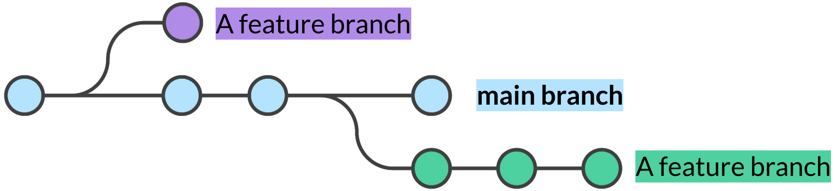
Working with branches in Git

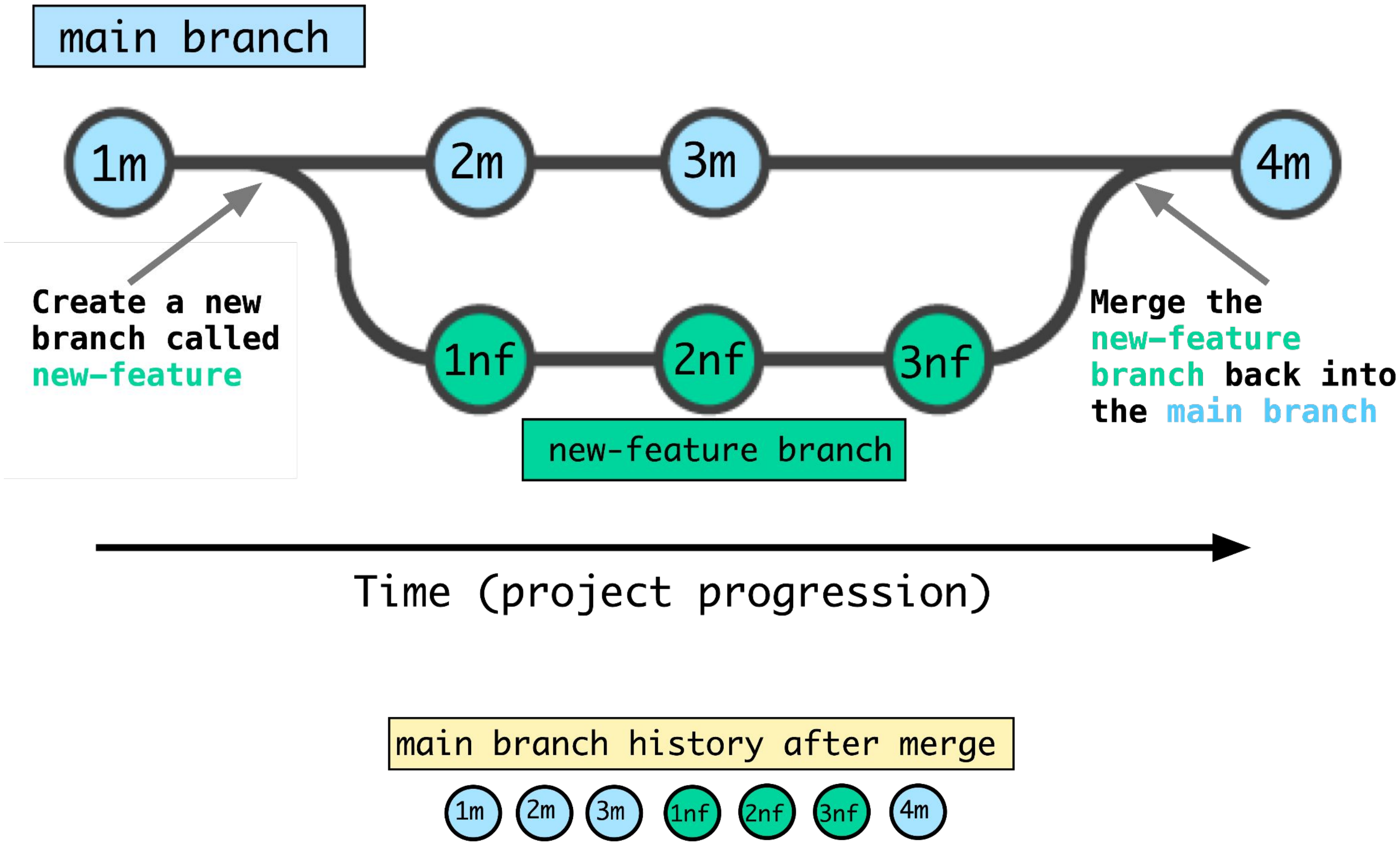
Childhood Cancer Data Lab

Branches in git



- Branches are like "repositories within repositories" 🤯
- Useful when you want to make changes (maybe experimental!) but you don't want to break the rest of your code
  - You can always switch back to a "clean" branch!
- Keep related changes together
  - All commits for a given new analysis or "feature" can be made within the same branch for easier tracking
  - Helps you to identify which commits are relevant to a given analysis
- If you wreck code in a branch, you've *only wrecked that branch!* Just delete it!
- Branches provide a great framework for collaboration and team science

Source: https://www.atlassian.com/git/tutorials/using-branches



Create a new branch called new-feature

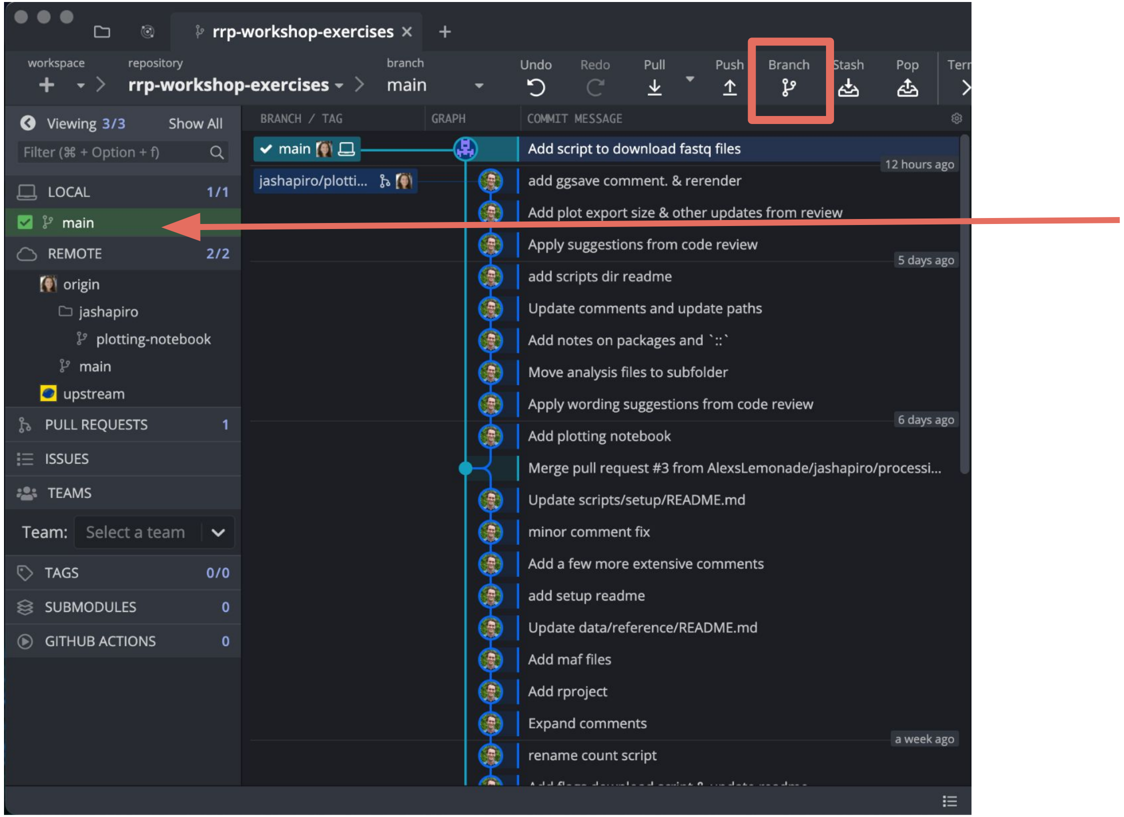
Merge the new-feature branch back into the main branch

Time (project progression)

main branch history after merge

Modified from https://www.atlassian.com/git/tutorials/using-branches/git-merge

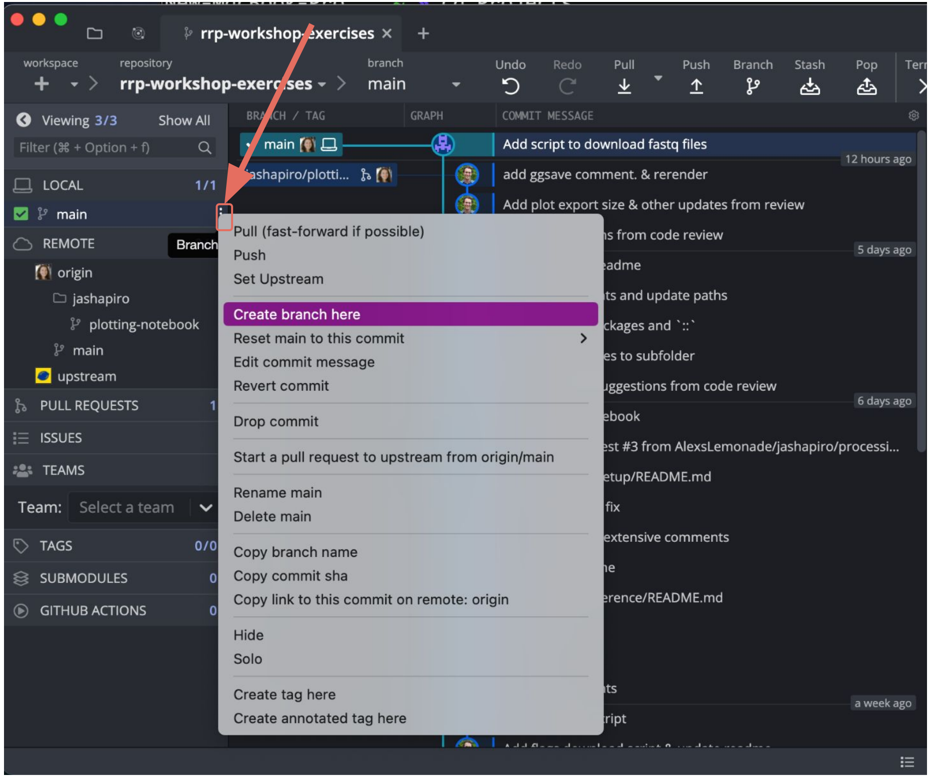
Creating a new branch



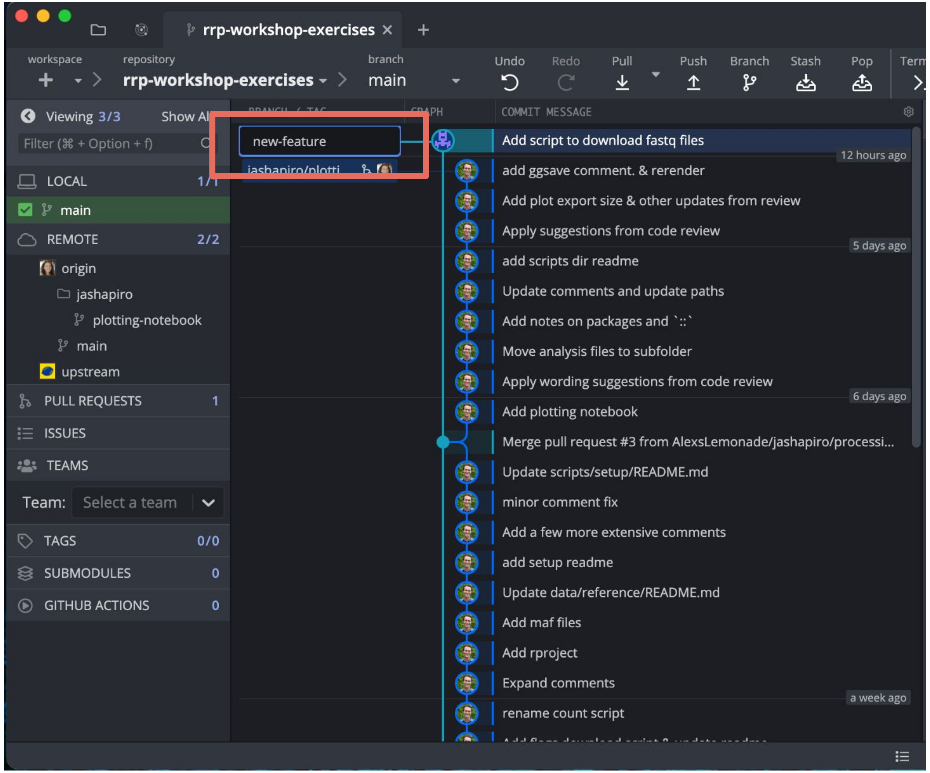
```
Add script to download fastq files
add ggsave comment. & rerender
Add plot export size & other updates from review
Apply suggestions from code review
add scripts dir readme
Update comments and update paths
Add notes on packages and `::`
Move analysis files to subfolder
Apply wording suggestions from code review
Add plotting notebook
Merge pull request #3 from AlexsLemonade/jashapiro/processi...
Update scripts/setup/README.md
minor comment fix
Add a few more extensive comments
add setup readme
Update data/reference/README.md
Add maf files
Add rproject
Expand comments
rename count script
Add flags download script & update readme
```

Because we are currently on the `main` branch, this new branch will be created off of the `main` branch's history.

Alternatively…



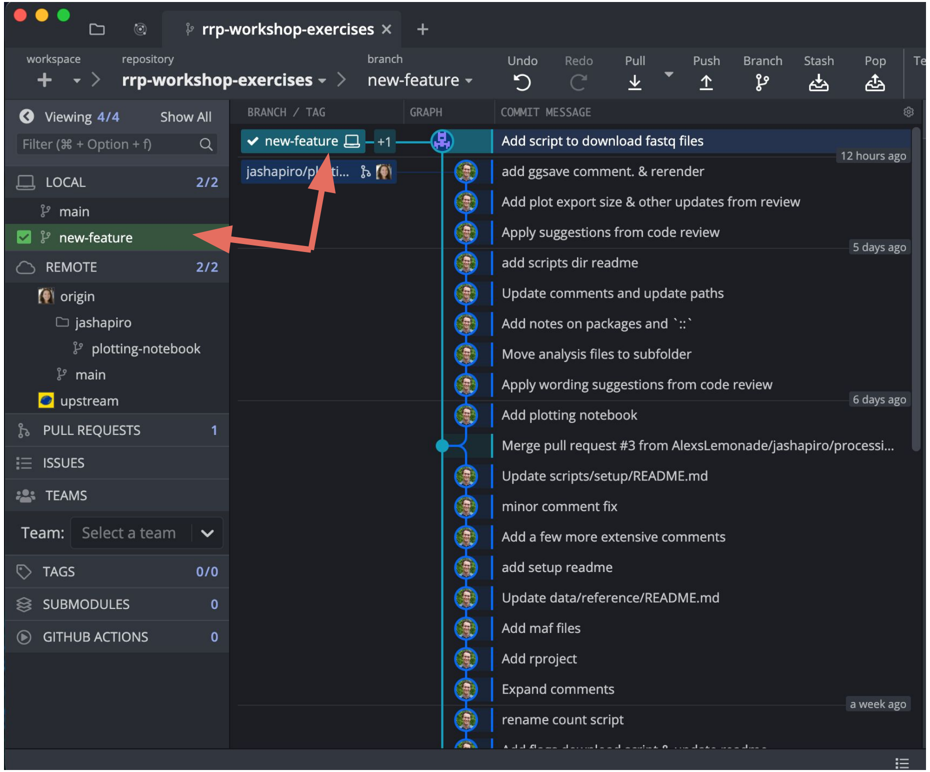
Name your new branch by typing it in here



new-feature

```
Add script to download fastq files
                                                12 hours ago
add ggsave comment. & rerender
Add plot export size & other updates from review
Apply suggestions from code review
                                                5 days ago
add scripts dir readme
Update comments and update paths
Add notes on packages and `::`
Move analysis files to subfolder
Apply wording suggestions from code review
                                                6 days ago
Add plotting notebook
Merge pull request #3 from AlexsLemonade/jashapiro/processi...
Update scripts/setup/README.md
minor comment fix
Add a few more extensive comments
add setup readme
Update data/reference/README.md
Add maf files
Add rproject
Expand comments
                                                a week ago
rename count script
```

Now you're in your new branch!



Add script to download fastq files
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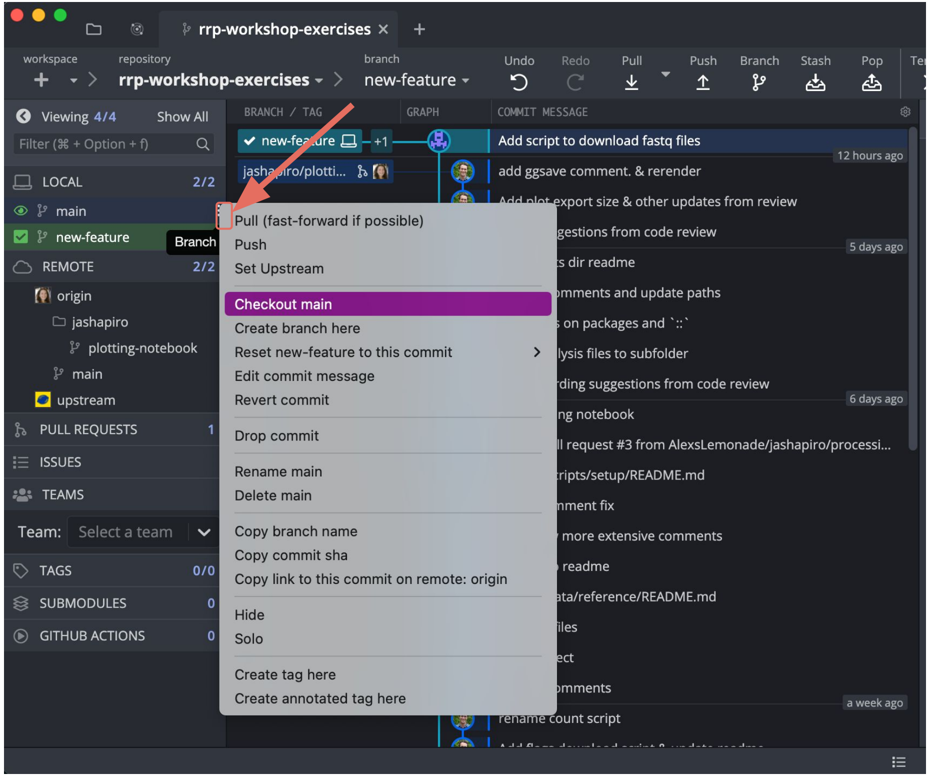
Expand comments
rename count script
Add flags download script & update readme

Note the different *icons* associated with **local** vs. **remote** repositories

- Local is a laptop icon
- *In this case*, remote is Stephanie's GitHub profile picture (but you aren't Stephanie!)

We created `new-feature` *locally*, so it does not (yet!) exist on our *remote*.

We can switch between branches with **checkout**



Add script to download fastq files
add ggsave comment. & rerender
Add plot export size & other updates from review
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s dir readme
omments and update paths
s on packages and `::`
lysis files to subfolder
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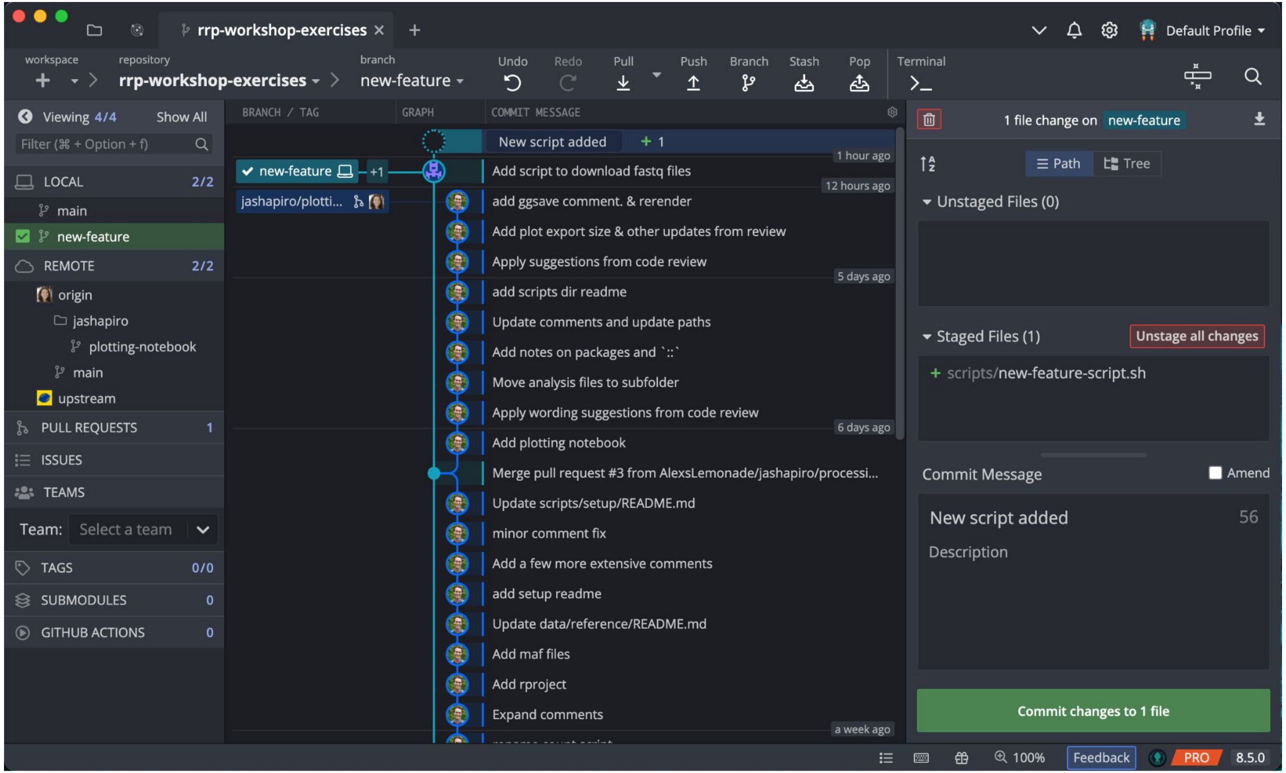
ng notebook
ll request #3 from AlexsLemonade/jashapiro/processi...
ripts/setup/README.md
mment fix
more extensive comments
readme
ata/reference/README.md
files
ect
omments
rename count script

You can also double-click on a branch in GitKraken!

Hurray for GitKraken!

Make commits within your new branch as usual



New script added + 1

Commit message	Time
Add script to download fastq files	1 hour ago
add ggsave comment. & rerender	12 hours ago
Add plot export size & other updates from review	
Apply suggestions from code review	
add scripts dir readme	5 days ago
Update comments and update paths	
Add notes on packages and `::`	
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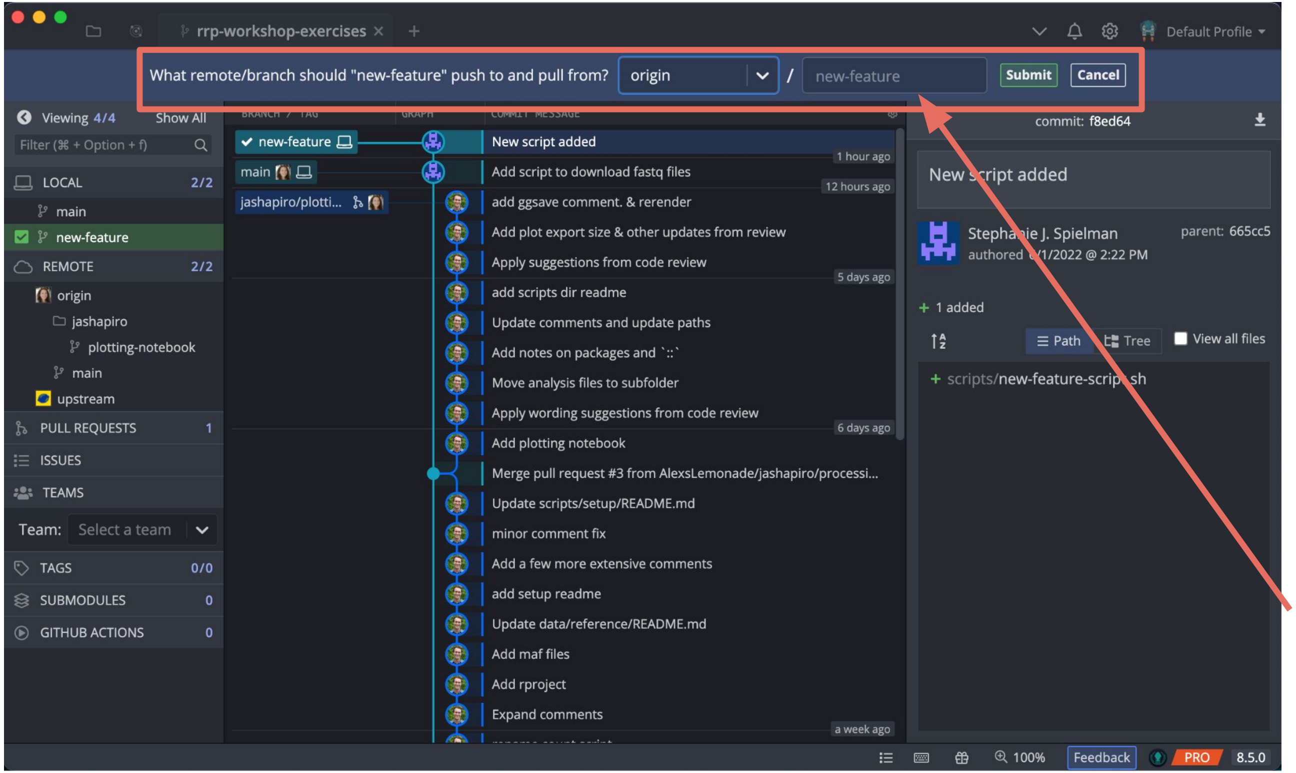
Merge pull request #3 from AlexsLemonade/jashapiro/processi...	
Update scripts/setup/README.md	
minor comment fix	
Add a few more extensive comments	
add setup readme	
Update data/reference/README.md	
Add maf files	
Add rproject	
Expand comments	
	a week ago

+ scripts/new-feature-script.sh

New script added 56

Description

Pushing prompts you to specify the remote branch



What remote/branch should "new-feature" push to and pull from? origin / new-feature **Submit** **Cancel**

BRANCH / TAG	COMMIT MESSAGE	
✓ new-feature	New script added	1 hour ago
main	Add script to download fastq files	12 hours ago
jashapiro/plotti...	add ggsave comment. & rerender	
	Add plot export size & other updates from review	
	Apply suggestions from code review	5 days ago
	add scripts dir readme	
	Update comments and update paths	
	Add notes on packages and `::`	
	Move analysis files to subfolder	
	Apply wording suggestions from code review	6 days ago
	Add plotting notebook	
	Merge pull request #3 from AlexsLemonade/jashapiro/processi...	
	Update scripts/setup/README.md	
	minor comment fix	
	Add a few more extensive comments	
	add setup readme	
	Update data/reference/README.md	
	Add maf files	
	Add rproject	
	Expand comments	a week ago

commit: f8ed64

New script added

Stephanie J. Spielman authored 6/1/2022 @ 2:22 PM parent: 665cc5

+ 1 added

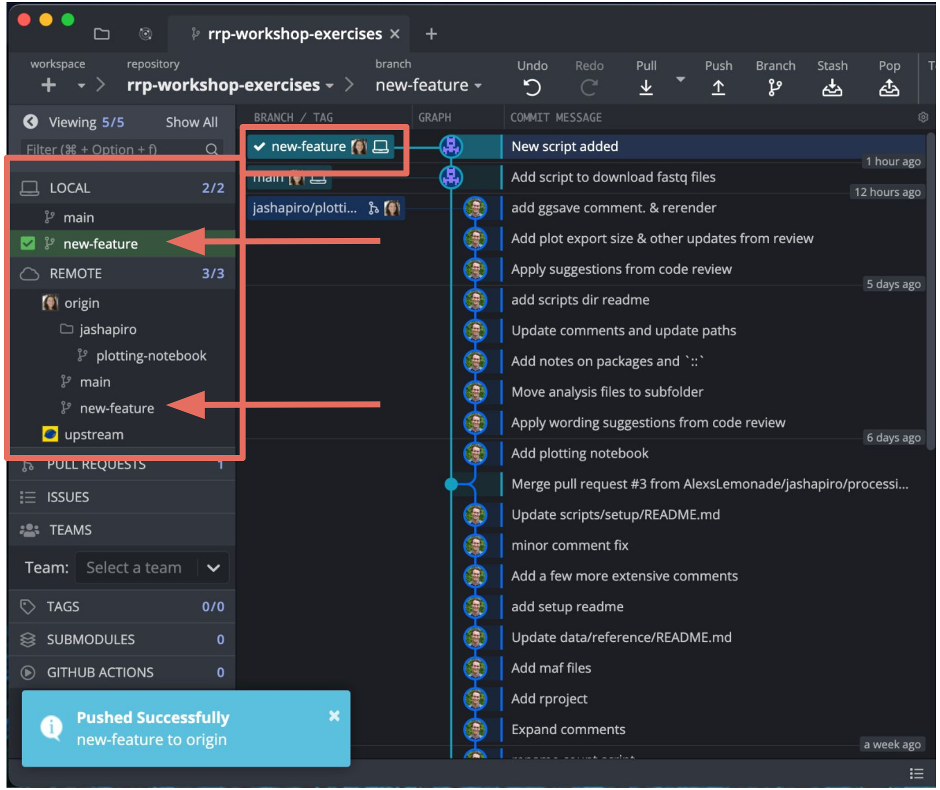
+ scripts/new-feature-script.sh

Because this `new-feature` branch doesn't exist (yet!) on the remote, Git needs more info about where to push to.

This prompt will always occur *the first time* you push from a brand new branch.

GitKraken helpfully guesses what you want your remote branch to be named! Click "Submit."

Pushing has created a corresponding *remote* branch



New script added
1 hour ago
Add script to download fastq files
12 hours ago
add ggsave comment. & rerender
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Apply suggestions from code review
5 days ago
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Add plotting notebook
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Update scripts/setup/README.md
minor comment fix
Add a few more extensive comments
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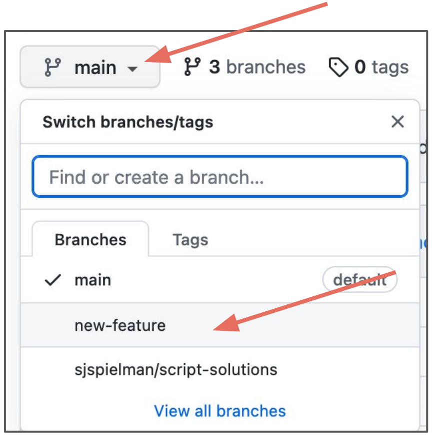
Update data/reference/README.md
Add maf files
Add rproject
Expand comments
a week ago

Pushed Successfully
new-feature to origin

Have a look at the icons! `new-feature` is now fully "synced" between local and remote.

Viewing branches on GitHub



main ▾ 3 branches 0 tags

Switch branches/tags ✕

Find or create a branch...

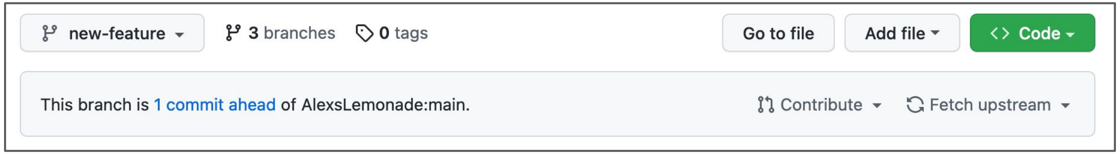
Branches Tags

✓ main default

new-feature

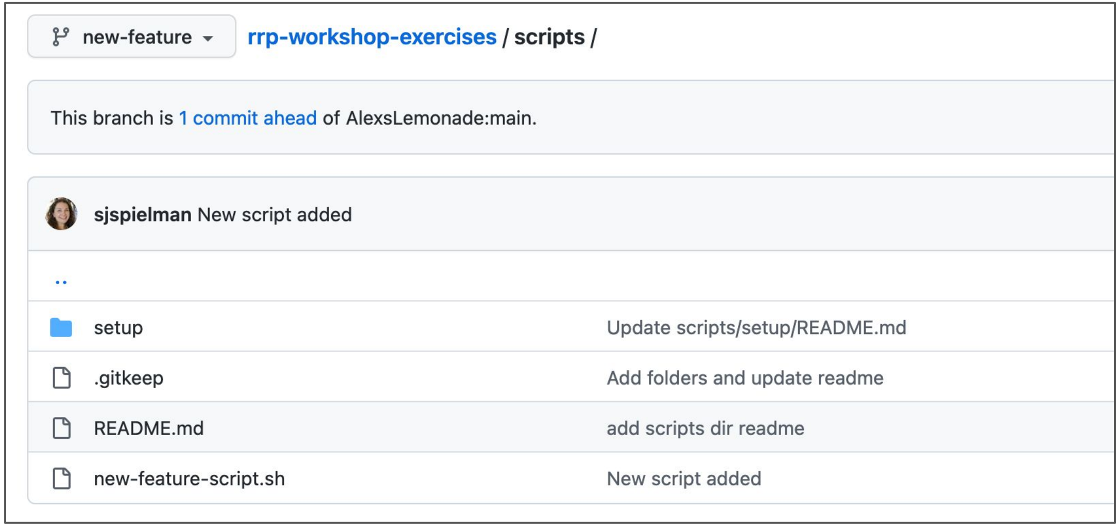
sjspielman/script-solutions

View all branches



new-feature ▾ 3 branches 0 tags Go to file Add file ▾ <> Code ▾

This branch is 1 commit ahead of AlexsLemonade:main.



new-feature ▾ rrp-workshop-exercises / scripts /

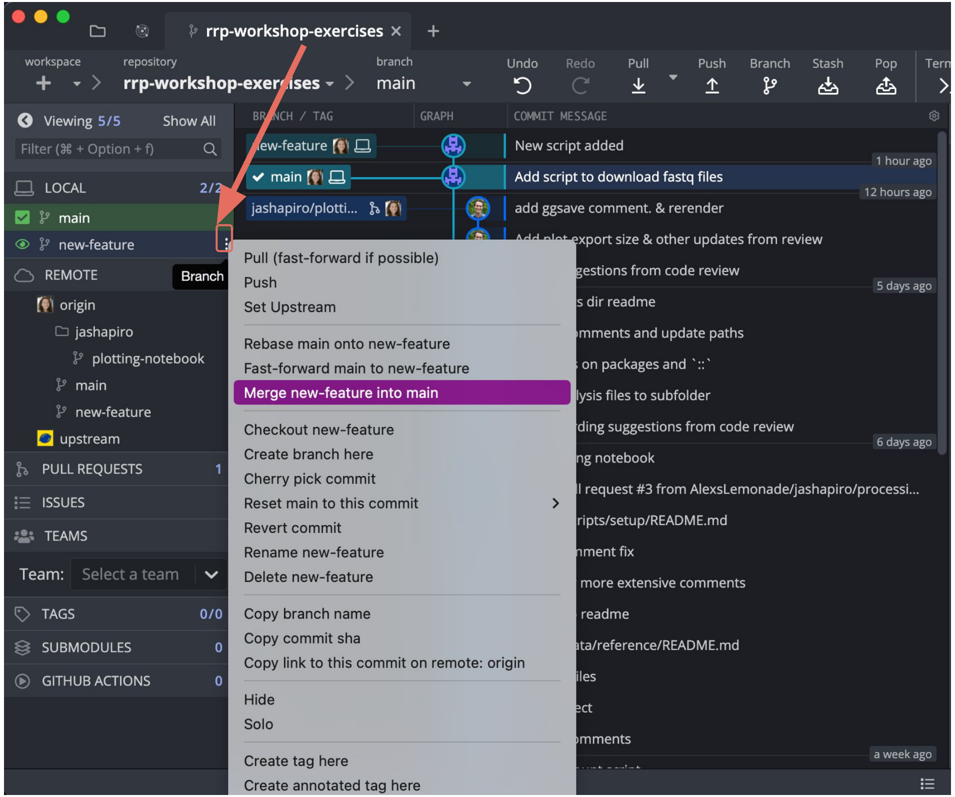
This branch is 1 commit ahead of AlexsLemonade:main.

sjspielman New script added

..

setup	Update scripts/setup/README.md
.gitkeep	Add folders and update readme
README.md	add scripts dir readme
new-feature-script.sh	New script added

Merge into your main branch



New script added
Add script to download fastq files
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ripts/setup/README.md
nment fix
more extensive comments
readme
ata/reference/README.md
iles
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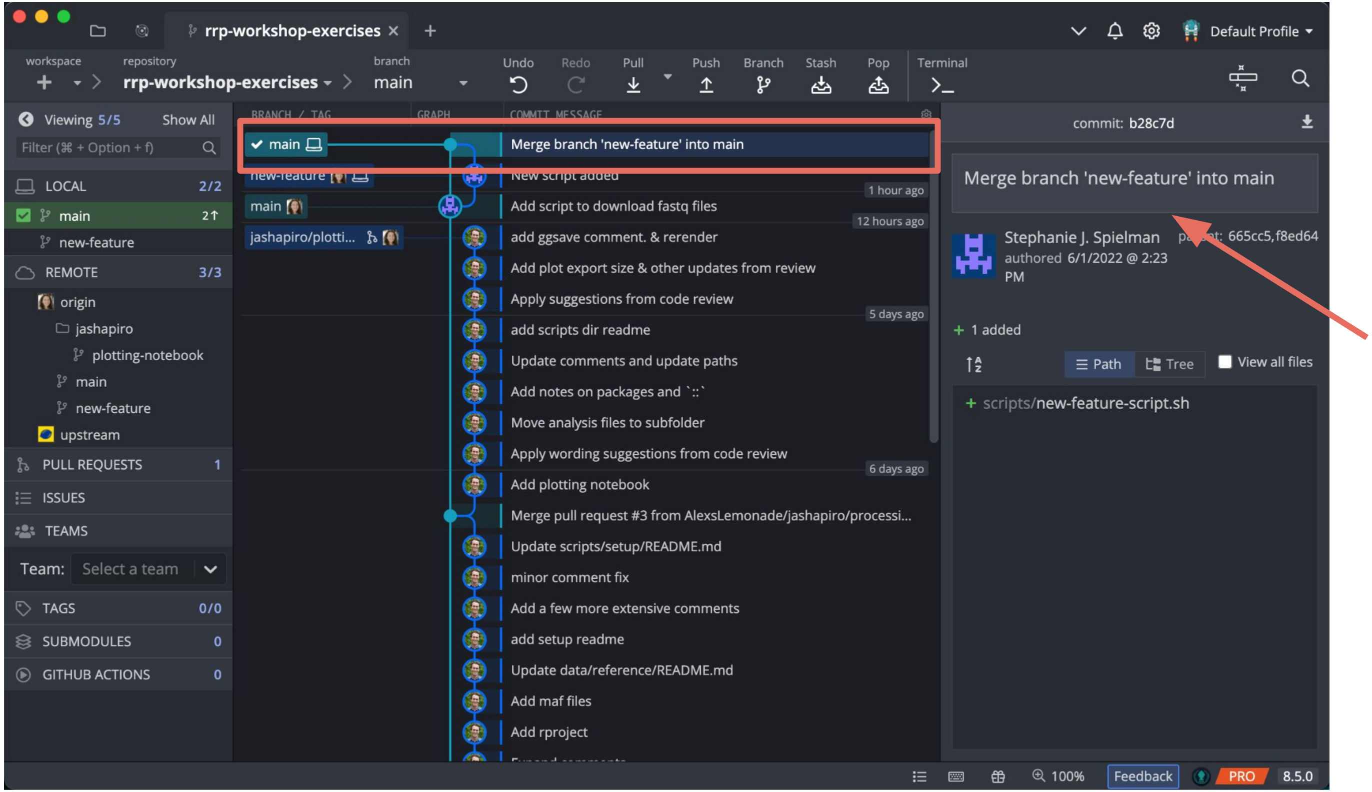
mments

But note!! You have to be in the branch you are merging into (see how `main` is highlighted?)

Bonus!! You can also point-and-click *drag* branches to merge them. Here, drag `new-feature` into `main` in the sidebar

Voila, your local histories have merged!



Merge branch 'new-feature' into main
New script added
1 hour ago
Add script to download fastq files
12 hours ago
add ggsave comment. & rerender
Add plot export size & other updates from review
Apply suggestions from code review
5 days ago
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Add plotting notebook
Merge pull request #3 from AlexsLemonade/jashapiro/processi...
Update scripts/setup/README.md
minor comment fix
Add a few more extensive comments
add setup readme
Update data/reference/README.md
Add maf files
Add rproject

commit: b28c7d

Merge branch 'new-feature' into main

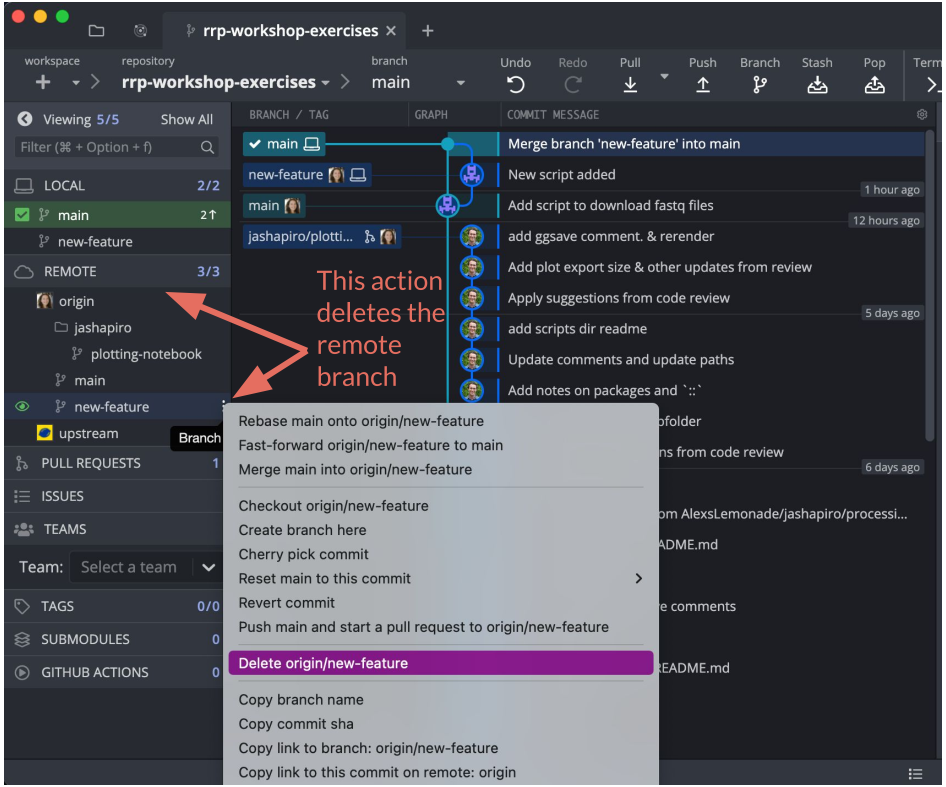
Stephanie J. Spielman
authored 6/1/2022 @ 2:23 PM
parent: 665cc5, f8ed64

+ 1 added

+ scripts/new-feature-script.sh

The merge itself is a commit to the `main` branch, with an automatic commit message

You can now safely delete your branch



Merge branch 'new-feature' into main

New script added

Add script to download fastq files

add ggsave comment. & rerender

Add plot export size & other updates from review

Apply suggestions from code review

add scripts dir readme

Update comments and update paths

Add notes on packages and `::`

bfolder

ns from code review

om AlexsLemonade/jashapiro/processi...

ADME.md

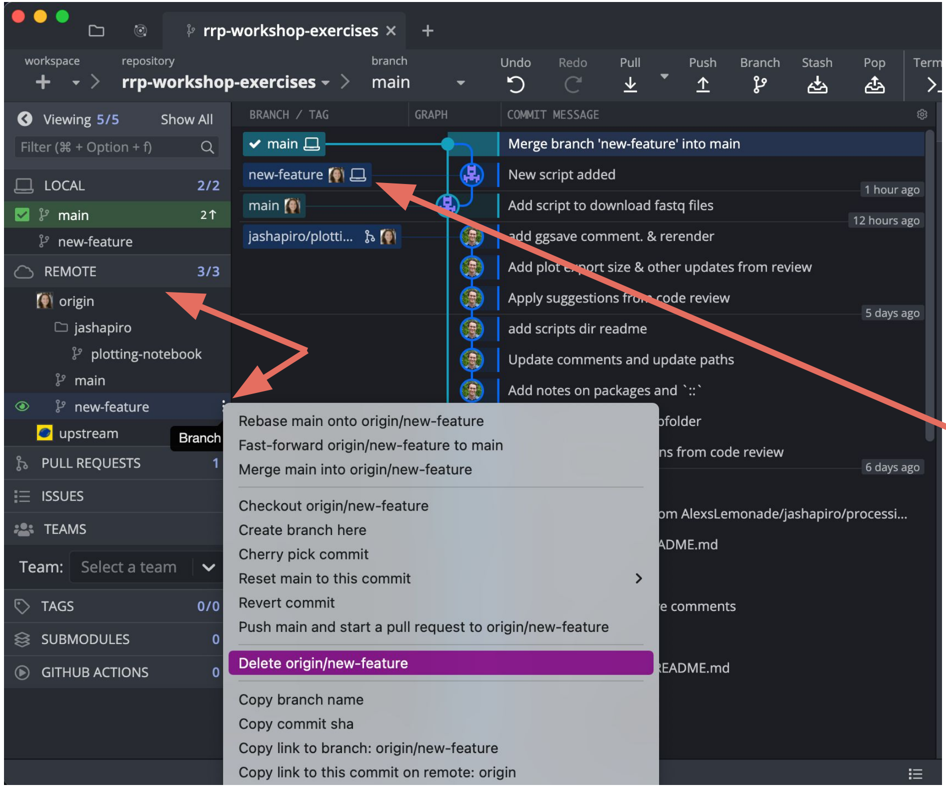
e comments

README.md

This action deletes the remote branch

Importantly, deleting branches that have been merged *does not* delete their commits! Those commits are part of the `main` branch's history now.

You can now safely delete your branch

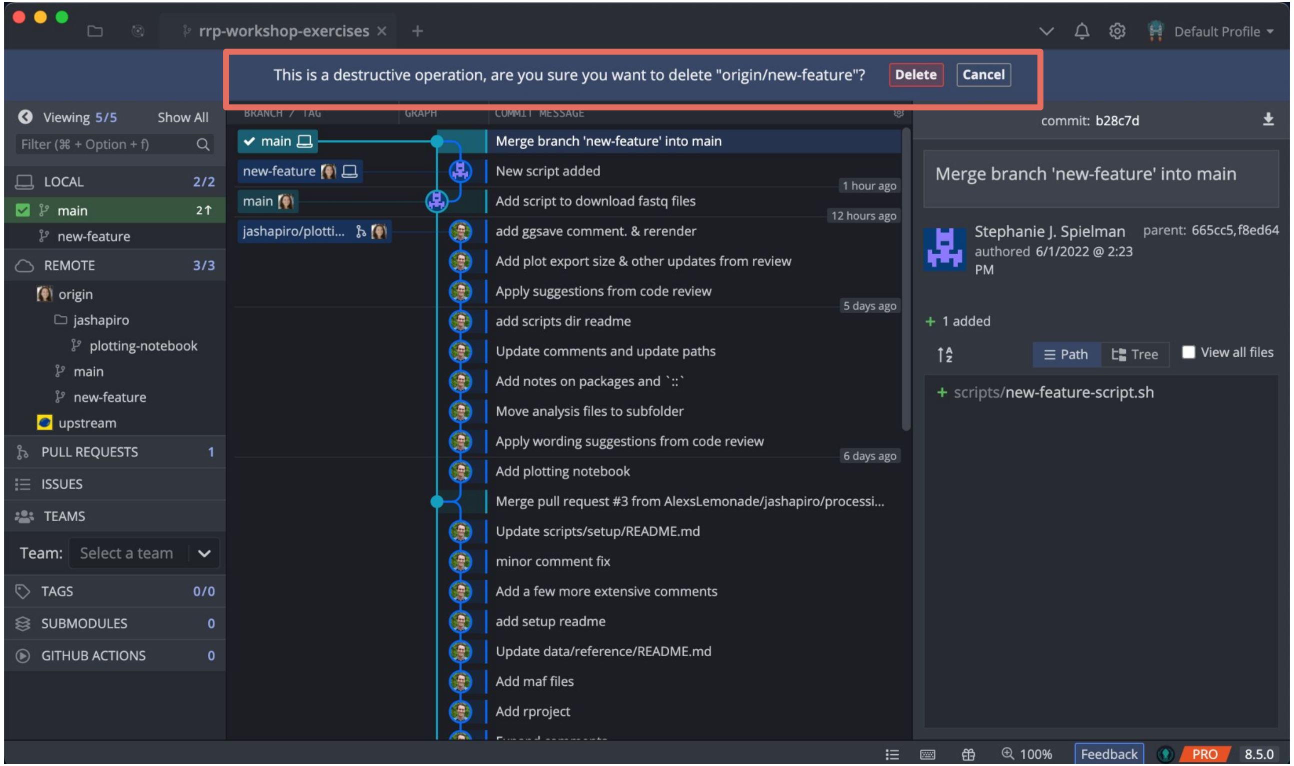


Merge branch 'new-feature' into main
New script added
Add script to download fastq files
add ggsave comment. & rerender
Add plot export size & other updates from review
Apply suggestions from code review
add scripts dir readme
Update comments and update paths
Add notes on packages and `::`

Deleting branches that have been merged *does not* delete their commits! Those commits are part of the `main` branch's history now.

You can also conveniently delete *both* remote and local branches at once by right-clicking the joint label in the *source graph*.

Are you sure?? If you've merged: yes, you're sure.



This is a destructive operation, are you sure you want to delete "origin/new-feature"? **Delete** **Cancel**

Merge branch 'new-feature' into main
New script added
Add script to download fastq files
add ggsave comment. & rerender
Add plot export size & other updates from review
Apply suggestions from code review
add scripts dir readme
Update comments and update paths
Add notes on packages and `::`
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Add plotting notebook
Merge pull request #3 from AlexsLemonade/jashapiro/processi...
Update scripts/setup/README.md
minor comment fix
Add a few more extensive comments
add setup readme
Update data/reference/README.md
Add maf files
Add rproject

Merge branch 'new-feature' into main

Stephanie J. Spielman parent: 665cc5,f8ed64
authored 6/1/2022 @ 2:23 PM

+ scripts/new-feature-script.sh

A quick note about merging branches

- When you are working *independently*, merging directly into `main` on your own is probably fine!

- When you are working *collaboratively*, it can get dangerous because your collaborators won't be in the loop, and conflicts will probably emerge
    - We recommend using *pull requests* (and maybe code review!) to merge code into `main` in collaborative projects. Learn more:
        - Pull Requests
        - Preprint about collaborative coding: Parker 2017
        - Slack blog: "On empathy and pull requests"

Branches and merging on the command line

```
# Make new branches, and change branches

# Step 1: Create new branch called `feature`
git branch feature

# Step 2: Go to your new branch
git switch feature      # git >=2.23
git checkout feature

# OR, do it all in one step!!
git switch -c feature   # git >=2.23
git checkout -b feature
```

```
# Merge `feature` into `main`

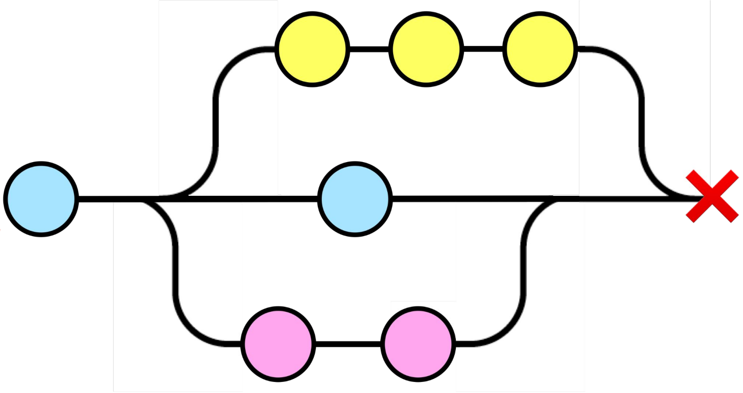
# Step 1: Be in `main`
git switch main      # git >=2.23
git checkout main

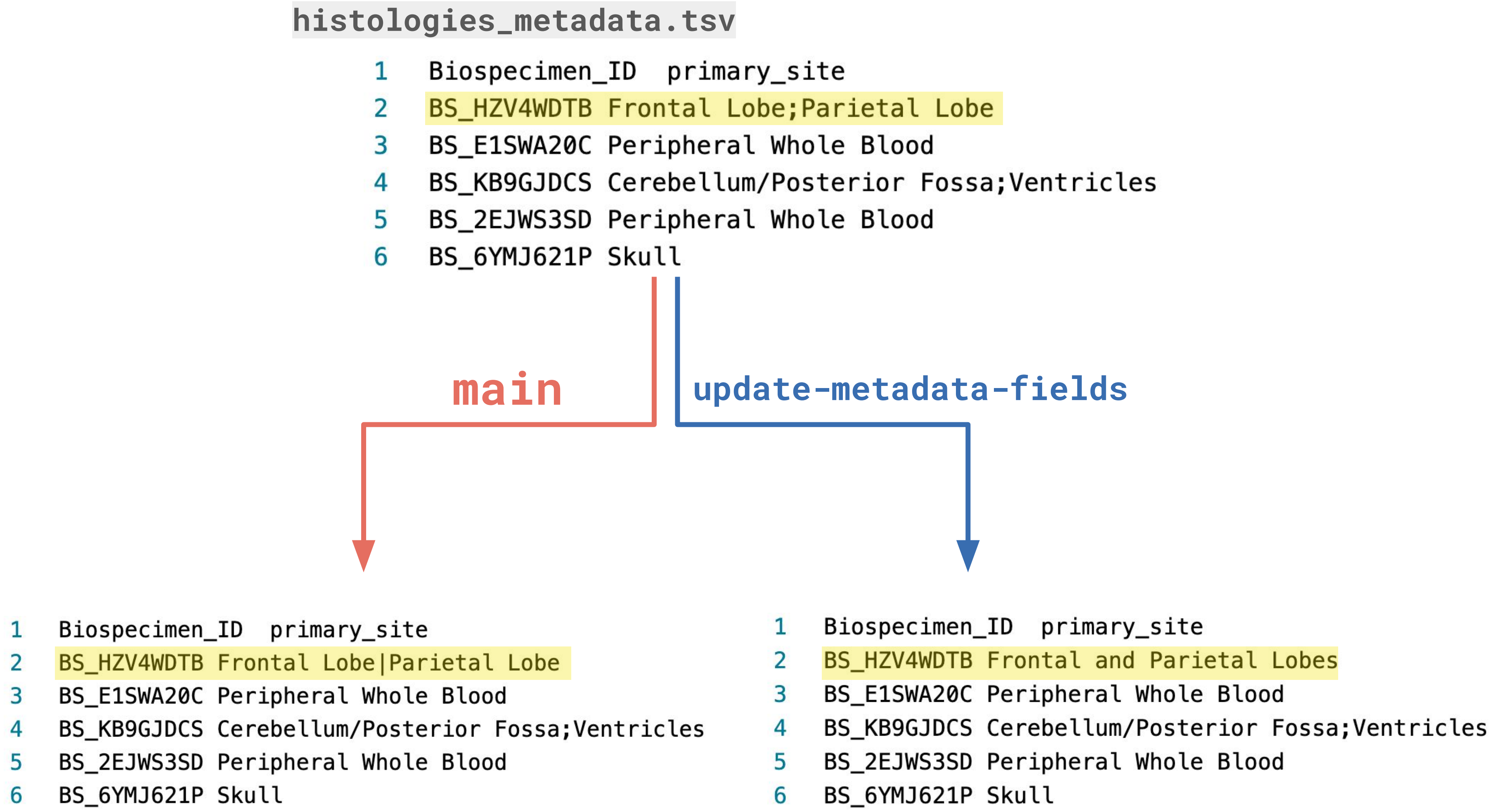
# Step 2: Merge `feature` into `main`
git merge feature
```

Merge conflicts can happen!

- If a given file has been *heavily* modified, `git` may not be able to merge the different file versions across branches together automatically
  - This is especially a problem if there are many branches floating around getting merged into each other
  - Imagine if each of these branches modified the same file in drastically incompatible ways……..

→ You will have to *manually fix the* ***merge conflicts!***





`histologies_metadata.tsv`

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe;Parietal Lobe
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

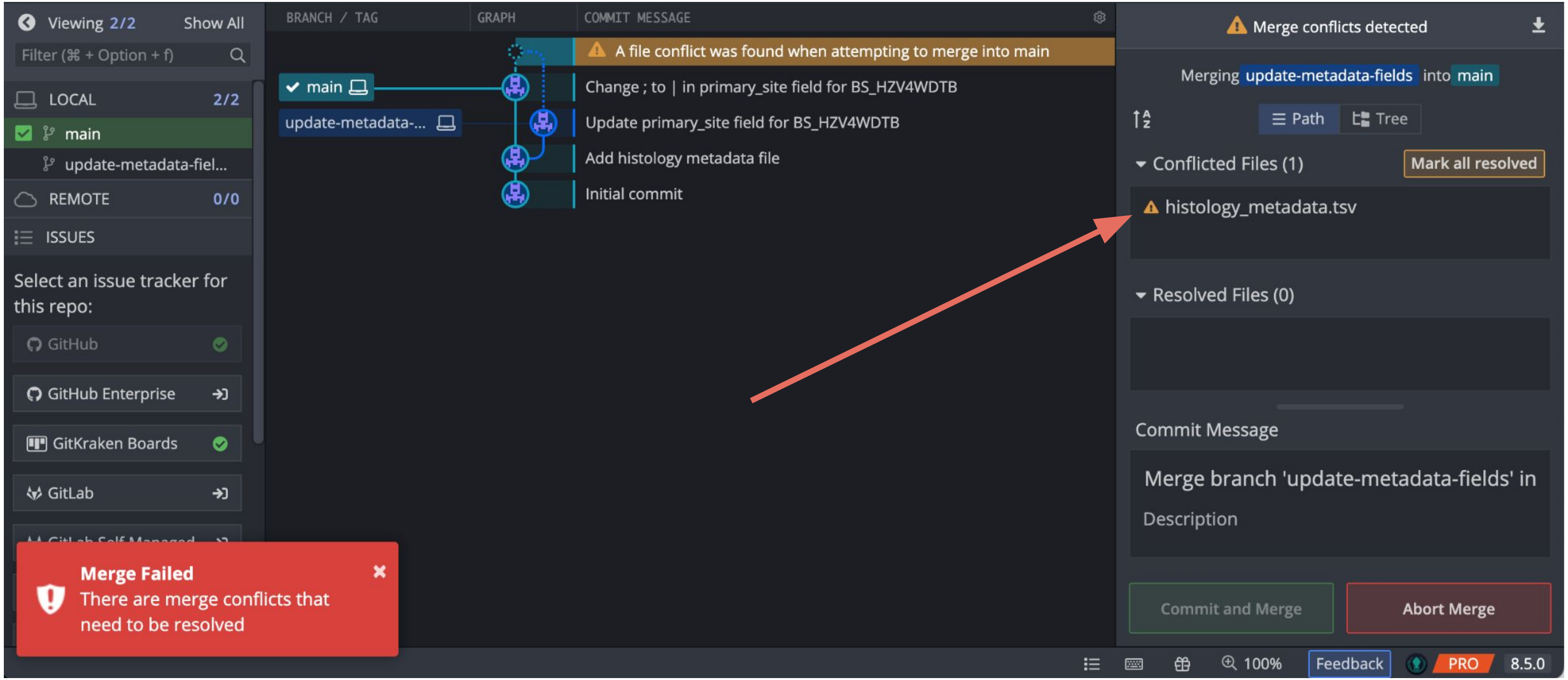
main

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe|Parietal Lobe
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

update-metadata-fields

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal and Parietal Lobes
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

Merging `update-metadata-fields` into `main` causes a **merge conflict**



Select an issue tracker for this repo:

A file conflict was found when attempting to merge into main

Change ; to | in primary_site field for BS_HZV4WDTB

Update primary_site field for BS_HZV4WDTB

Add histology metadata file

Initial commit

Merging update-metadata-fields into main

Conflicted Files (1)

histology_metadata.tsv

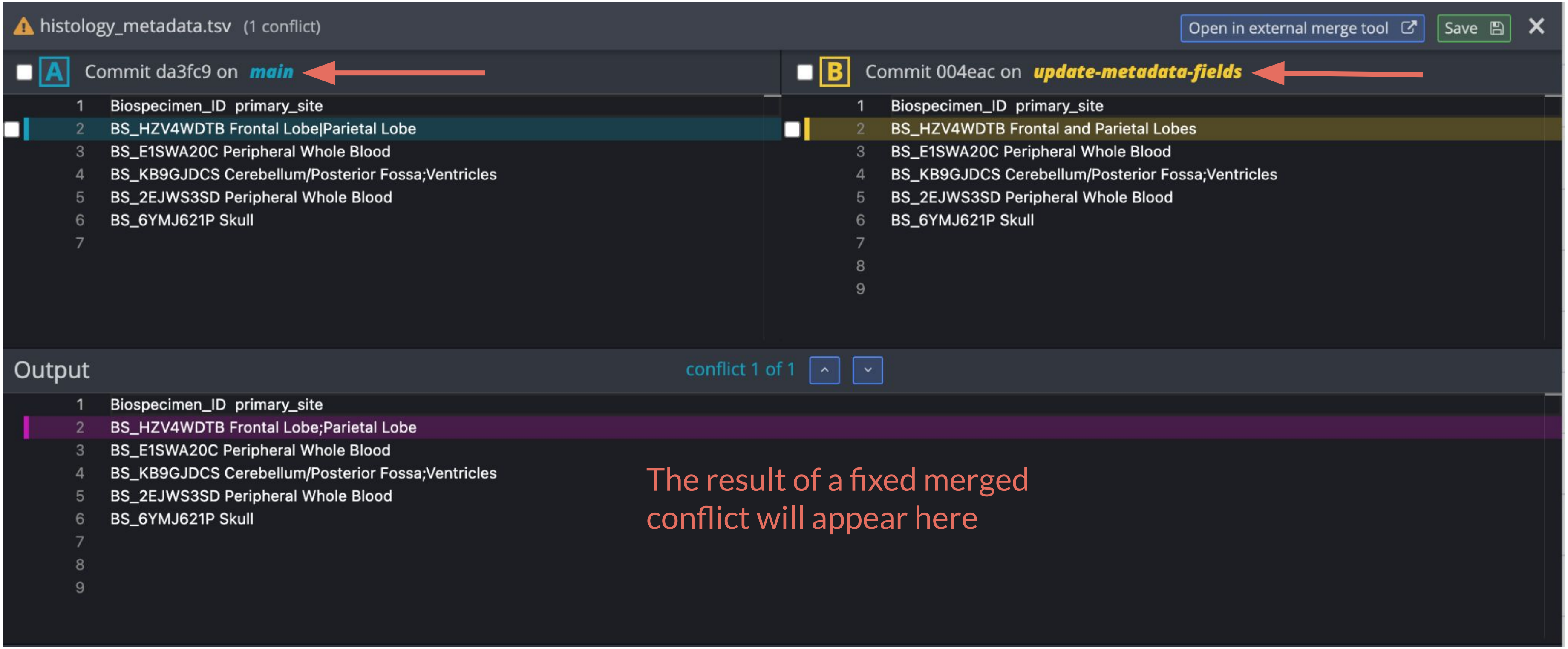
Resolved Files (0)

Commit Message

Merge branch 'update-metadata-fields' in

Description

Merge Failed
There are merge conflicts that need to be resolved



histology_metadata.tsv (1 conflict)

□ Commit da3fc9 on *main*

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe|Parietal Lobe
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

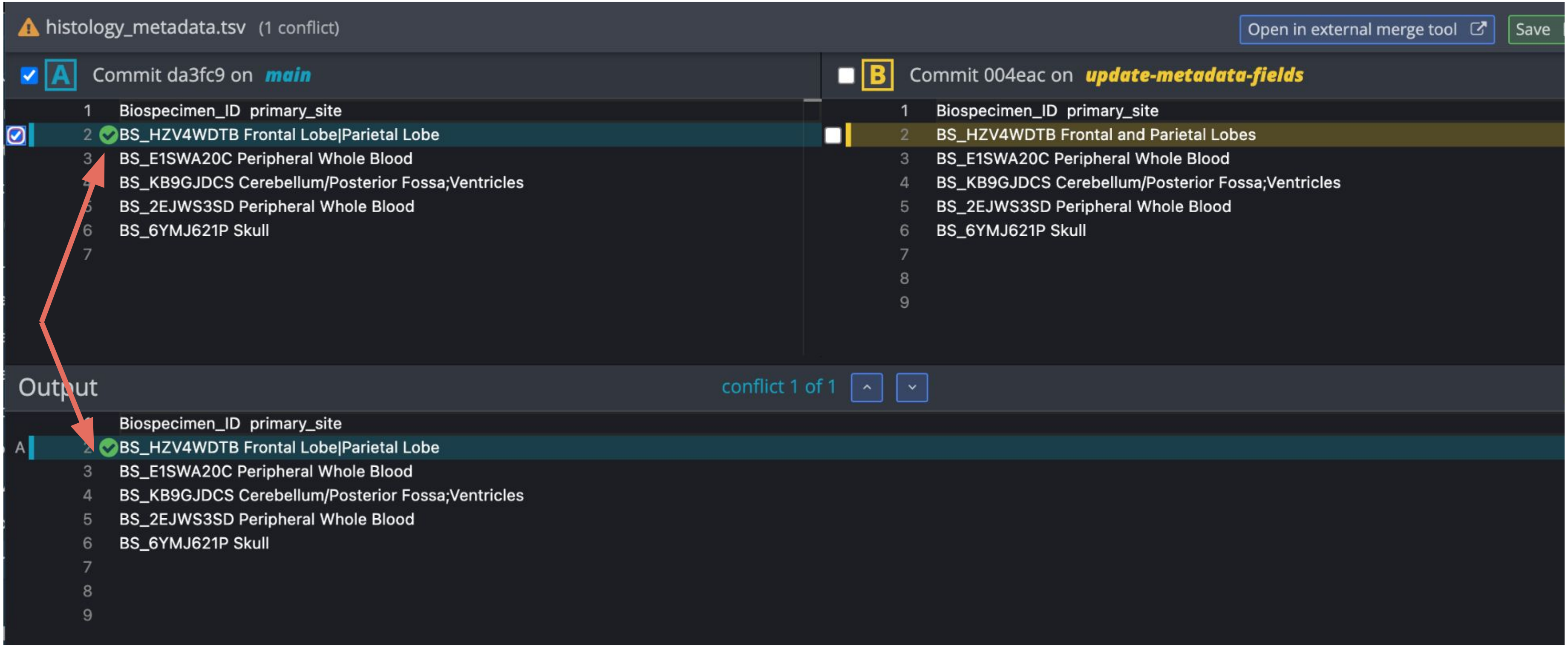
□ Commit 004eac on *update-metadata-fields*

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal and Parietal Lobes
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

Output

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe;Parietal Lobe
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

The result of a fixed merged conflict will appear here


histology_metadata.tsv (1 conflict)
Open in external merge tool
Save
conflict 1 of 1

☑ A Commit da3fc9 on *main*

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe|Parietal Lobe
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

□ B Commit 004eac on *update-metadata-fields*

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal and Parietal Lobes
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
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```

Output

```
Biospecimen_ID  primary_site
BS_HZV4WDTB Frontal Lobe|Parietal Lobe
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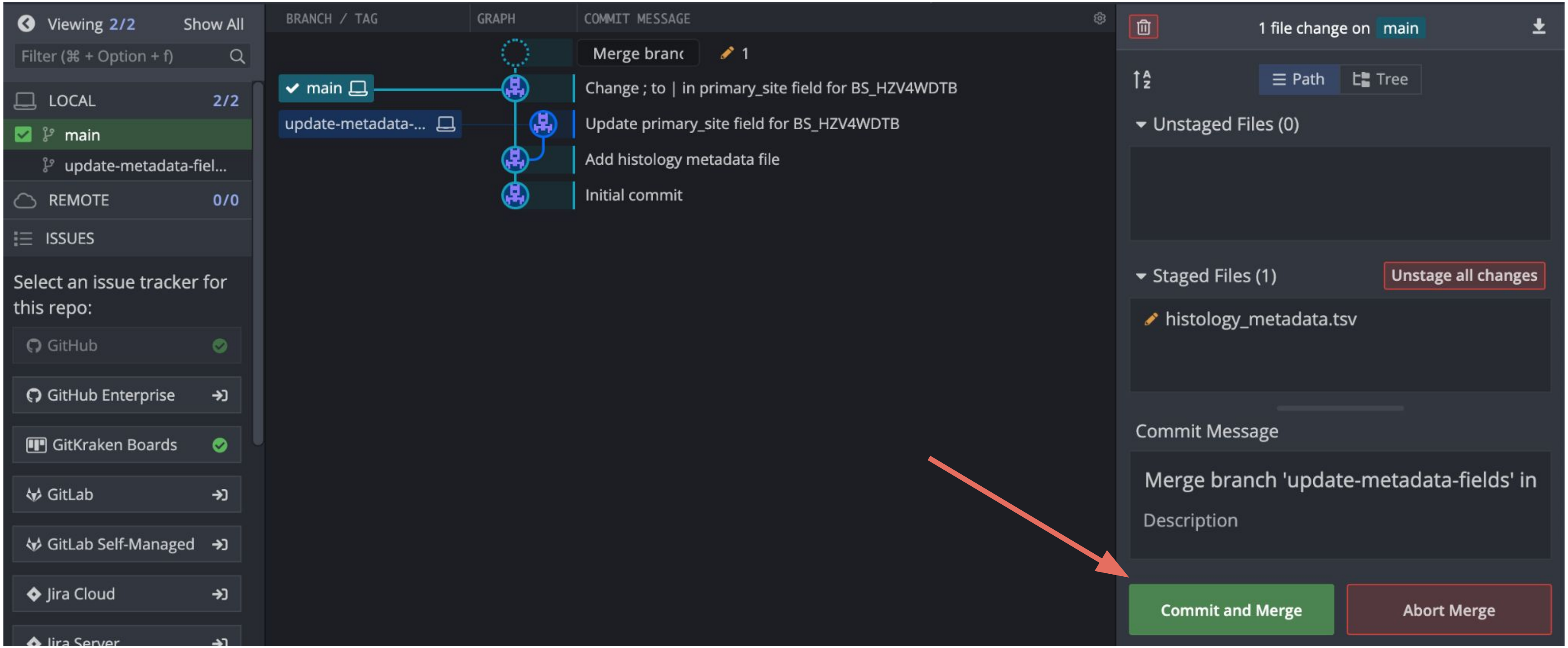


Merge branc 1

Change ; to | in primary_site field for BS_HZV4WDTB

Update primary_site field for BS_HZV4WDTB

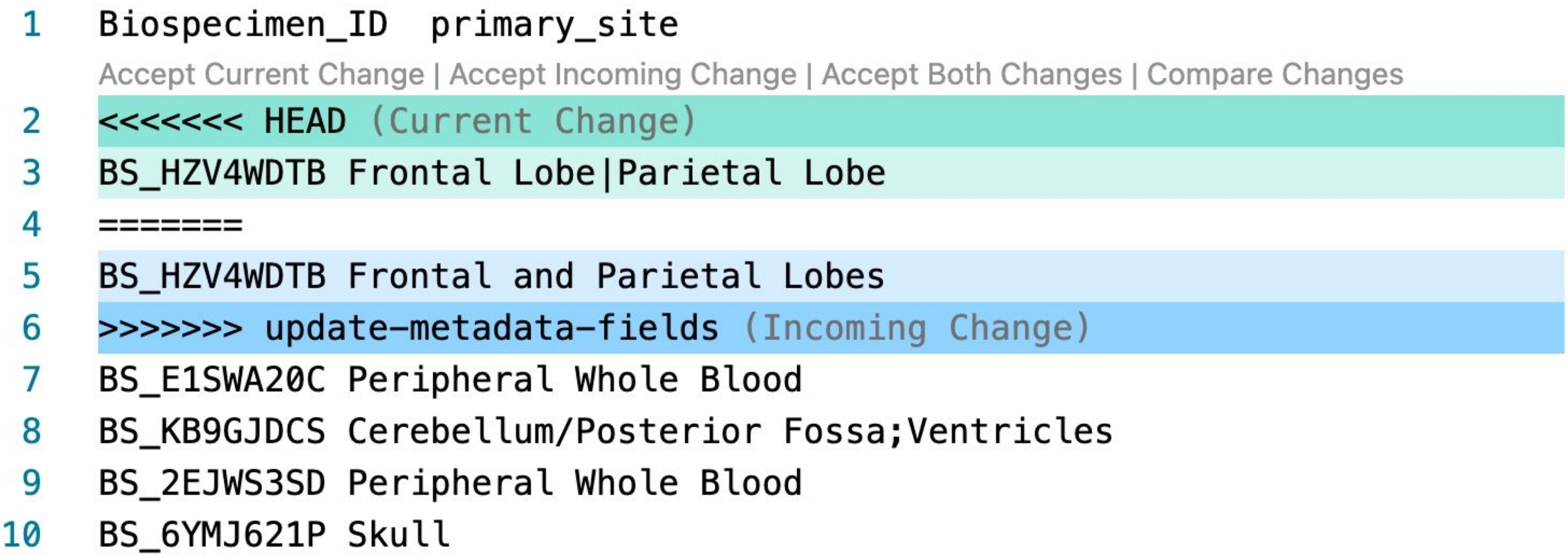
Add histology metadata file

Initial commit

histology_metadata.tsv

Merge branch 'update-metadata-fields' in

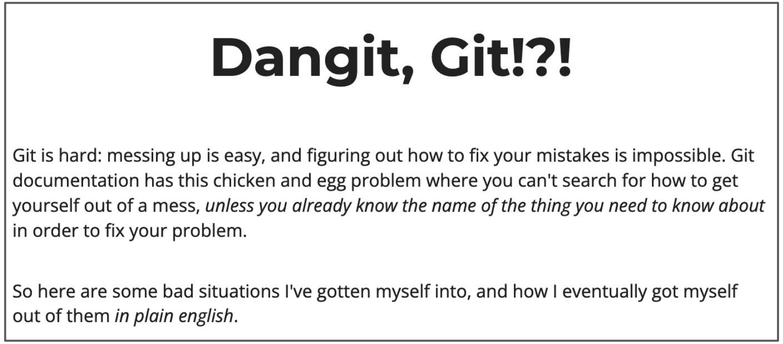
VS Code also has helpful git integration!


Accept Current Change | Accept Incoming Change | Accept Both Changes | Compare Changes

```
Biospecimen_ID  primary_site
<<<<<<< HEAD (Current Change)
BS_HZV4WDTB Frontal Lobe|Parietal Lobe
=======
BS_HZV4WDTB Frontal and Parietal Lobes
>>>>>>> update-metadata-fields (Incoming Change)
BS_E1SWA20C Peripheral Whole Blood
BS_KB9GJDCS Cerebellum/Posterior Fossa;Ventricles
BS_2EJWS3SD Peripheral Whole Blood
BS_6YMJ621P Skull
```

A reminder: Everyone agrees Git is tricky.

- You will make mistakes
  - *That's ok! So do we, and so does everyone else!*
  - Git and GitKraken error messages will try to help you
- But sometimes you will just want to curse



Dangit, Git!?!

Git is hard: messing up is easy, and figuring out how to fix your mistakes is impossible. Git documentation has this chicken and egg problem where you can't search for how to get yourself out of a mess, *unless you already know the name of the thing you need to know about* in order to fix your problem.

So here are some bad situations I've gotten myself into, and how I eventually got myself out of them *in plain english*.

https://dangitgit.com/en

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Translated into over 20 languages, and counting!

(and its other version, https://ohs**tgit.com, but with those letters filled in!)