COGS138: Neural Data Science

Lecture 6

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(Based on a course created by Prof. Bradley Voytek)

Plan for today

- Announcements
- Assignment 1 overview
- Review - Last time
- NWB data and BIDS data - definition, accessing, usage and relevance
- DANDI - putting datasets together and making it all available, reusable and documented
- Version control, git, github review

Announcements

- Final reminder to check on your FinAID status
- A1 - due **a week from release**, which will be tonight or tomorrow
- Reading 1 - Released on canvas and in web site password protected area soon, lecture quiz due **a week from release**, released tonight
- **Group formation** - time to start choosing who you want to work with for your project group

Last time

Course links

Website	http://casimpkinsjr.radiantdolphinpress.com/pages/cogs138_sp23	Main face of the course and everything will be linked from here. Lectures, Readings, Handouts, Files, links
GitHub	https://github.com/drsimpkins-teaching	files/data, additional materials & final projects
datahub	https://datahub.ucsd.edu	assignment submission
Piazza	https://piazza.com/ucsd/spring2023/cogs138_sp23_a00/home (course code on canvas home page)	questions, discussion, and regrade requests
Canvas	https://canvas.ucsd.edu/courses/44897	grades, lecture videos
Anonymous Feedback	Will be able to submit via google form	If I ever offend you, use an example you are uncomfortable with, or to provide general feedback. Please remain constructive and polite

So far we have discussed

- Neural Data science
- Programming
- Tools for data exploration, modeling, visualization (Python, Jupyter, Matlab, others)
- NLP
- EEG, MEG, associated analysis and tools (at a high level), other imaging
- MOCAP
- Eye tracking
- Other behavioral observations

That’s a lot of data!

- How do you deal with it all, standardize, organize, communicate it?
- How can you talk across disciplines?
- How do you collaborate and work in teams with this?
- How can you ask questions with all that data and the results generated?

Data science questions, hypothesis generation (automated), Genes/gene expression, animal models, FAIR, Neurodata Without Borders (NWB), Brain Imaging Data Structure (BIDS), DANDI

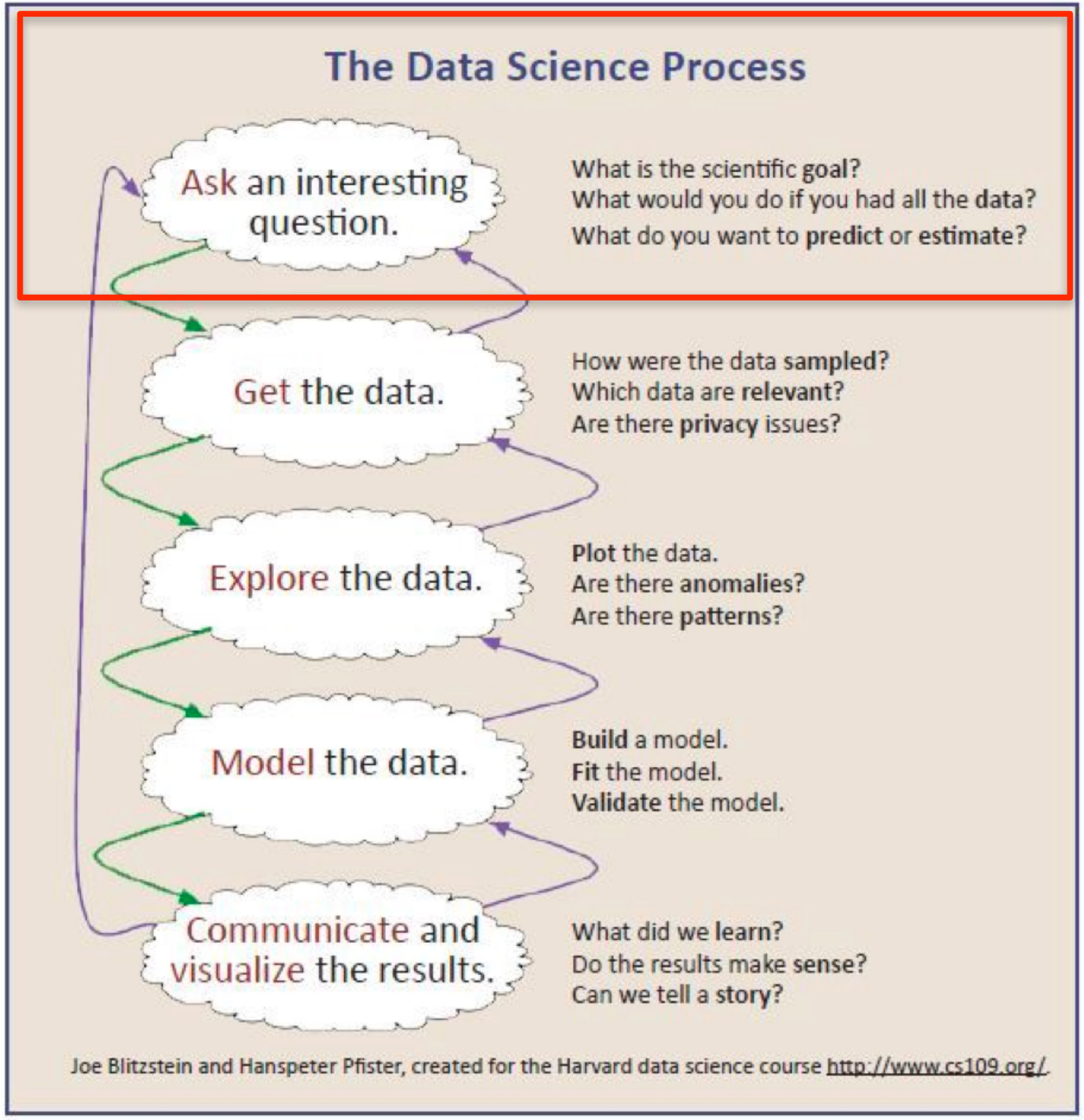
Formulating Data Science Questions

When you and your group sit down to figure out what you're going to do for your final project in this class, you'll have to formulate a strong question. It should be:

1. **Specific**,

2. Can be answered with **data**,

3. And makes **clear what** exactly **is** being **measured**.


The Data Science Process
Ask an interesting question.
What is the scientific goal?
What would you do if you had all the data?
What do you want to predict or estimate?
Get the data.
How were the data sampled?
Which data are relevant?
Are there privacy issues?
Explore the data.
Plot the data.
Are there anomalies?
Are there patterns?
Model the data.
Build a model.
Fit the model.
Validate the model.
Communicate and visualize the results.
What did we learn?
Do the results make sense?
Can we tell a story?
Joe Blitzstein and Hanspeter Pfister, created for the Harvard data science course http://www.cs109.org/

Hypothesis testing

-Cannot prove hypothesis

-Can only reject or fail to reject null hypothesis

-Why?

Data Science questions should...

- Be specific
- Be answerable with data
- Specify what's being measured

What makes a question a good question?

Specifying what you're going to measure is important

Examples of poor questions that leave wiggle room for useless answers:

- What can my data tell me about the brain?
- What should I do about the brain?
- How can I increase my neuroscience?

Examples of good questions where the answer is impossible to avoid:

- Does a subject's reaching trajectory change when put under a static force field? Is this change static or dynamic?
- What is the average/maximum grip strength required to manipulate a pen during writing tasks (pen and paper)?
- What is the minimum light intensity perceptible by the average subject of age range 18-24yrs in pitch black darkness for a point light at a distance of 2m?

Working toward a strong data science question

Working toward a strong data science question

Vague: How does the brain change when you have a brain injury?

Better: What neurological changes are there after a stroke?

Even better: What neurological and behavioral changes can be measured with EEG and motion capture between an average normal subject and a stroke patient who had a recent stroke that impaired motor function?

Best?

Practicing asking questions…

- Could reflex be measured with brain activity

Previous questions asked during this class's projects…

Genes and text, LISC

()

- Leveraging LISC and NLTK for research like gene expression studies
- Creating gene dictionaries
- Looking through literature to collect information about topics of interest, data and results using python (LISC)

LISC project

- Open source python module “Literature Scanner”
  - https://github.com/lisc-tools/lisc
- Donoghue, Thomas. (2019). LISC: A Python Package for Scientific Literature Collection and Analysis. Journal of Open Source Software. 4. 1674. 10.21105/joss.01674.
- https://www.researchgate.net/publication/336082537_LISC_A_Python_Package_for_Scientific_Literature_Collection_and_Analysis
- LISC is based on BRAIN-SCANR by Voytek (2012)

LISC- Automated methods for digesting vast information

()

- Scientific literature is vast, expanding and beyond a single researcher's ability to digest completely
- By the time an article is read, more are published
- >30M published articles as of 2019 in biomedical sciences alone!
- Automated methods for curation and digestion of literature has been explored to enhance a researcher's abilities to absorb information
- "Knowledge discovery, literature-based discovery, hypothesis generation"

LISC- Automated methods for digesting vast information

()

- Easily accessible
- Connects to several external resources through APIs
- e.g. PubMed, OpenCitations database
- Supports utilities to analyze collected data

LISC- types of data collection

()

- **Counts**: tools to collect and analyze data on the co-occurrence of specified search terms

- **Words**: tools to collect and analyze text and meta-data from scientific articles

- **Citations**: tools to collect and analyze citation and reference data

LISC- includes for supporting use cases

()

- URL management and requesting for interacting with integrated APIs
- Custom data objects for managing collected data
- A database structure, as well as save and load utilities for storing collected data
- Functions and utilities to analyze collected data
- Data visualization for plotting collected data and analysis outputs

LISC vs. Moliere

()

- LISC takes a lightweight, fast and efficient approach to hypothesis generation
- A complement for other tools like Moliere or Meta (www.meta.org)
- More customizable (LISC), tools included for efficient analysis on the results
- Connective interface to Natural Language Processing (NLP) tools such as NLTK
- Moliere/Meta better for more complex analyses

Caveats

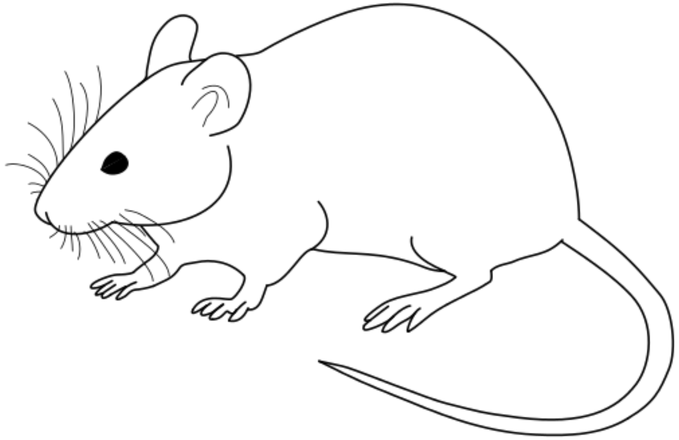
- Take care using automated systems since they don't "understand" the literature as a human does
- Programming biases are inevitable
  - Chatbot knowledge biases
  - Programmer biases
- Statistics can be biased
- Use with a grain of salt - it's a tool
  - ***"The hammer does not make the building" [Simpkins 2023]***

Gene expression studies

- **Gene expression definition** - *the process by which the information encoded in a gene is turned into a function. This mostly occurs via the transcription of RNA molecules that code for proteins or non-coding RNA molecules that serve other functions.*

Why Animal Models?

- We use ***animal models*** for gene expression because, unless a human is undergoing brain surgery where tissue can be sampled, ***we cannot currently measure*** gene expression in the brain otherwise
  - So to avoid harming a human (ethics are complicated!)
- Animals are found that have certain genomic similarities and assumptions are made about mapping behaviors, diseases and gene patterns into insights about humans
- Often an animal is bred for the study with specific genes or “knockouts” are created with certain genes removed in order to understand effects



(Source: https://en.wikipedia.org/wiki/Laboratory_mouse)

Why ***Not*** Animal Models?

- Ethical considerations
- Differences between animals and humans
- Time
- Cost
- Space, resources, pollution, energy use

Alternatives to animal models

- Simulation/computational modeling
- Artificial hardware systems/embodied systems
- Organoids
- Others?

F.A.I.R.

Findable **A**ccessible **I**nteroperable **R**eusable

Data

Science and reproducibility

- Understanding the brain requires broad, diverse and complex sets of data taken from many species of creatures, simulation, models and worldwide contributors
- The data must be findable, accessible, interoperable and reusable (FAIR)

The FAIR Data Principles

- https://force11.org/info/the-fair-data-principles/

- “One of the grand challenges of data-intensive science is to facilitate knowledge discovery by assisting humans and machines in their discovery of, access to, integration and analysis of, task-appropriate scientific data and their associated algorithms and workflows. Here, we describe FAIR – a set of guiding principles to make data Findable, Accessible, Interoperable, and Reusable. The term FAIR was launched at a Lorentz workshop in 2014, the resulting FAIR principles were published in 2016.”

To be Findable

- F1. (meta)data are assigned a globally unique and eternally persistent identifier.
- F2. data are described with rich metadata.
- F3. (meta)data are registered or indexed in a searchable resource.
- F4. metadata specify the data identifier.

To be Accessible

- A1 (meta)data are retrievable by their identifier using a standardized communications protocol.
- A1.1 the protocol is open, free, and universally implementable.
- A1.2 the protocol allows for an authentication and authorization procedure, where necessary.
- A2 metadata are accessible, even when the data are no longer available.

To be Interoperable

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles.
- I3. (meta)data include qualified references to other (meta)data.

To be Re-usable

- R1. (meta)data have a plurality of accurate and relevant attributes.
- R1.1. (meta)data are released with a clear and accessible data usage license.
- R1.2. (meta)data are associated with their provenance.
- R1.3. (meta)data meet domain-relevant community standards.

FAIR Principles Working Detailed Document

- https://force11.org/guiding-principles-for-findable-accessible-interoperable-and-re-usable-data-publishing-version-b1-0/

On to today…

Neurodata **W**ithout **B**orders (N.W.B.)

Introduction, tools, definitions and relevance

Use **NWB** for

- Use this for **cellular neurophysiology**, such as electrophysiology and optical physiology

NWB Definition

- https://www.nwb.org/
- “**Neurodata Without Borders (NWB)** is a ***data standard*** for neurophysiology, providing neuroscientists with a common standard to share, archive, use, and build analysis tools for neurophysiology data. NWB is designed to store a variety of neurophysiology data, including data from intracellular and extracellular electrophysiology experiments, data from optical physiology experiments, and tracking and stimulus data.” [www.nwb.org]

NWB Introduction

- https://www.nwb.org/
- https://nwb-overview.readthedocs.io/en/latest/
- So essentially
  - A data format for sharing/archiving
  - Standardized (set of rules and best practices)
  - Packages Data and Metadata together so human- and machine-readable

NWB Introduction

- Take advantage of established techniques for processing, analysis, visualization tools
- Makes data easier to reuse - additional scientific insights
- Essential step to getting data into the DANDI archive (https://dandiarchive.org/)

Brain **I**maging **D**ata **S**tructure
(B.I.D.S.)

Introduction, tools, definitions and relevance

Use **BIDS** for

- Use for **neuroimaging data** such as MRI

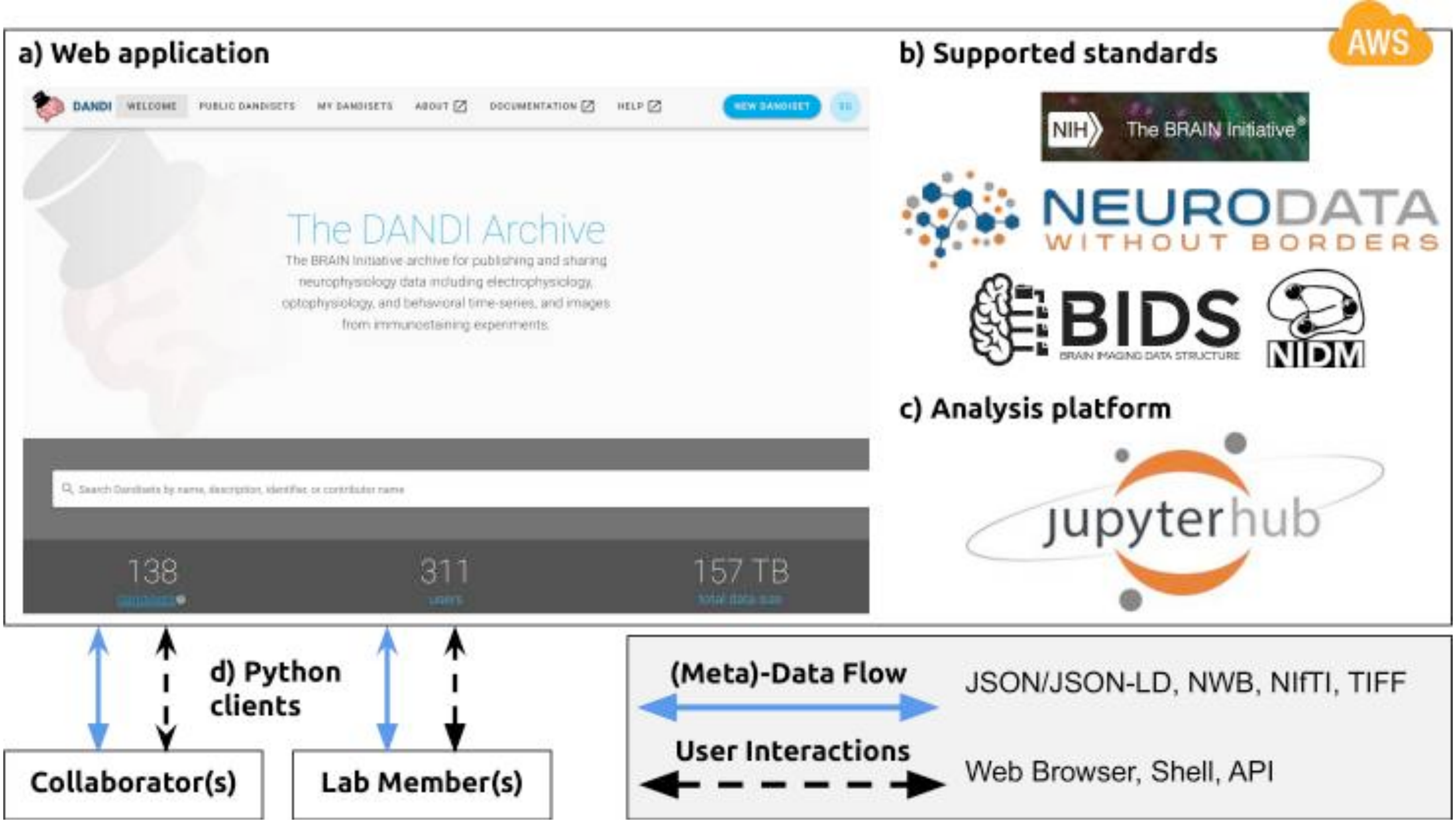
Brain Imaging Data Structure

- https://bids.neuroimaging.io/
- A second data standard

Distributed **A**rchives for **N**europhysiology **D**ata **I**ntegration (D.A.N.D.I.)

What is DANDI?

- The BRAIN Initiative archive for publishing and sharing neurophysiology data including
  - Electrophysiology, Optophysiology, Behavioral time-series, Images from immunostaining experiments.
- A persistent, versioned, and growing collection of standardized datasets
- A place to house data to collaborate across research sites
- Supported by the BRAIN Initiative and the AWS Public dataset programs


a) Web application
DANDI
WELCOME
PUBLIC DANDISETS
MY DANDISETS
ABOUT
DOCUMENTATION
HELP
NEW DANDISET
The DANDI Archive
The BRAIN Initiative archive for publishing and sharing neurophysiology data including electrophysiology, optophysiology, and behavioral time-series, and images from immunostaining experiments.
Search Dandisets by name, description, identifier, or contributor name
138
311
157 TB
b) Supported standards
AWS
NIH
The BRAIN Initiative
NEURODATA
WITHOUT BORDERS
BIDS
BRAIN IMAGING DATA STRUCTURE
NIDM
c) Analysis platform
jupyterhub
d) Python clients
Collaborator(s)
Lab Member(s)
(Meta)-Data Flow
JSON/JSON-LD, NWB, NIfTI, TIFF
User Interactions
Web Browser, Shell, API

Benefits of DANDI

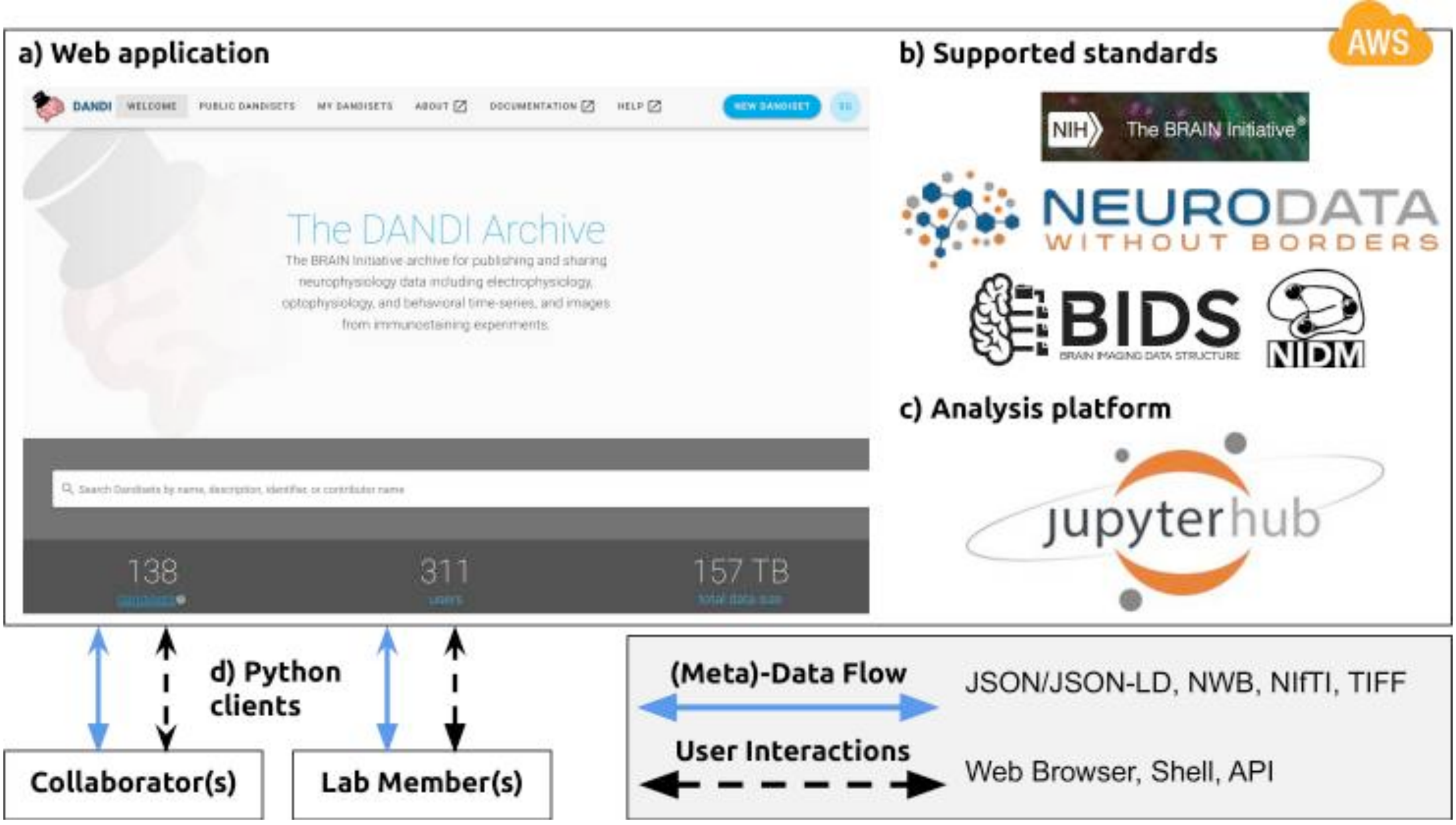
- A FAIR (Findable, Accessible, Interoperable, Reusable) data archive to house standardized neurophysiology and associated data
- Rich metadata to support search across data
- Consistent and transparent data standards to simplify data reuse and software development.
  - Uses NWB, BIDS, Neuroimaging Data Model (NIDM), and other BRAIN Initiative standards to organize and search the data.
  - The data can be accessed programmatically allowing for software to work directly with data in the cloud
- The infrastructure is built on a software stack of open source products, thus enriching the ecosystem

DANDI compatibility

- Uses NWB for core data language
- “Dandisets” - DANDI datasets - collection of NWB files recorded over multiple sessions, organized together
- Viewable from a web browser
- Can interact through Jupyterhub interface for exploring, visualizing and analyzing the data stored in the archive

DANDI python client

- Organize data locally into the required structure
- Download/upload data from/to the DANDI archive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DANDI archive

- **Public DANDI sets:** https://dandiarchive.org/dandiset
- **Documentation:** https://www.dandiarchive.org/handbook/10_using_dandi/

DANDI Properties

- **Data identifiers:** The archive provides persistent identifiers for versioned datasets and assets, thus improving reproducibility of neurophysiology research

- **Data storage:** Cloud-based platform on AWS. Data are available from a public S3 bucket. Data from embargoed datasets are available from a private bucket to owners only

- **Type of data:** The archive accepts cellular neurophysiology data including electrophysiology, optophysiology, and behavioral time-series, and images from immunostaining experiments and other associated data (e.g. participant information, MRI or other modalities)

- **Accepted Standards** and Data File Formats: NWB (HDF5), BIDS (NIfTI, JSON, PNG, TIF, OME.TIF, OME.BTF, OME.ZARR) (see Data Standards for more details)

Neurophysiology Informatics Challenges and DANDI Solutions

Challenges	Solutions
Most raw data stays in laboratories.	DANDI provides a public archive for dissemination of raw and derived data.
Non-standardized datasets lead to significant resource needs to understand and adapt code to these datasets.	DANDI standardizes all data using NWB and BIDS standards.
The multitude of different hardware platforms and custom binary formats requires significant effort to consolidate into reusable datasets.	The DANDI ecosystem provides tools for converting data from different instruments into NWB and BIDS.
There are many domain general places to house data (e.g. Open Science Framework, G-Node, Dropbox, Google drive), but it is difficult to find relevant scientific metadata.	DANDI is focused on neurophysiology data and related metadata.
Datasets are growing larger, requiring compute services to be closer to data.	DANDI provides Dandihub, a JupyterHub instance close to the data.
Neurotechnology is evolving and requires changes to metadata and data storage.	DANDI works with community members to improve data standards and formats.
Consolidating and creating robust algorithms (e.g. spike sorting) requires varied data sources.	DANDI provides access to many different datasets.

DANDI archive

- https://elifesciences.org/articles/78362

- **Oliver Rübel, Andrew Tritt, Ryan Ly, Benjamin K Dichter, Satrajit Ghosh, Lawrence Niu, Pamela Baker, Ivan Soltesz, Lydia Ng, Karel Svoboda, Loren Frank, Kristofer E Bouchard (2022) The Neurodata Without Borders ecosystem for neurophysiological data science eLife 11:e78362**

- https://doi.org/10.7554/eLife.78362

This sucks

main_simple_bak9-pretty-good.c	Aug 1, 2008, 1:01 AM	33 KB	C Source
main_simple_bak9-pretty-good.o	Aug 1, 2008, 1:00 AM	303 KB	object code
main_simple_bak9-pretty-goodv2.c	Aug 2, 2008, 1:16 AM	33 KB	C Source
main_simple_bak10.c	Sep 28, 2008, 1:16 PM	33 KB	C Source
main_simple_bak11-workingUART_correctspeed.c	Aug 30, 2008, 2:49 AM	27 KB	C Source
main_simple_bak11-workingUART_correctspeed.o	Aug 2, 2008, 1:17 AM	303 KB	object code
main_simple_bak12_willspin.c	Aug 2, 2008, 1:30 AM	28 KB	C Source
main_simple_bak12_willspin.o	Aug 2, 2008, 2:35 AM	301 KB	object code
main_simple_bak13-worksA-D-nonoise-spins.c	Aug 7, 2008, 12:57 PM	26 KB	C Source
main_simple_bak14-widersinefunctionsworkingrotation.c	Aug 8, 2008, 5:02 PM	26 KB	C Source
main_simple_bak15-spins-stillneedsquadrantfixed.c	Aug 15, 2008, 7:32 PM	30 KB	C Source
main_simple_bak16-15backup-spins-needs-improvement.c	Oct 15, 2008, 8:54 PM	31 KB	C Source
main_simple_bak17-smoother-stillnostandingstart.c	Aug 16, 2008, 6:50 PM	30 KB	C Source
main_simple_bak17-smoother-stillnostandingstart.o	Aug 18, 2008, 9:41 PM	305 KB	object code
main_simple_bak18-notgood.c	Aug 18, 2008, 9:42 PM	31 KB	C Source
main_simple_bak20SIMPLE-DCnotbrushless.c	Sep 17, 2009, 11:02 PM	27 KB	C Source
main_simple_bak20WORKS_PWM_COMMAND_CONTROL.c	Aug 19, 2008, 12:54 AM	29 KB	C Source
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main_simple_timer_intrpt_bak2.c	Aug 12, 2008, 2:00 PM	13 KB	C Source
main_simple_timer_intrpt_bak3.c	Aug 18, 2008, 12:14 AM	13 KB	C Source
main_simple_timer_intrpt.c	Aug 18, 2008, 12:17 AM	13 KB	C Source
main_simple_workingHWPWM.c	Aug 18, 2008, 7:19 PM	15 KB	C Source
main_simple.c	Sep 17, 2009, 11:02 PM	29 KB	C Source

Yup, this sucks too.

Thanks for chatting with me earlier today. I added the link to the visualization project into my resume and attached the resume. Thanks for any connections you can make for me. I'd love to know where you send it, so I can keep track of that. Thanks again!

Best,

May 11

[redacted]

May 11

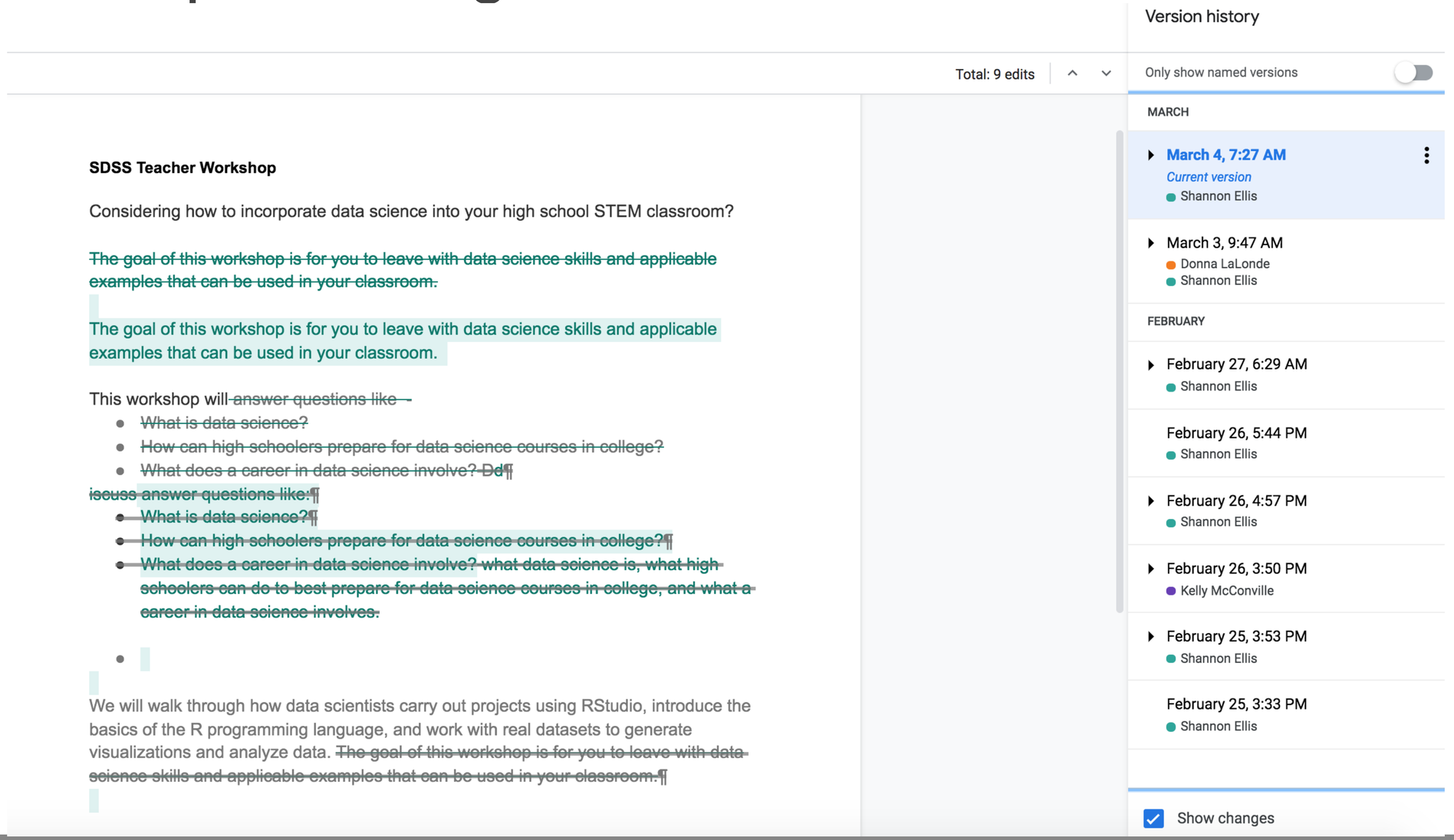
Actually, please use this one. I fixed a typo that was previously missed. Thanks!

[redacted]

May 11

Final copy, I swear. Thanks for helping out.

This is a step in the right direction



Version Control

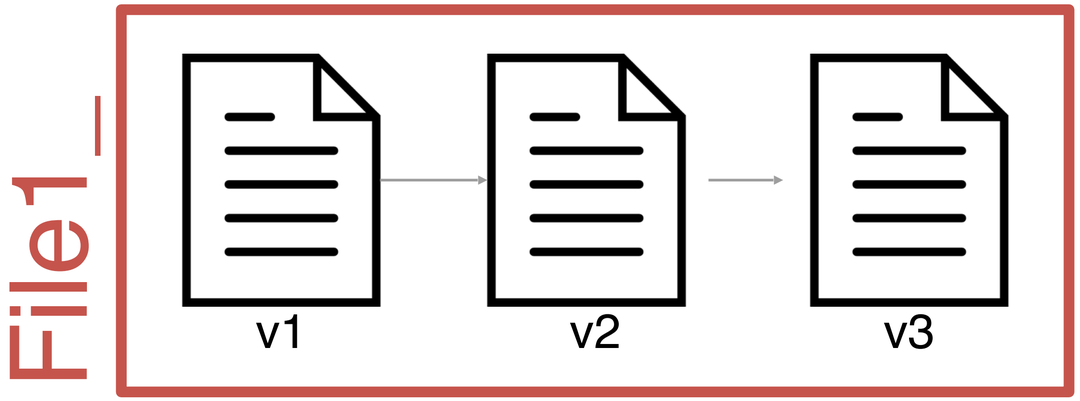
- Enables multiple people to simultaneously work on a single project.
- Each person edits their own copy of the files and chooses when to share those changes with the rest of the team.
- Thus, temporary or partial edits by one person do not interfere with another person's work

What is version control?

A way to manage the evolution of a set of files

What is version control?

A way to manage the evolution of a set of files



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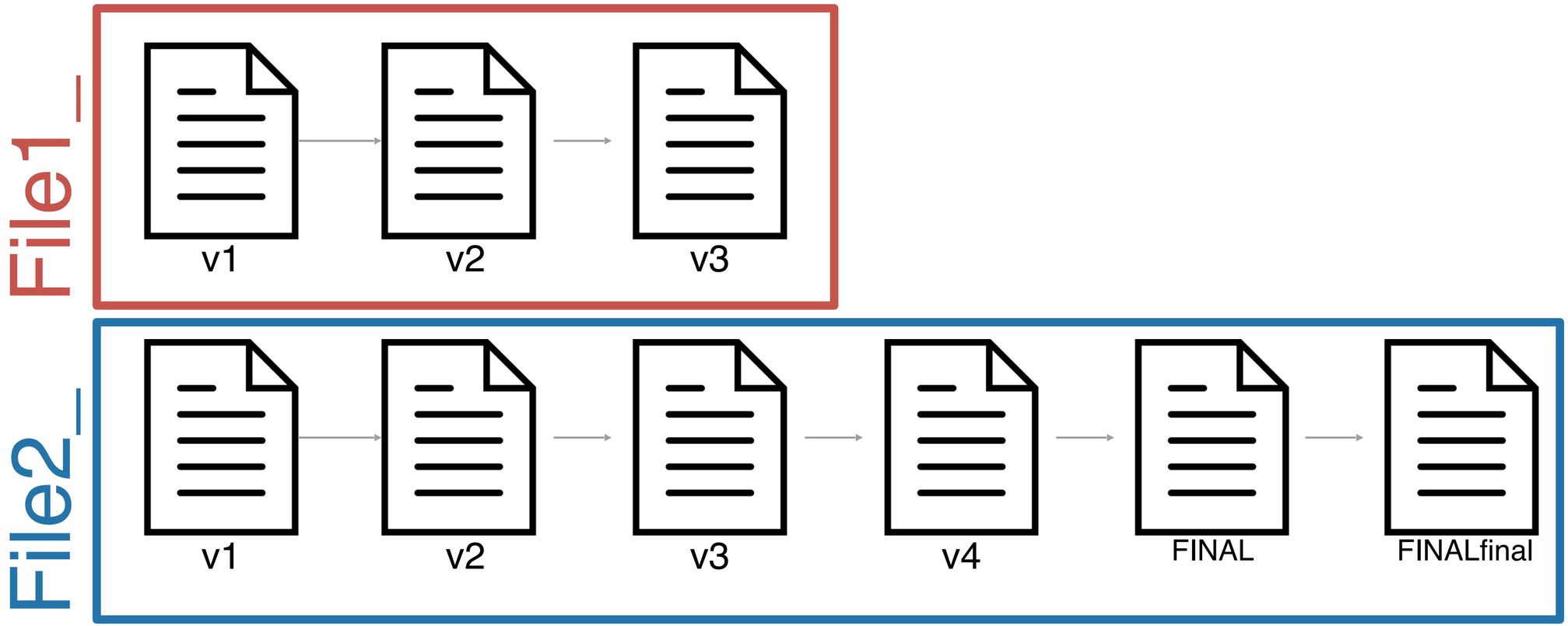
A way to manage the evolution of a set of files



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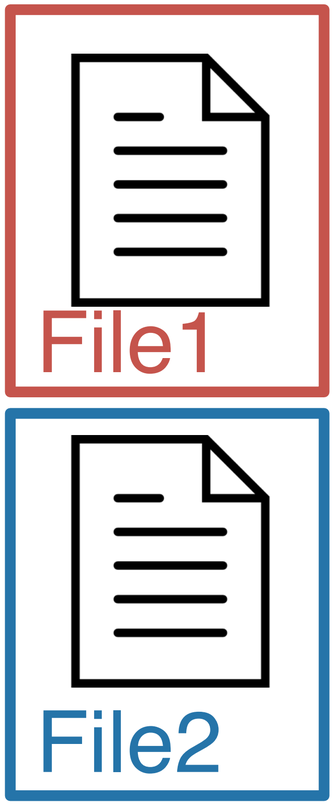
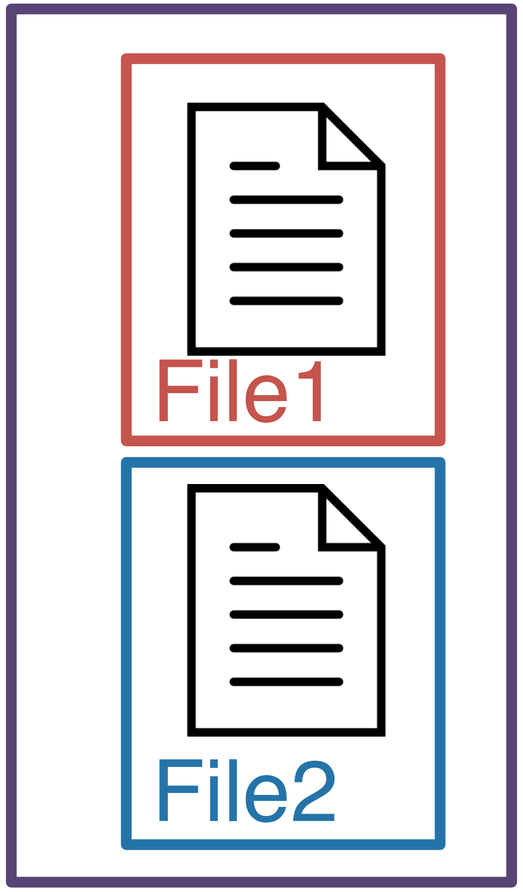
A way to manage the evolution of a set of files



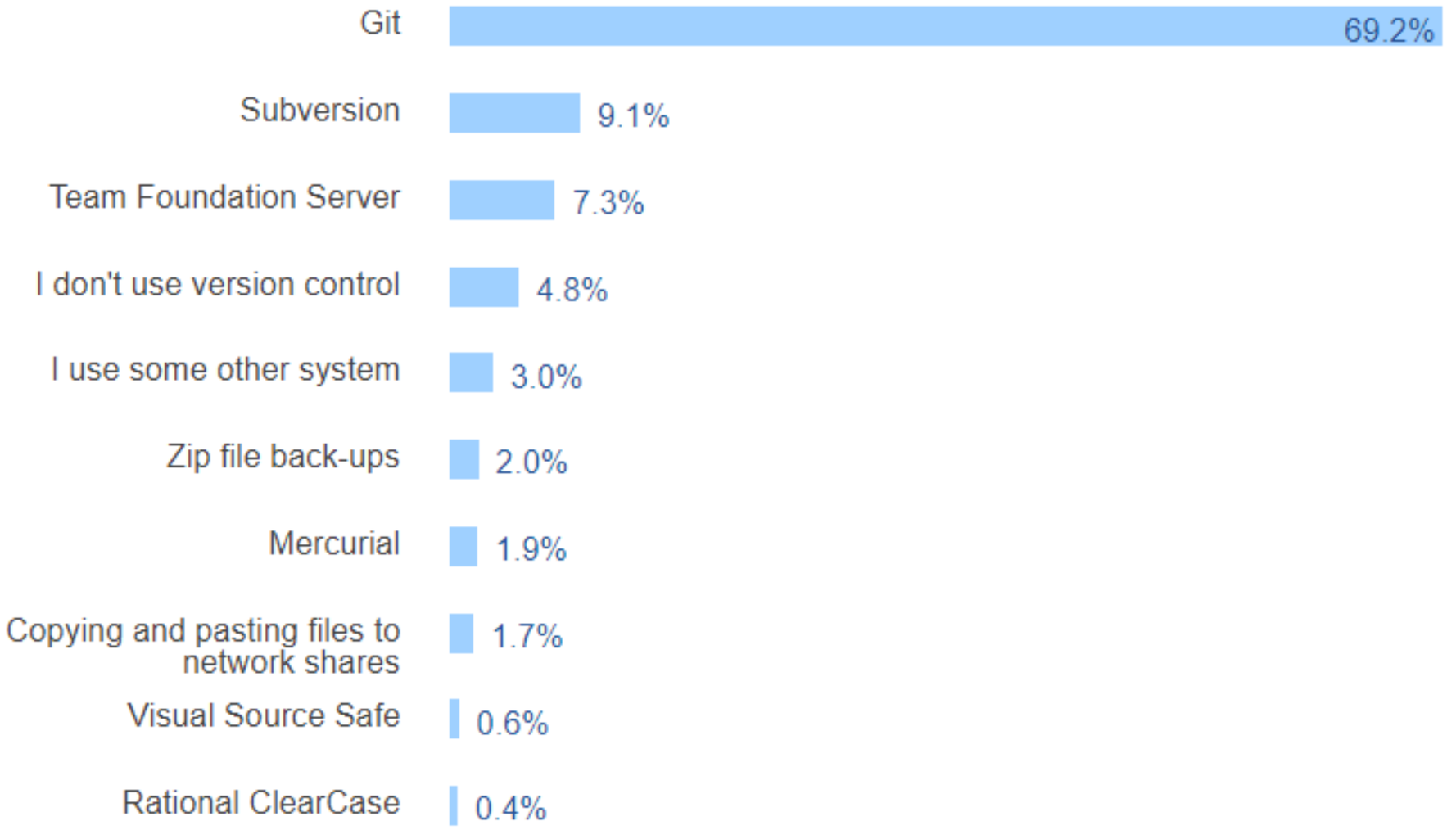
When using a version control system, you have **one copy of each file** and the *version control system tracks the changes* that have occurred over time

What is version control?

A way to manage the evolution of a set of files



The set of files is referred to as a **repository (repo)**



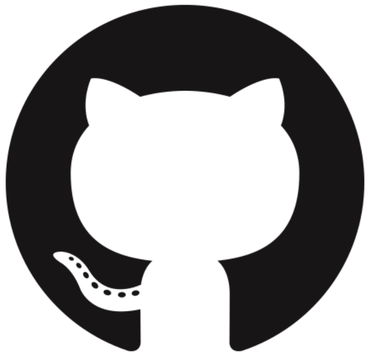
https://insights.stackoverflow.com/survey/2017#work-version-control

git & GitHub

git

the version control system

~ Track Changes from Microsoft Word….on steroids



GitHub (or Bitbucket or GitLab) is the home **where your git-based projects live** on the Internet.

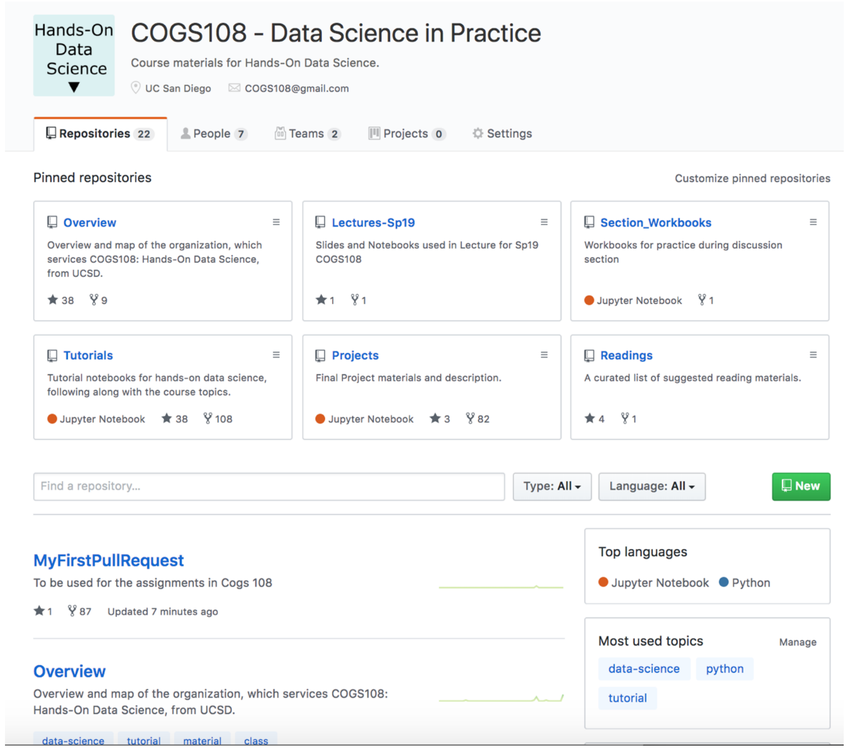
~ Dropbox….but way better

What version control looks like

```
$ git clone https://www.github.com/username/repo.git
$ git pull
$ git add -A
$ git commit -m “informative commit message”
$ git push
```

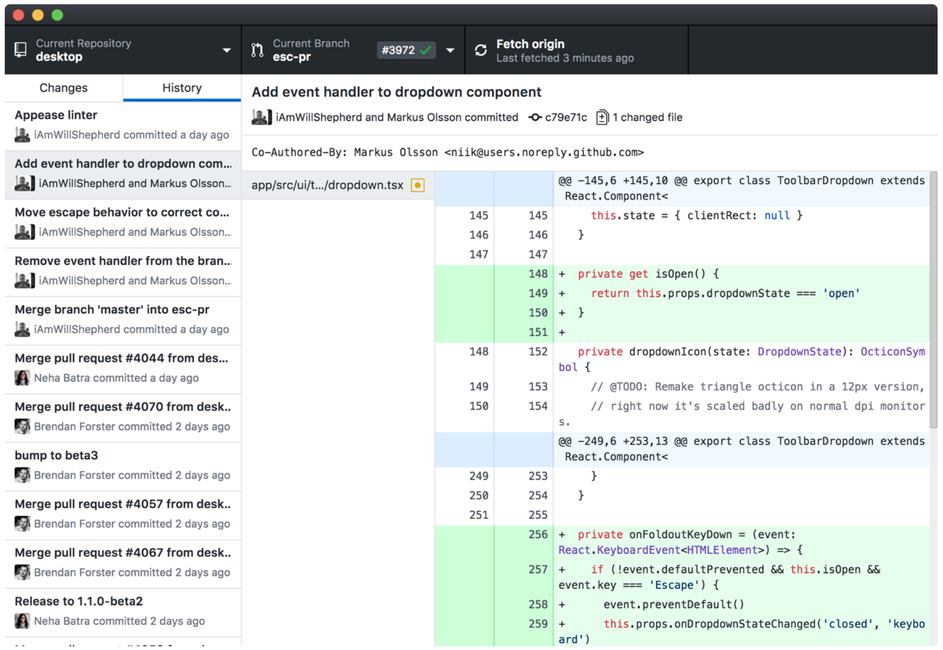
Terminal

git

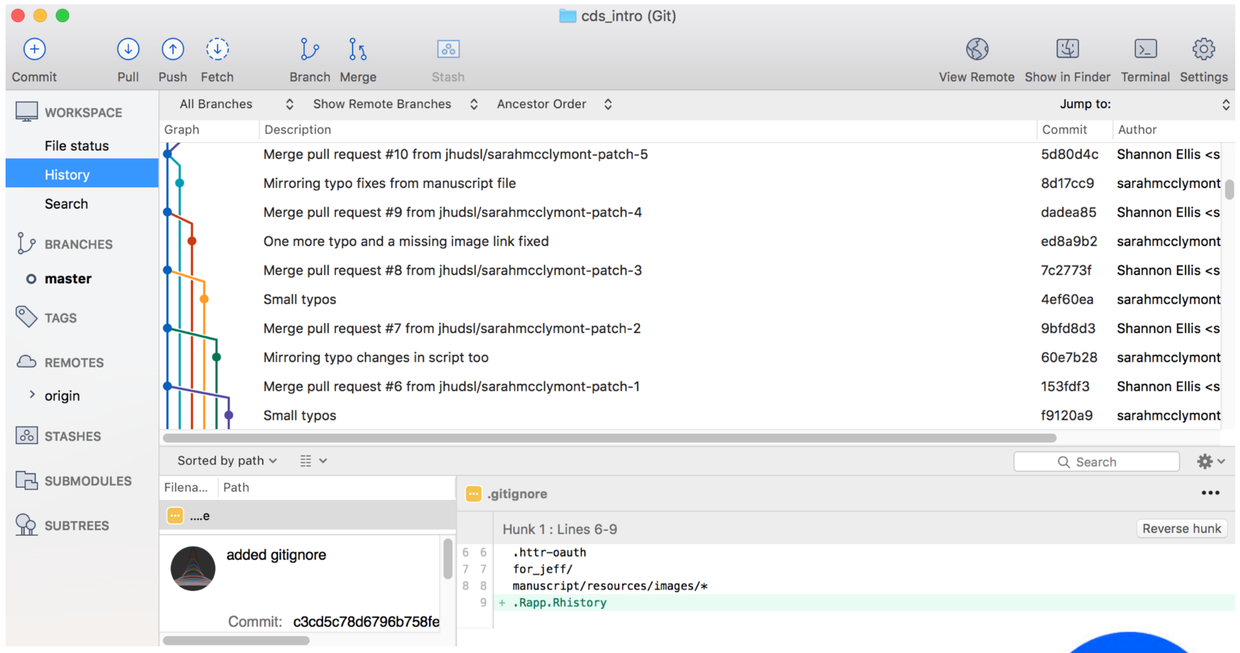


iitHub

GUIs can be helpful when working with version control



GitHub Desktop



SourceTree

Version Controller a

How do you typically interact with git?

A
I don’t

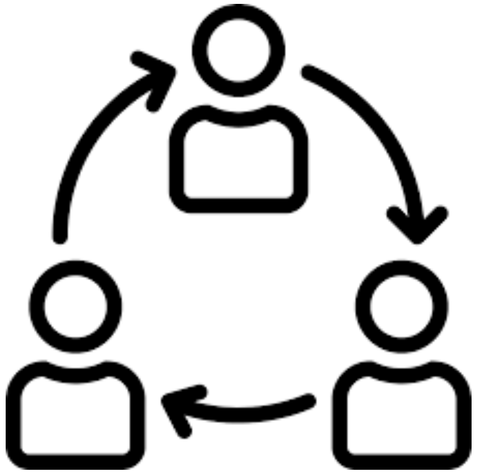
B
command line

C
GUI: GitHub Desktop

D
GUI: SourceTree

E
GUI: other

Why version control with git and GitHub?



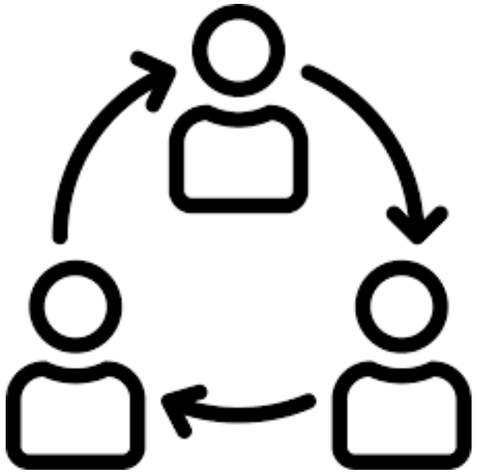
Collaboration

Returning to a safe state

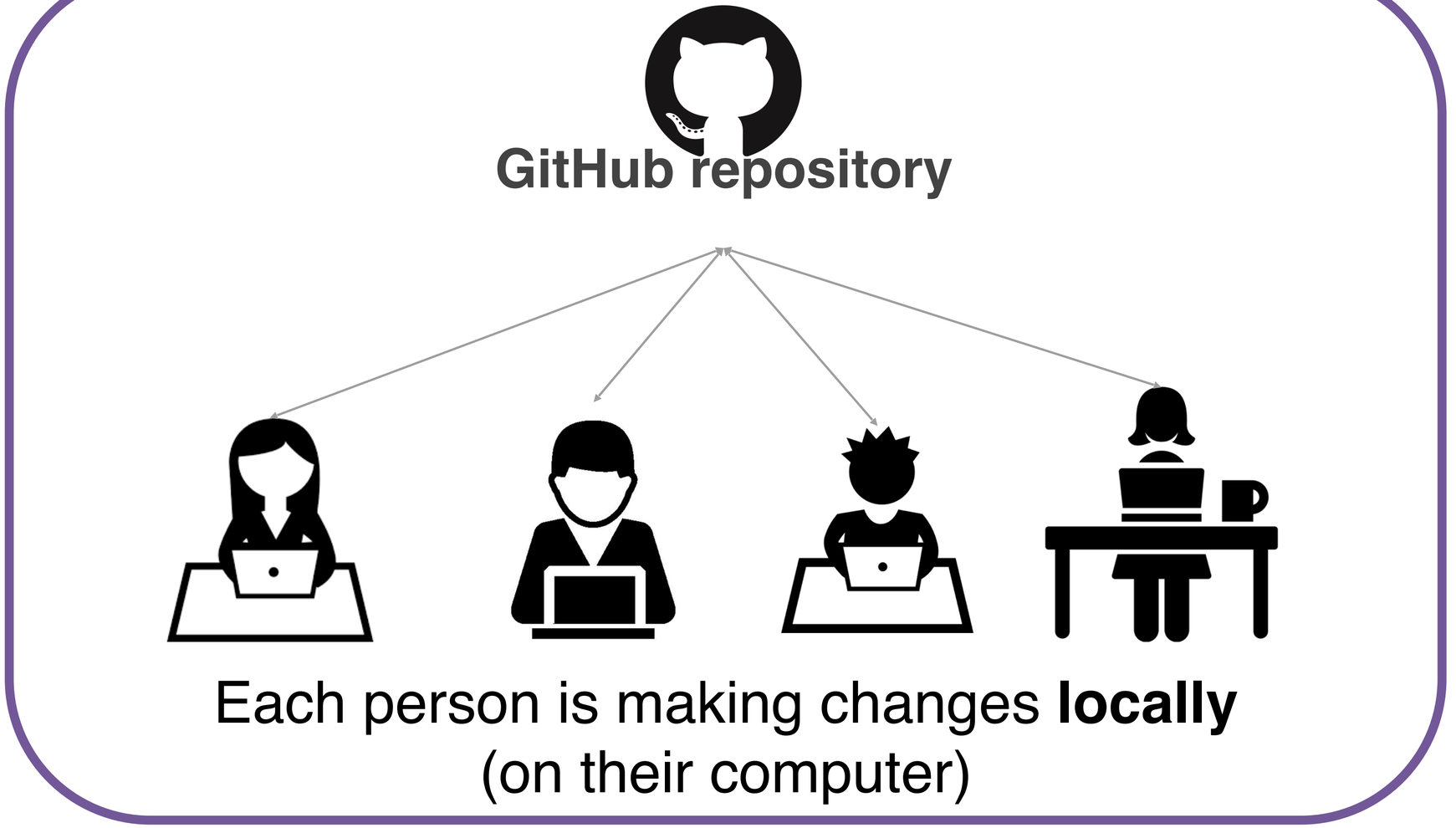
Exposure for your work

Tracking others' work

Collaborate like you do with Google Docs



Collaboration



Make changes locally, while knowing a stable copy exists

Returning to a safe state

You're free and safe to **try things out locally**. You'll only send changes to the repo when you're at a stable point

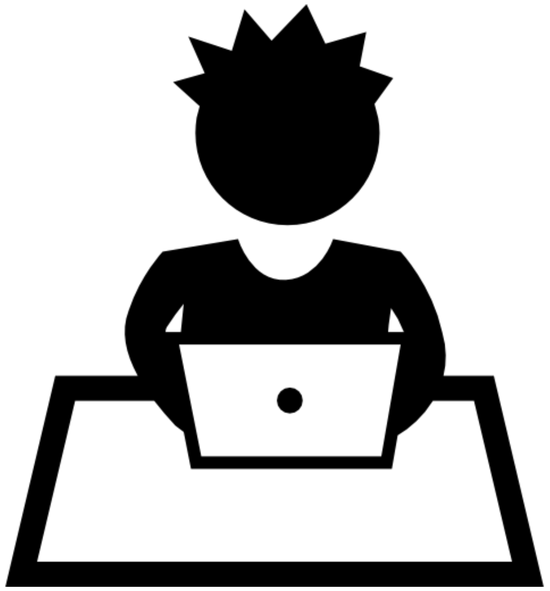
Your repositories will be visible to others!

Exposure for your work

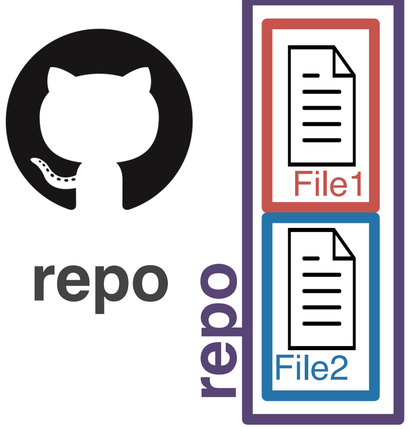
Your public GitHub repos are your coding social media

Keep up with others' work easily

Tracking others' work

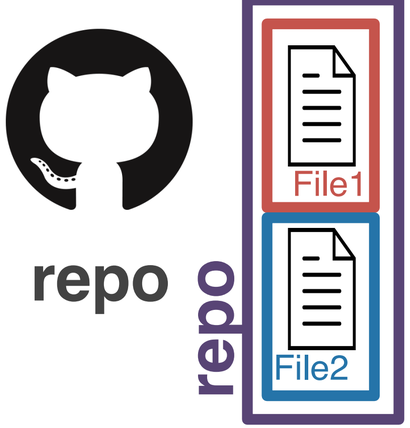


As a social platform, you can see others' work too!



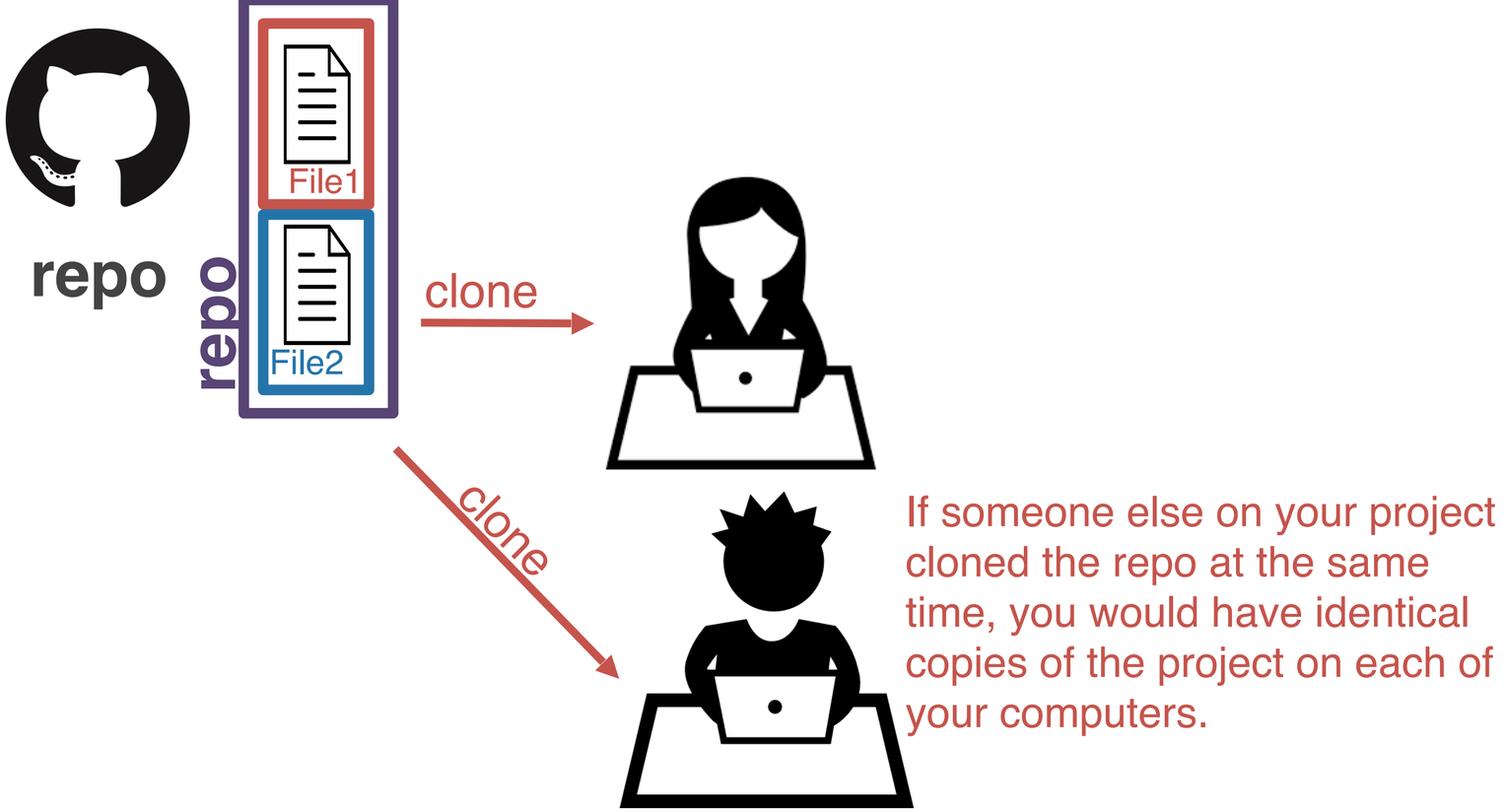
A **GitHub repo** contains all the files and folders for your project.

GitHub is a **remote host**. The files are geographically distant from any files on your computer.

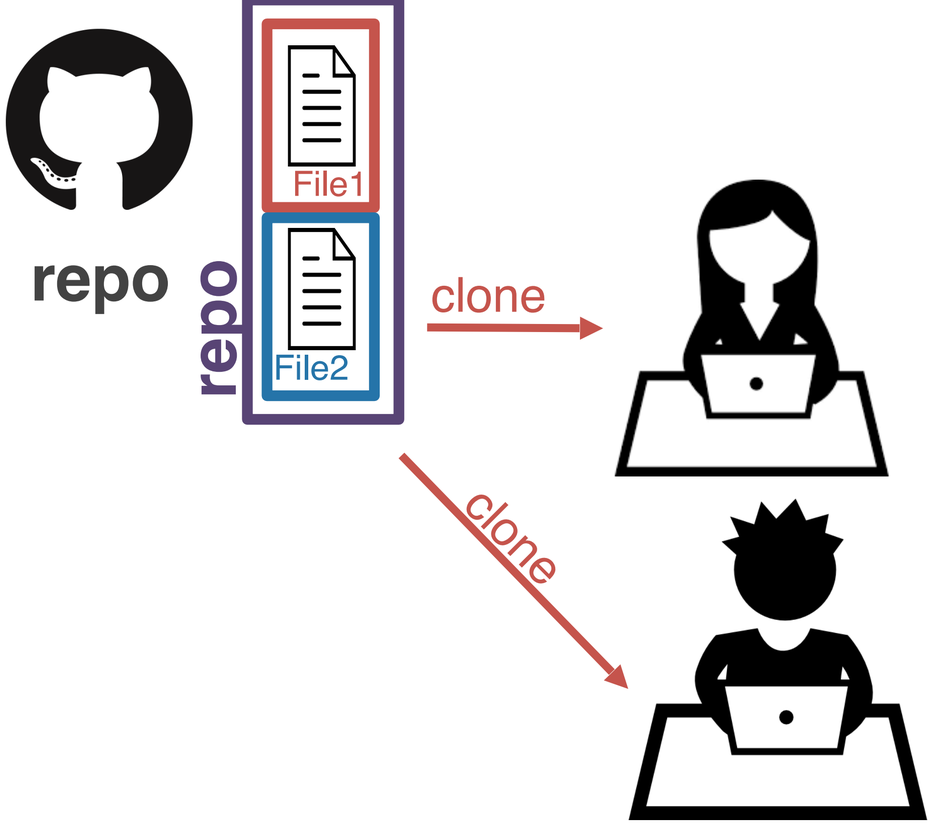


clone

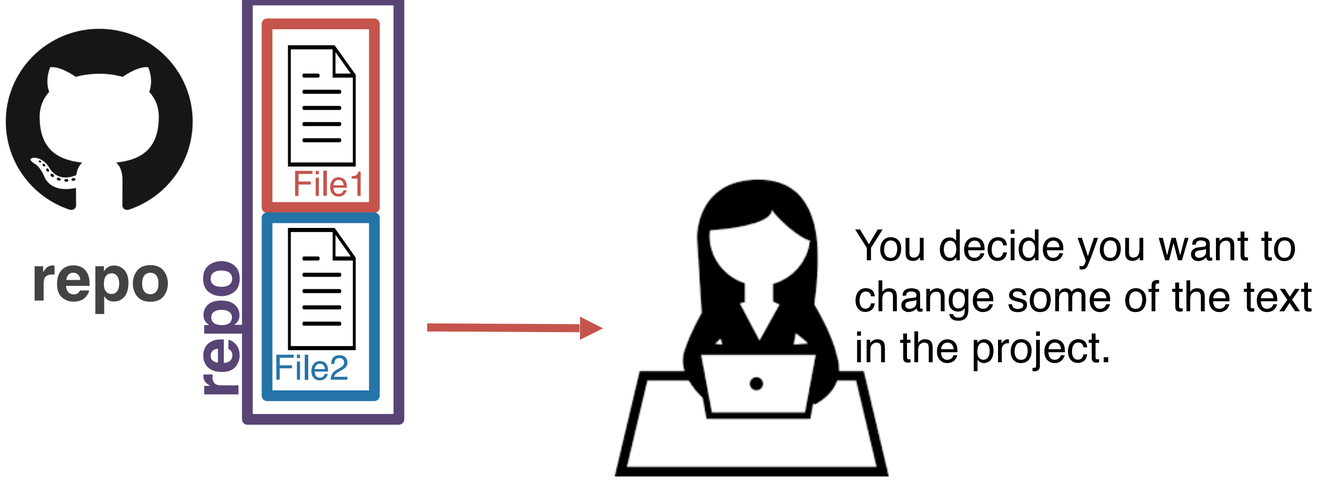
When you first make a copy onto your local computer (read: laptop), you **clone** the repository.

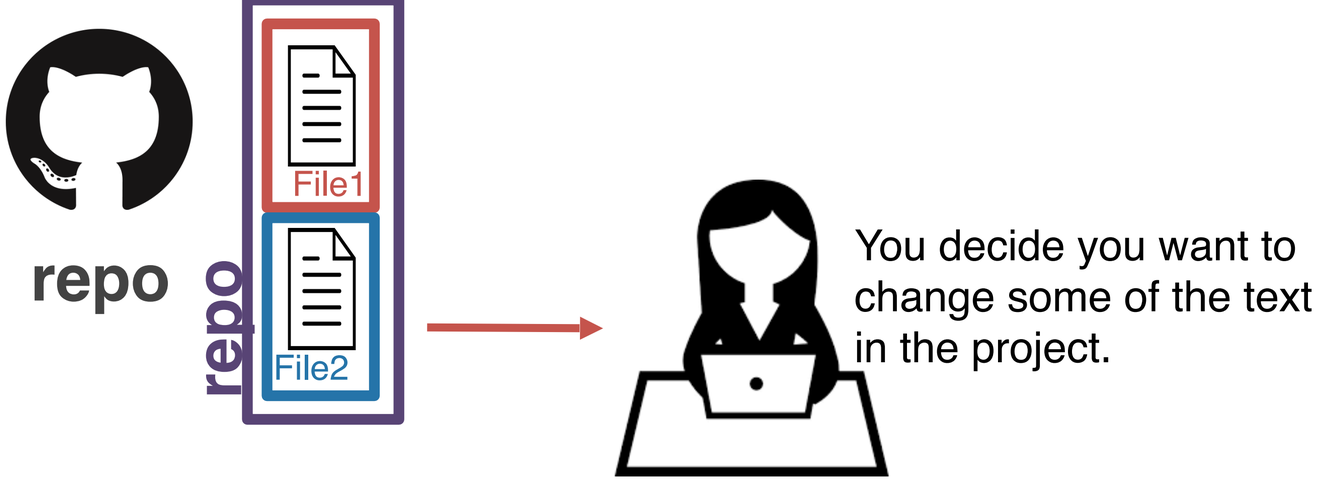


If someone else on your project cloned the repo at the same time, you would have identical copies of the project on each of your computers.



Yay! Everyone can work on the project!


repo
repo
File1
File2
You decide you want to change some of the text in the project.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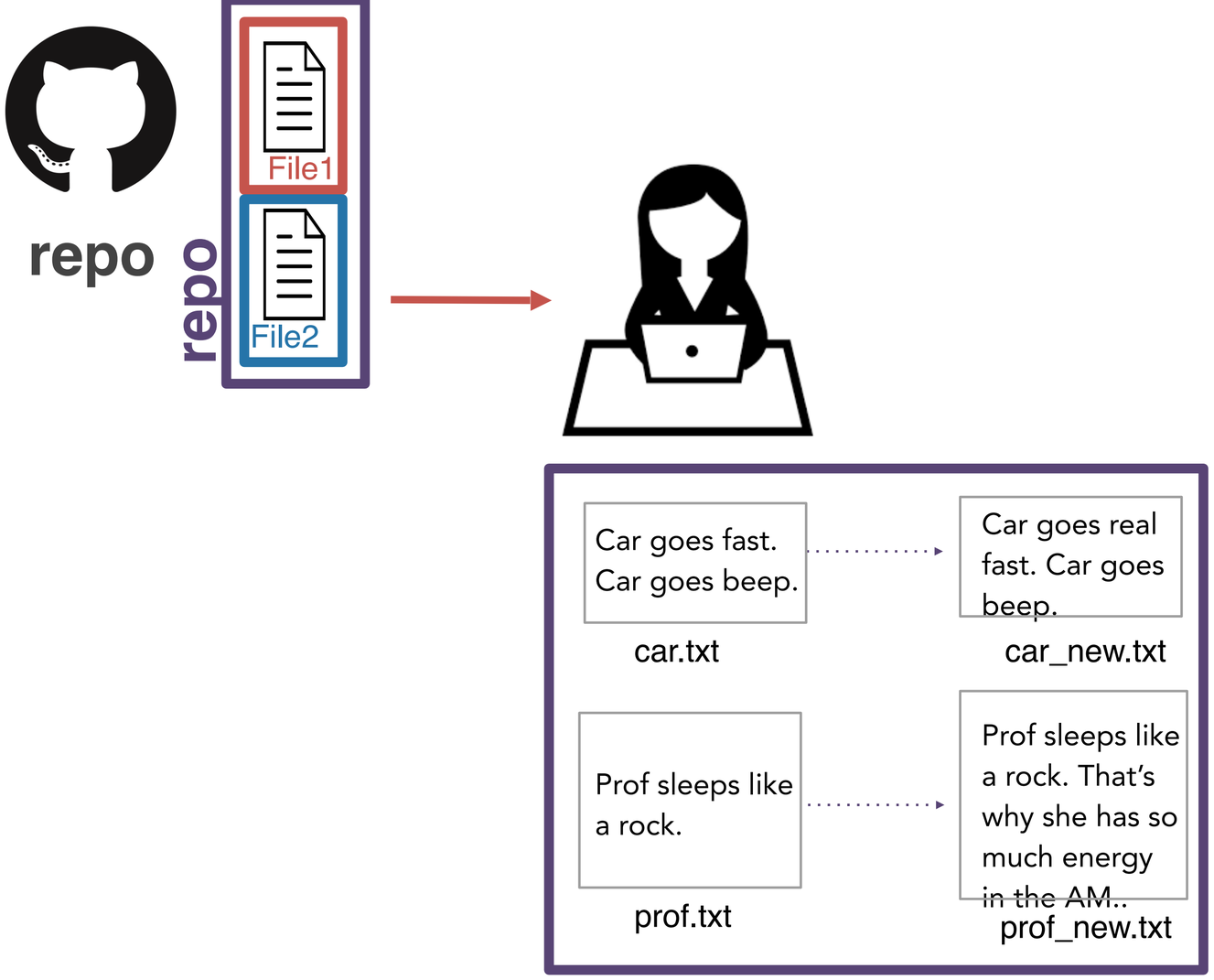
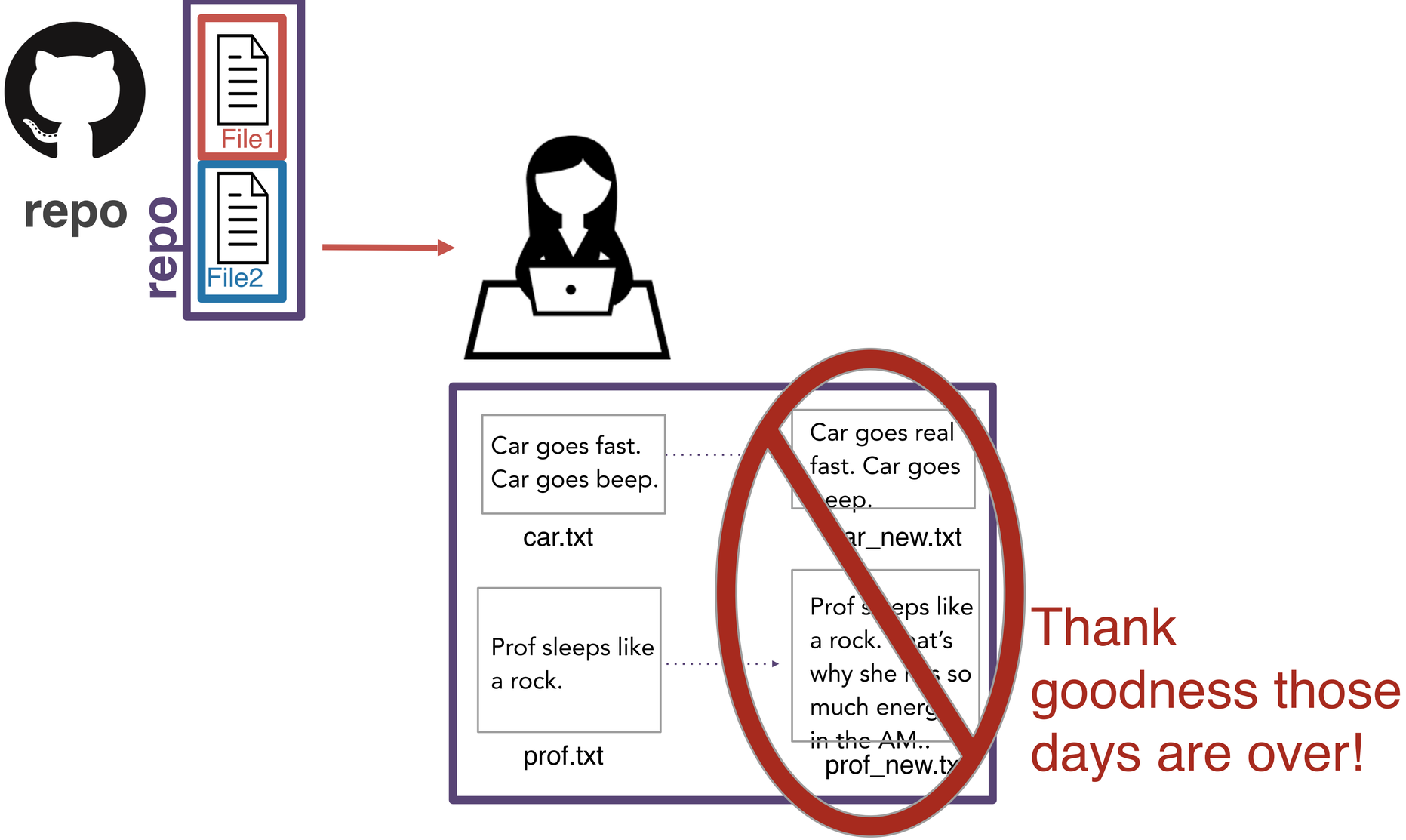
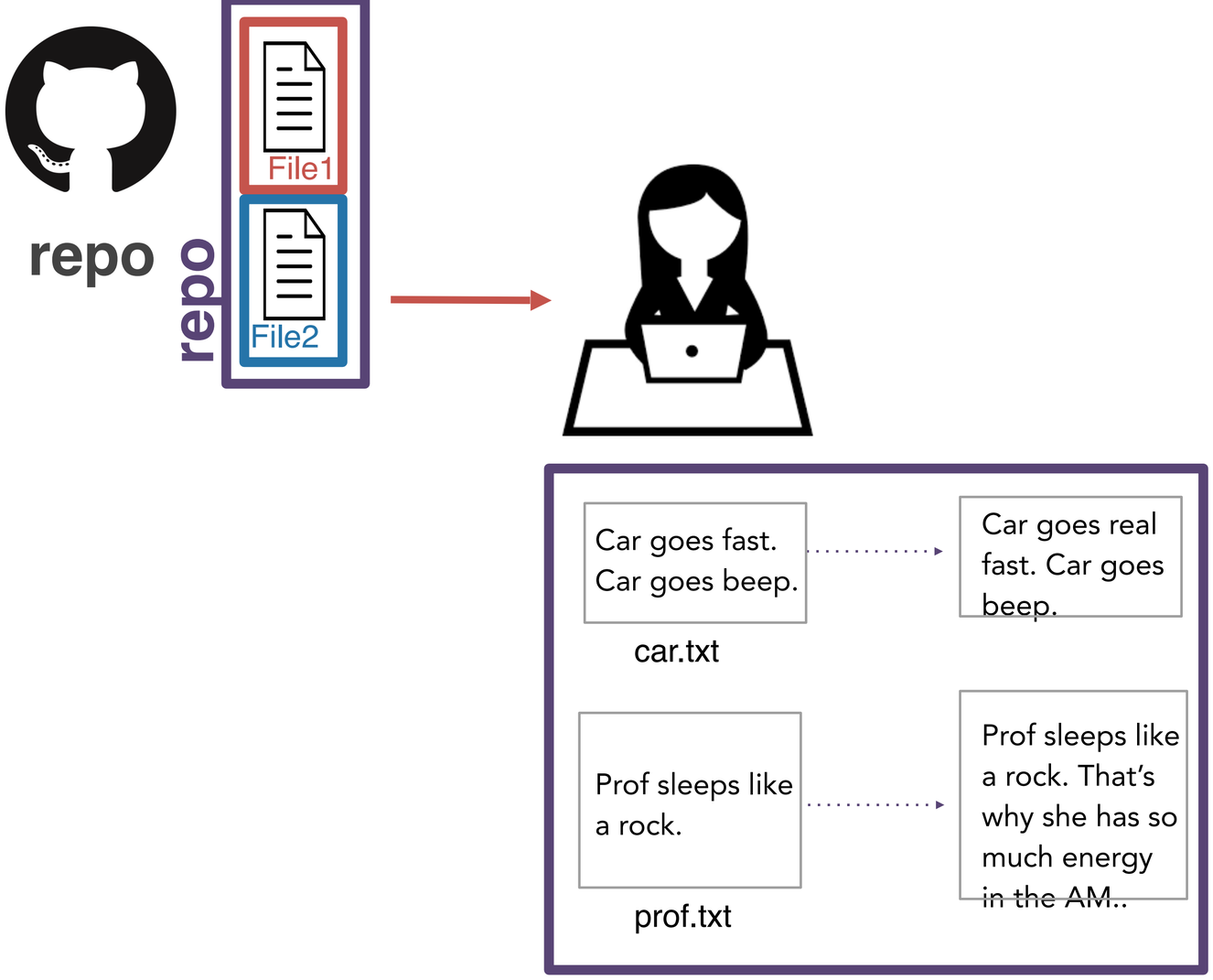
You decide you want to change some of the text in the project.



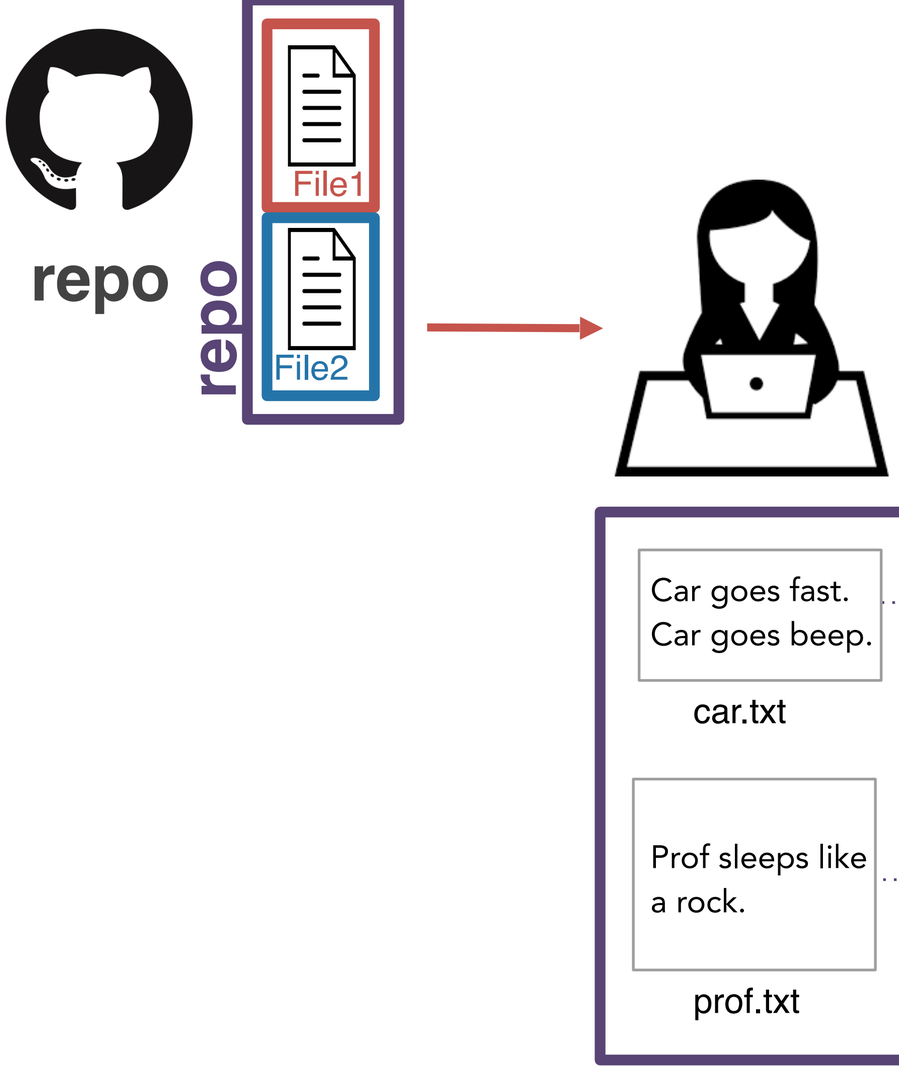
without git…you'd likely rename these files….



Thank goodness those days are over!

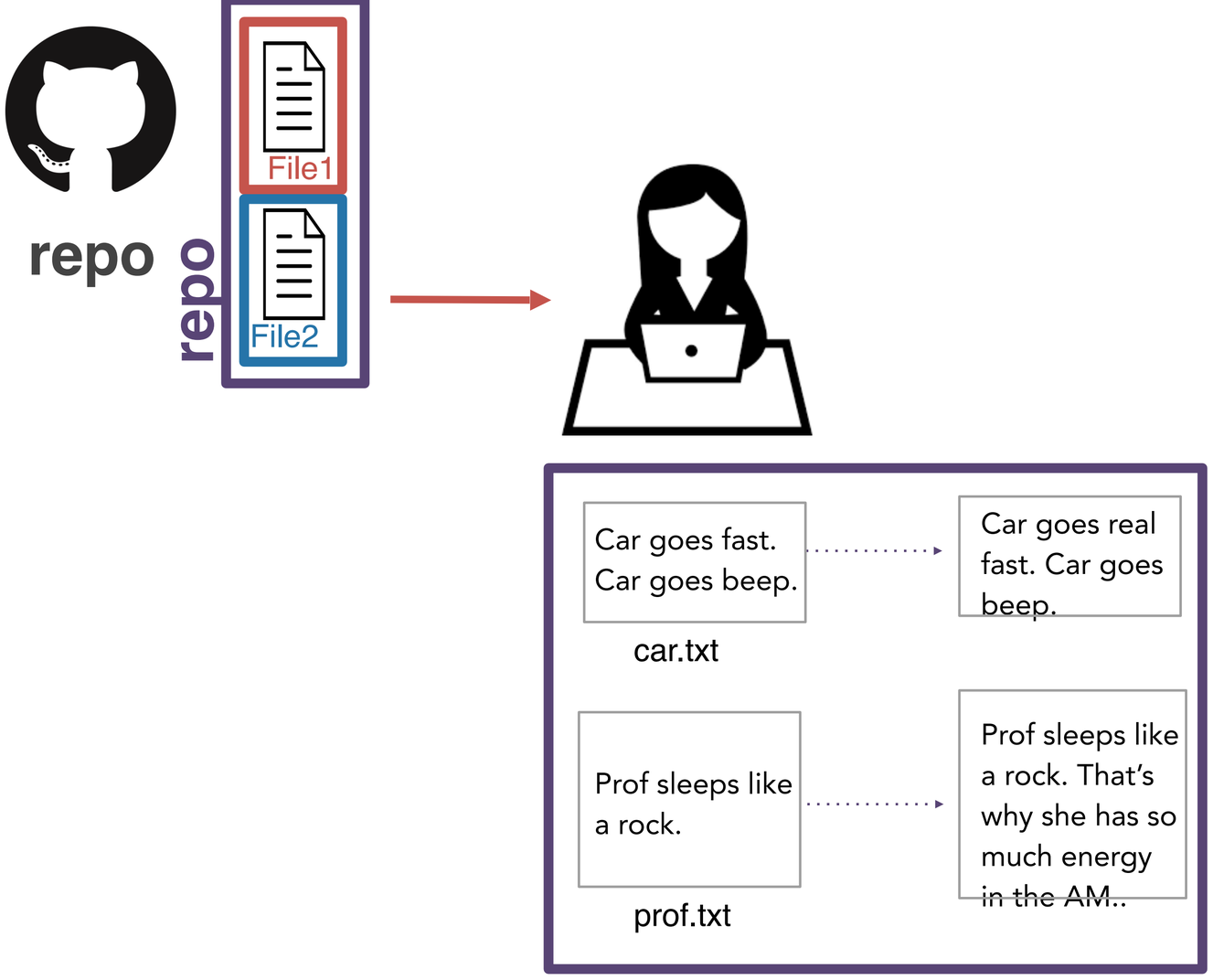


Instead, you tell git which files you'd like to keep track of using **add**. This process is called *staging*.



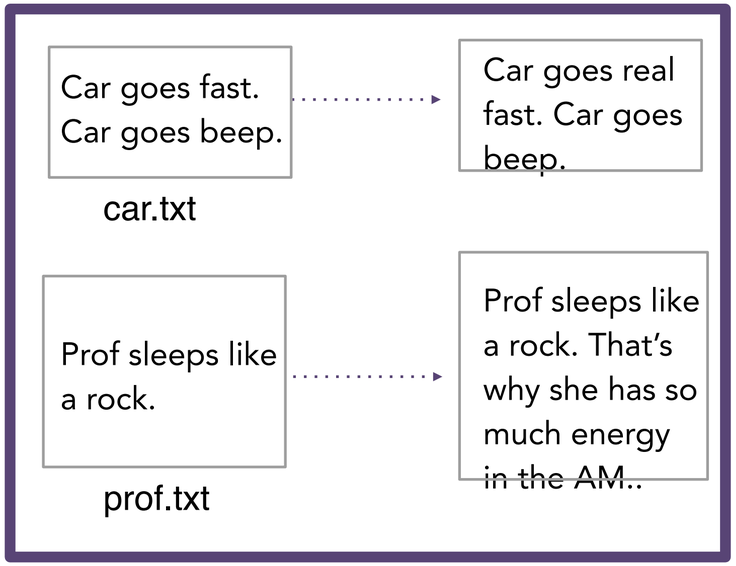
`git add file`	stages specified file (or folder)
`git add .`	stages new and modified files
`git add -u`	stages modified and deleted files
`git add -A`	stages new, modified, and deleted files
`git add *.csv`	Stages any files with .csv extension
`git add *`	Use with caution: stages everything

Instead, you tell git which files you'd like to keep track of using **add**. This process is called *staging*.



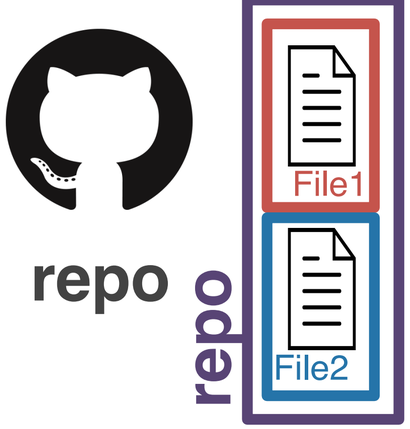
Then, you create a snapshot of your files at this point. This snapshot is called a **commit**.

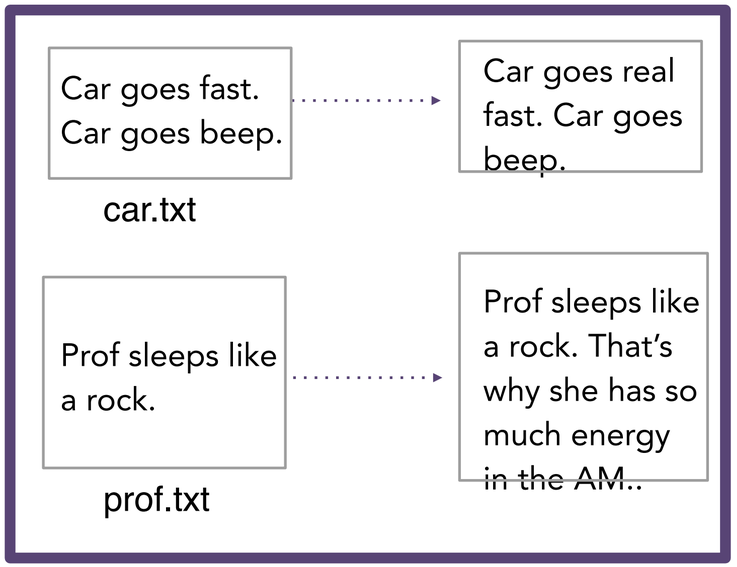
repo



Then, you create a snapshot of your files at this point. This snapshot is called a **commit**.

A **commit** tracks who, what, and when



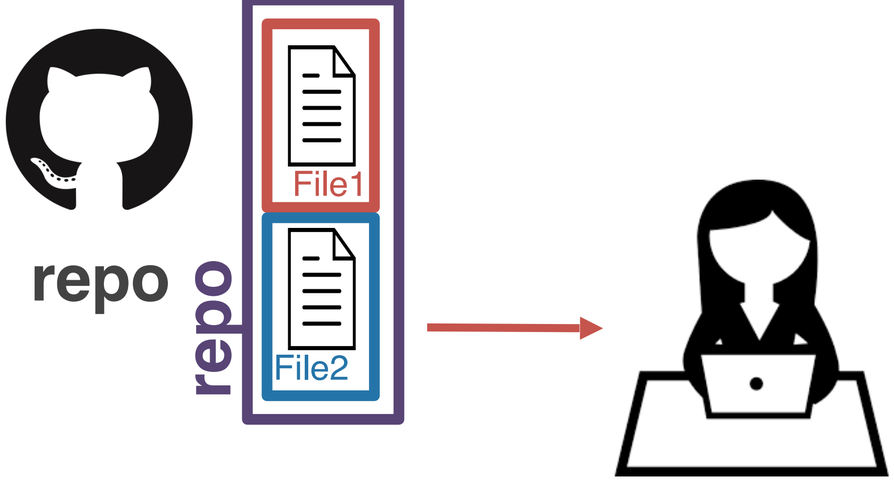


You can make commits more informative by adding a **commit message**.

Example: `git commit -m 'fix typos in car and prof'`

Then, you create a snapshot of your files at this point. This snapshot is called a **commit**.

A **commit** tracks who, what, and when

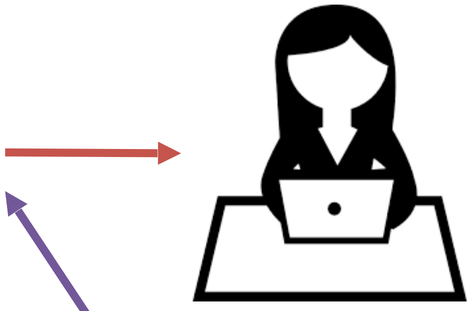


Shannon Ellis
3/28/21 3:28pm

fix typos in car and prof

repo

repo



push

Remember, you're not the only one working on this project though! You want your teammates to have access to these changes! You **push** these changes back to the remote.

Shannon Ellis
3/28/21 3:28pm

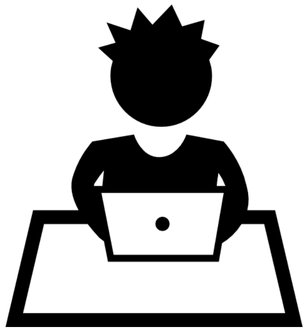
fix typos in car and prof

repo

repo

Shannon Ellis
3/28/21 3:28pm

fix typos in car and prof



Your teammate is still working with the (out-of-date) copy he cloned earlier!

Shannon Ellis
3/28/21 3:28pm

fix typos in car and prof

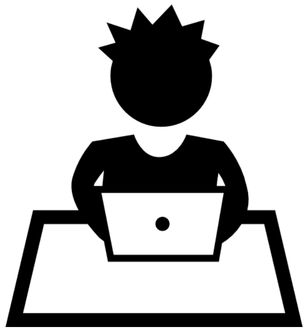
repo

repo

To catch up, your teammate will have to **pull** the changes from GitHub (remote)

Shannon Ellis
3/28/21 3:28pm

fix typos in car and prof



Your teammate is still working with the (out-of-date) copy he cloned earlier!

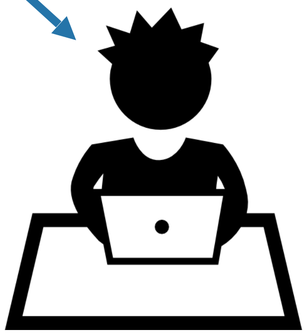
Shannon Ellis
3/28/21 3:28pm

fix typos in car and prof

repo

repo

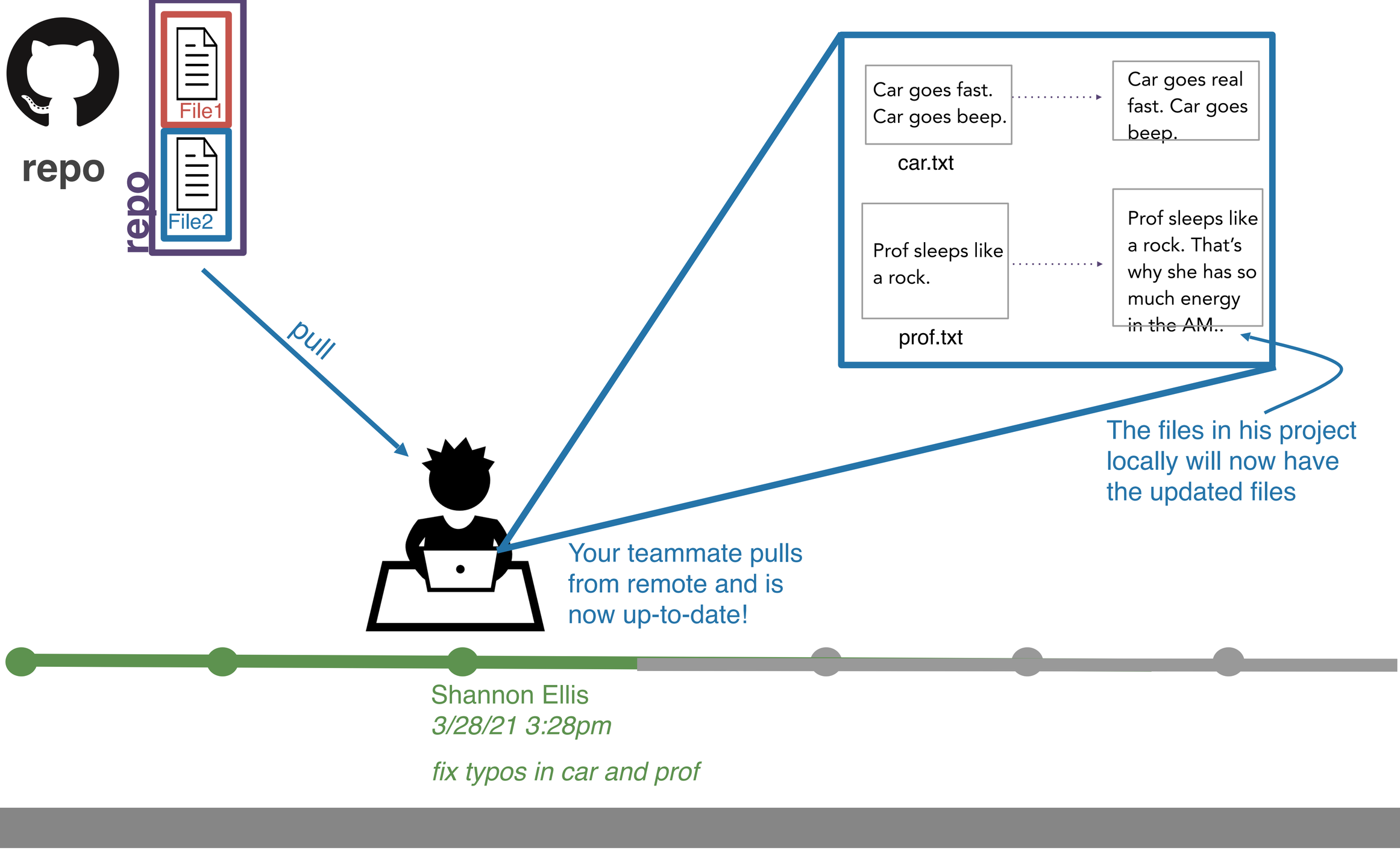
pull

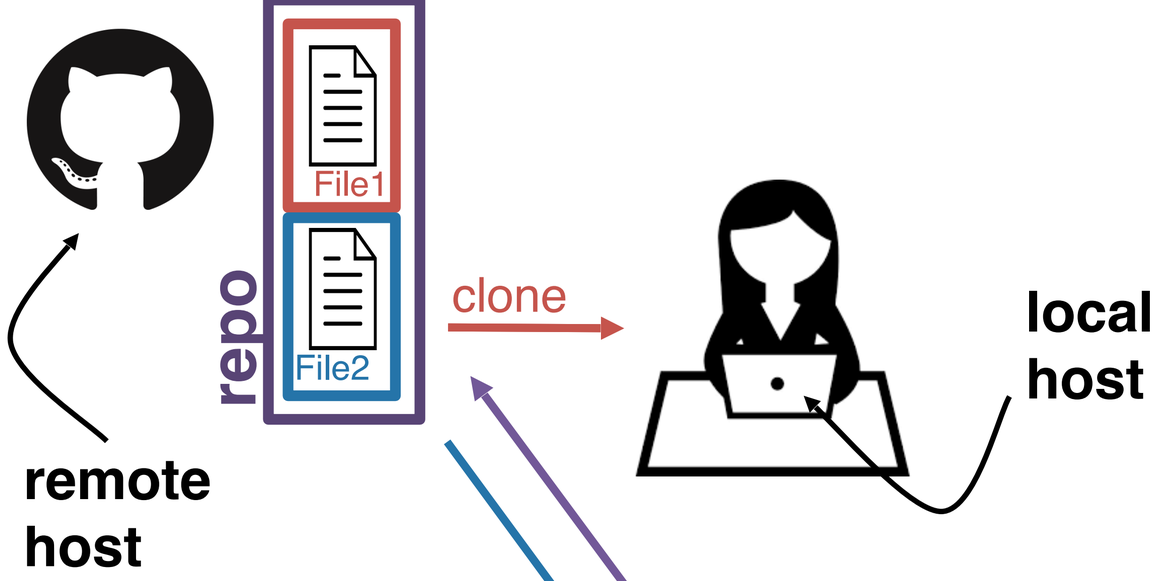


Your teammate pulls from remote and is now up-to-date!

Shannon Ellis
3/28/21 3:28pm

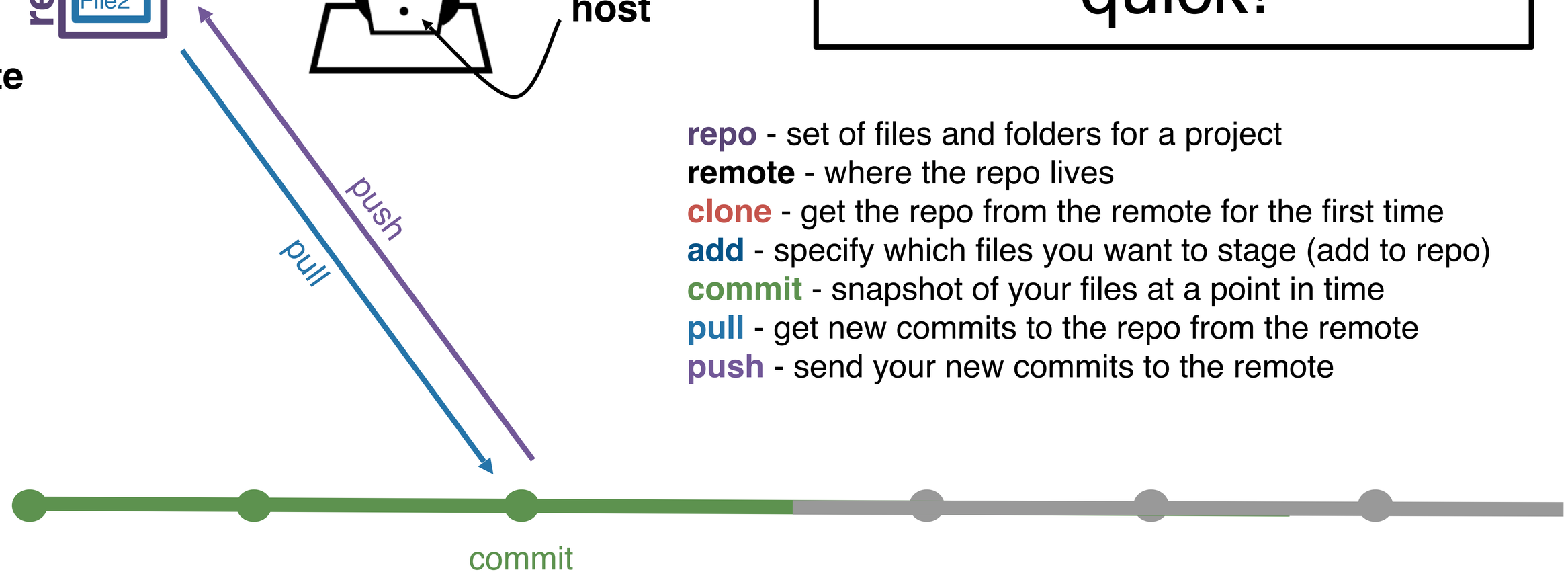
fix typos in car and prof


repo
repo
File1
File2
pull
Car goes fast.
Car goes beep.
car.txt
Car goes real fast. Car goes beep.
Prof sleeps like a rock.
prof.txt
Prof sleeps like a rock. That's why she has so much energy in the AM..
The files in his project locally will now have the updated files
Your teammate pulls from remote and is now up-to-date!
Shannon Ellis
3/28/21 3:28pm
fix typos in car and prof



Let's recap real quick!

repo - set of files and folders for a project
remote - where the repo lives
clone - get the repo from the remote for the first time
add - specify which files you want to stage (add to repo)
commit - snapshot of your files at a point in time
pull - get new commits to the repo from the remote
push - send your new commits to the remote



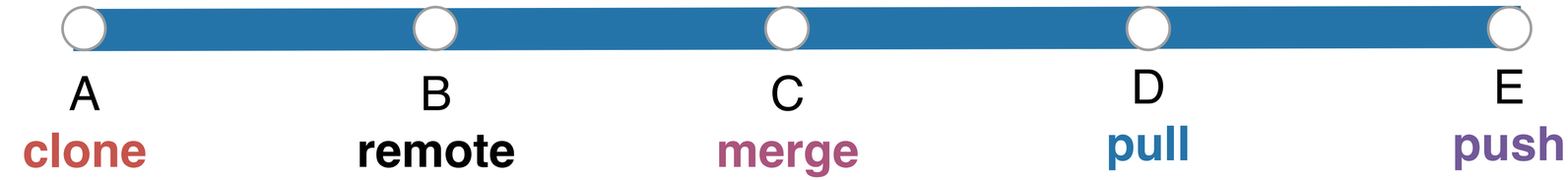
```
(base) sellis:Projects shannonellis$ git status
On branch master
Your branch is up to date with 'origin/master'.

Untracked files:
  (use "git add <file>..." to include in what will be committed)

        FinalProject_Guidelines.pdf

nothing added to commit but untracked files present (use "git add" to track)
(base) sellis:Projects shannonellis$ git add FinalProject_Guidelines.pdf
(base) sellis:Projects shannonellis$ git commit -m "update Project Guidelines"
[master 264e91a] update Project Guidelines
 1 file changed, 0 insertions(+), 0 deletions(-)
 create mode 100644 FinalProject_Guidelines.pdf
(base) sellis:Projects shannonellis$ git push
Counting objects: 3, done.
Delta compression using up to 8 threads.
Compressing objects: 100% (3/3), done.
Writing objects: 100% (3/3), 148.21 KiB | 29.64 MiB/s, done.
Total 3 (delta 1), reused 0 (delta 0)
remote: Resolving deltas: 100% (1/1), completed with 1 local object.
To https://github.com/COGS108/Projects.git
   6931768..264e91a  master -> master
```

Review & Question Time

Version Controller I

You've been working with a team on a project in a repo. You've made changes locally and you want to see them on the remote.

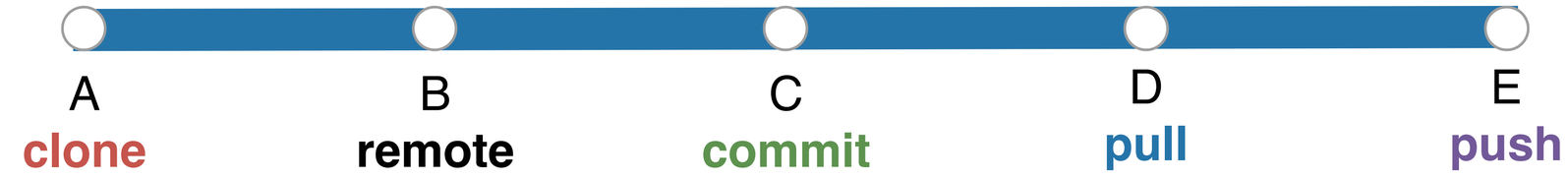
What do you do to get them on the remote?

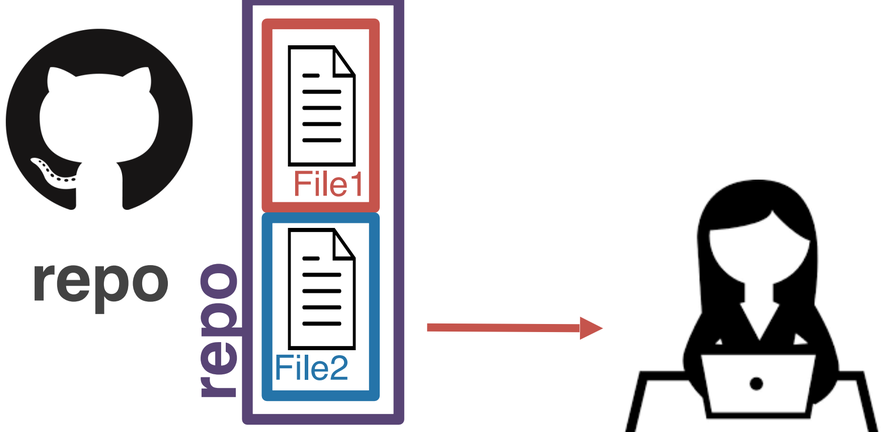


Version Controller II

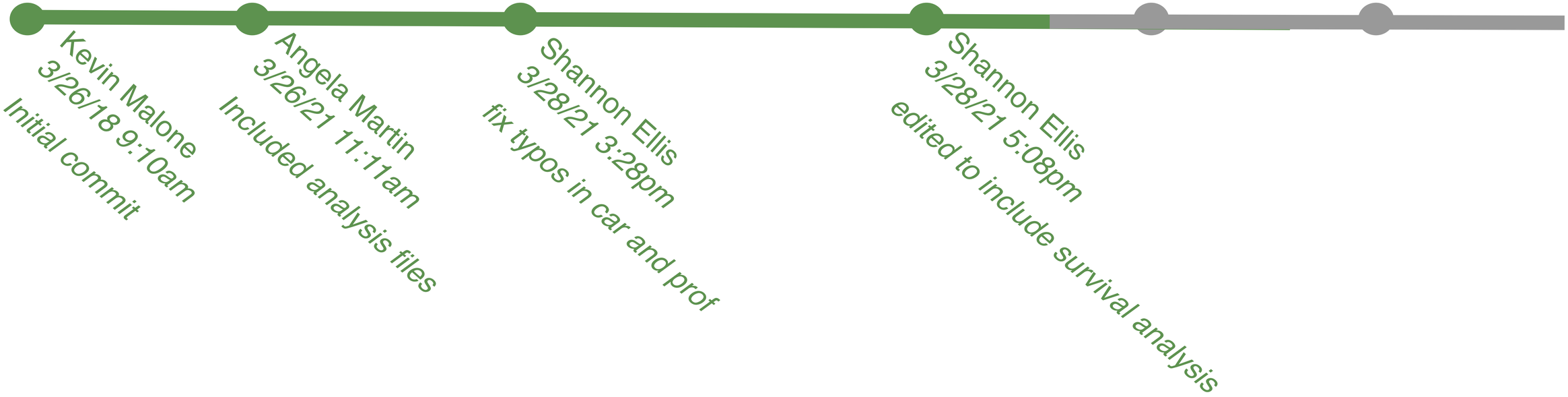
Your teammate has given you access to a GitHub repository to work on a project together. You want to get them for the first time on your computer locally.

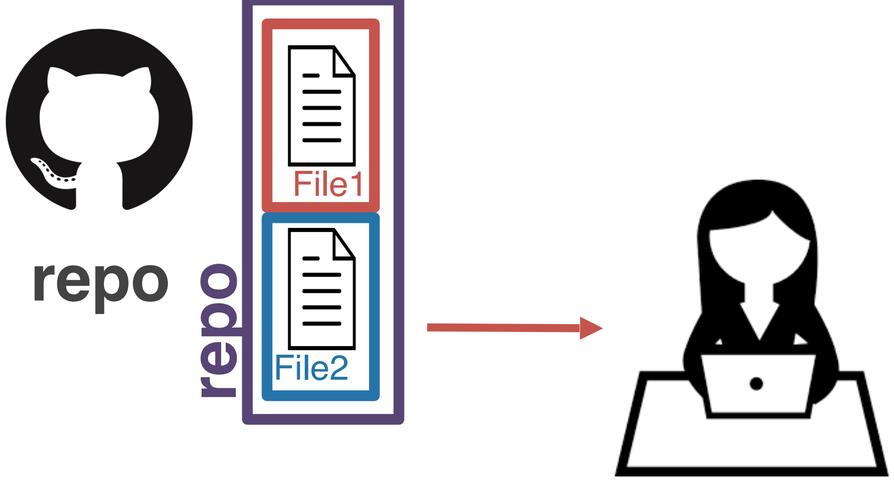
What do you do to get the repo on your computer?



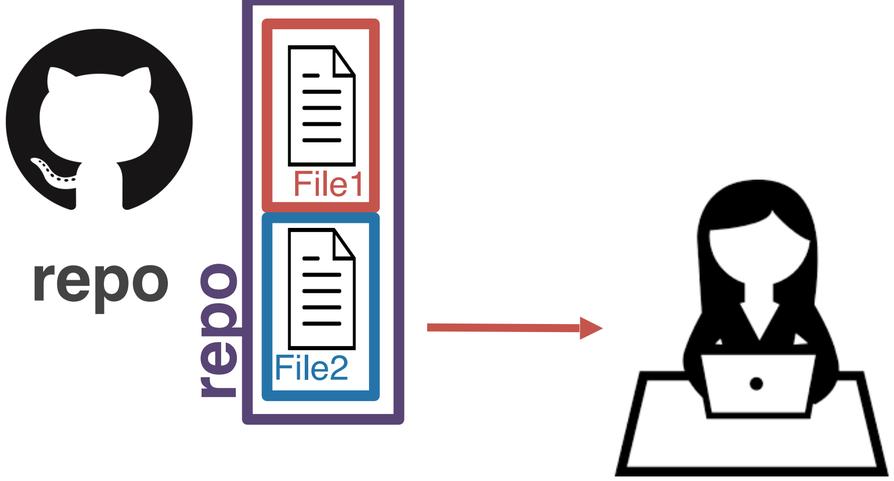


Each time you create a commit, git tracks the changes made automatically.





By committing each time you make changes, git allows you to time travel!



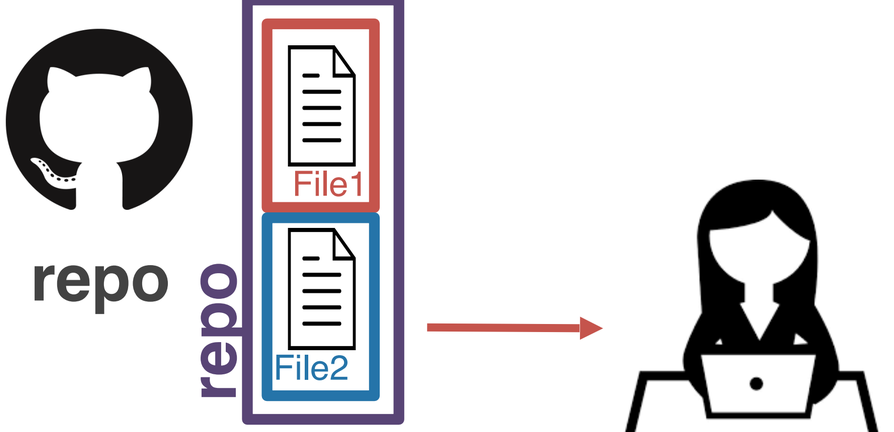
By committing each time you make changes, git allows you to time travel!

377dfcd00dd057542b112cf13be6cf1380b292ad

439301fe69e8f875c049ad0718386516b4878e22

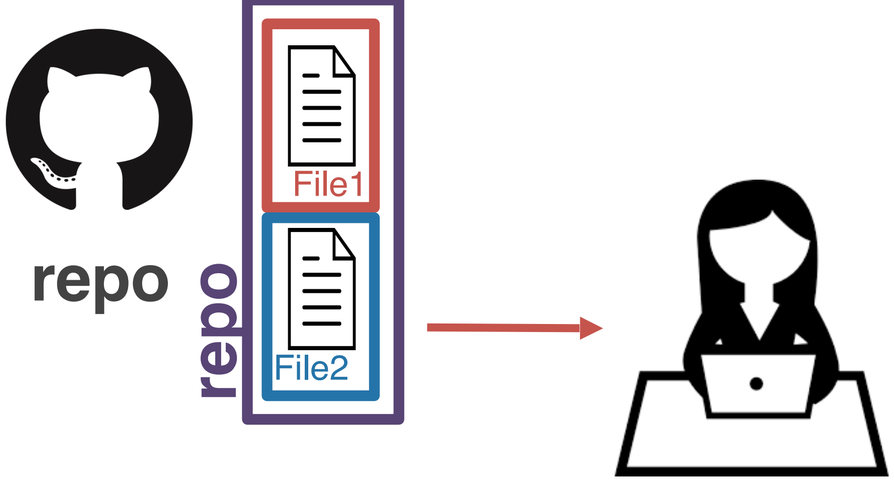
456722223e9f9e0ee0a92917ba80163028d89251

There's a unique id, known as a **hash**, associated with each commit.

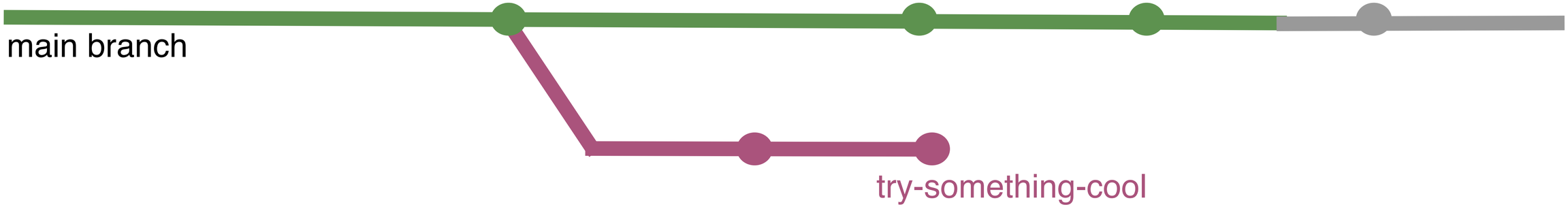


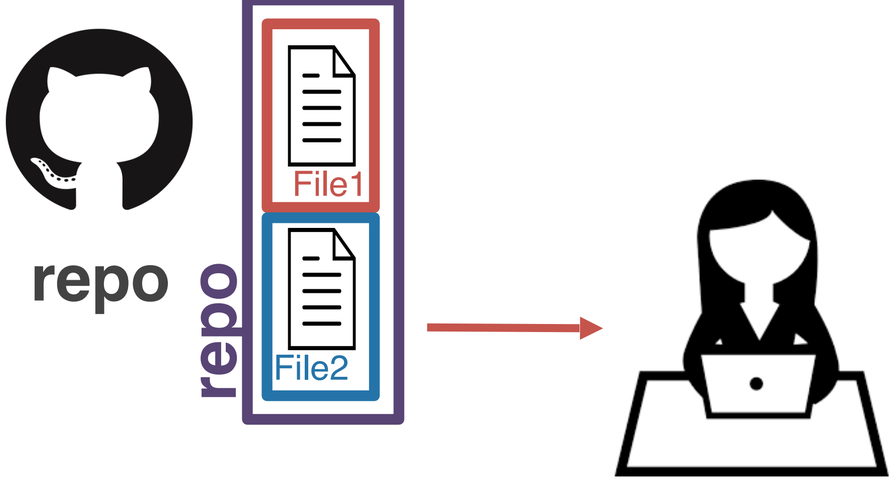
You can return to the state of the repository at any commit. Future commits don't disappear. They just aren't visible when you **check out** an older commit.

377dfcd00dd057542b112cf13be6cf1380b292ad

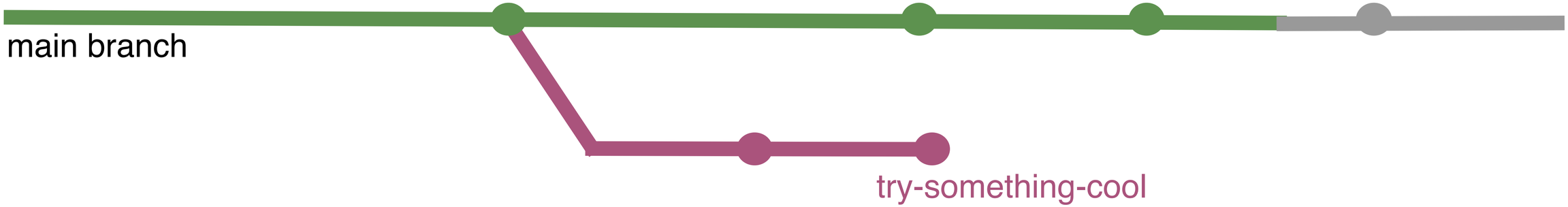


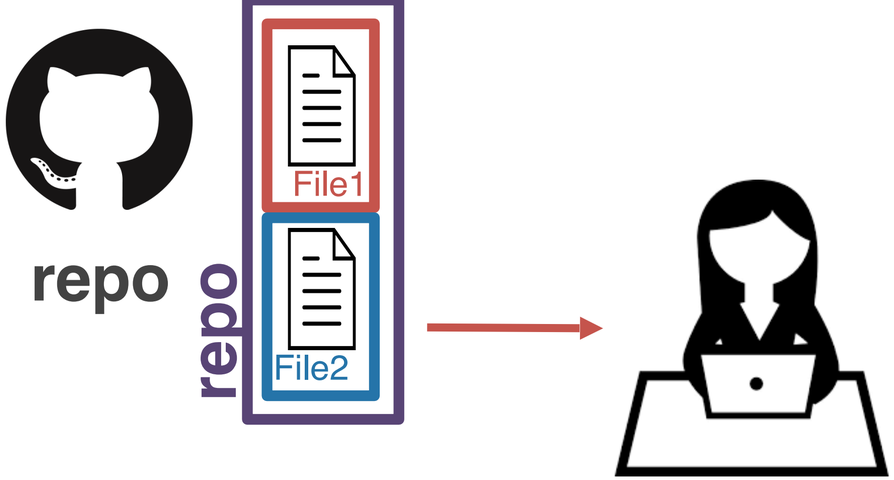
But...not everything is always linear. Sometimes you want to try something out and you're not sure it's going to work. This is where you'll want to use a **branch**.



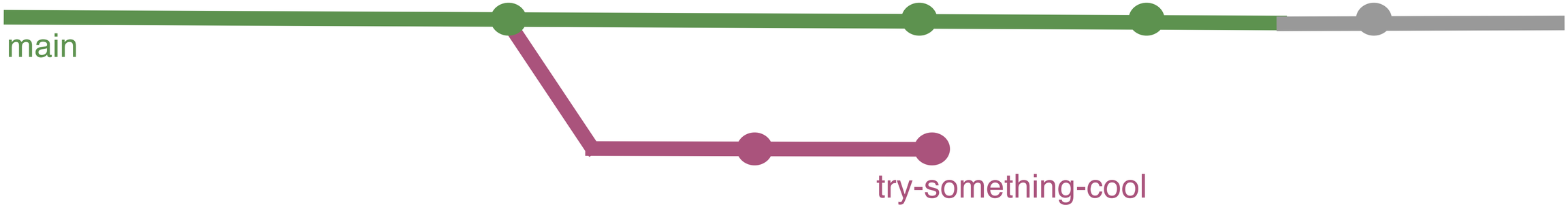


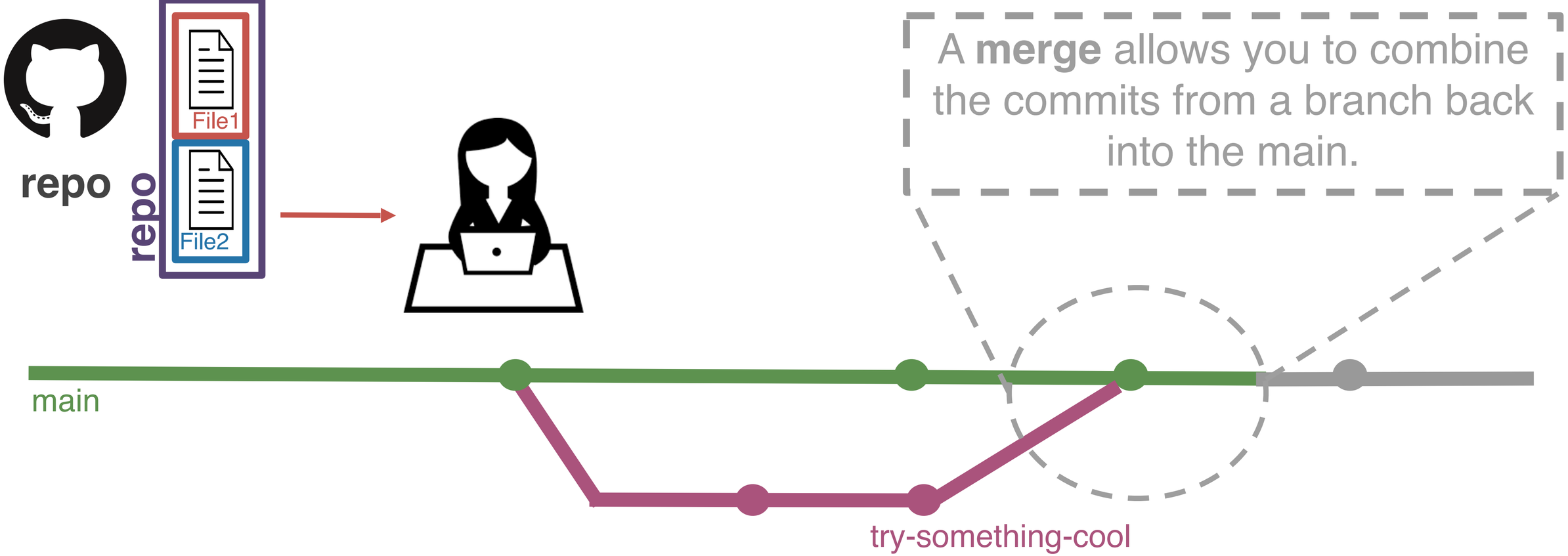
It’s a good way to experiment. It’s pretty easy to get rid of a branch later on should you not want to include the commits on that branch.



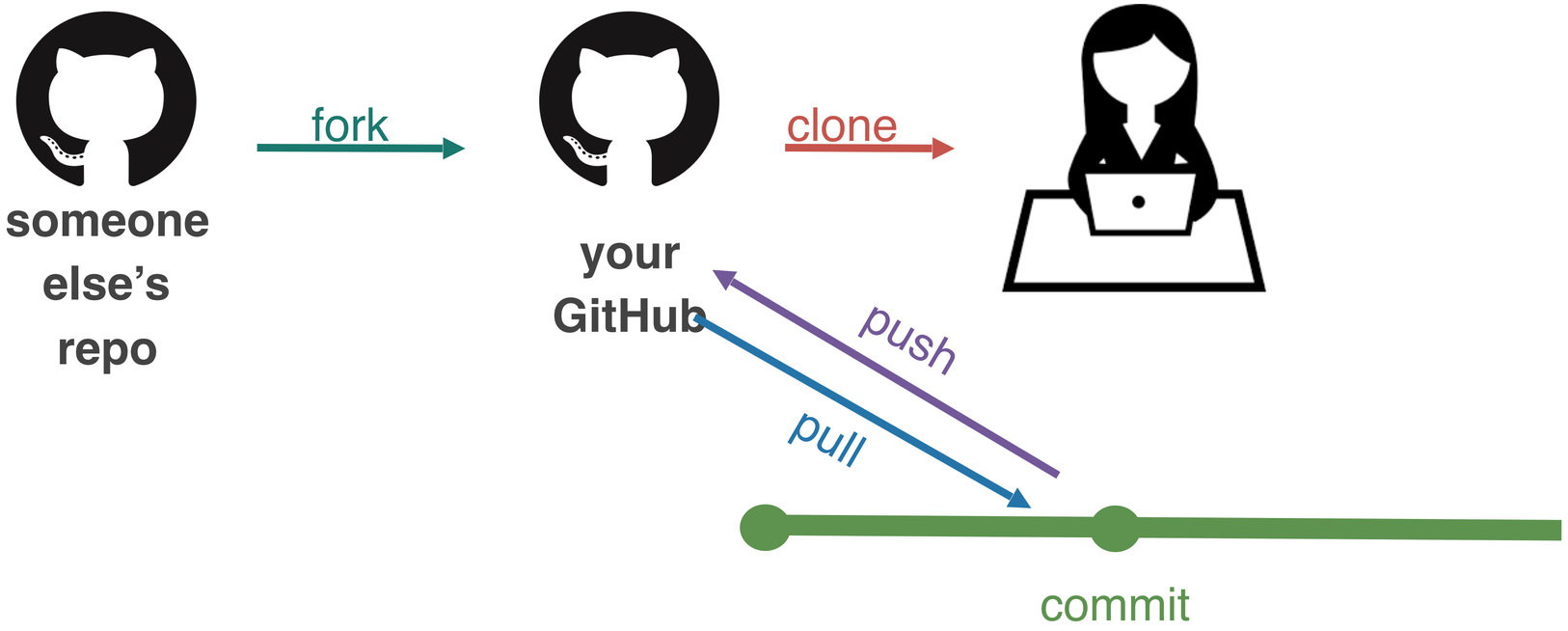


But...what if you DO want to include the changes you've made on your try-something-cool branch into the main branch?

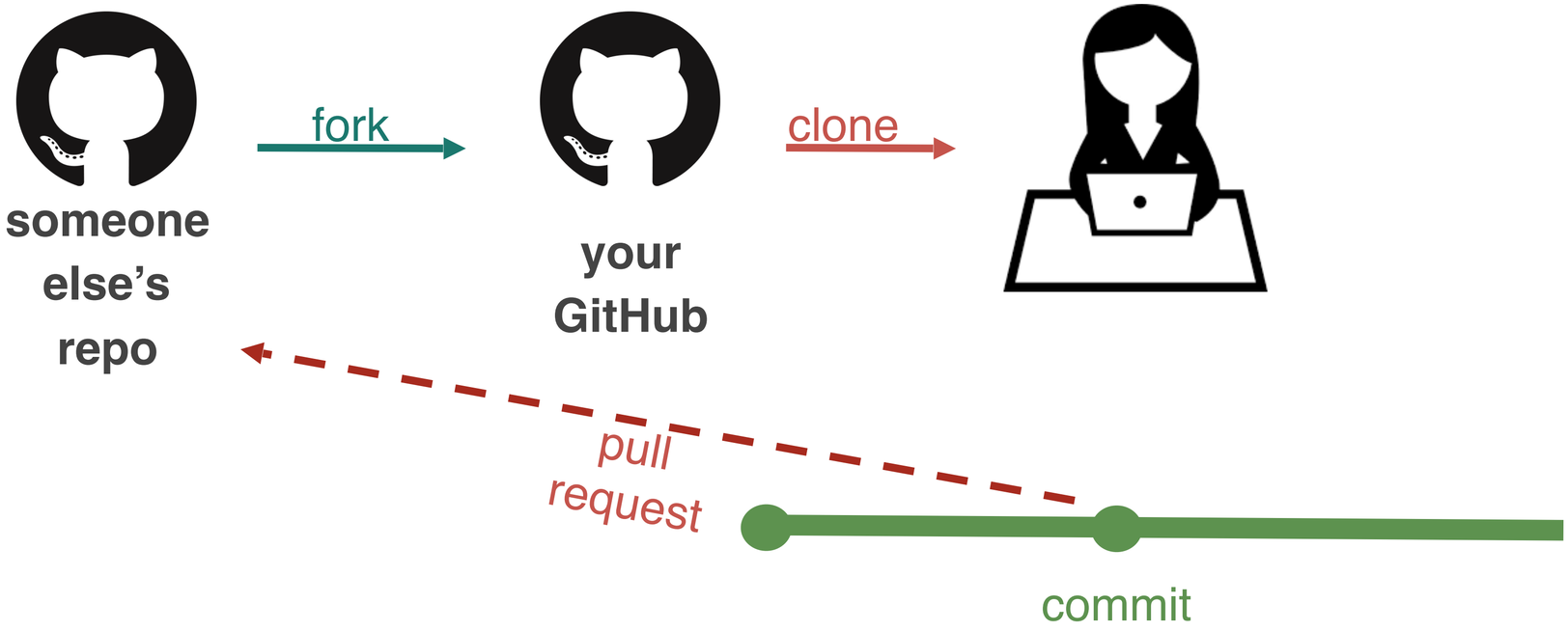



repo
repo
File1
File2
A **merge** allows you to combine the commits from a branch back into the main.
main
try-something-cool

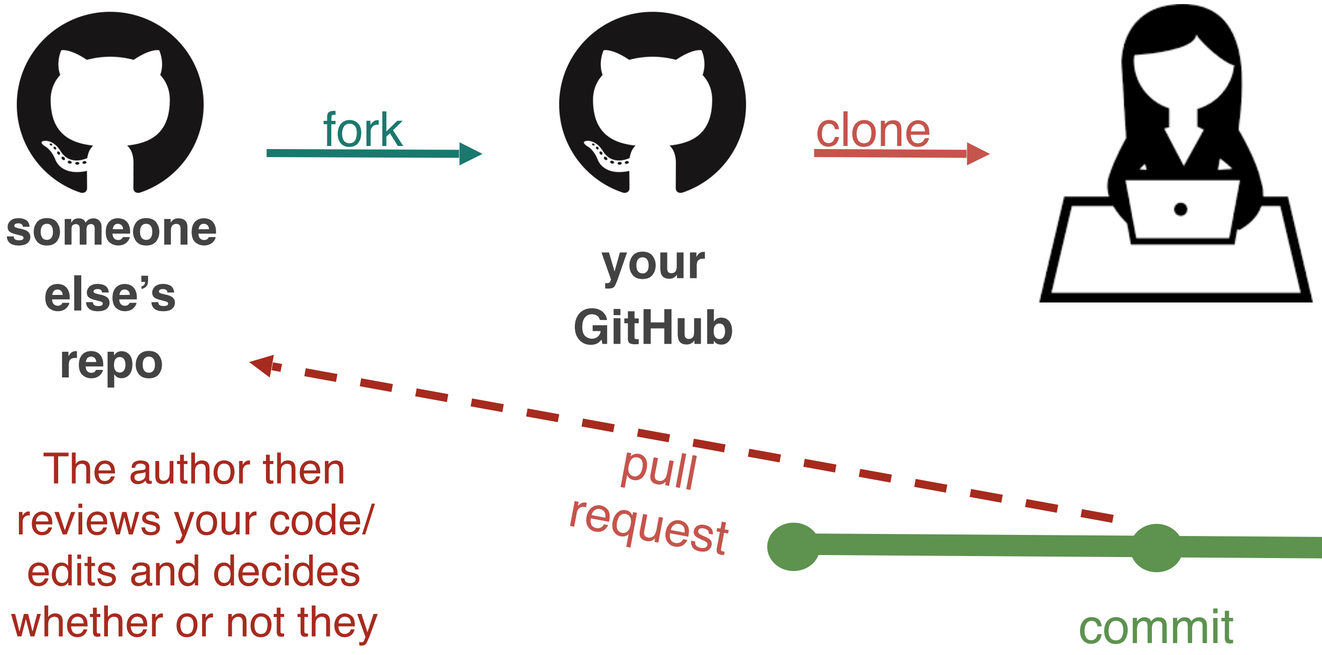
What if someone else is working on something cool and you want to play around with it? You'll have to **fork** their repo.



After you fork their repo, you can play around with it however you want, using the workflow we've already discussed.



But what if you think you've found a bug in their code, a typo, or want to add a new feature to their software? For this, you'll submit a **pull request** (aka **PR**).



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someone else's repo

Last but not least...what if you find a bug in someone else's code OR you want to make a suggestion but aren't going to submit a suggestion with a PR. For this, you can file an **issue** on GitHub.

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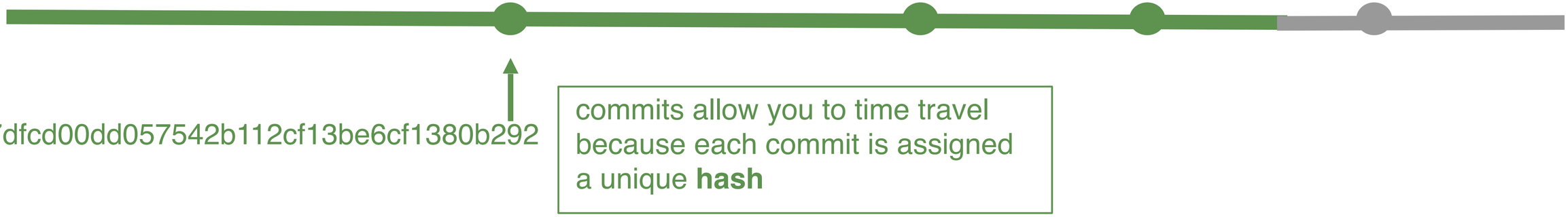
Last but not least...what if you find a bug in someone else's code OR you want to make a suggestion but aren't going to submit a suggestion with a PR. For this, you can file an **issue** on GitHub.

Issues are *bug trackers*. While, they can include bugs, they can also include feature requests, to-dos, whatever you want, really!

They can be assigned to people.

They can be closed once addressed ….or if the software maintainer doesn't like the suggestion



One more git recap...

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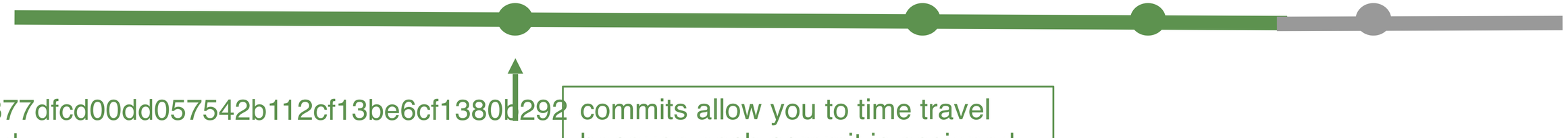
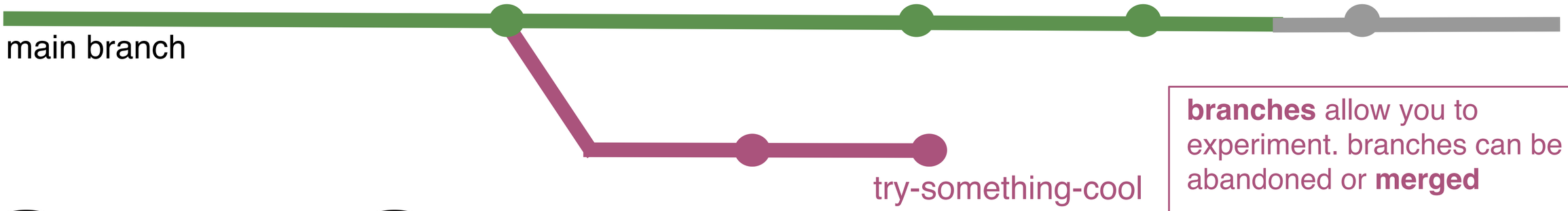


377dfcd00dd057542b112cf13be6cf1380b292ad

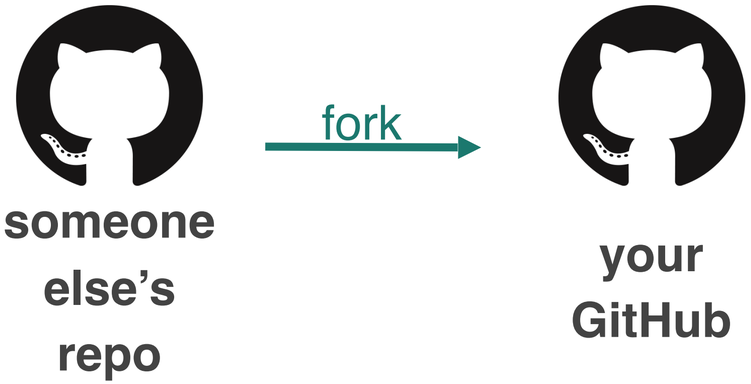
commits allow you to time travel because each commit is assigned a unique **hash**



branches allow you to experiment. branches can be abandoned or **merged**

You can work on others' repos by first **forking** their repository onto your GitHub

One more git recap...



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Pull requests allow you to make specific edits to others' repos

Issues allow you to make general suggestions to your/others' repos

One more git recap...