysis and compare differences. (N.B. Helps fix software regression bugs!)
- Keeps track of changes to code you use from others such as fixed bugs & new features
- Provides a mechanism for sharing, updating and collaborating (like a social network)
- Helps keep your work and software organized and available

Obtaining Git

Note: You hopefully already have git installed!

To check open the “**Terminal**” tab in RStudio and type:

- 1 **which git**
- 2 **git --version**

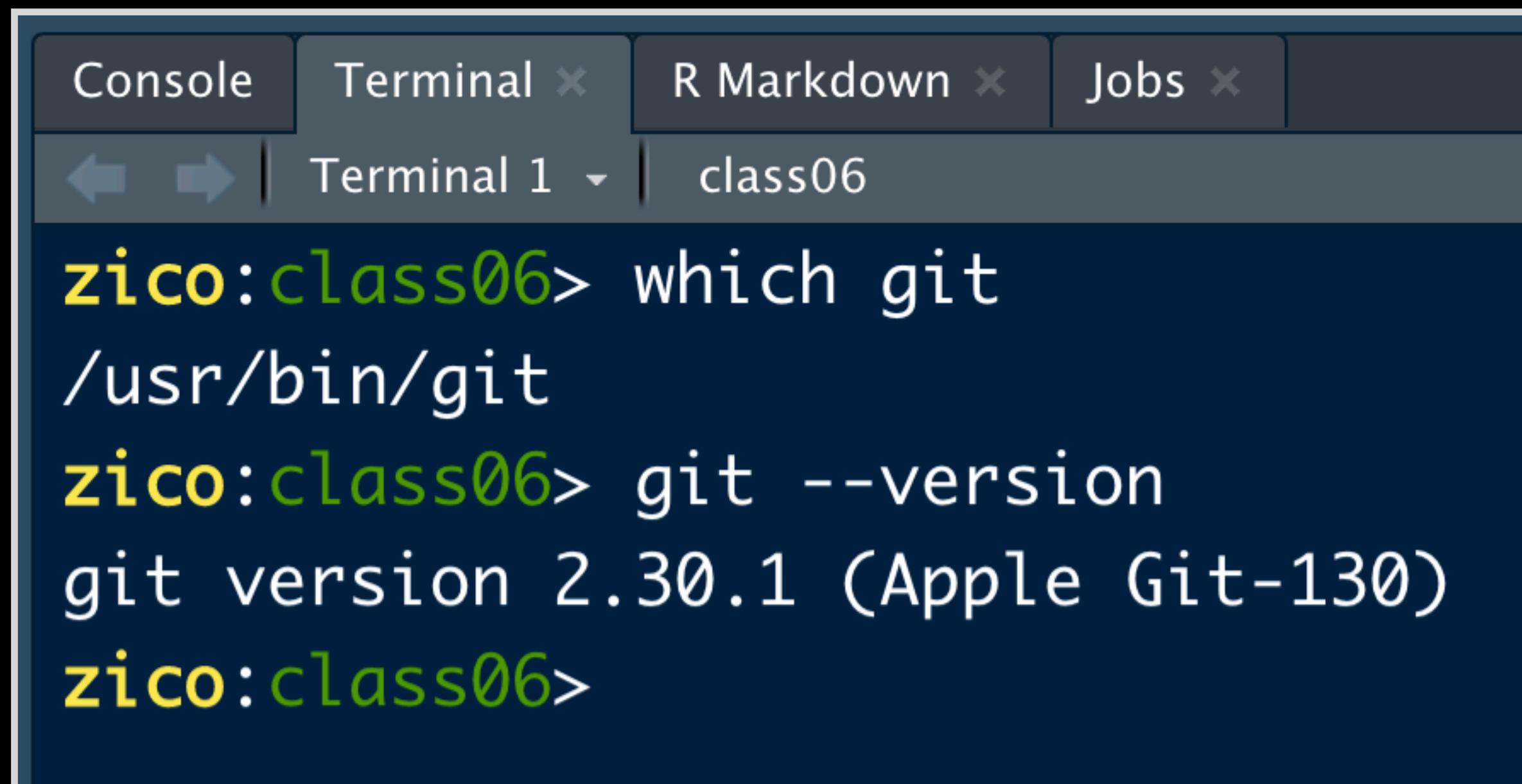
Obtaining Git

Note: You hopefully already have git installed!

To check open the “**Terminal**” tab in RStudio and type:

- 1 **which git**
- 2 **git --version**

Obtaining Git



The screenshot shows the RStudio interface with the Terminal tab active. The terminal window title is "Terminal 1 - class06". The terminal output shows the results of running the "which git" and "git --version" commands.

```
zico:class06> which git
/usr/bin/git
zico:class06> git --version
git version 2.30.1 (Apple Git-130)
zico:class06>
```

Note: You might already have git installed
To check open the “**Terminal**” tab in RStudio and type:

- 1 **which git**
- 2 **git --version**

Obtaining Git

Windows Only (if you have problems)

If the “**which git**” command did not work, try:

where git

If this works see next slide. If not then you need to install **GitBash**, instructions here:

Class Computer Setup Page

Mac Only (if you have problems)

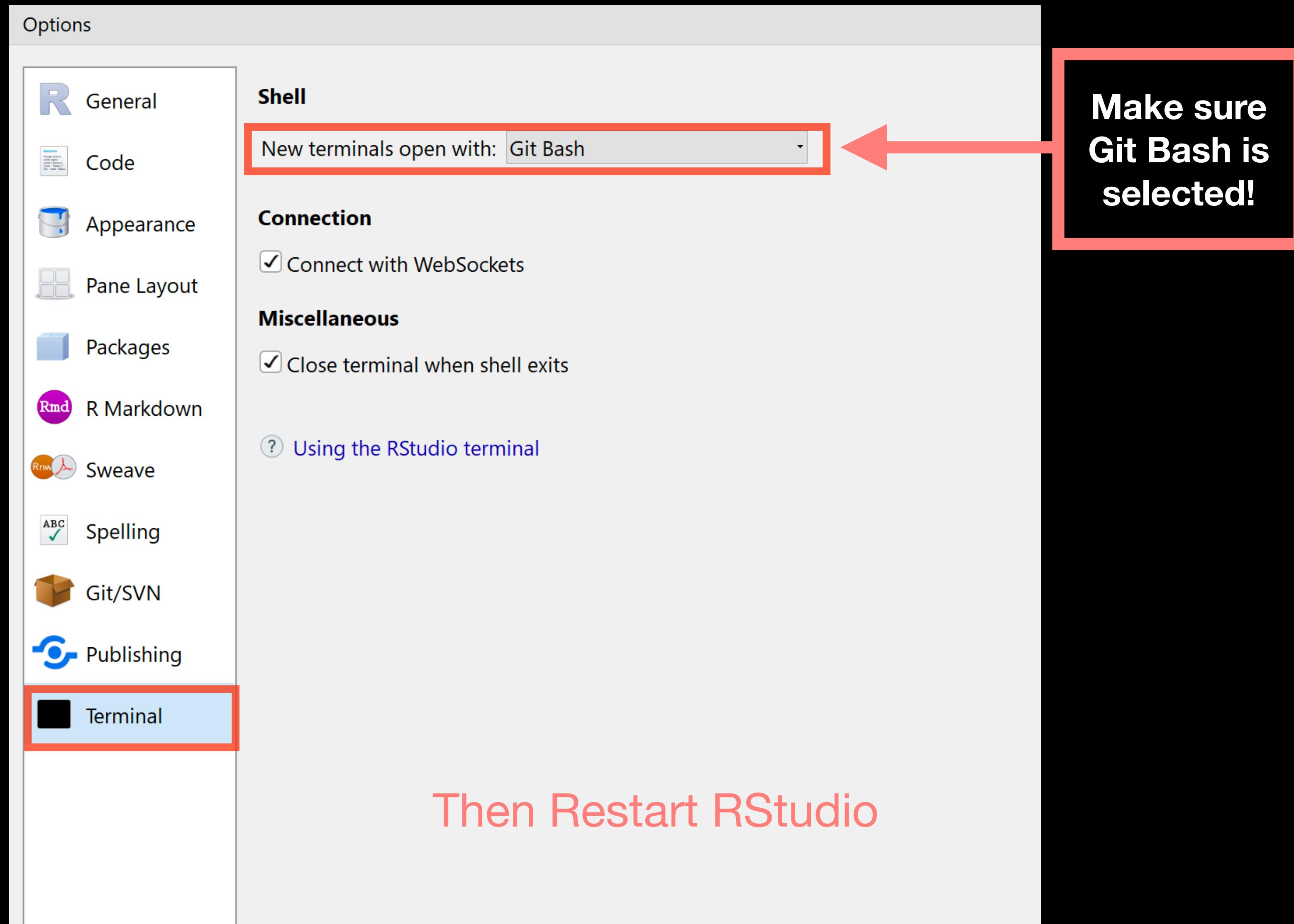
If the “**which git**” command did not work, you may need to install select developer tools.

In your Terminal type:

xcode-select --install

On a Windows PC Only!

Go to: RStudio > Tools > Global Options > Terminal



Note: You might already have git installed
To check open the “**Terminal**” tab in RStudio and type:

- 1 **which git**
- 2 **git --version**

Installing Git

Windows (if you have problems)

Follow the GitBash instructions here:

Class [Computer Setup Page](#)

Mac (if you have problems)

In the **Terminal** instal select developer tools

xcode-select --install

Configuring Git

Configuring Git

(RStudio **Terminal** Tab)
(...or *RStudio > Tools > Shell*)

First tell Git who you are

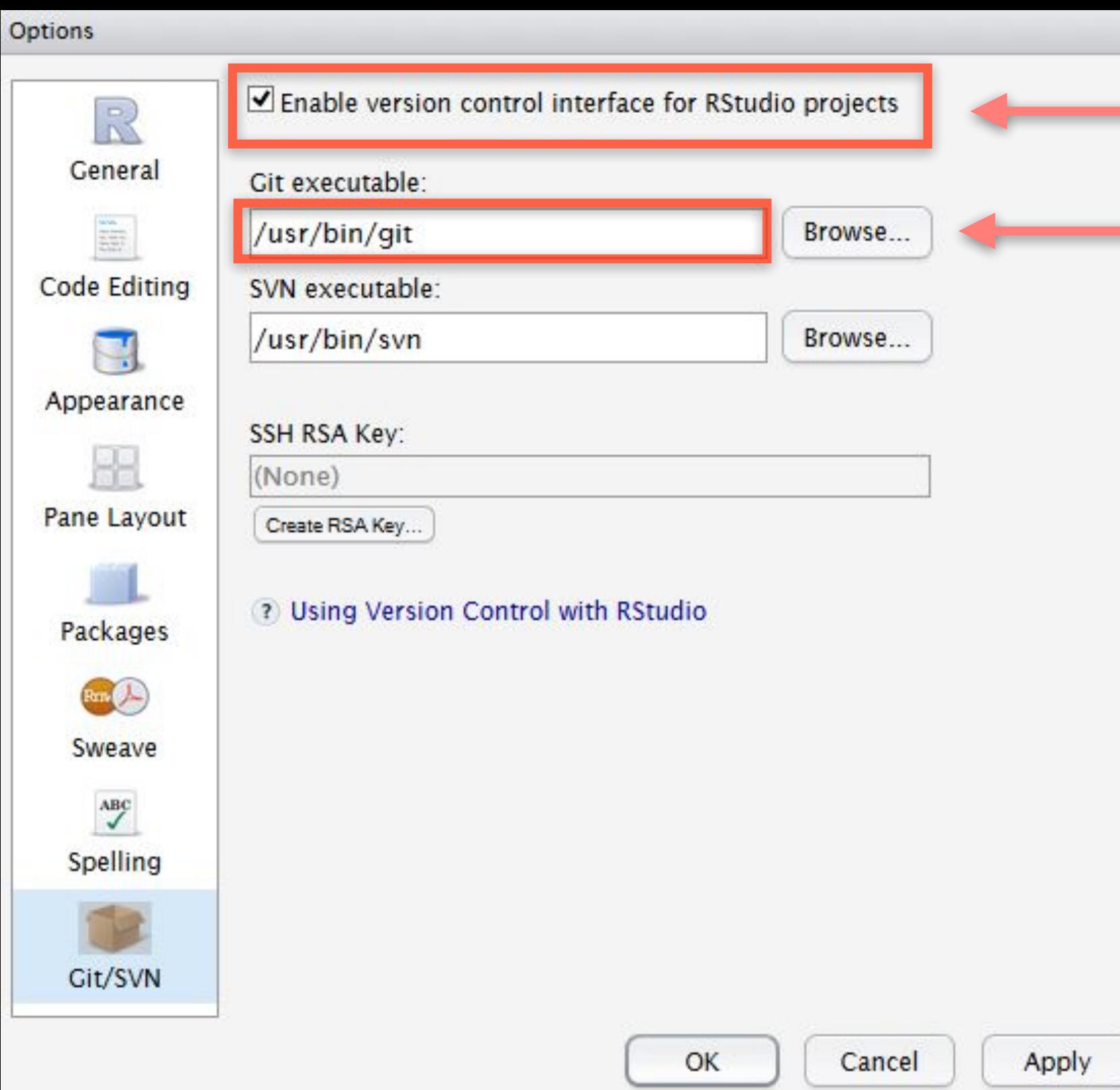
- > git config --global user.name "Barry Grant"
- > git config --global user.email "bjgrant@ucsd.edu"

Configuring RStudio

For Mac & Linux

(PC on next slide)

Go to: RStudio > Tools > Global Options > Git/SVN



- 1 *Make sure this is **ticked**!*
- 2 *Make sure this is **correct**!*

Check in your RStudio “Terminal” tab:

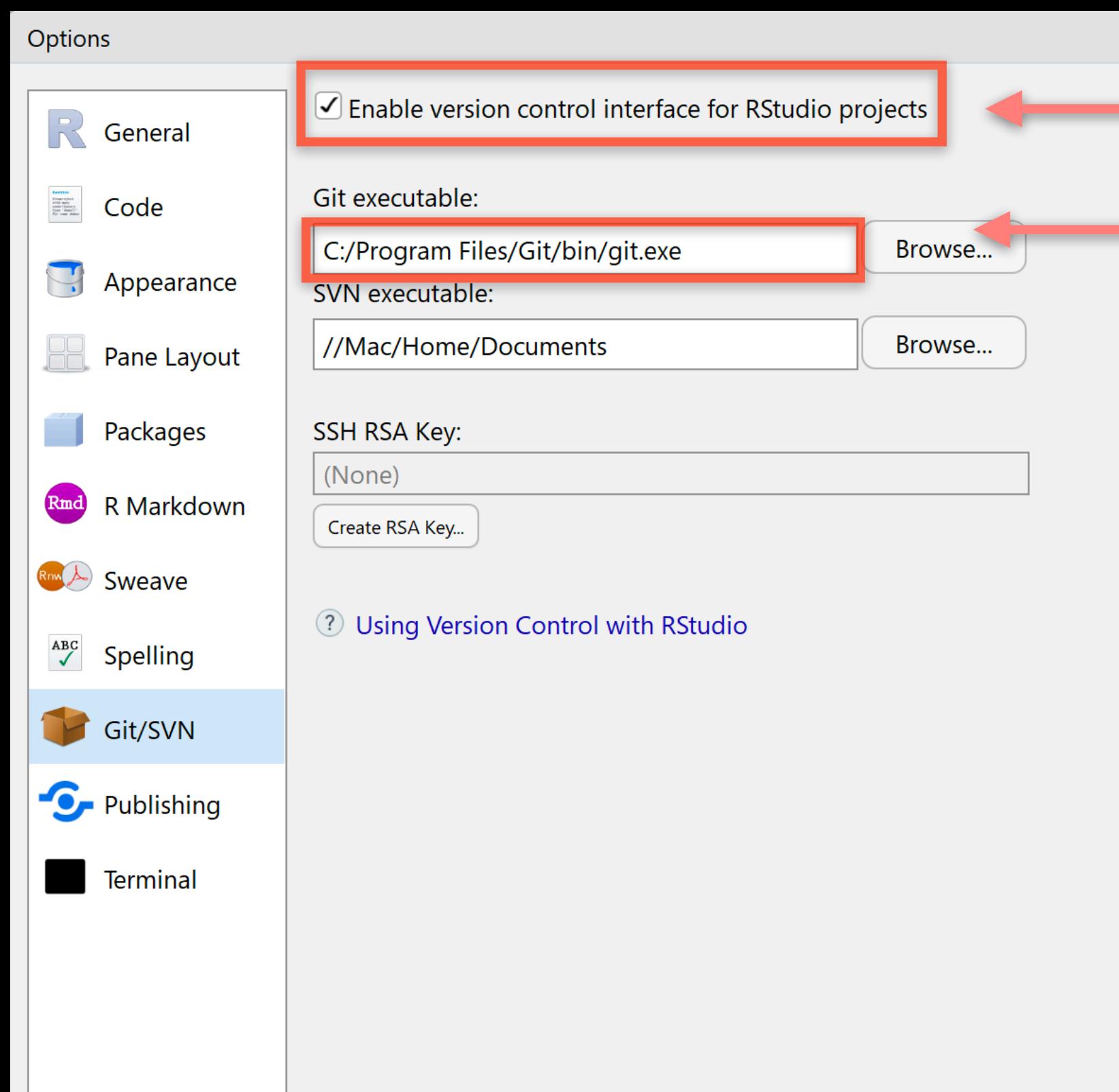
The screenshot shows the RStudio interface with multiple tabs: Console, Terminal x, R Markdown x, Terminal 1, and another. The Terminal 1 tab is active, displaying the following text in a dark blue terminal window:

```
blitz:another> which git
/usr/local/bin/git
blitz:another>
```

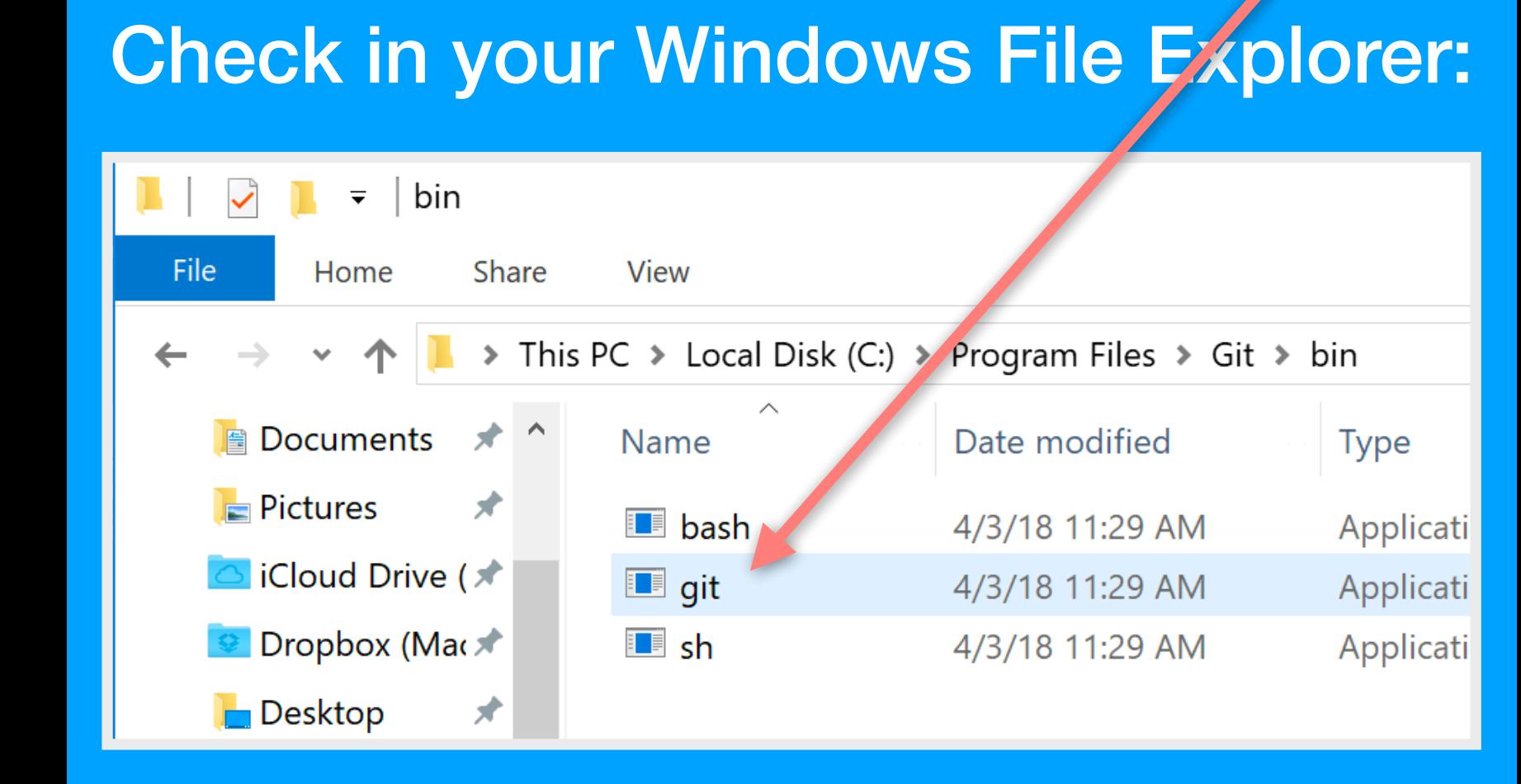
A large red arrow points from the 'Git executable' field in the options dialog to the '/usr/local/bin/git' line in the terminal output.

On a PC!

Go to: RStudio > Tools > Global Options > Git/SVN



- 1 *Make sure this is **ticked**!*
- 2 This is the PATH for PC!



Restart RStudio!

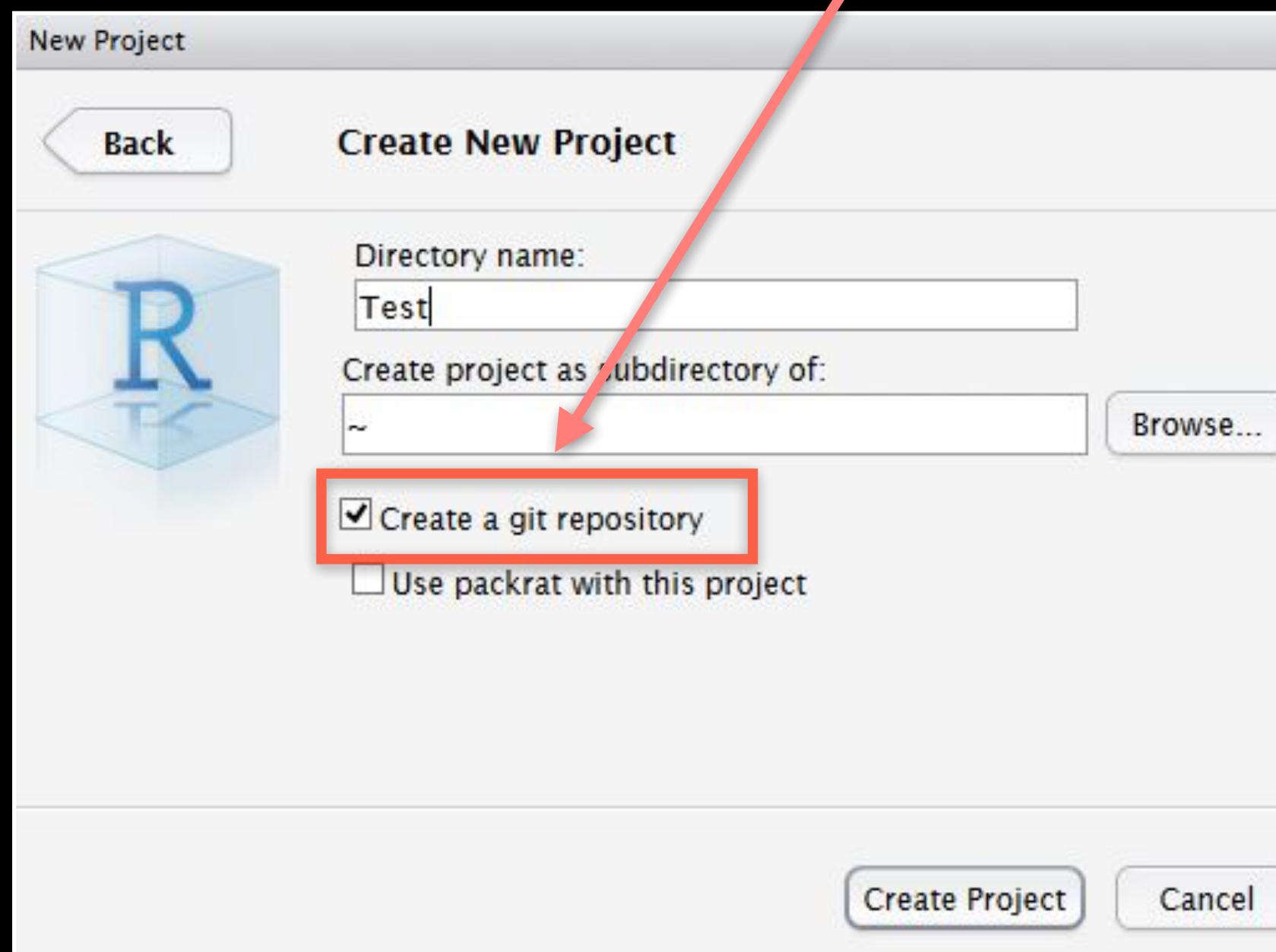
Using Git

Using Git

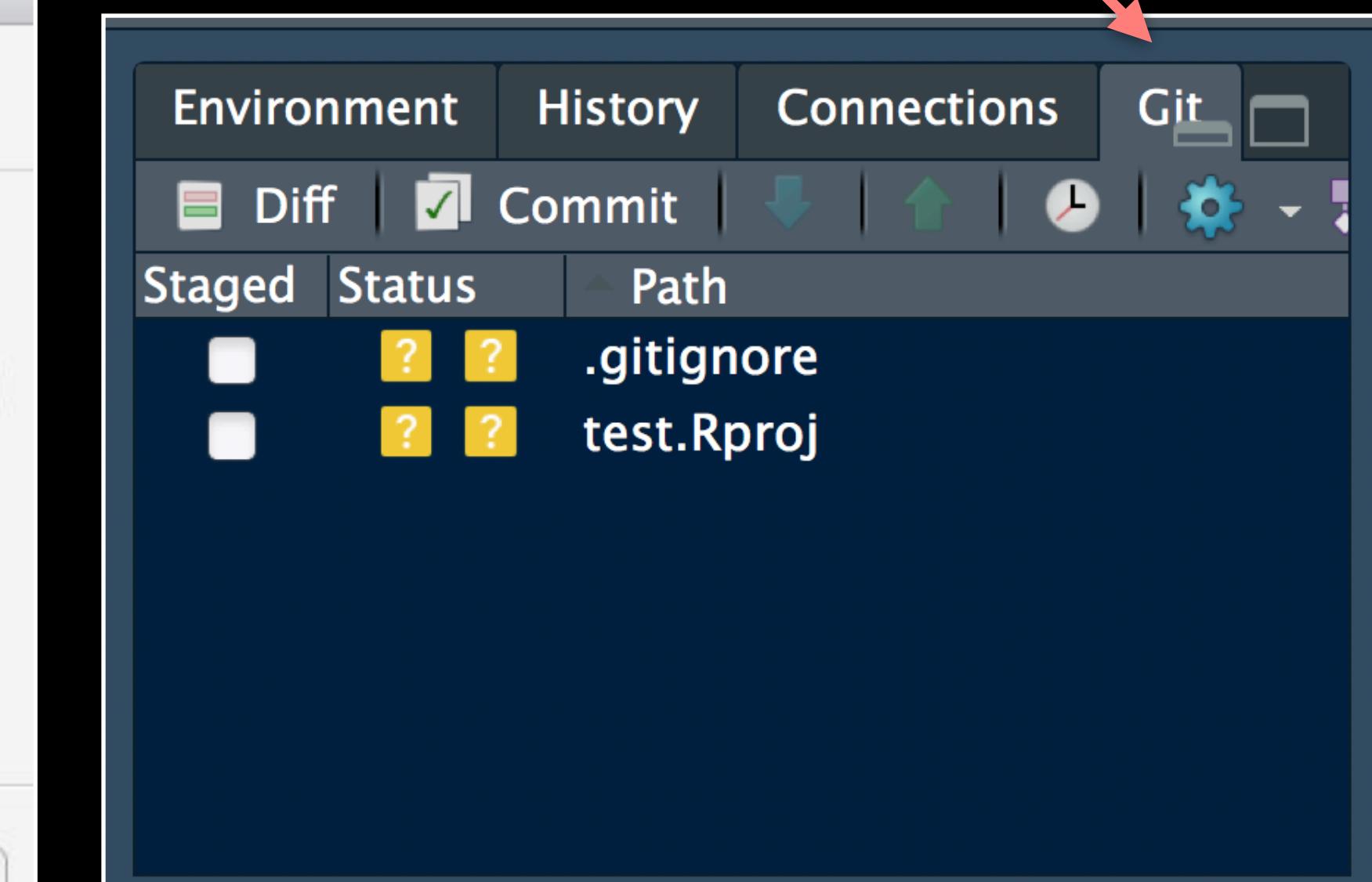
1. Initiate a Git repository.
2. Edit content (i.e. change some files).
3. Store a 'snapshot' of the current file state.*

Create a new **Test** RStudio project

1 New option to create a Git repository...



2 New Git tab...



Check if new Git options appear in RStudio?

Using Git in RStudio

1. **Initiate** a git repository for an RStudio Project
2. Do your work and edit content as normal
3. Store a ‘snapshot’ of the current file state
 - (a) Periodically **add** important files to git “Staging Area”
 - (b) **Commit** changes to your “git repository”

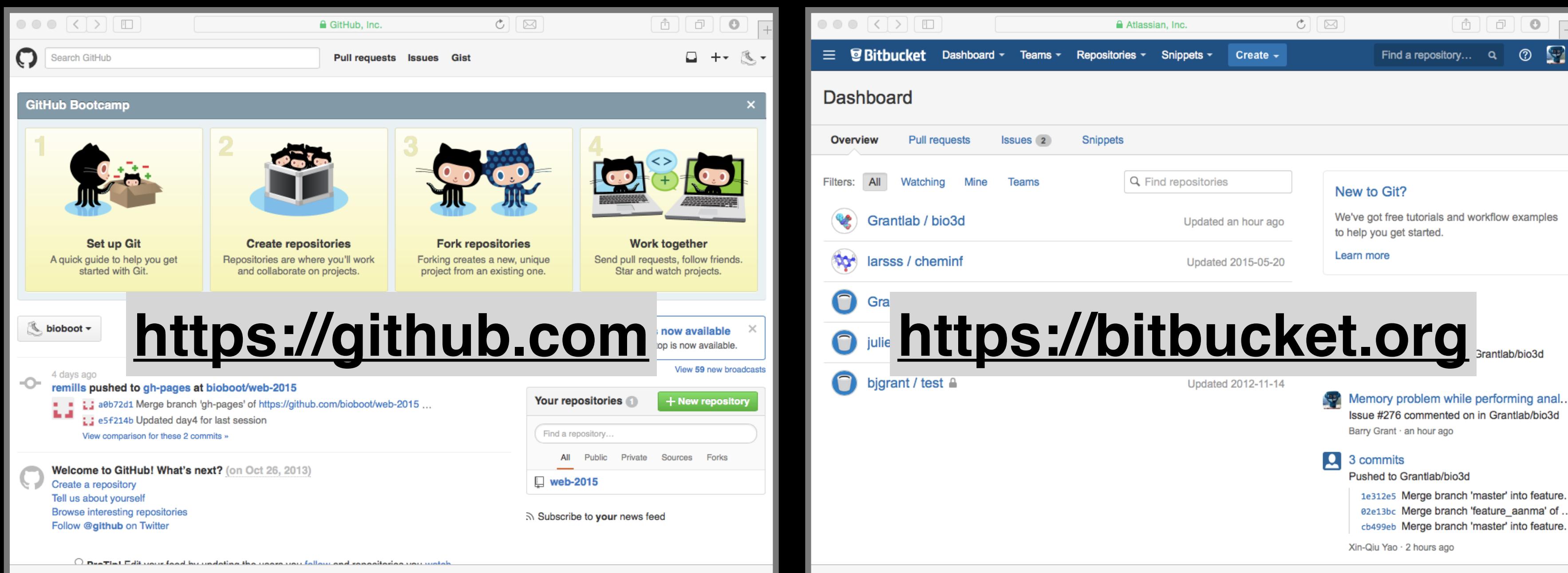
Rinse and repeat....

Follow along!

Demo:

GitHub & Bitbucket

GitHub and **Bitbucket** are two popular hosting services for Git repositories. These services allow you to share your projects and collaborate with others using both '**public**' and '**private**' repositories*.



wsj.com

Nikkei
17893.73 0.49% Hang Seng
21404.96 0.72% U.S. 10 Yr
-0/32 Yield 2.074% Crude Oil
39.17 -0.36% Yen
119.16 0.26% EXPAND

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TECH

GitHub Raises \$250 Million at \$2 Billion Valuation

Capital raise puts company's total funding at \$350 million





Analytics
How does your organization's talent measure up to its technology?
[Read the MIT Sloan report](#) 

www.bbc.com/news/technology-44351214

Home Gmail Gcal Bitbucket GitHub BIMM143_F18 BGGN213_S18 BIMM-194 GDocs Disqus Blink News Atmosphere Galaxy + MMTF

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NEWS

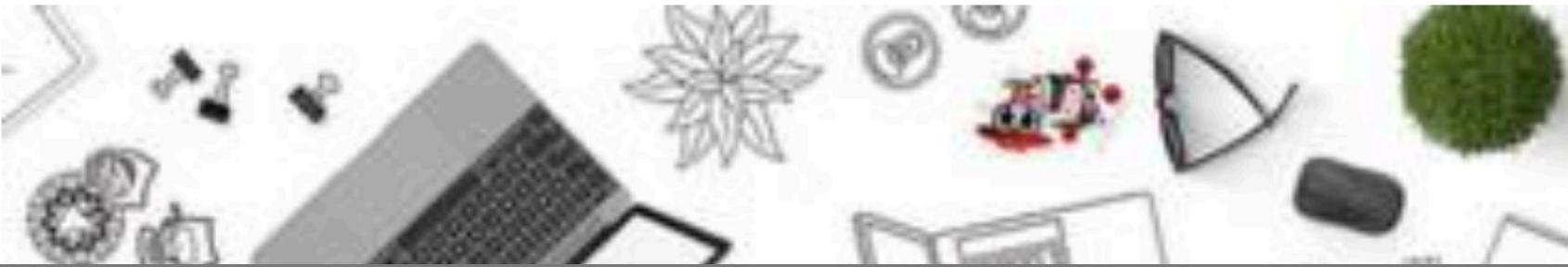
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Microsoft buys Github code-sharing site for \$7.5bn

 **Dave Lee**
North America technology reporter

4 June 2018 | [Comment](#)

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Top Stories

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Bulger was severely beaten by one or more inmates shortly after arriving at the prison, sources say.
30 October 2018

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30 October 2018

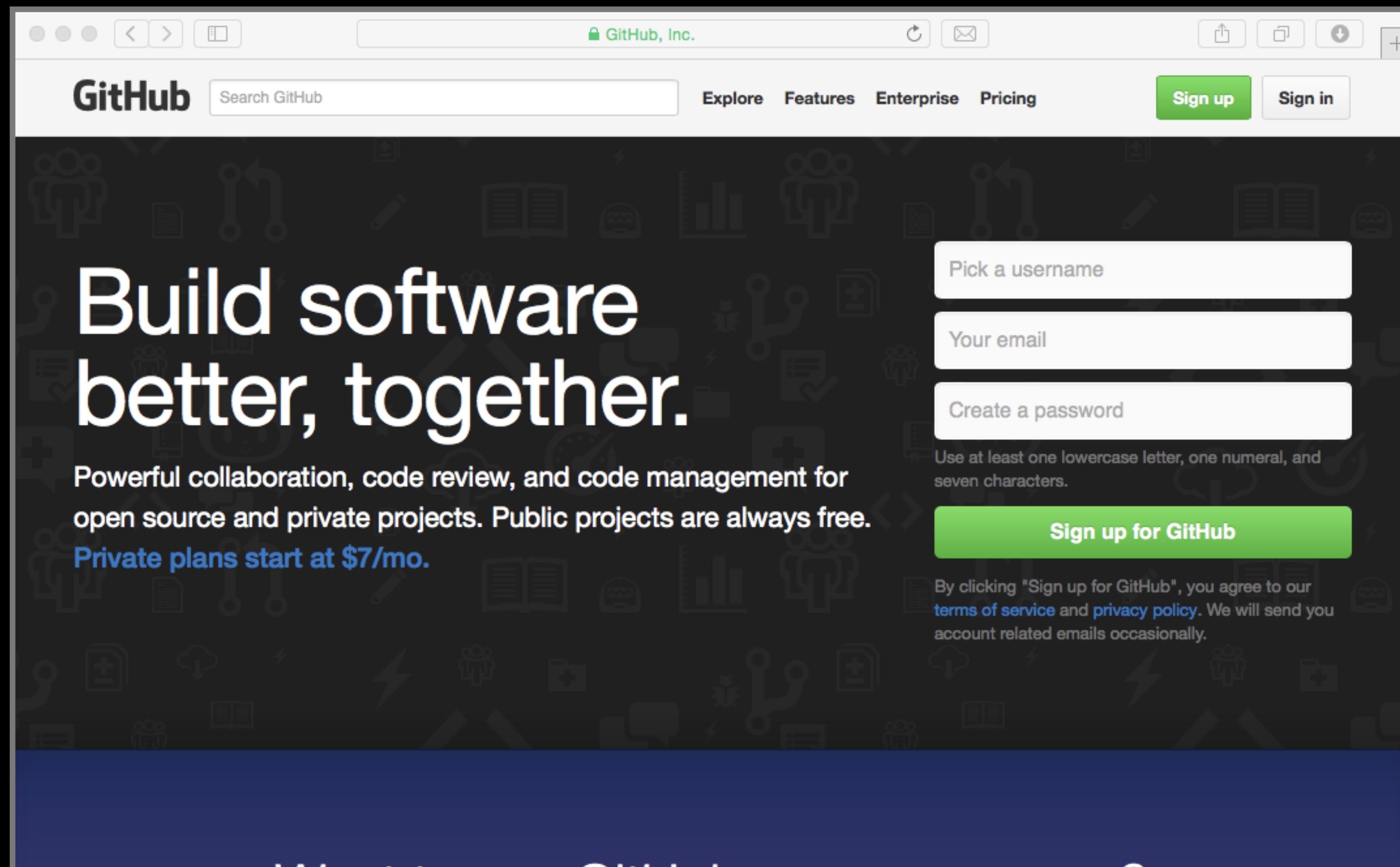
What do American voters care about?
30 October 2018

What is the big deal?

- At the simplest level GitHub and Bitbucket offer **backup** of your projects history and a centralized mechanism for **sharing** with others by putting **your Git repo online**.
 - GitHub in particular is often referred to as the “nerds FaceBook and LinkedIn combined”.
- At their core both services **offer a new paradigm for open collaborative project development**, particularly for software.
 - In essence they allow anybody to contribute to any public project and get acknowledgment.

First sign up for a GitHub account

<https://github.com>



Pick the FREE plan!

The screenshot shows the GitHub account setup process. At the top, there are three steps: 'Completed' (Set up a personal account), 'Step 2: Choose your plan' (which is highlighted in blue), and 'Step 3: Go to your dashboard'. The main area is titled 'Choose your personal plan' and lists five plans: Large (\$50/month, 50 repos), Medium (\$22/month, 20 repos), Small (\$12/month, 10 repos), Micro (\$7/month, 5 repos), and Free (\$0/month, 0 repos). The 'Free' plan is circled in red and has a 'Chosen' button next to it. To the right, a box lists 'Each plan includes:' with items like Unlimited collaborators, Unlimited public repositories, Free setup, HTTPS Protection, Email support, and Wikis, Issues, Pages, & more.

Plan	Cost	Private repositories	Action
Large	\$50/month	50	Choose
Medium	\$22/month	20	Choose
Small	\$12/month	10	Choose
Micro	\$7/month	5	Choose
Free	\$0/month	0	Chosen

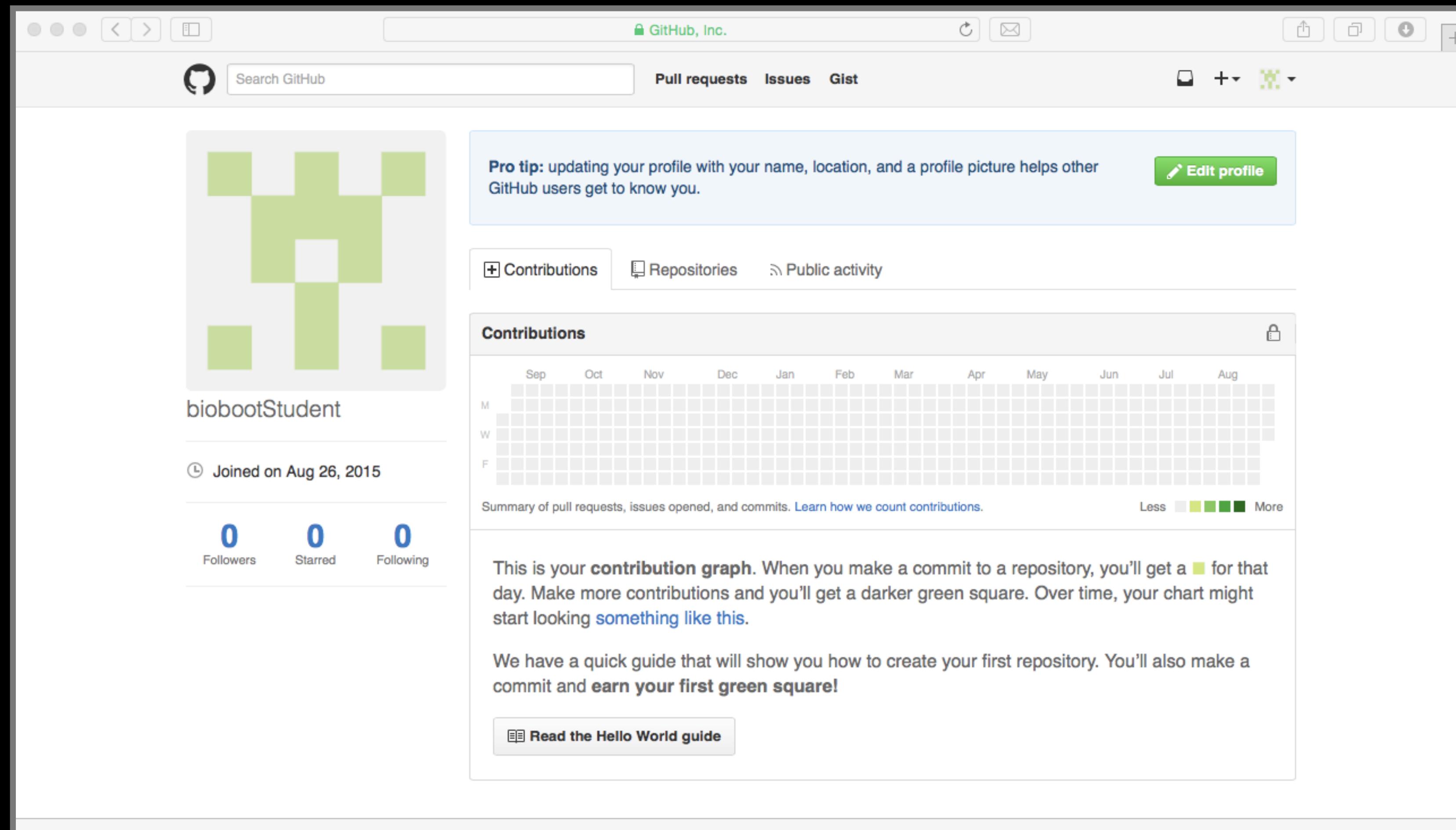
Each plan includes:

- Unlimited collaborators
- Unlimited public repositories
- ✓ Free setup
- ✓ HTTPS Protection
- ✓ Email support
- ✓ Wikis, Issues, Pages, & more

Charges to your account will be made in **US Dollars**. Converted prices are provided as a convenience and are only an estimate based on current exchange rates. Local prices will change as the exchange rate fluctuates.
Don't worry, you can cancel or upgrade at any time.

Your GitHub homepage

Check your email for verification request



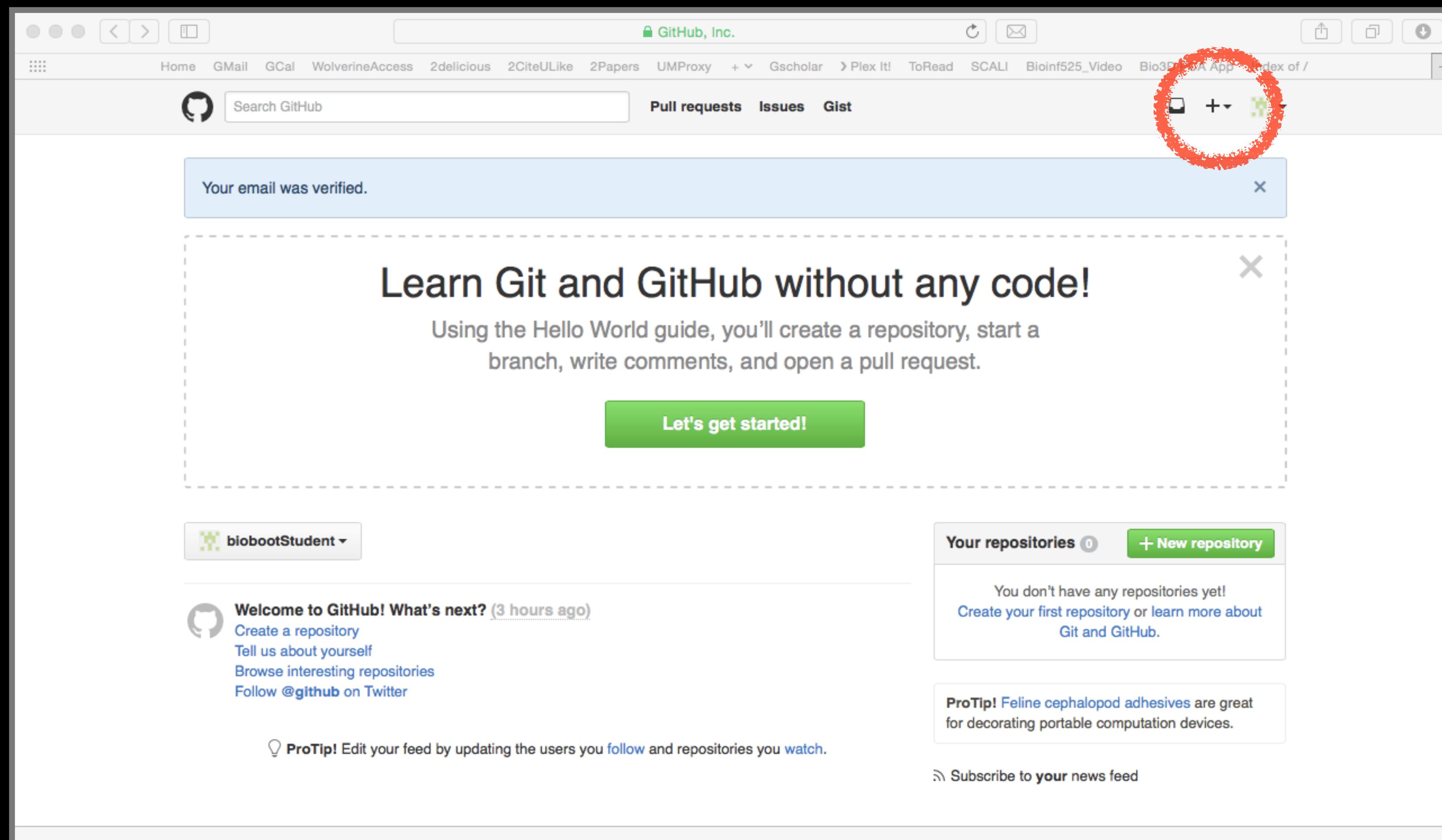
Connecting RStudio to GitHub

Create a **Personal Access Token** (PAT) on GitHub

See **section 4** of lab worksheet

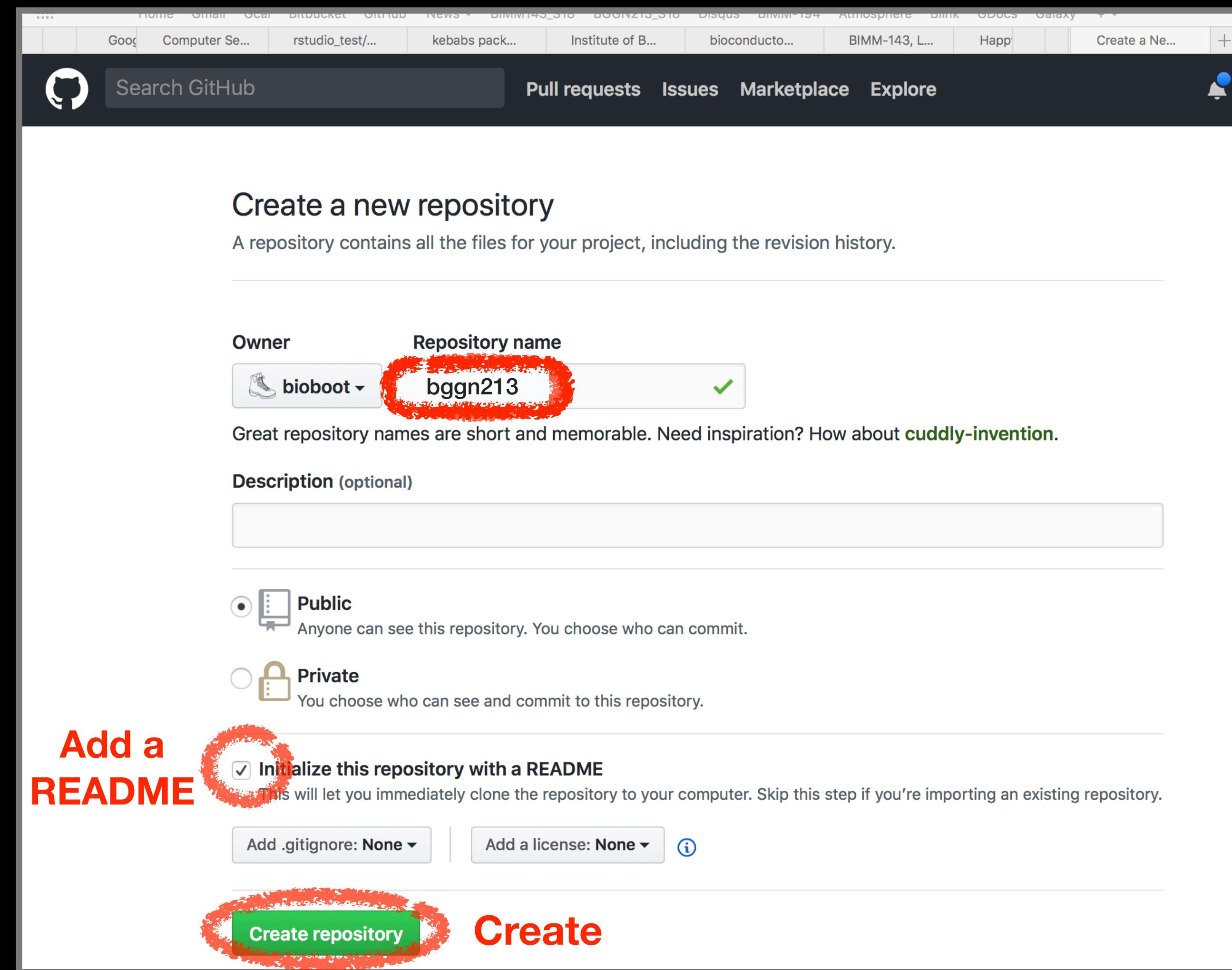
Skip the hello-world tutorial

<https://guides.github.com/activities/hello-world/>

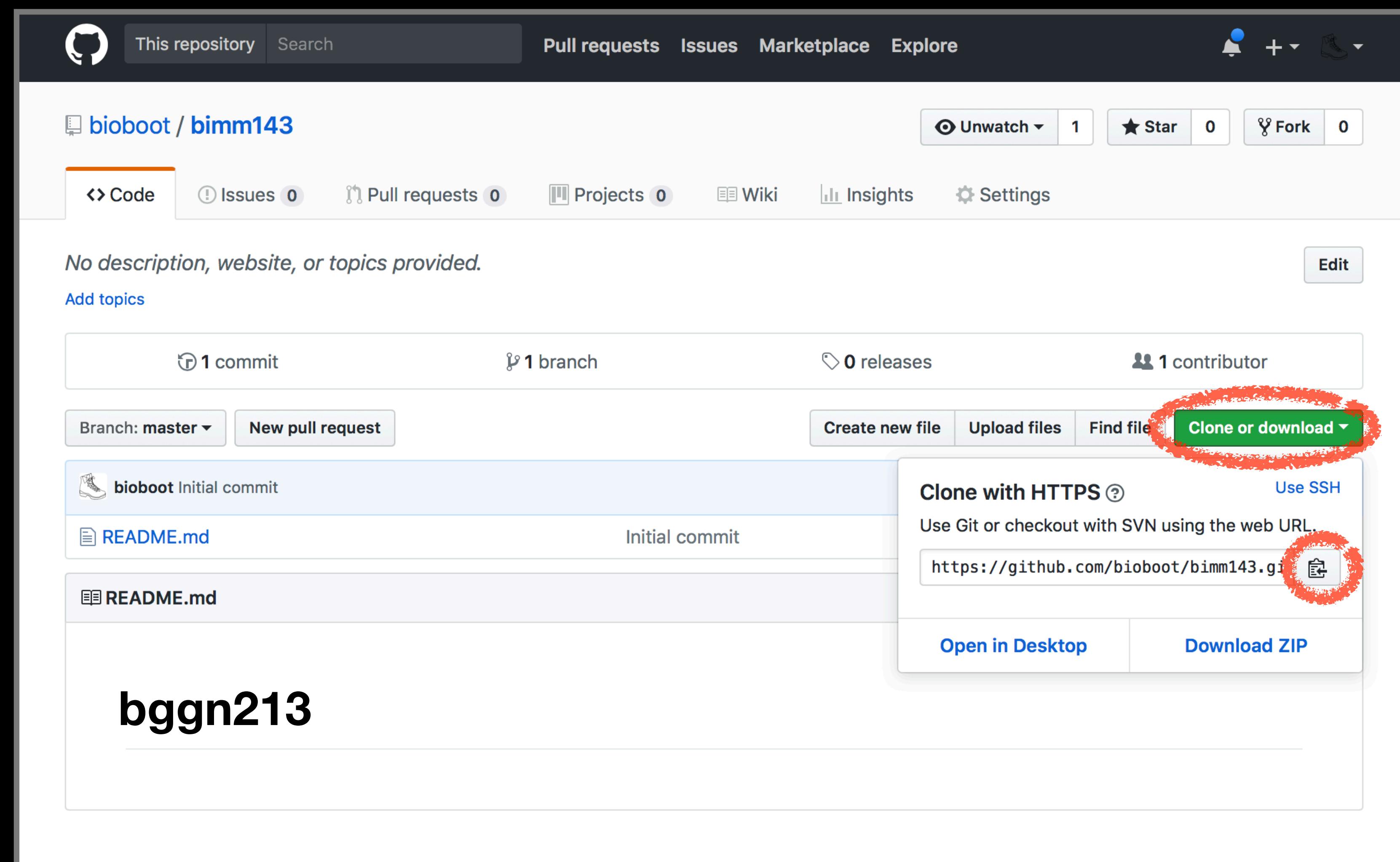


Name your repo

bggn213



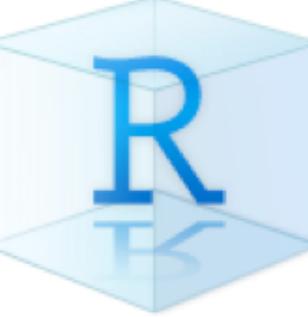
Copy the “Clone” HTTPS link



RStudio > New Project > Version Control

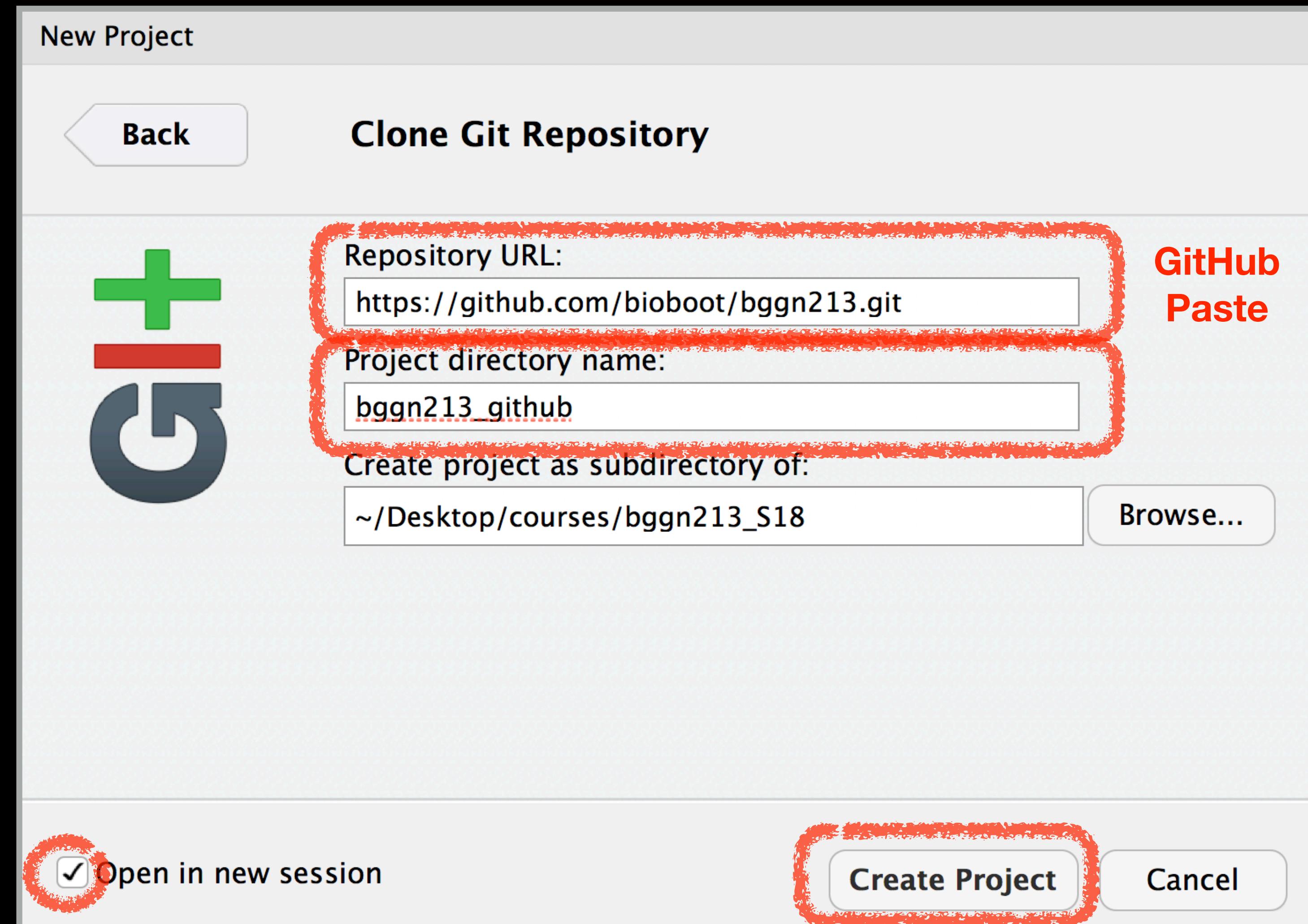
New Project

Create Project

- **New Directory**
Start a project in a brand new working directory >
- **Existing Directory**
Associate a project with an existing working directory >
- **Version Control**
Checkout a project from a version control repository >

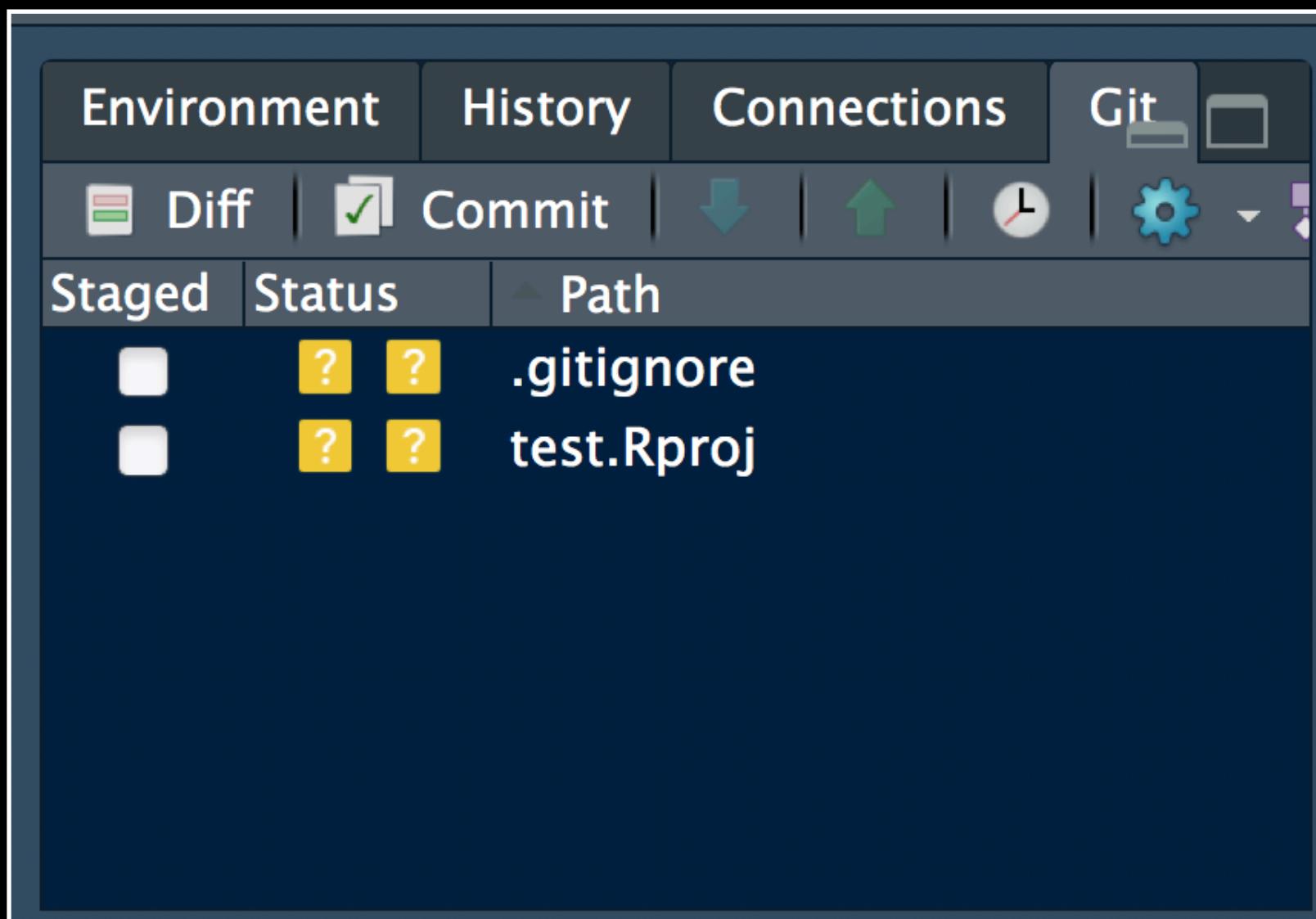
Cancel

RStudio > New Project > Version Control



Demo of editing, adding committing and pushing

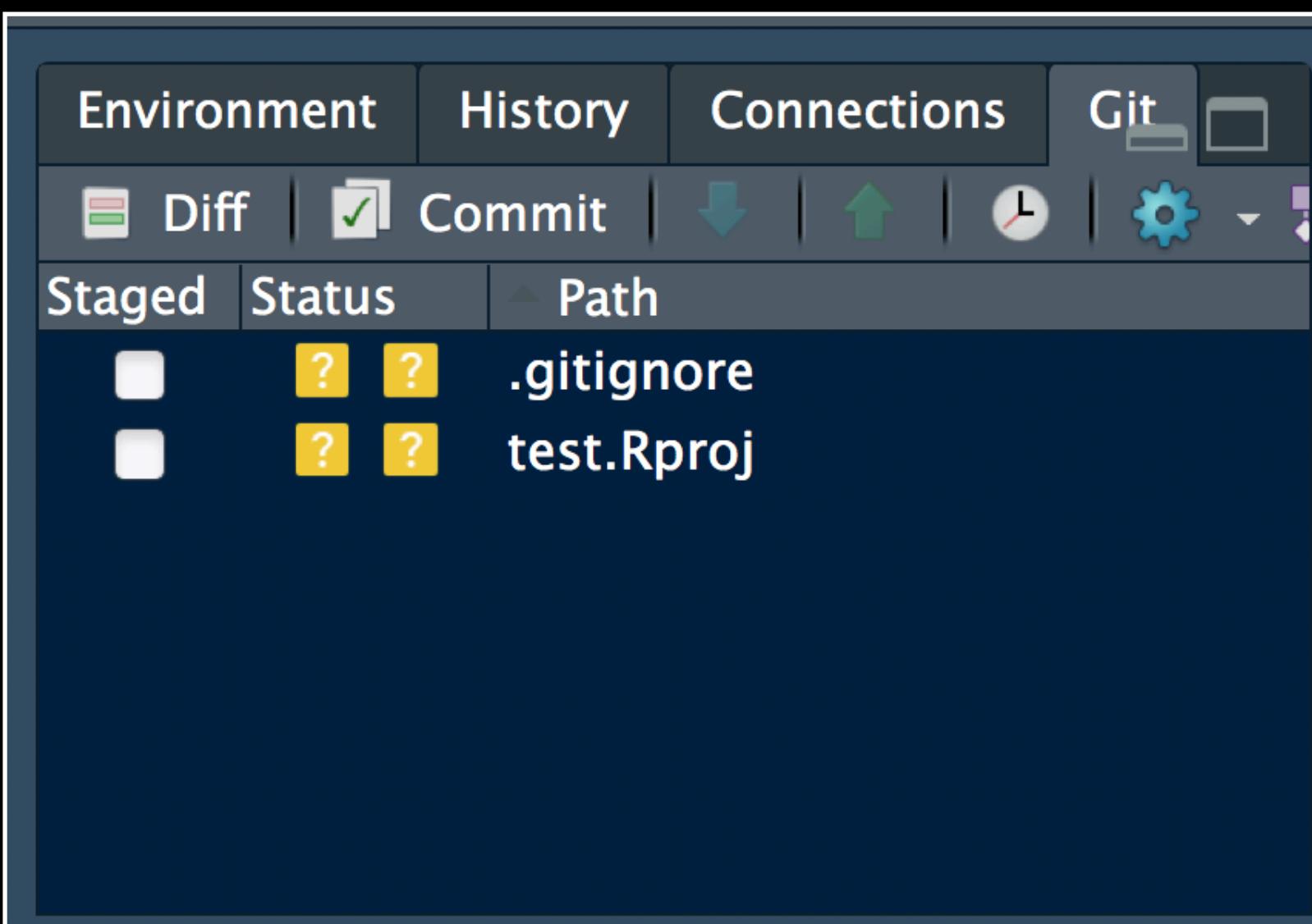
**Check if new Git tab
Appears in RStudio?**



Now experiment editing the
README.md file in RStudio
and adding, committing and
pushing changes to GitHub
via this tab

Demo of *editing, adding committing and pushing*

**Check if new Git tab
Appears in RStudio?**



Now experiment editing the README.md file in RStudio and adding, committing and pushing changes to GitHub via this tab

When you are ready copy your different class directories/projects to this new GitHub tracked folder

Side-note: How to edit online

Specifically lets add some Markdown content

The screenshot shows a GitHub repository page for 'biobootStudent / demo1_github'. The 'Branch: master' dropdown is set to 'master'. The main content is the 'demo1_github / README' file, which contains the following text:

```
1 # My first Git repo is now online
2 This is a first line of text.
3 This is a 2nd line of text.
4
5 I am going to use **markdown** syntax from now on because it is _cool_!
6 I am a student in [bioboot camp](http://bioboot.github.io/web-2015/)
```

A red circle highlights the edit icon (a pencil) located in the top right corner of the code editor area. The GitHub interface includes a sidebar with various icons and links.

Summary

- Git is a popular ‘distributed’ version control system that is lightweight and free
- GitHub and BitBucket are popular hosting services for git repositories that have changed the way people contribute to open source projects
- Introduced basic git and GitHub usage within RStudio and encouraged you to adopt these ‘best practices’ for your future projects.

Bonus:
GitHub Spit & Polish

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](#)

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 GitHub repository page for 'bioboot / bimm143_fall18'. The page includes a navigation bar with links to Home, Gmail, Gcal, Bitbucket, GitHub, BIMM143_F18, BGNN213_S18, BIMM-194, GDocs, Disqus, Blink, News, Atmosphere, Galaxy, and MMTF. The main content area displays the repository details: 'bioboot / bimm143_fall18', 'Code' tab selected, 22 commits, 1 branch, 0 releases, 1 contributor, and a description 'My class repo for bimm143 at UCSD'. It also shows a 'Manage topics' link and a summary bar with 22 commits, 1 branch, 0 releases, and 1 contributor. At the bottom, there are buttons for 'Branch: master', 'New pull request', 'Create new file', 'Upload files', 'Find file', and 'Clone or download'. A list of recent commits is shown, including 'Add class18' by bioboot, 'Add class 5' by class05, and 'add class08' by class08.

GitHub, Inc. github.com/bioboot/bimm143_fall18

Search or jump to... / Pull requests Issues Marketplace Explore

Unwatch 1 Star 0 Fork 0

Code Issues 0 Pull requests 0 Projects 0 Wiki Insights Settings

My class repo for bimm143 at UCSD Edit

Manage topics

22 commits 1 branch 0 releases 1 contributor

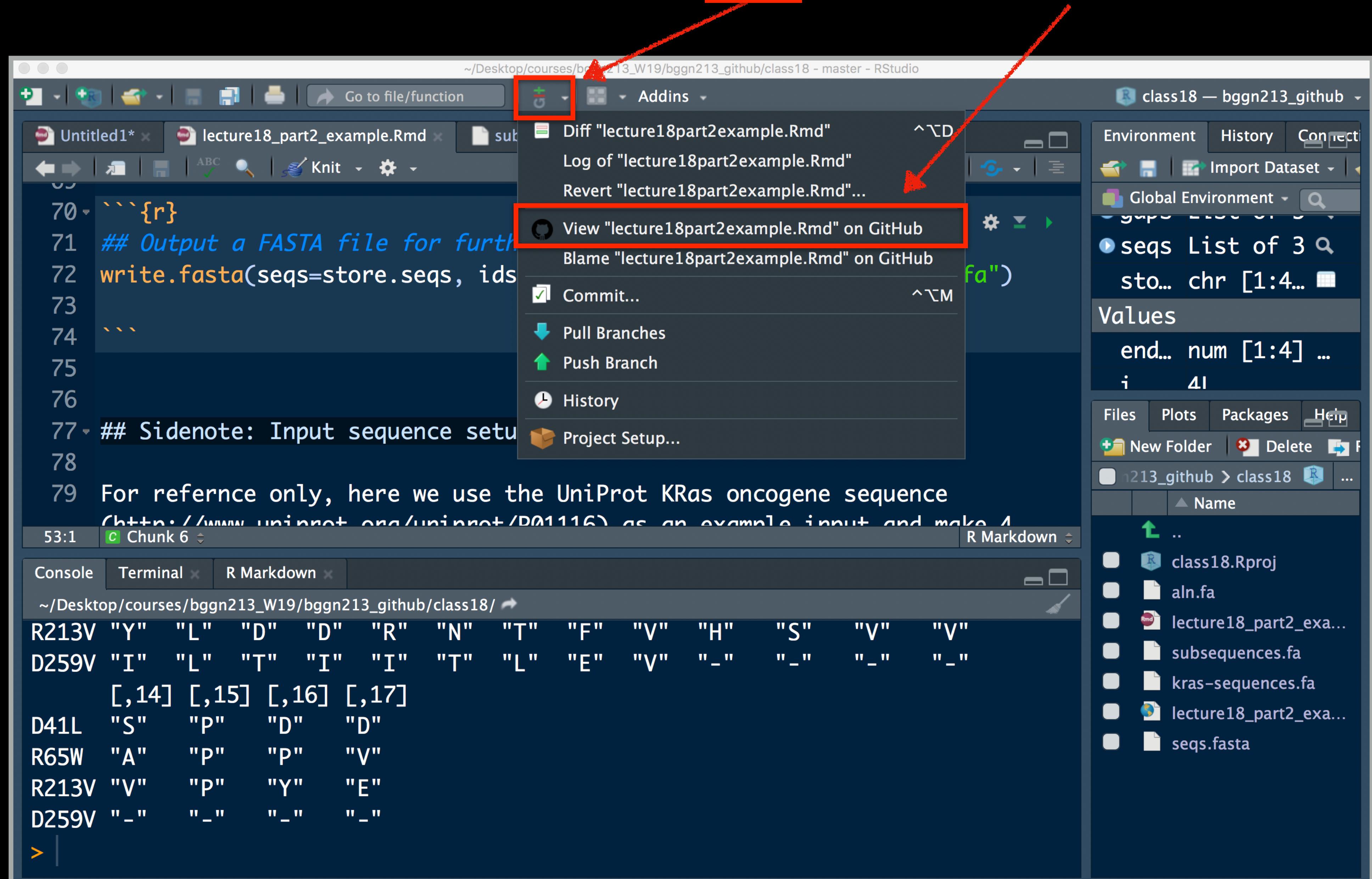
Branch: master New pull request Create new file Upload files Find file Clone or download

bioboot Add class18 Latest commit 959723b 7 minutes ago

class05 Add class 5 a month ago

class08 add class08 a month ago

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

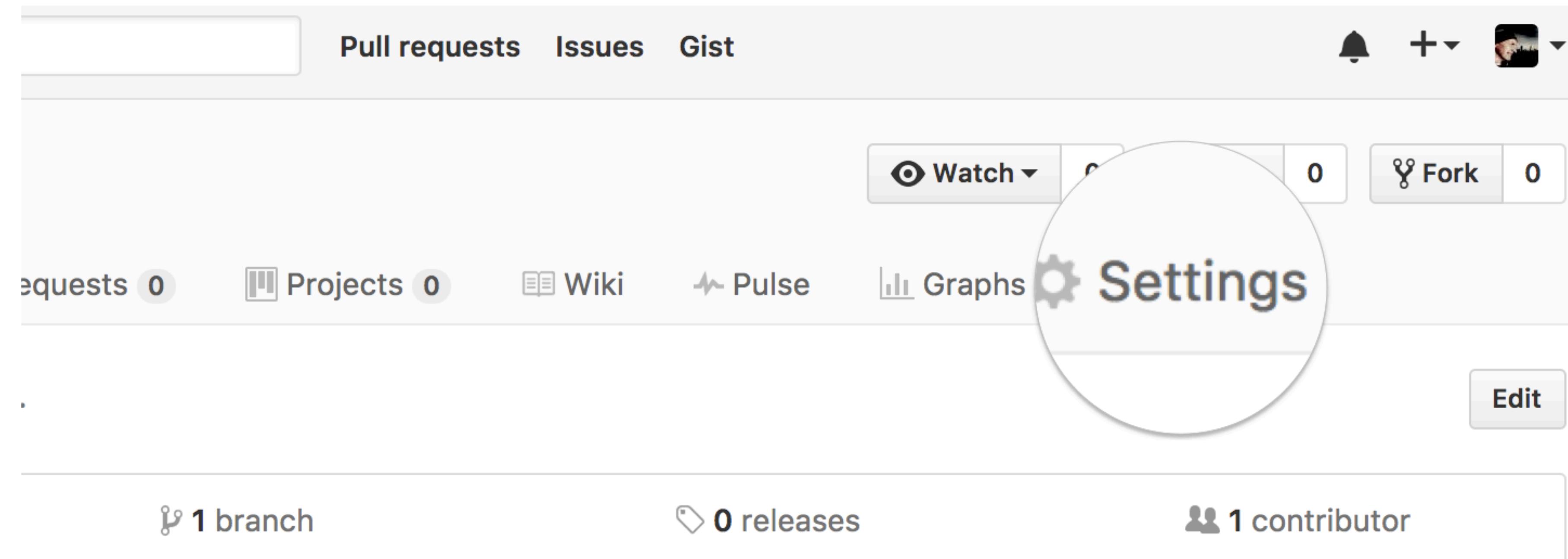


1

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”**

The screenshot shows the GitHub Pages settings for a repository. At the top, there's a heading for "GitHub Pages". Below it, a paragraph explains that GitHub Pages is designed to host personal, organization, or project pages from a GitHub repository. Under the "Source" heading, it says "GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository." It includes a "None" dropdown menu and a "Save" button. A horizontal line separates this from the "Theme chooser" section. The "Theme chooser" section has a heading and a paragraph stating "Select a theme to build your site with a Jekyll theme using the master branch." It includes a "Choose a theme" button.

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

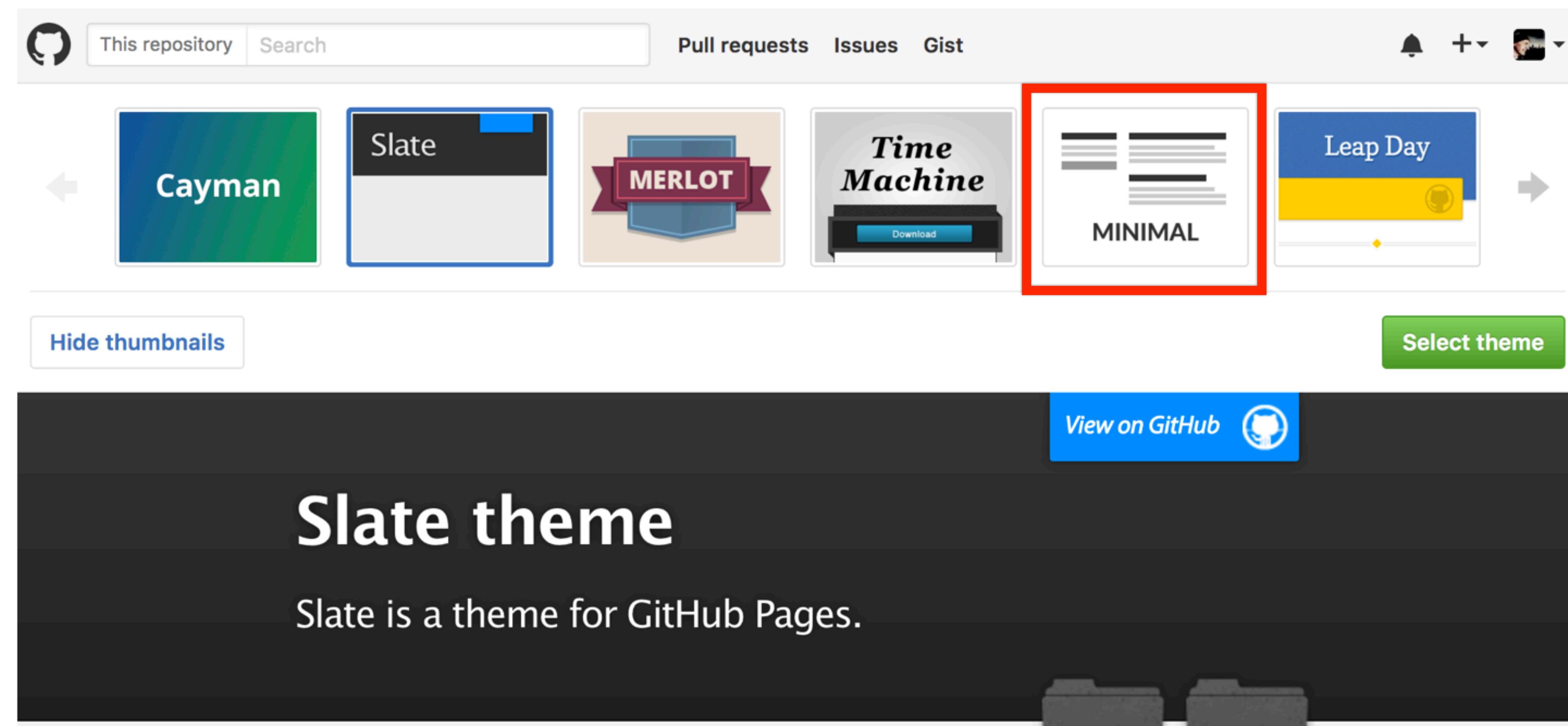
Select a theme to build your site with a Jekyll theme using the `master` branch. [Learn more](#).

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.



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 interface for 'jldec / new-pages-site'. The top navigation bar includes the repository name, a 'Watch' button (0), a 'Star' button (0), and a 'Fork' button (0). Below the navigation bar are links for 'Issues 0', 'Pull requests 0', 'Projects 0', 'Wiki', 'Pulse', 'Graphs', and 'Settings'. The main content area shows the 'new-pages-site / README.md' file being edited. The file contains the following Markdown content:

```
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 \[documentation\]\(https://help.github.com/categories/gi\)  
\(\) and we'll help you sort it out.  
38
```



Commit changes

Add content to new pages site

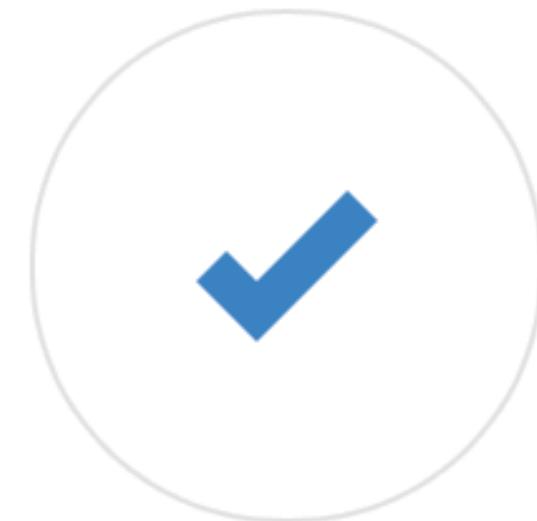
Add an optional extended description...

Commit directly to the `master` branch.

6

...and you're done!

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



The screenshot shows a web browser window with the URL bioboot.github.io/bimm143-1/ in the address bar. The page content is as follows:

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](#)

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

Y 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

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

BGPN213

This is my classwork from BGPN213 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) Edited README.md

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

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

The screenshot shows a web browser window with the URL `bioboot.github.io/bimm143-1/` in the address bar. The page content is as follows:

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Class 12 - [Drug Discovery: Techniques and Analysis](#)

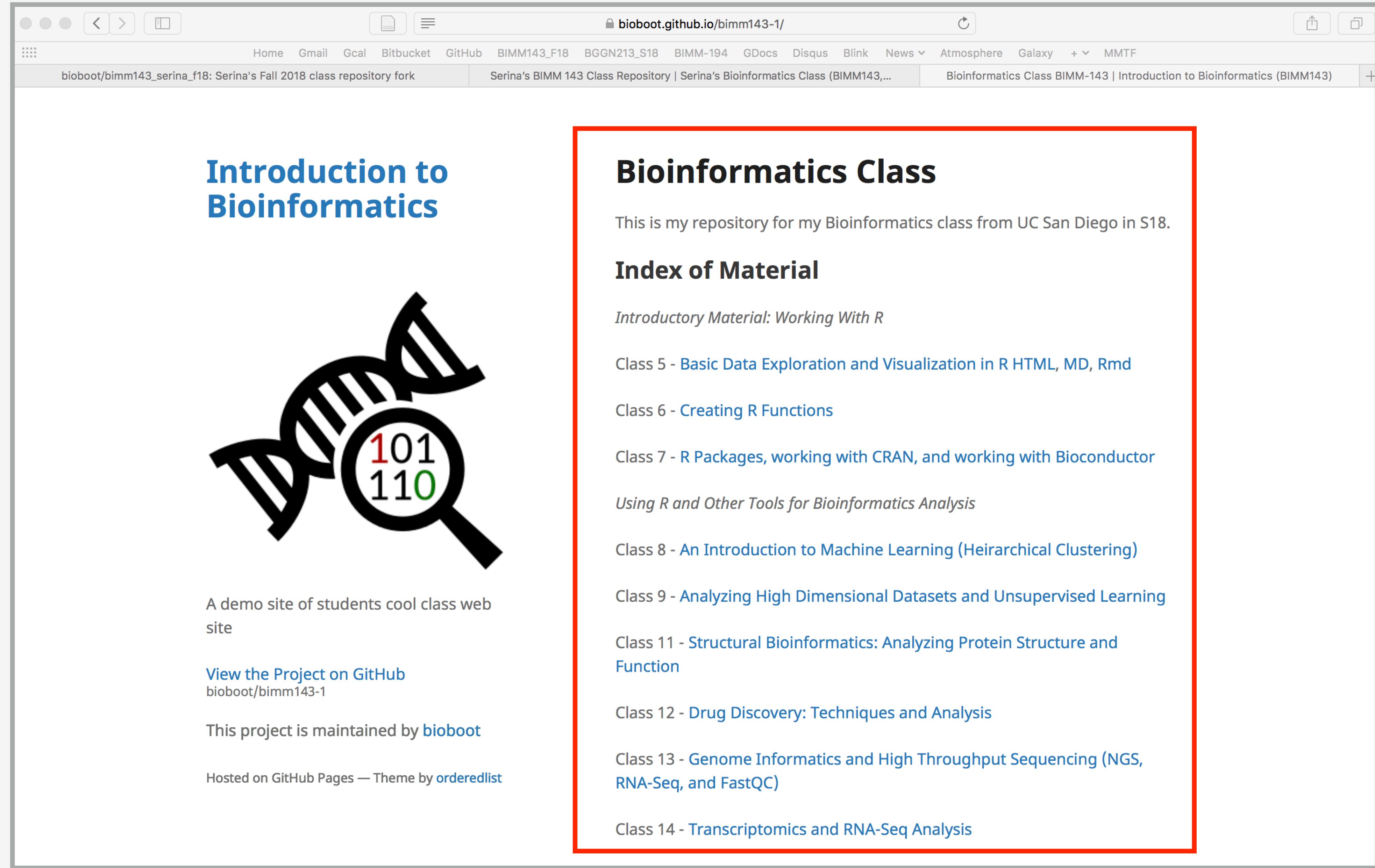
Class 13 - [Genome Informatics and High Throughput Sequencing \(NGS, RNA-Seq, and FastQC\)](#)

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

The screenshot shows a GitHub repository page for 'bioboot / tmp_test'. The repository has 1 unwatched star and 0 forks. The 'Code' tab is selected. The README.md file contains the following content:

```
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/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](#)

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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 chance.
It is important to the courses we offer in the future and how we teach them!

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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](#) with all classes by
this Friday and receive another 5pts credit!

Going Further With DataCamp

https://bioboot.github.io/bimm143_F19/class-material/datacamp_extras.pdf

The screenshot shows a web browser window for the DataCamp website (www.datacamp.com/tracks/custom-bioinformatics-extension). The page title is "CUSTOM TRACK Bioinformatics Extension". The main content area describes Barry's suggested DataCamp courses for delving deeper into R, Git, the Shell, data visualization, and Bioinformatics data analysis generally. It includes a yellow "Enroll" button, a DNA helix icon with a magnifying glass over binary code (101 110), and a summary of 111 hours and 26 Courses across R Language, Shell, Git, and Spreadsheets.

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**

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](#) with all classes by
this Friday and receive another 5pts credit!

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.

Learning git can be painful!

However in practice it is not nearly as crazy-making as the alternatives:

- Documents as email attachments
- Hair-raising ZIP archives containing file salad
- Am I working with the most recent data?
- Archaeological “digs” on old email threads and uncertainty about how/if certain changes have been made or issues solved

Finally Please remember that **GitHub** and **BitBucket** are **PUBLIC** and that you should cultivate your professional and scholarly profile with intention!



The End!

<http://thegrantlab.org>



Thank You!

<http://thegrantlab.org>

Reference Slides

Command Line GIT

Using Command Line Git

1. Initiate a Git repository.
2. Edit content (i.e. change some files).
3. Store a 'snapshot' of the current file state.*

Initiate a Git repository

Initiate a Git repository

```
> cd ~/Desktop  
> mkdir git_class # Make a new directory  
> cd git_class    # Change to this directory  
> git init      # Our first Git command!  
> ls -a          # what happened?
```

Side-Note: The `.git` directory

- Git created a ‘hidden’ `.git` directory inside your current working directory.
- You can use the ‘`ls -a`’ command to list (*i.e.* see) this directory and its contents.
- This is where Git stores all its goodies - **this is Git!**
- You should not need to edit the contents of the `.git` directory for now but do feel free to poke around.

Important Git commands

```
> git status      # report on content changes
```

```
> git add <filename>    # stage/track a file  
> git commit -m "message"  # snapshot
```

Important Git commands

```
> git status      # report on content changes
```

```
> git add <filename>    # stage/track a file  
> git commit -m "message"  # snapshot
```

You will use these three commands again and again in your Git workflow!

Git TRACKS your directory content

- To get a report of changes (since last commit) use:
> git status

- You tell Git which files to track with:
> git add <filename>

This adds files to a so called **STAGING AREA** (akin to a “shopping cart” before purchasing).

- You tell Git when to take an historical **SNAPSHOT** of your staged files (*i.e.* record their current state) with:
> git commit -m ‘Your message about changes’

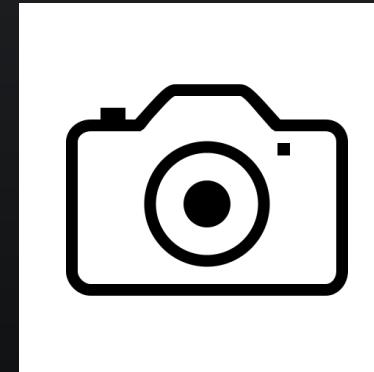
Example Git workflow



Eva creates a README text file
(this starts as untracked)



Adds file to STAGING AREA*
(tracked and ready to take a snapshot)



Commit changes*
(records snapshot of staged files!)

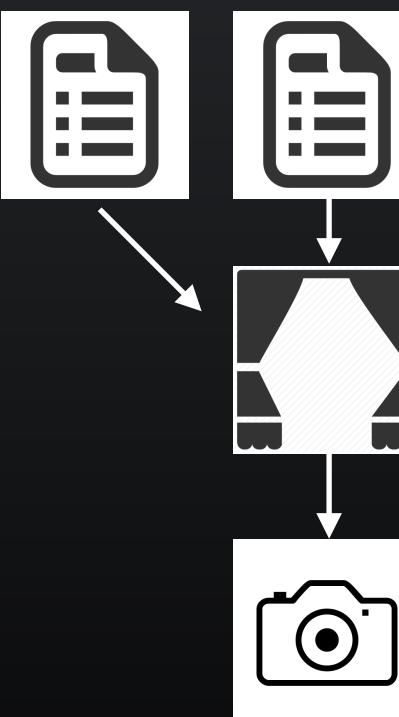
Example Git workflow



Eva creates a README text file

Adds file to STAGING AREA*

Commit changes*



Eva modifies README and adds a ToDo text file

Adds both to STAGING AREA*

Commit changes*

1. Eva creates a README file

```
> # cd ~/Desktop/git_class  
> # git init  
  
> echo "This is a first line of text." > README  
> git status      # Report on changes  
# On branch master  
#  
# Initial commit  
#  
# Untracked files:  
# (use "git add <file>..." to include in what will be committed)  
#  
# README  
#  
# nothing added to commit but untracked files present (use "git add" to track)
```

2. Adds to ‘staging area’

```
> git add README      # Add README file to staging area  
> git status          # Report on changes  
  
# On branch master  
#  
# Initial commit  
#  
# Changes to be committed:  
#   (use "git rm --cached <file>..." to unstage)  
#  
#       new file: README  
#
```

3. Commit changes

```
> git commit -m "Create a README file" # Take snapshot
```

```
# [master (root-commit) 8676840] Create a README file  
# 1 file changed, 1 insertion(+)  
# create mode 100644 README
```

```
> git status # Report on changes
```

```
# On branch master  
# nothing to commit, working directory clean
```

4. Eva modifies README file and adds a ToDo file

```
> echo "This is a 2nd line of text." >> README
> echo "Learn git basics" >> ToDo

> git status      # Report on changes
# On branch master
#
# Changes not staged for commit:
#   (use "git add <file>..." to update what will be committed)
#   (use "git checkout -- <file>..." to discard changes in working directory)
#
#       modified: README
#
# Untracked files:
#   (use "git add <file>..." to include in what will be committed)
#
#       ToDo
#
# no changes added to commit (use "git add" and/or "git commit -a")
```

5. Adds both files to ‘staging area’

```
> git add README ToDo      # Add both files to 'staging area'  
> git status                 # Report on changes  
  
# On branch master  
# Changes to be committed:  
#   (use "git reset HEAD <file>..." to unstage)  
#  
#       modified: README  
#       new file: ToDo  
#
```

6. Commits changes

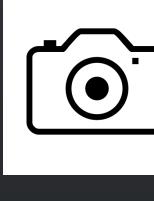
```
> git commit -m "Add ToDo and modify README"
```

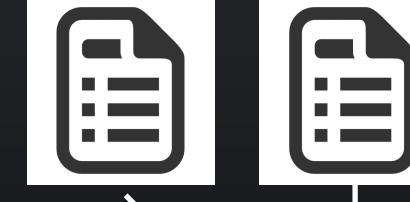
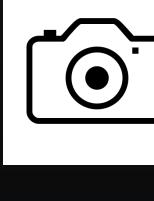
```
# [master 7b679fa] Add ToDo and modify README
# 2 files changed, 2 insertions(+)
# create mode 100644 ToDo
```

```
> git status
```

```
# On branch master
# nothing to commit, working directory clean
```

Example Git workflow

1.  Eva creates a README text file
2.  Adds file to STAGING AREA*
3.  Commit changes*

4.  Eva modifies README and adds a ToDo text file
5.  Adds both to STAGING AREA*
6.  Commit changes*

...But, how do we see the history of our project changes?

git log: Timeline history of snapshots (*i.e.* commits)

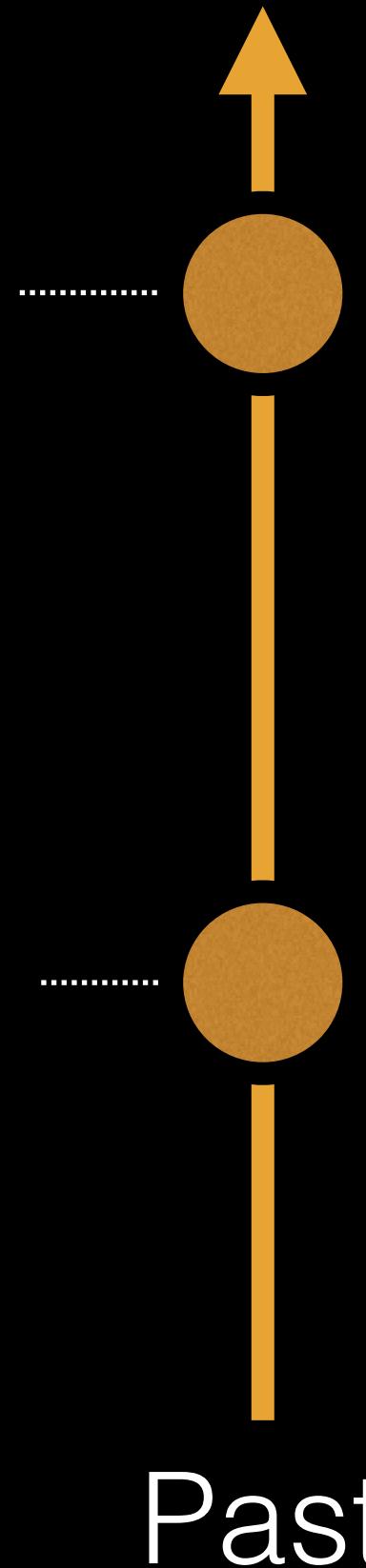
> **git log**

```
# commit 7b679fa747e8640918fcaad7e4c3f9c70c87b170
# Author: Barry Grant <bjgrant@umich.edu>
# Date:  Thu Jul 30 11:43:40 2015 -0400
#
#   Add ToDo and finished README
#
# commit 86768401610770ae32e2fd4faee07d1d5c68619c
# Author: Barry Grant <bjgrant@umich.edu>
# Date:  Thu Jul 30 11:26:40 2015 -0400
#
#   Create a README file
#
```

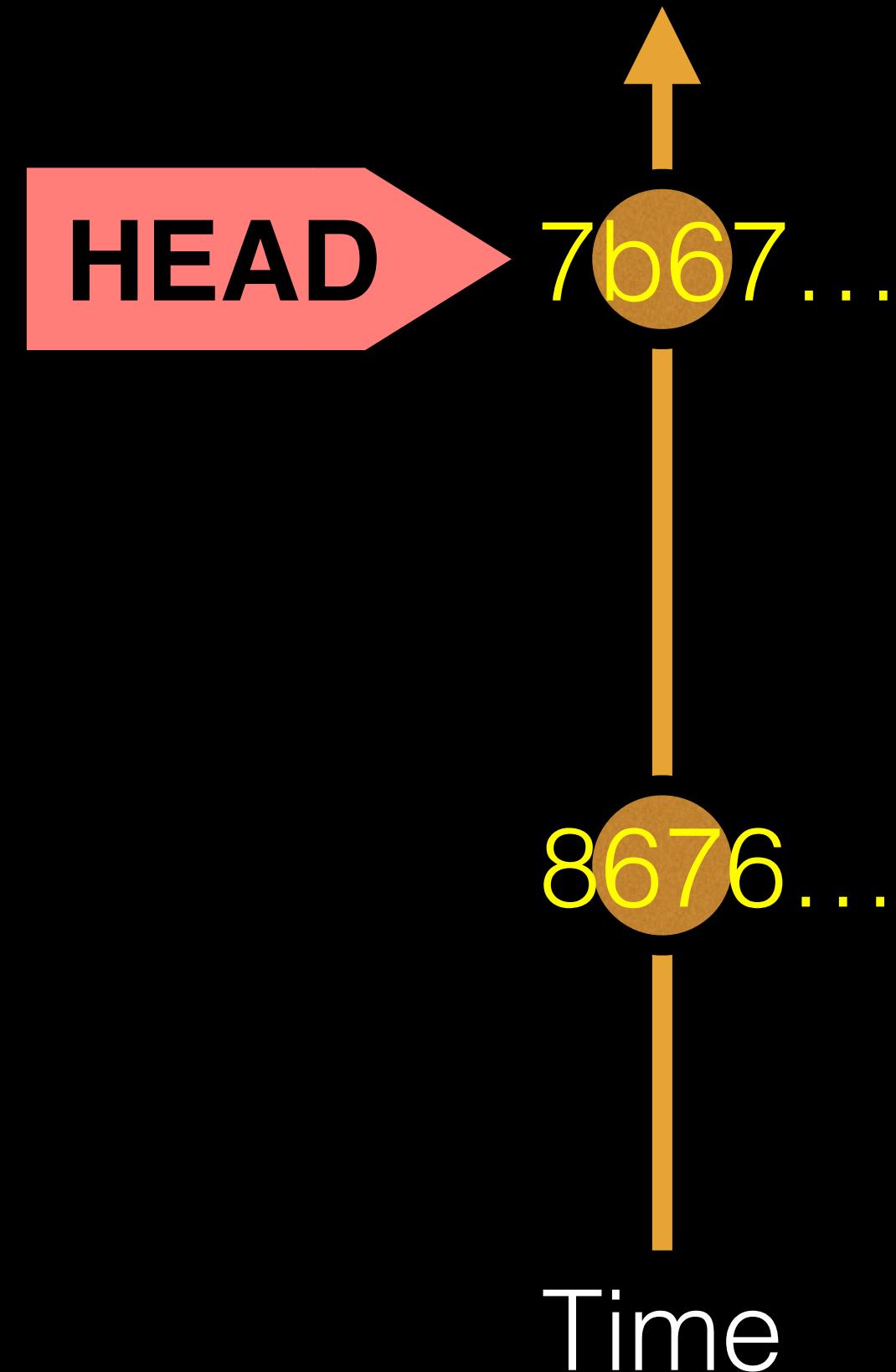
git log: Timeline history of snapshots (*i.e.* commits)

```
> git log
```

```
# commit 7b679fa747e8640918fcaad7e4c3f9c70c87b170
# Author: Barry Grant <bjgrant@umich.edu>
# Date:  Thu Jul 30 11:43:40 2015 -0400
#
#   Add ToDo and finished README
#
# commit 86768401610770ae32e2fd4faee07d1d5c68619c
# Author: Barry Grant <bjgrant@umich.edu>
# Date:  Thu Jul 30 11:26:40 2015 -0400
#
#   Create a README file
#
```



Side-Note: Git history is akin to a graph

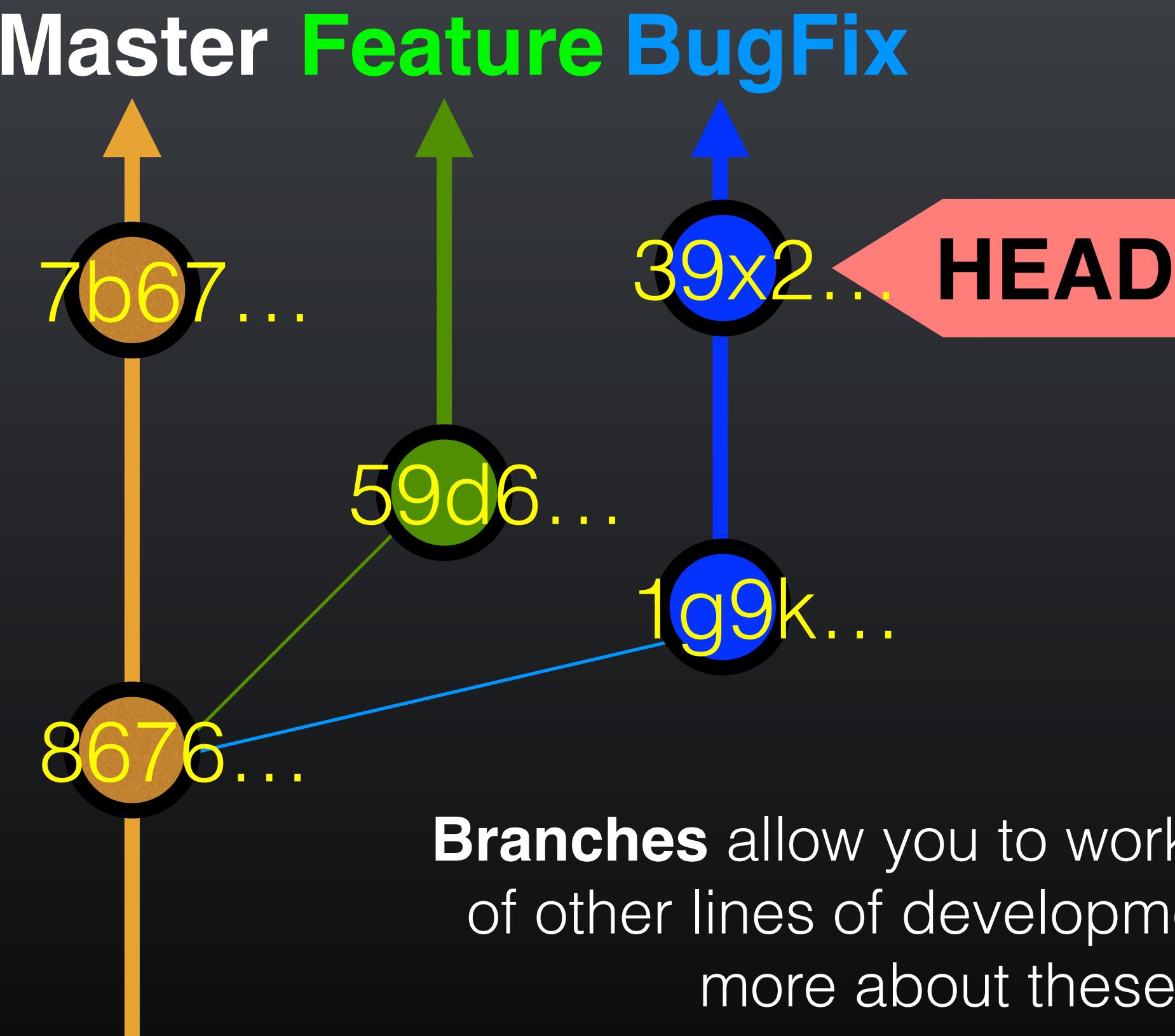


Nodes are **commits** labeled by their unique '**commit ID**'.

(This is a **CHECKSUM** of the commits author, time, commit msg, commit content and previous commit ID).

HEAD is a reference (or '**pointer**') to the currently checked out commit (typically the most recent commit).

Projects can have complicated graphs due to **branching**



Branches allow you to work independently of other lines of development we will talk more about these later!

Key Points:

You explicitly and iteratively tell git what files to track (“**git add**”) and snapshot (“**git commit**”).

Git keeps an historical log “(**git log**)” of the content changes (and your comments on these changes) at each past commit.

It is good practice to regularly check the status of your working directory, staging arena repo (“**git status**”)

Break

Summary of key Git commands:

```
> git status      # Get a status report of changes since last commit
```

```
> git add <filename>      # Tell Git which files to track/stage
```

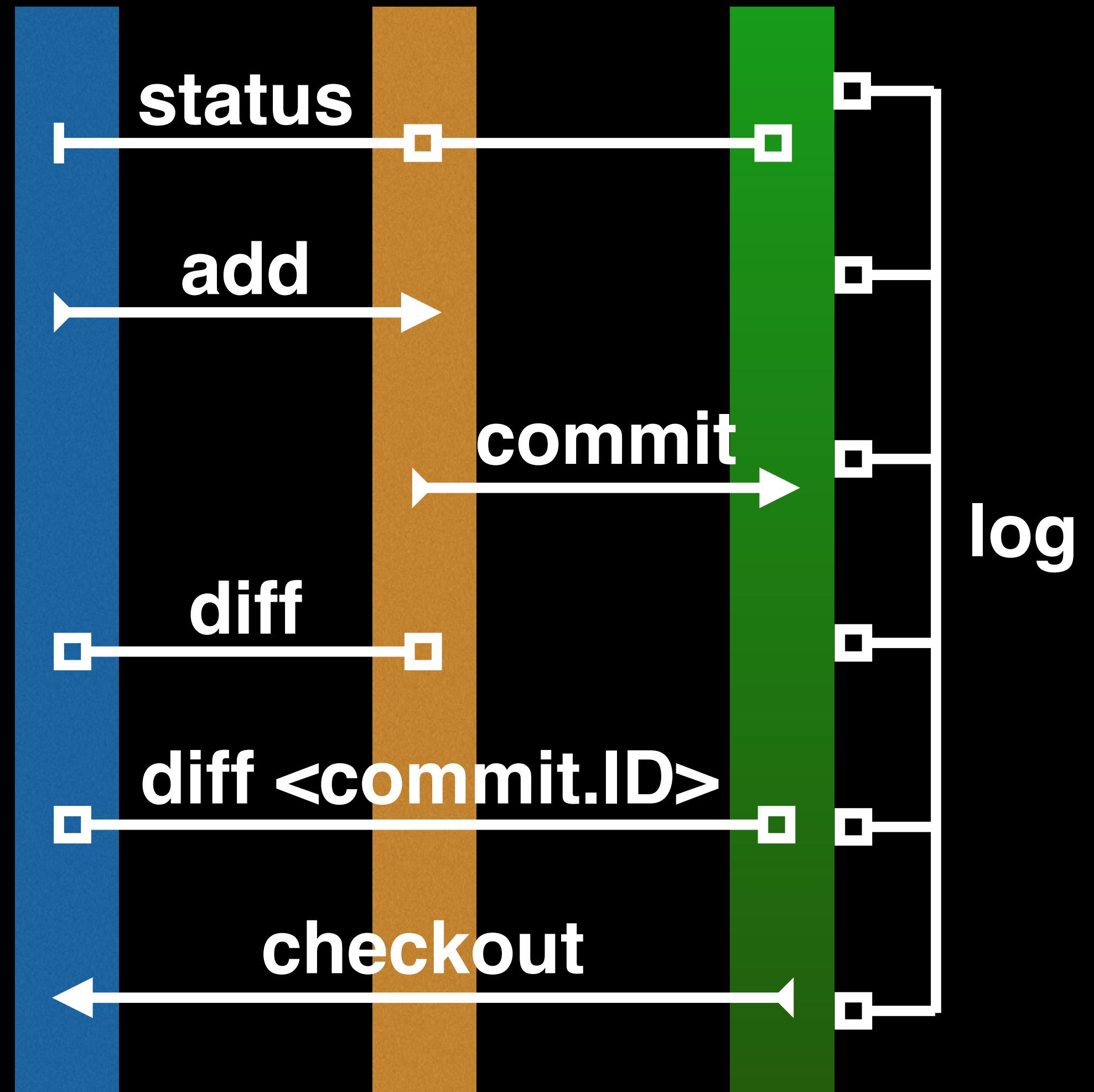
```
> git commit -m 'Your message'    # Take a content snapshot!
```

```
> git log          # Review your commit history
```

```
> git diff <commit.ID> <commit.ID> # Inspect content differences
```

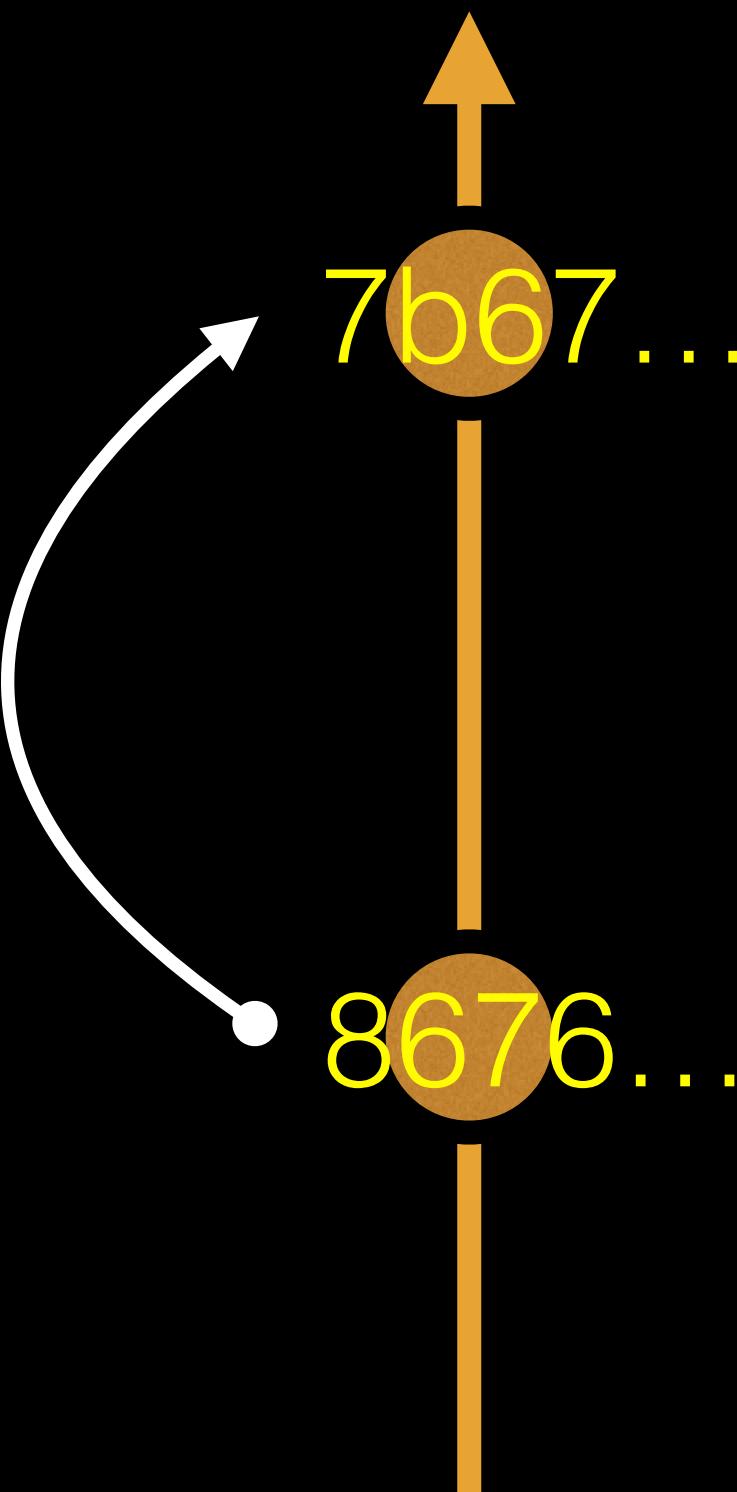
```
> git checkout <commit.ID> # Navigate through the commit history
```

Your 'Staging Local
Directory Area' Repository



git diff: Show changes between commits

```
> git diff 8676 7b67  
# diff --git a/README b/README  
# index 73bc85a..67bd82c 100644  
# --- a/README  
# +++ b/README  
# @@ -1 +1,2 @@  
# This is a first line of text.  
# +This is a 2nd line of text.  
  
# diff --git a/ToDo b/ToDo  
# new file mode 100644  
# index 0000000..14fb56  
# --- /dev/null  
# +++ b/ToDo  
# @@ -0,0 +1 @@  
# +Learn git basics
```



git diff: Show changes between commits

```
> git diff 7b67 8676
```

```
# diff --git a/README b/README
# index 67bd82c..73bc85a 100644
# --- a/README
# +++ b/README
# @@ -1,2 +1 @@
# This is a first line of text.
# -This is a 2nd line of text.

# diff --git a/ToDo b/ToDo
# deleted file mode 100644
# index 14fb5d6..0000000
# --- a/ToDo
# +++ /dev/null
# @@ 1 +0,0 @@
# -Learn git basics
```



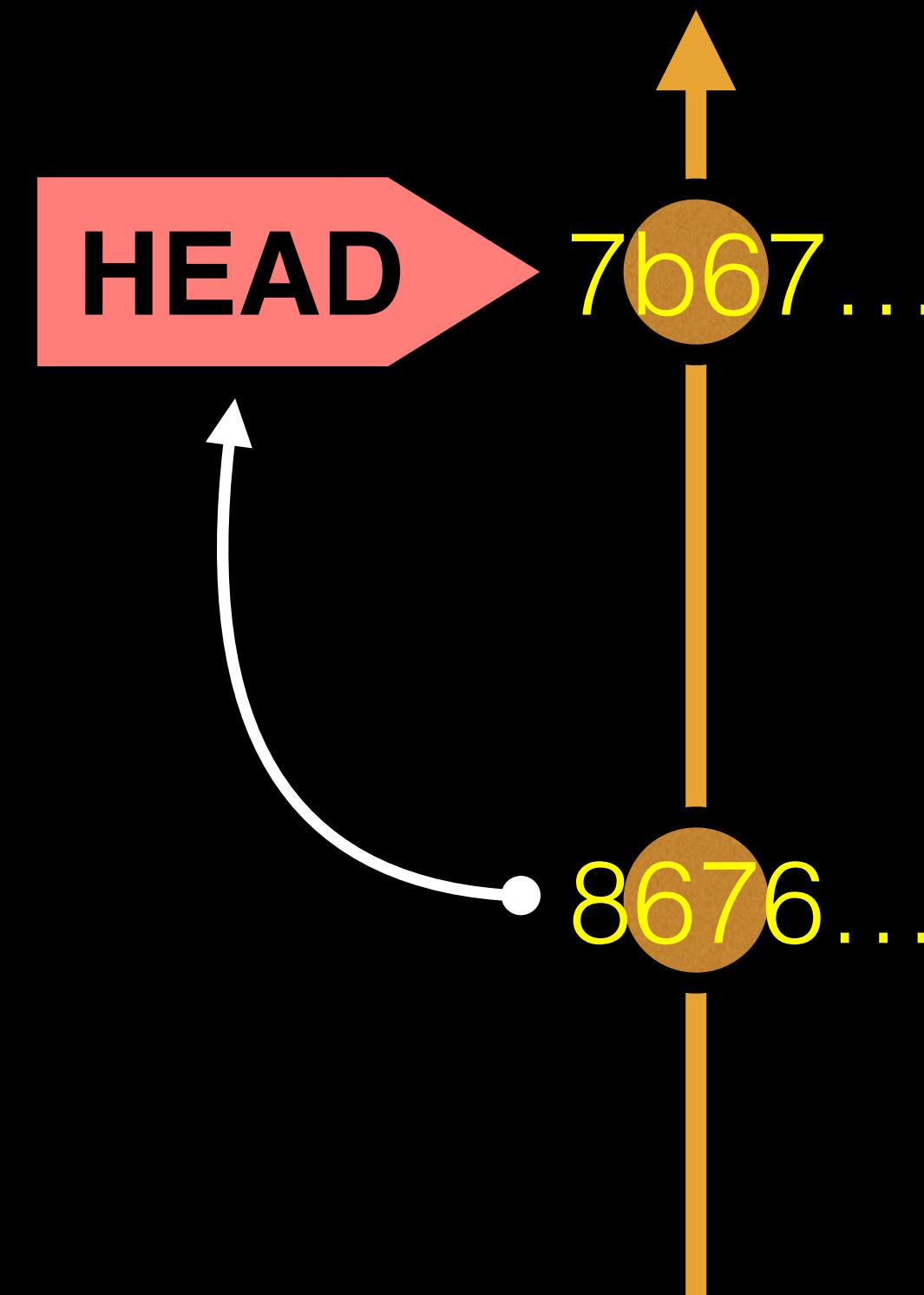
git diff: Show changes between commits

```
> git diff 8676
```

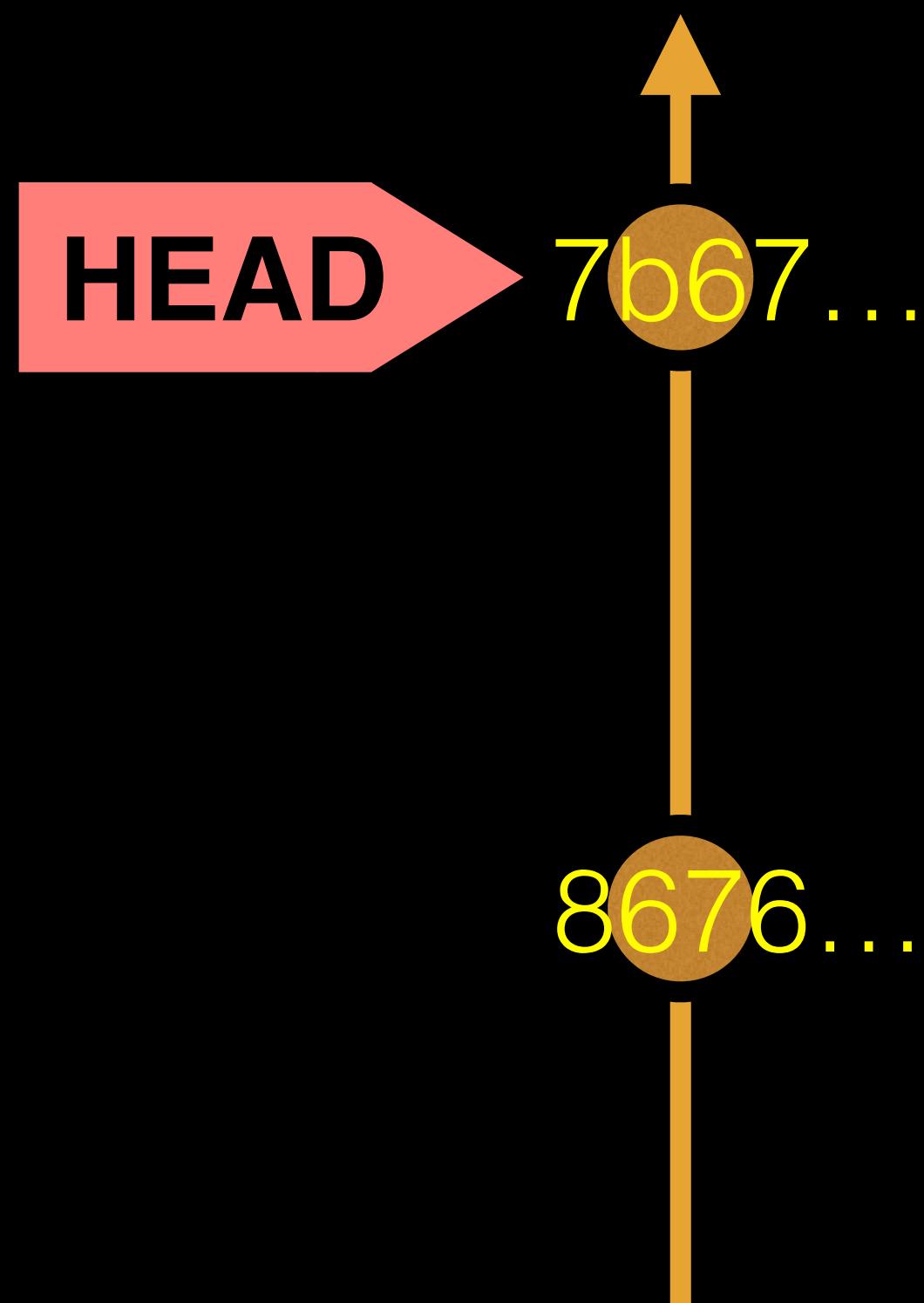
Difference to current HEAD position!

```
# diff --git a/README b/README
# index 73bc85a..67bd82c 100644
# --- a/README
# +++ b/README
# @@ -1 +1,2 @@
# This is a first line of text.
# +This is a 2nd line of text.

# diff --git a/ToDo b/ToDo
# new file mode 100644
# index 0000000..14fb56
# --- /dev/null
# +++ b/ToDo
# @@ -0,0 +1 @@
# +Learn git basics
```



HEAD advances automatically with each new commit



To move **HEAD** (back or forward) on the Git graph (and retrieve the associated snapshot content) we can use the command:

> `git checkout <commit.ID>`

git checkout: Moves HEAD

> **more README**

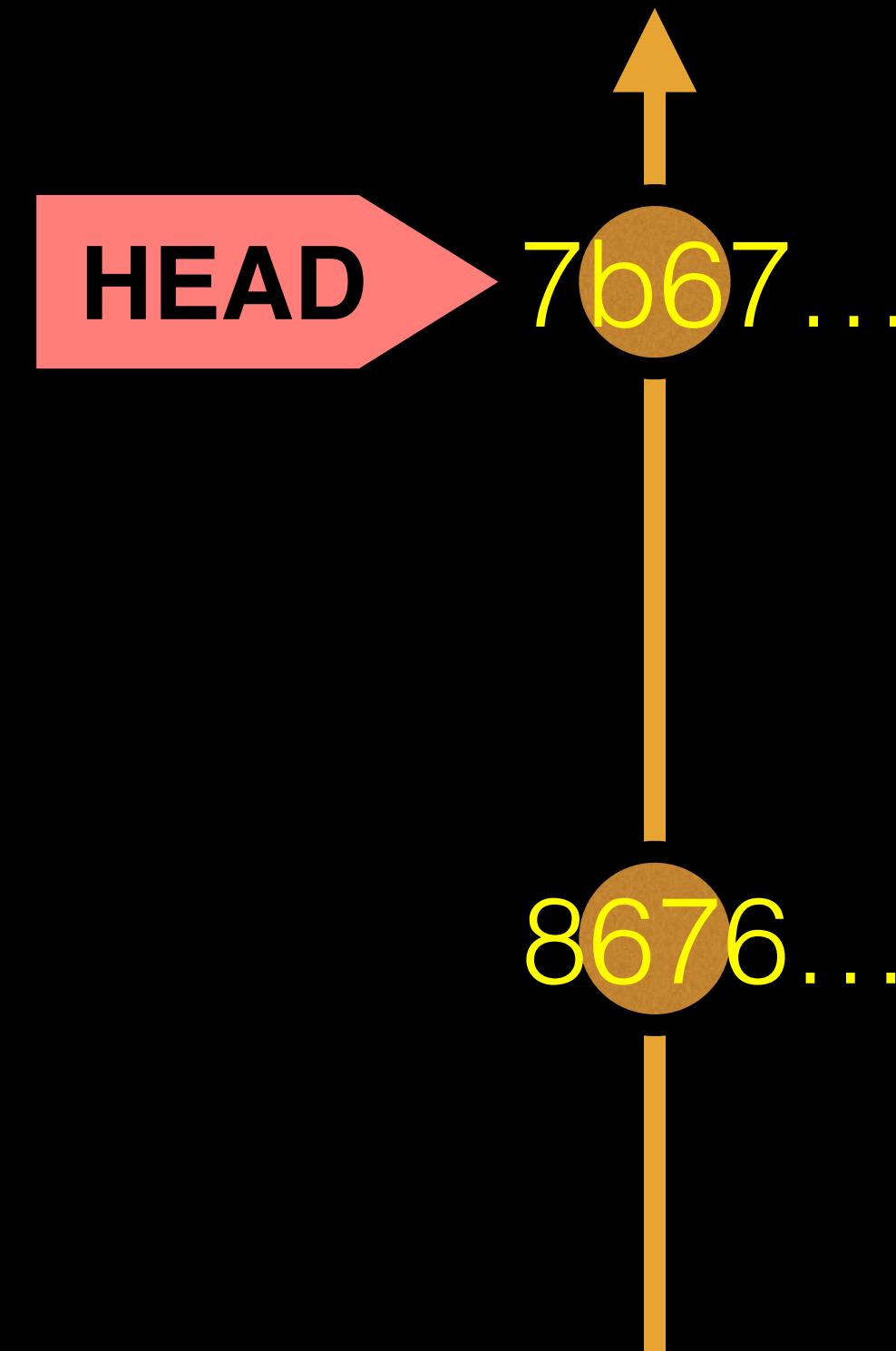
This is a first line of text.

This is a 2nd line of text.

> **git log --oneline**

7b679fa Add ToDo and finished README

8676840 Create a README file



git checkout: Moves HEAD (e.g. back in time)

> **more README**

This is a first line of text.

This is a 2nd line of text.

> **git log --oneline**

7b679fa Add ToDo and finished README

8676840 Create a README file

> **git checkout 8676840**

You are in 'detached HEAD' state...<cut>...

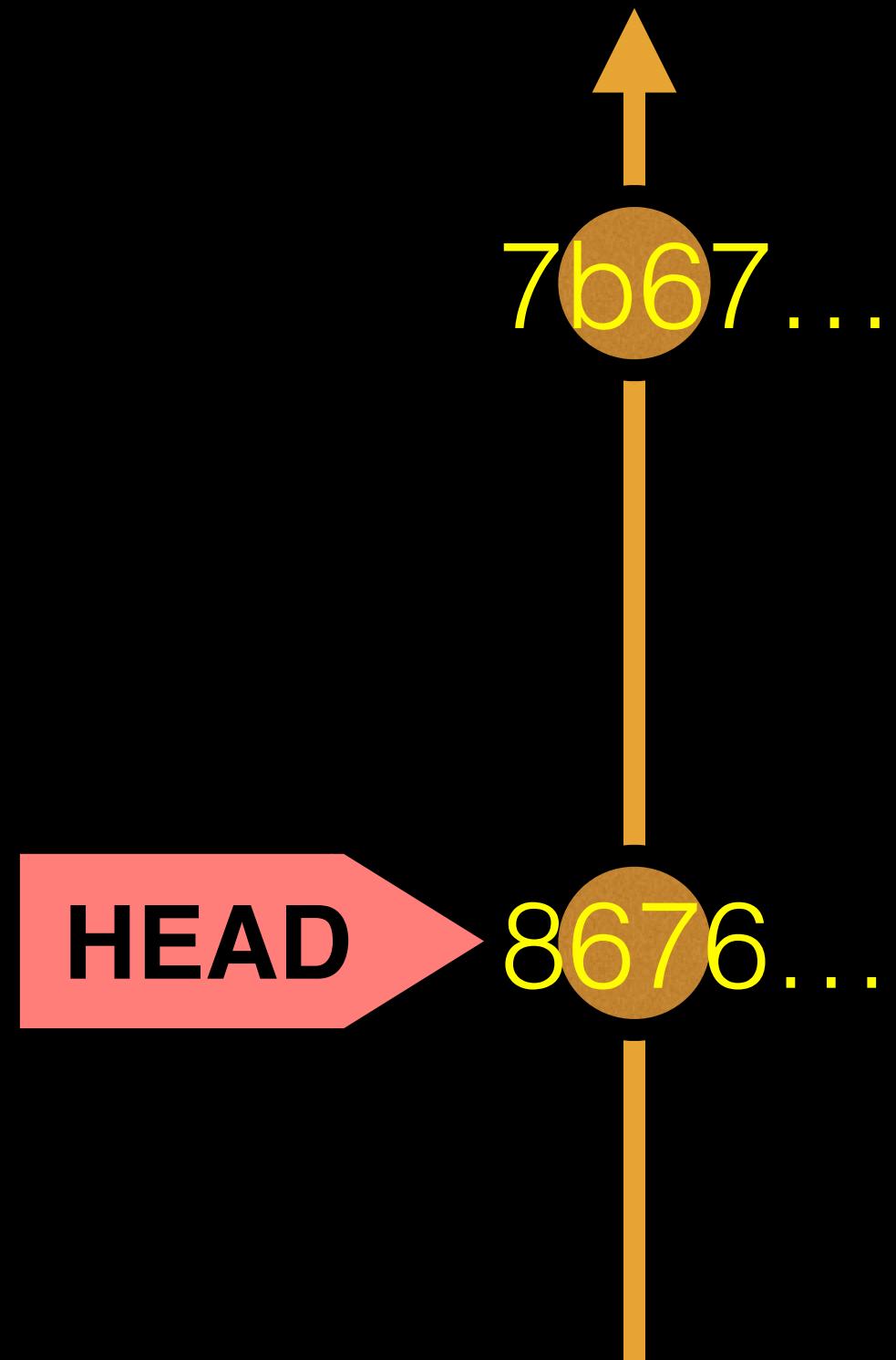
HEAD is now at 8676840... Create a README file

> **more README**

This is a first line of text.

> **git log --oneline**

8676840 Create a README file



git checkout: Moves HEAD (e.g. back to the future!)

> **git checkout master**

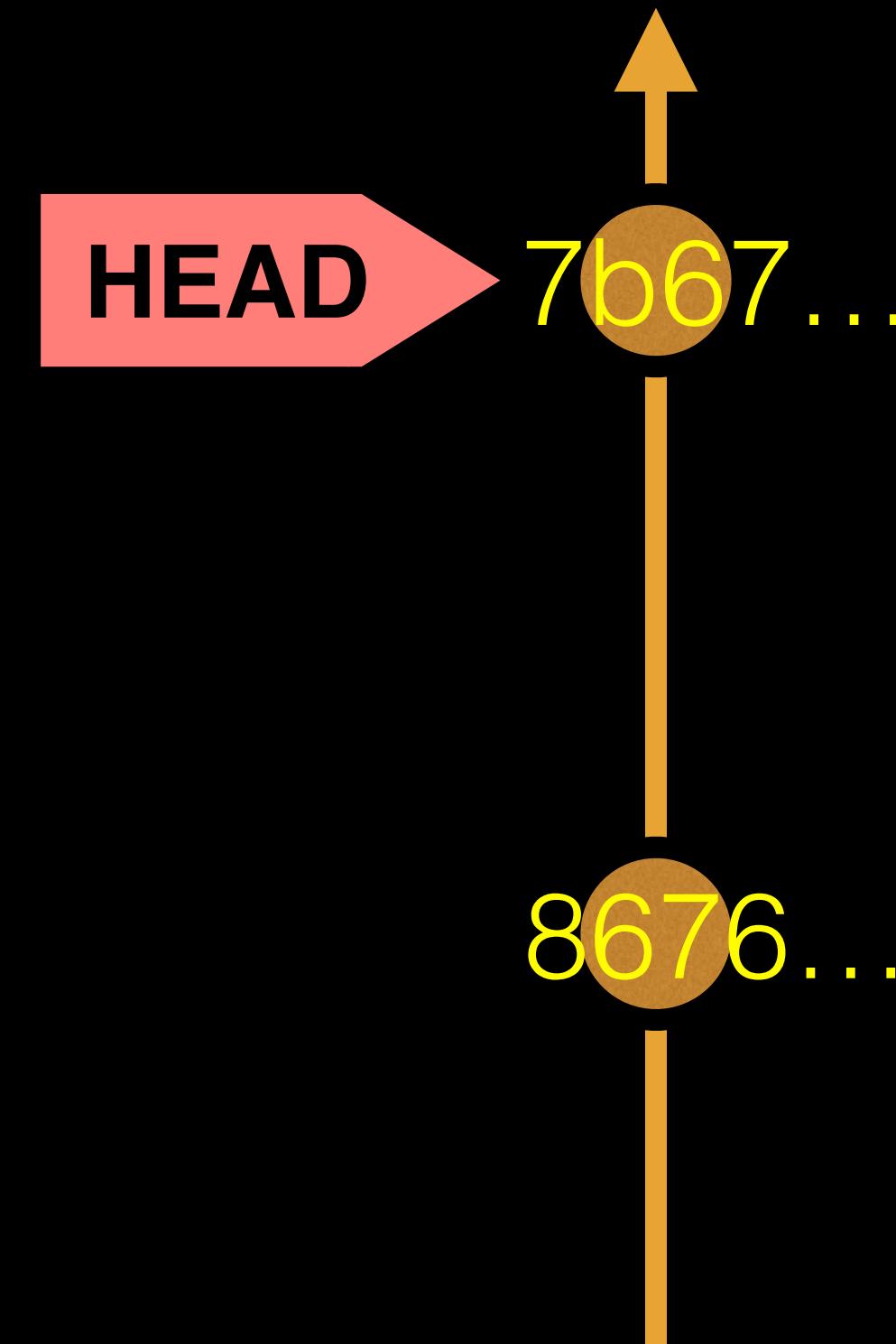
```
# Previous HEAD position was 8676840... Create a README file
# Switched to branch 'master'
```

> **git log --oneline**

```
# 7b679fa Add ToDo and finished README
# 8676840 Create a README file
```

> **more README**

This is a first line of text.
This is a 2nd line of text.



Side-Note: There are two* main ways to use **git checkout**

- Checking out a **commit** makes the entire working directory match that commit. This can be used to view an old state of your project.

> `git checkout <commit.ID>`

- Checking out a **specific file** lets you see an old version of that particular file, leaving the rest of your working directory untouched.

> `git checkout <commit.ID> <filename>`

You can discard revisions with **git revert**

- The **git revert** command undoes a committed snapshot.
- But, instead of removing the commit from the project history, it figures out how to **undo the changes** introduced by the commit and **appends a new commit** with the resulting content.

```
> git revert <commit.ID>
```

- This prevents Git from losing history!

Removing untracked files with **git clean**

- The **git clean** command removes untracked files from your working directory.
- Like an ordinary **rm** command, **git clean** is not undoable, so make sure you really want to delete the untracked files before you run it.

> `git clean -n` # dry run display of files to be ‘cleaned’

> `git clean -f` # remove untracked files

GUIs

Tower (Mac only)

GitHub_Desktop (Mac, Windows)

SourceTree (Mac, Windows)

SmartGit (Linux)

RStudio

<https://git-scm.com/downloads/guis>