Cleveland Clinic

IBM

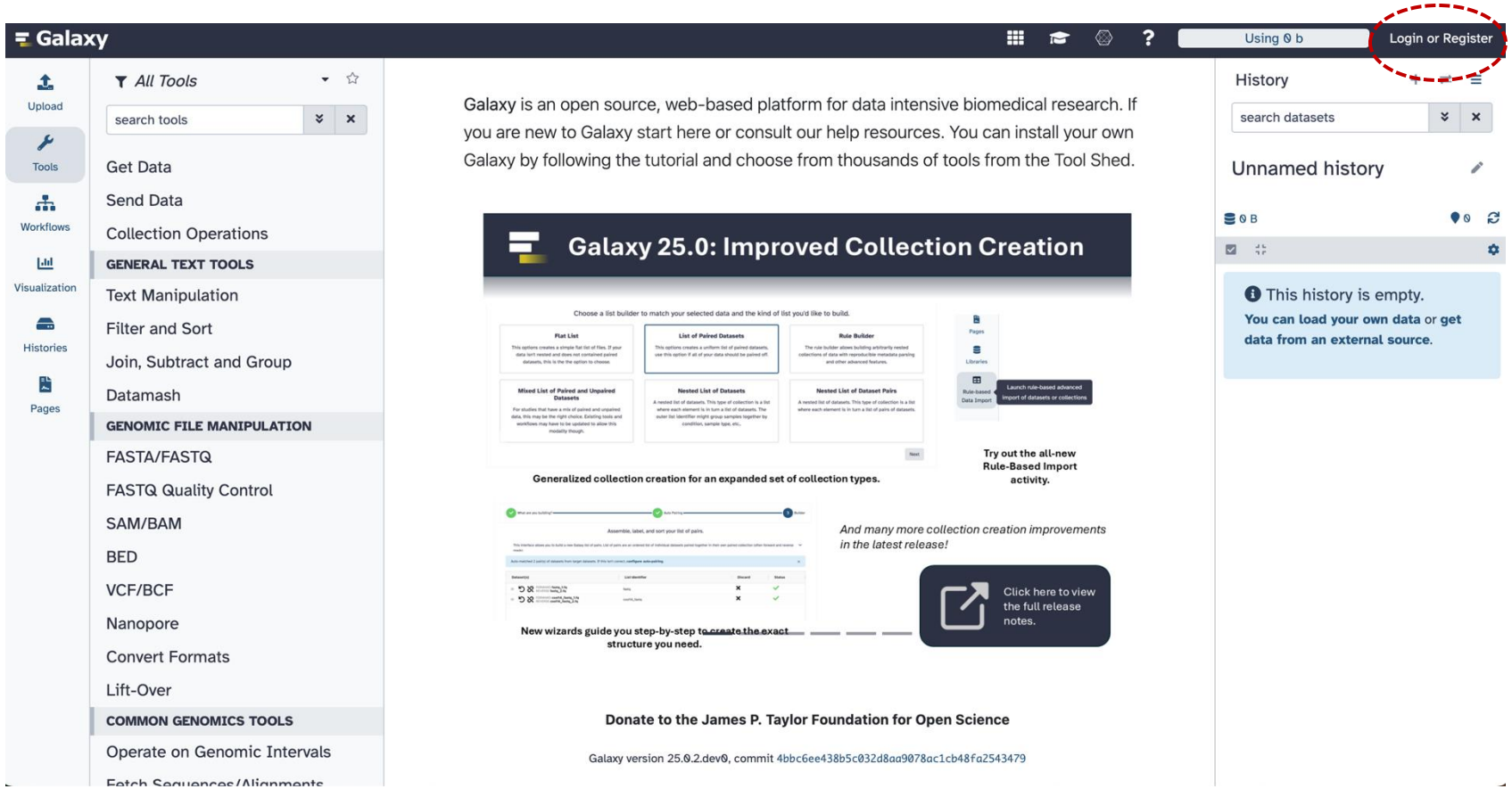
QBioCode with JupyterLab *in Galaxy*

Qiskit

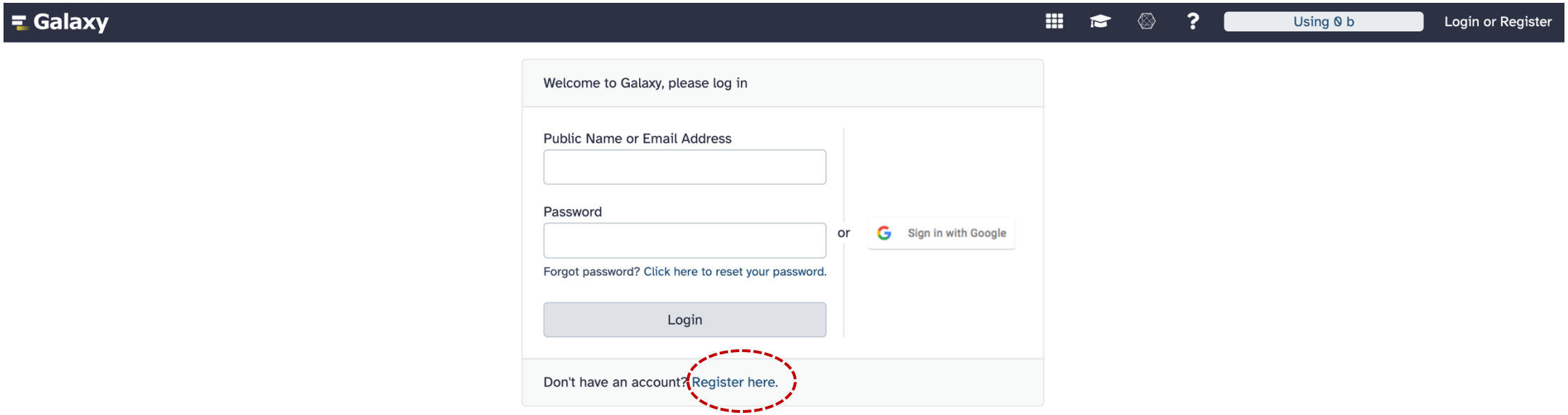
Galaxy

Create Account

- If new to Galaxy, create a new account on usegalaxy.org or usegalaxy.eu

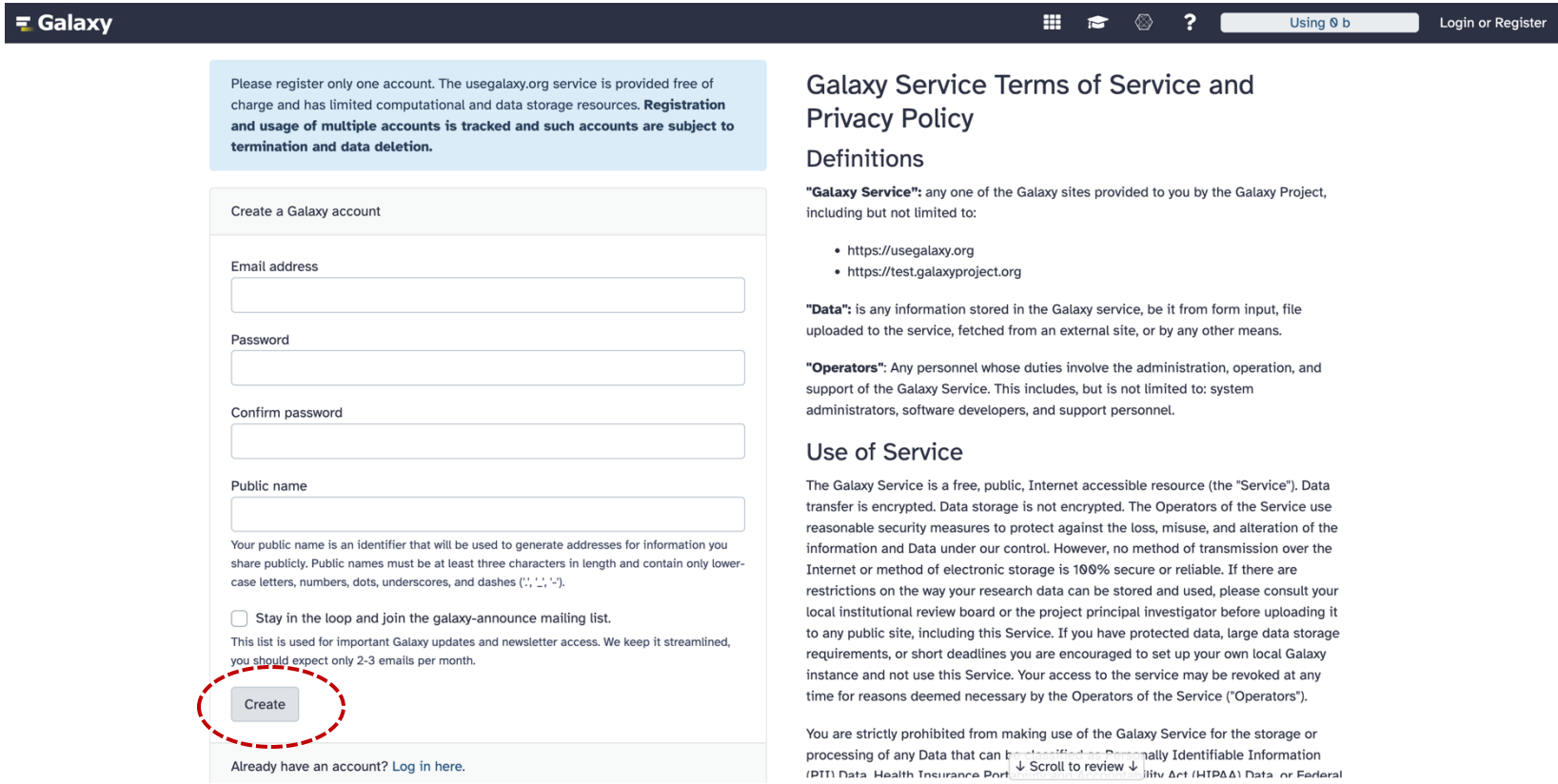


Create Account



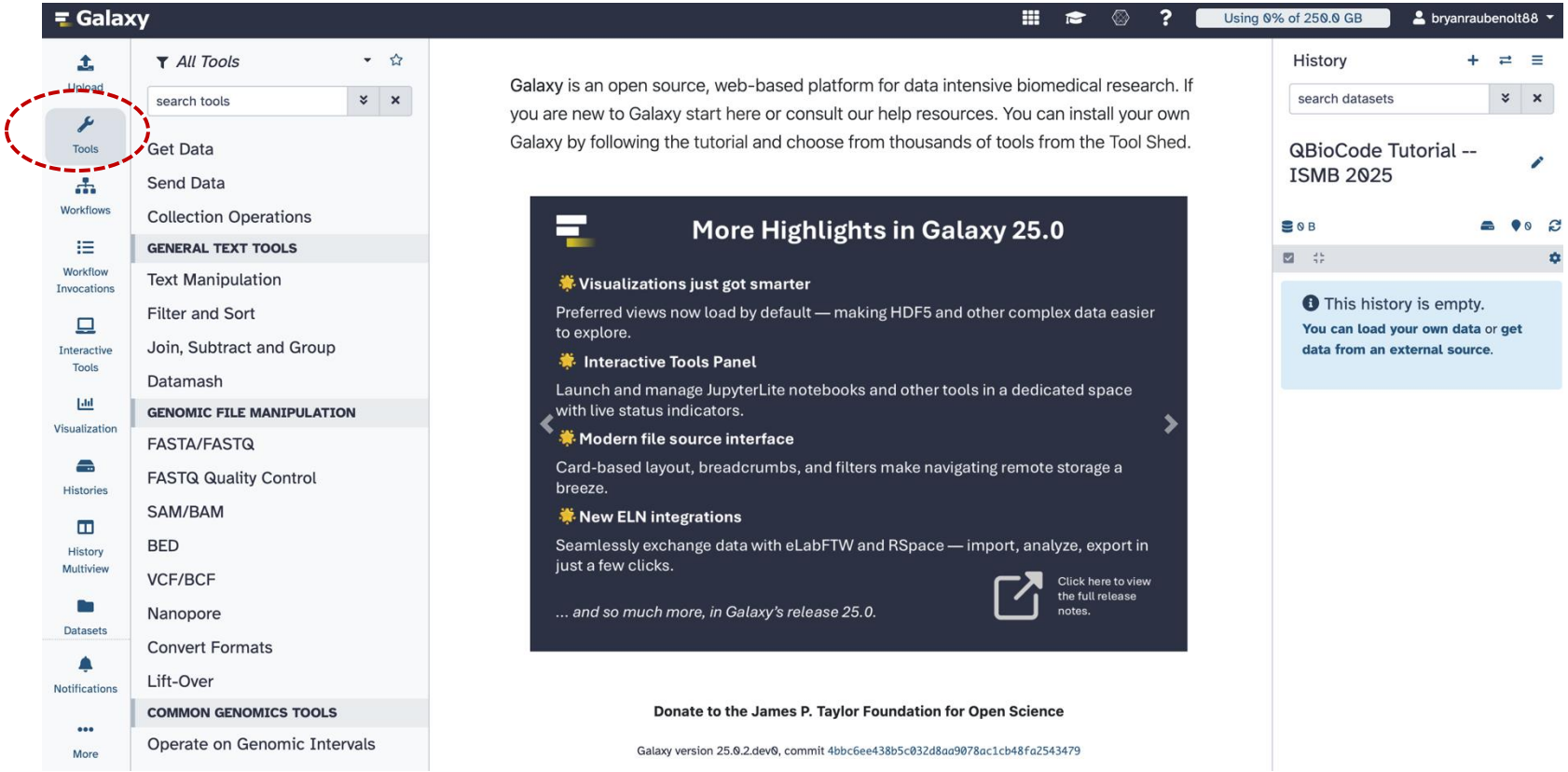
Create Account

- Fill in your user information and then wait for confirmation email.
- Follow instructions in confirmation email.
- Be sure to check your spam/junk folder if you don’t receive it.



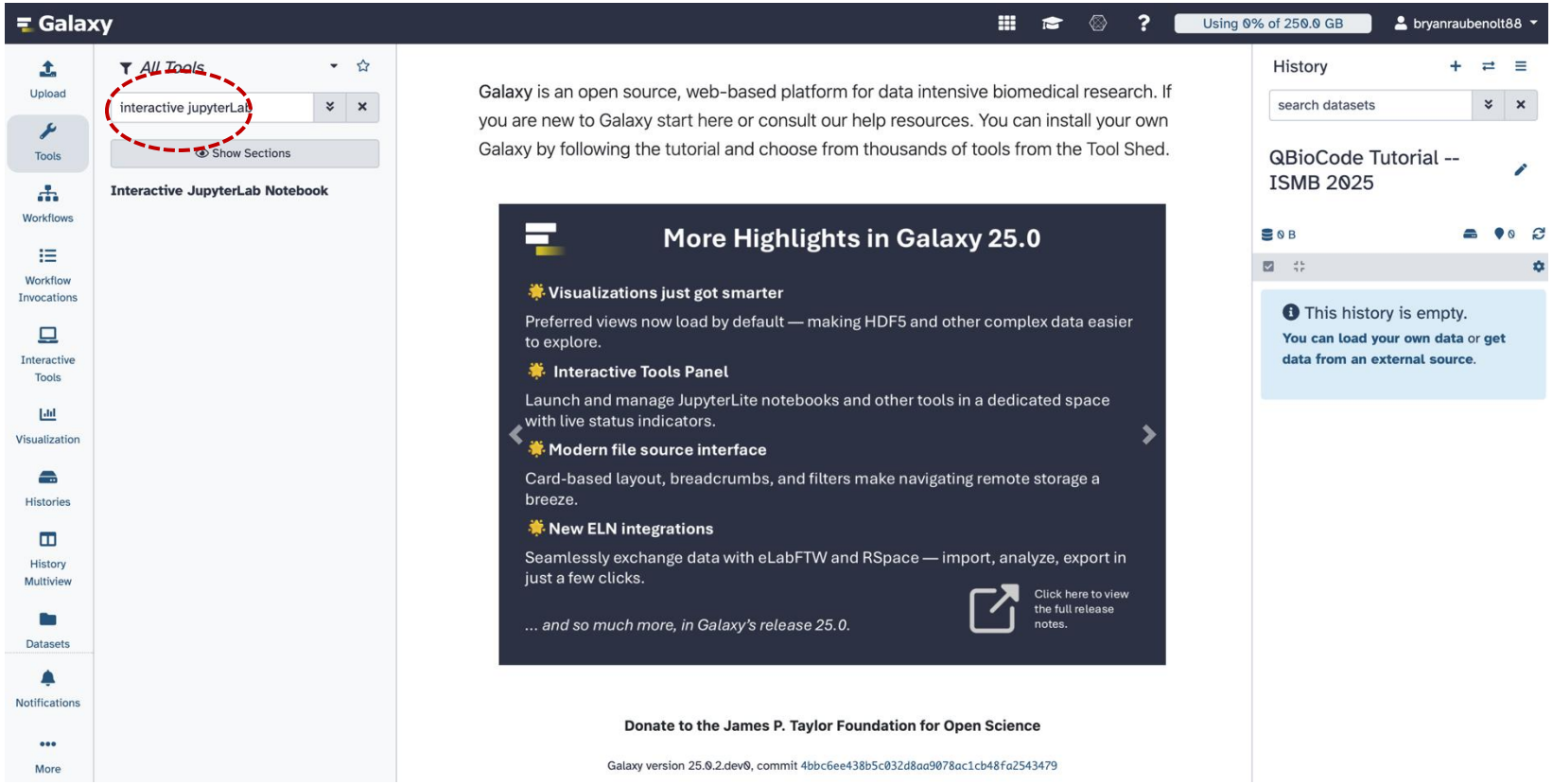
Find the Tool

- Bring up the tool panel by clicking the “Tools” icon



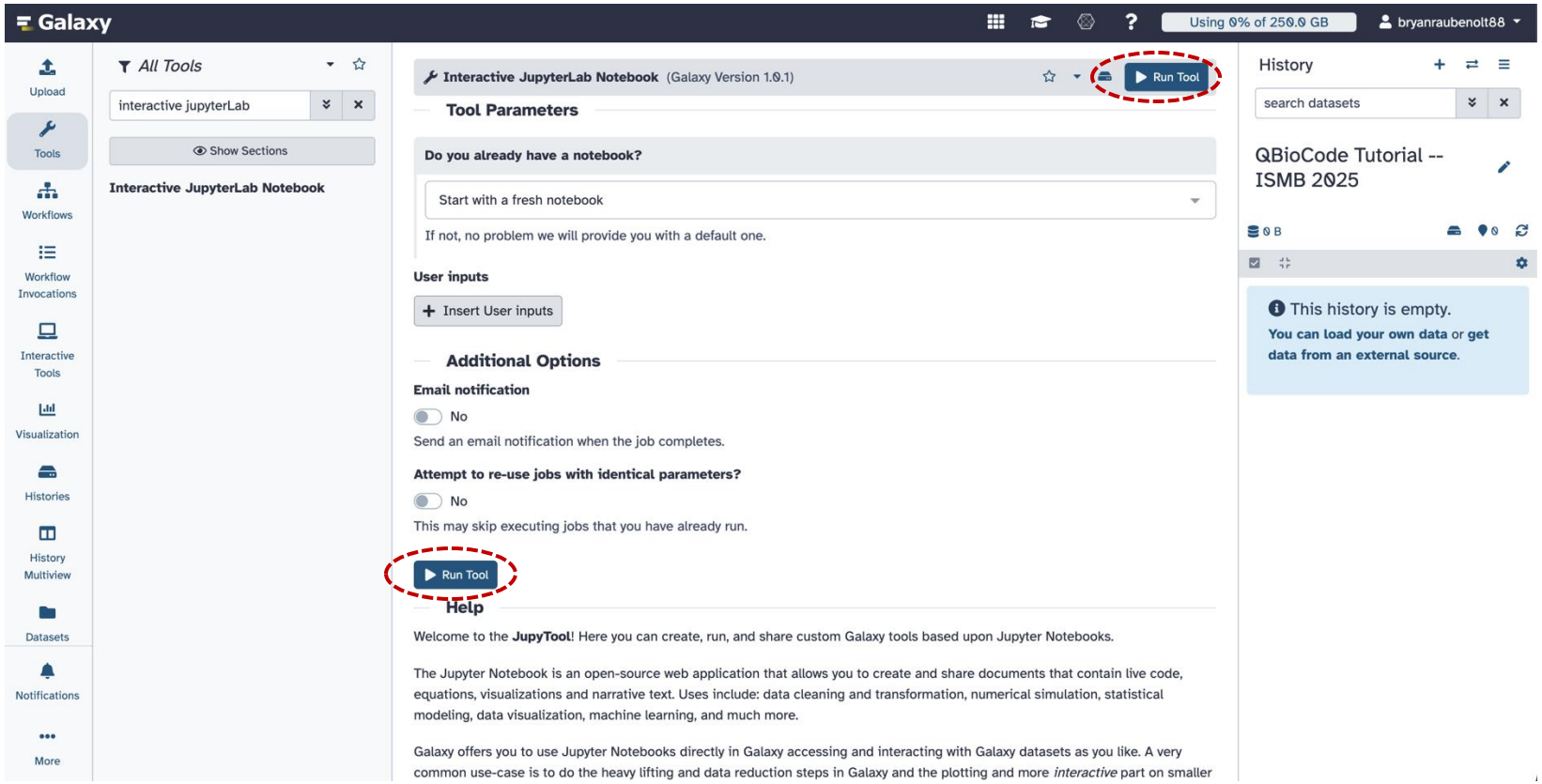
Find the Tool

- Search for “Interactive JupyterLab…” and click on the tool that comes up



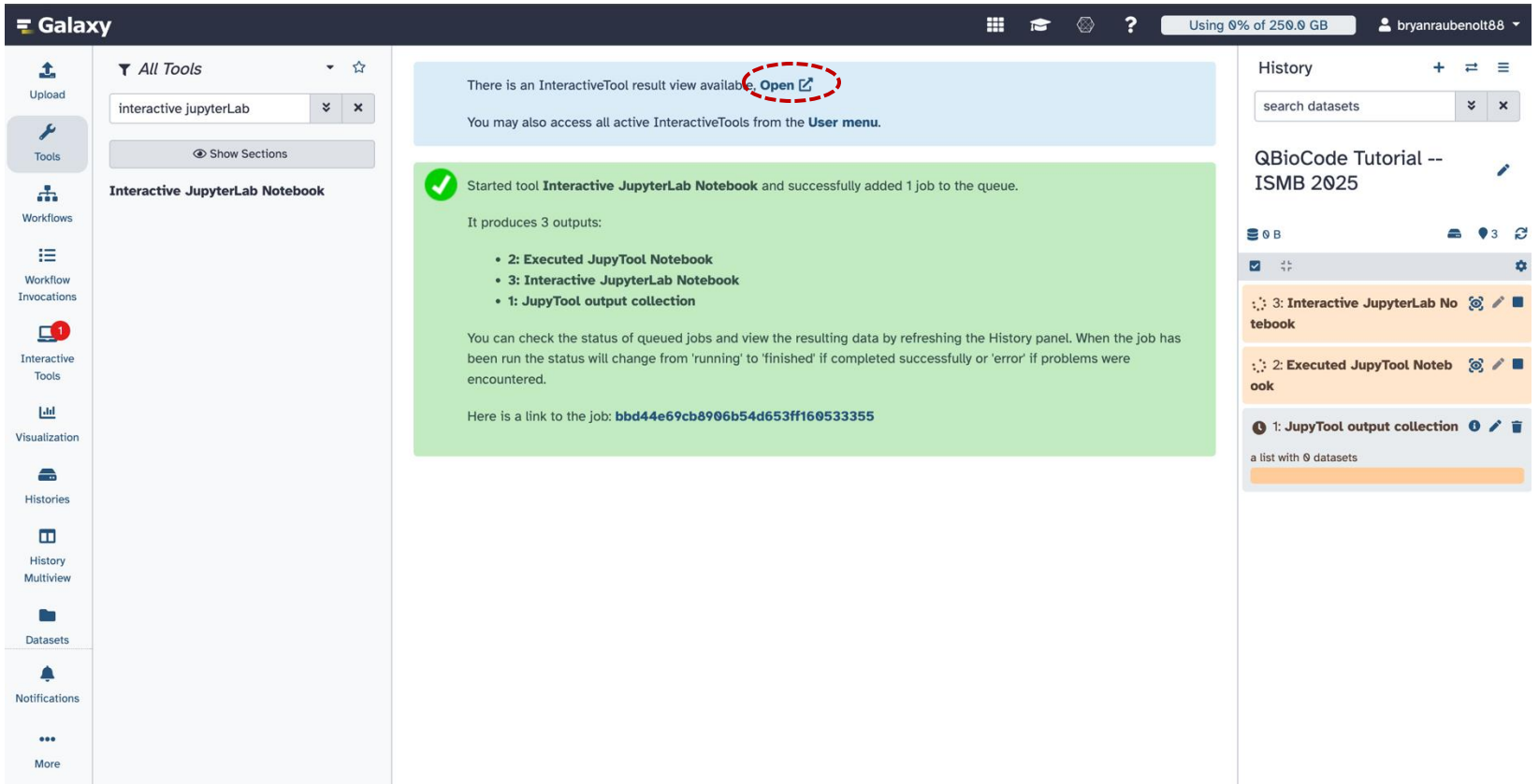
Run the Tool

- Click on “Run Tool”.



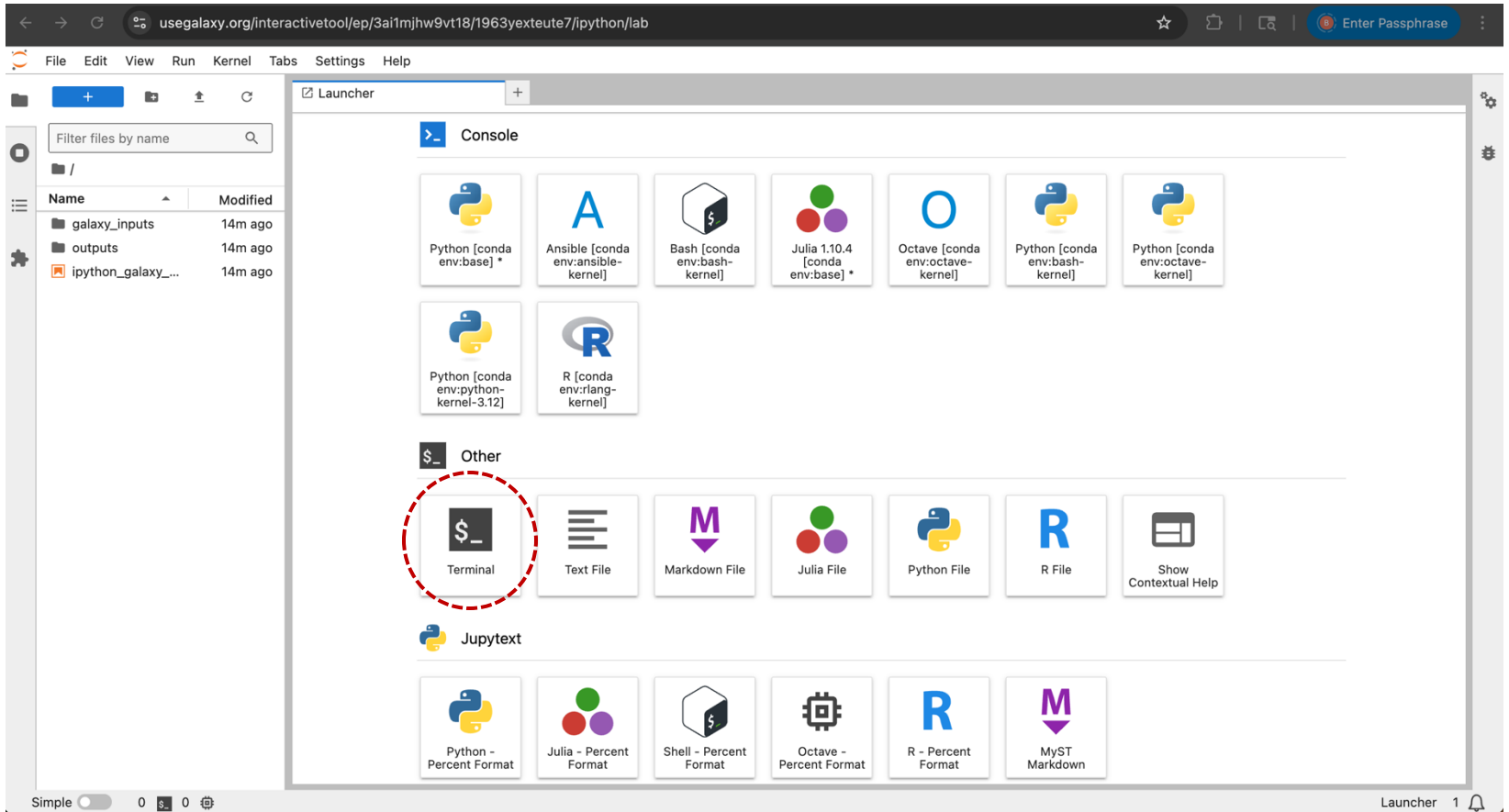
Run the Tool

- Wait until tool becomes active (orange colors in your history items) and then click open.

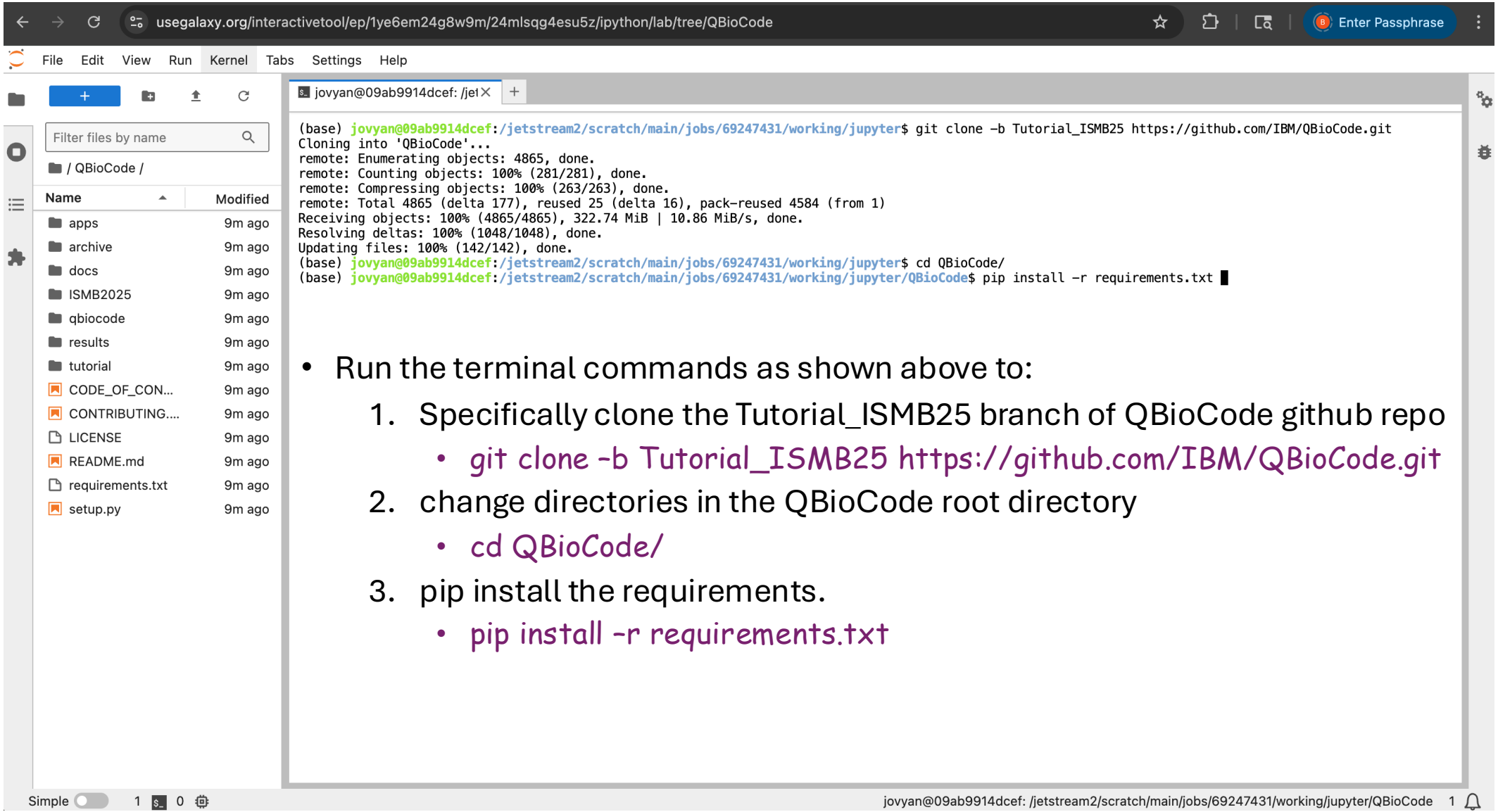


Run the Tool

- A new browser window opens up containing the tool's jupyter lab instance. Open a terminal window to get started.



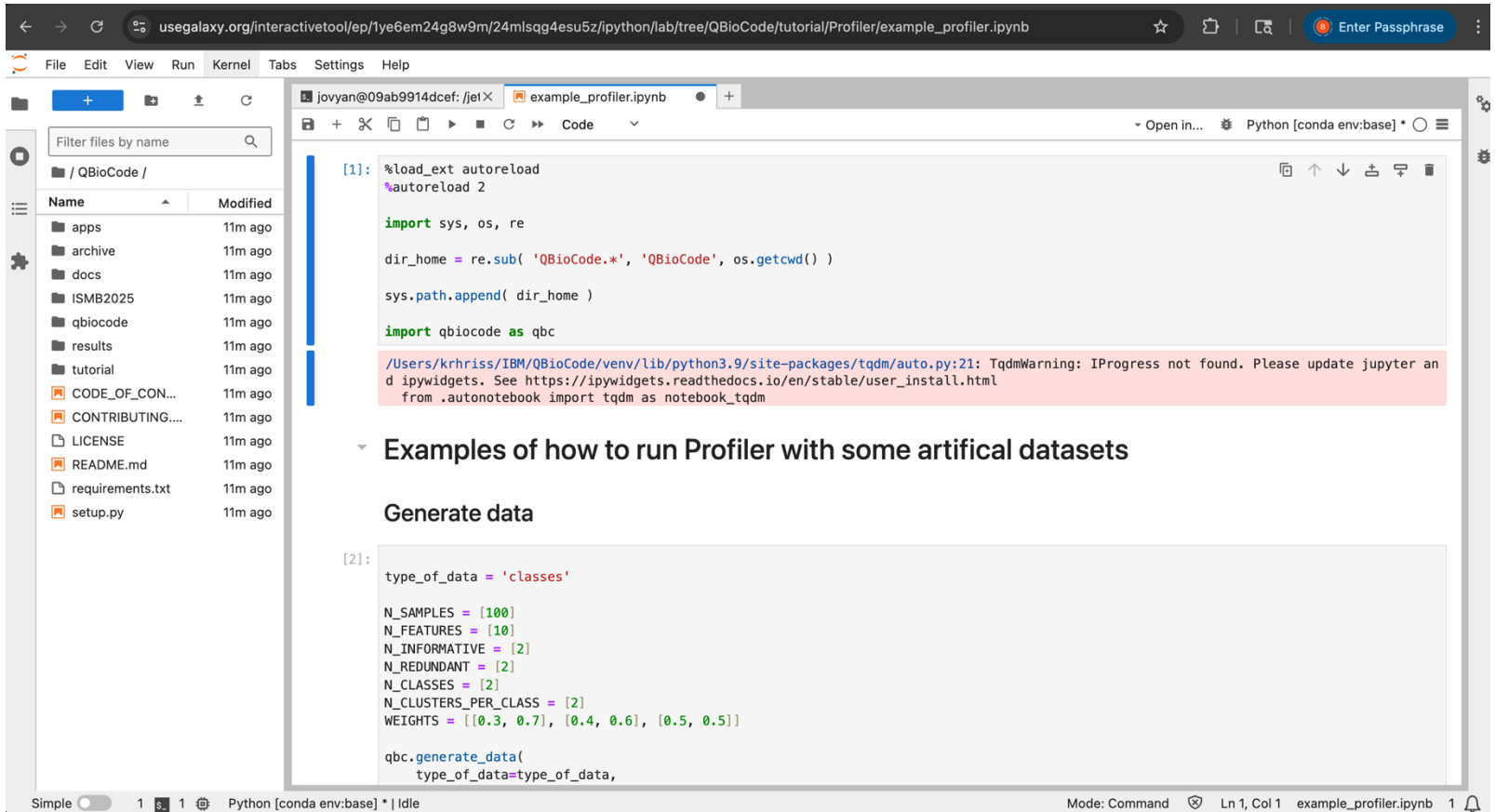
Run the Tool



- Run the terminal commands as shown above to:
  1. Specifically clone the Tutorial_ISMB25 branch of QBioCode github repo
     - git clone -b Tutorial_ISMB25 https://github.com/IBM/QBioCode.git
  2. change directories in the QBioCode root directory
     - cd QBioCode/
  3. pip install the requirements.
     - pip install -r requirements.txt

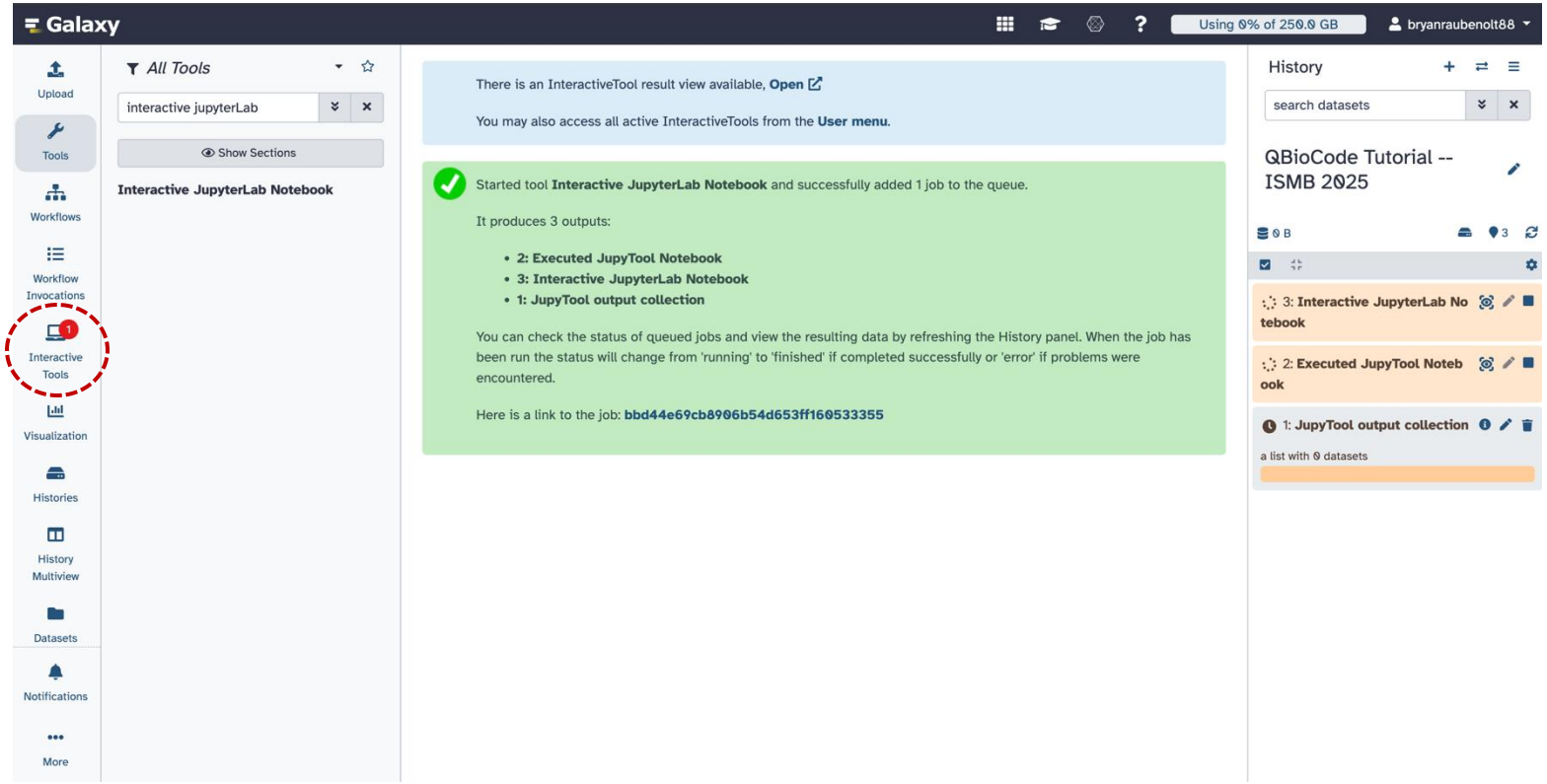
Begin the QBioCode Tutorial!

- Your environment should now have all the packages installed, and you can now go through the whole QBioCode Tutorial, using Galaxy!



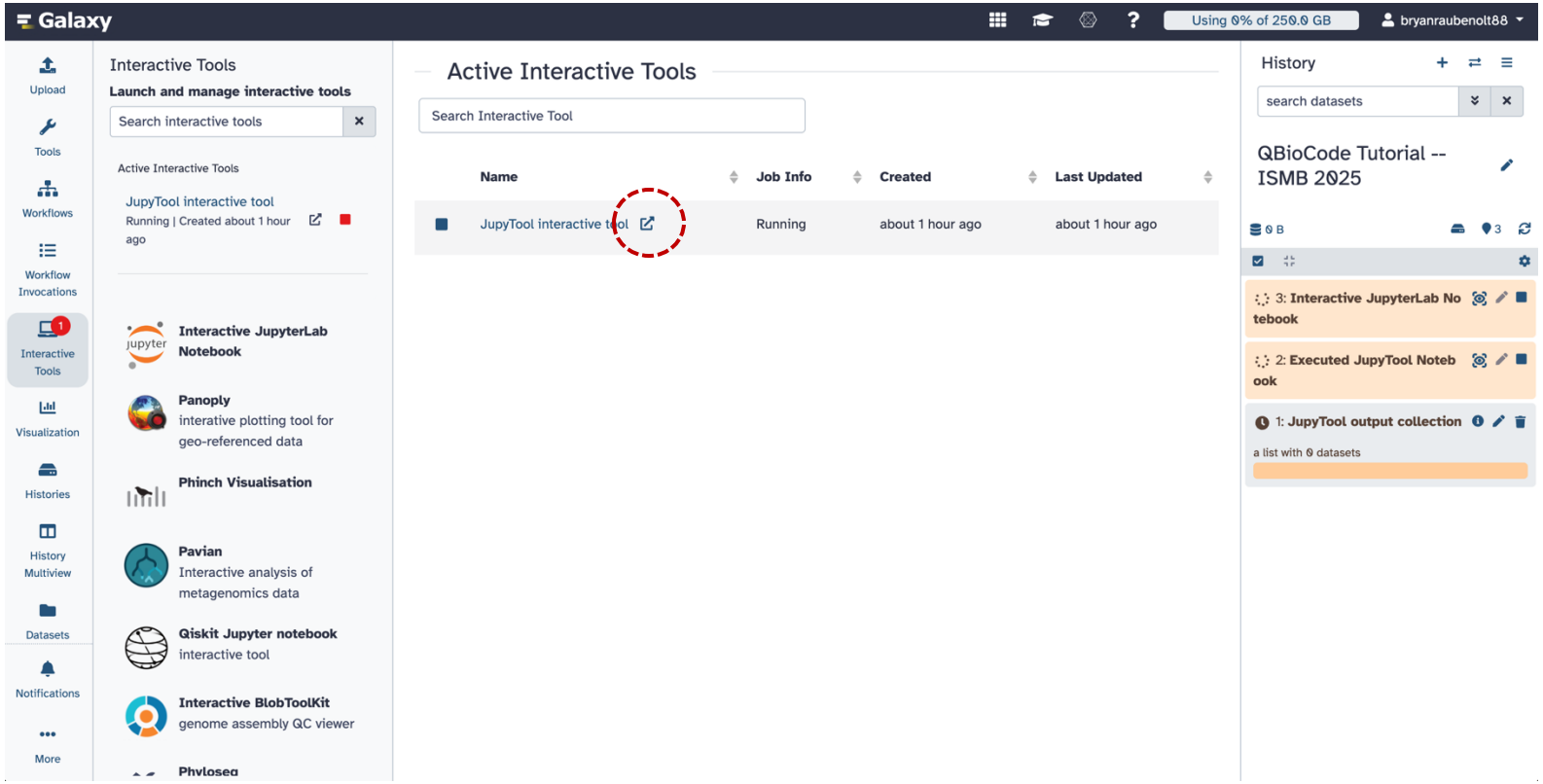
Reopening your session

- We recommend to not close your browser, but if you do and need to come back to your JupyterLab instance: Go back to the Galaxy server you signed up with (usegalaxy.org or usegalaxy.eu) and click on *Interactive Tools*.



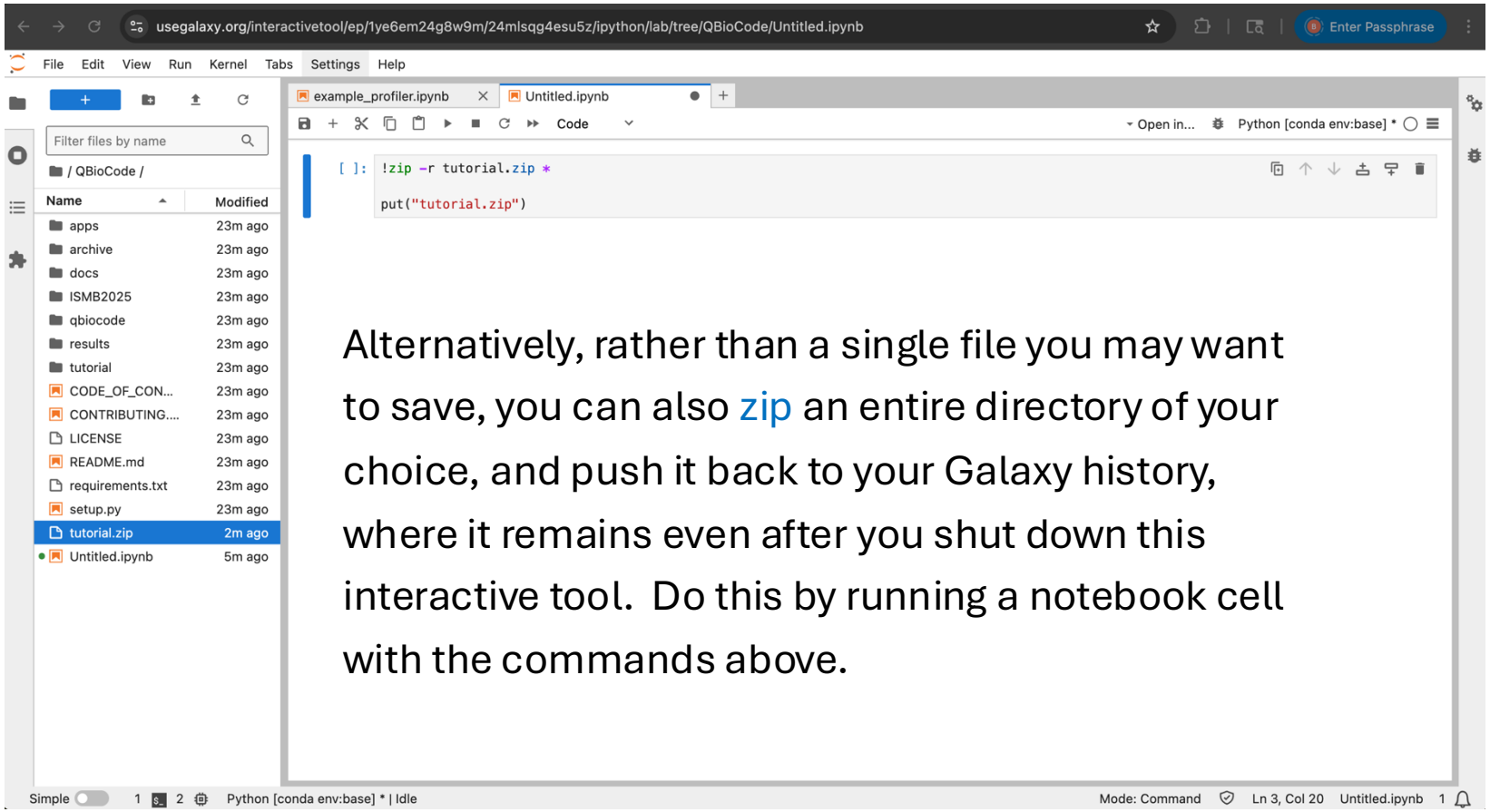
Reopening your session

- Click on your current running tool and a new tab should reopen your JupyterLab session.



Saving your files

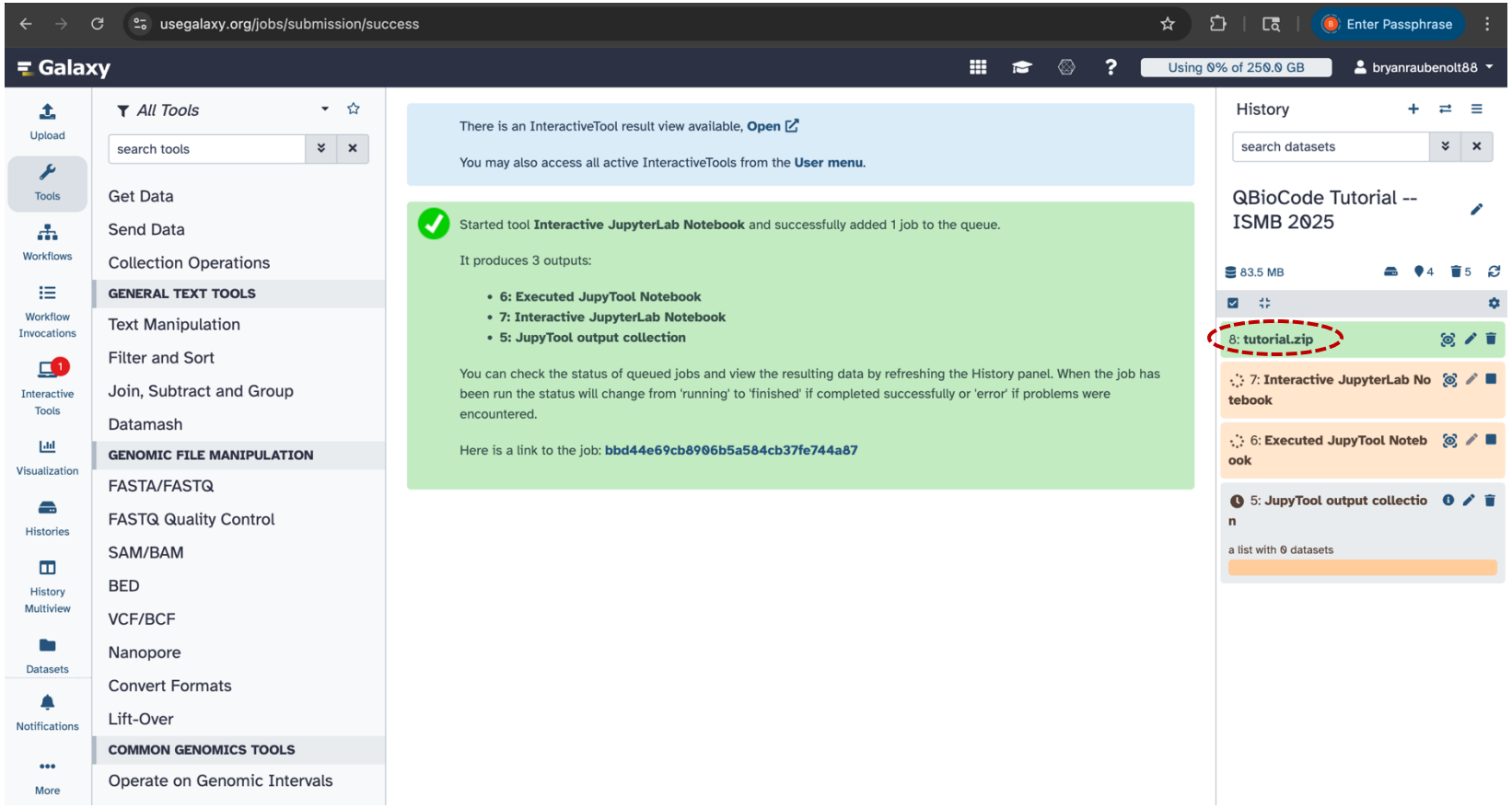
- If there are any files you want to keep, you can either download them to your computer directly from the JupyterLab instance (right click + Download), or you can push into your Galaxy history, by simply running this command in a notebook cell:
  - put("file.ext")



Alternatively, rather than a single file you may want to save, you can also zip an entire directory of your choice, and push it back to your Galaxy history, where it remains even after you shut down this interactive tool. Do this by running a notebook cell with the commands above.

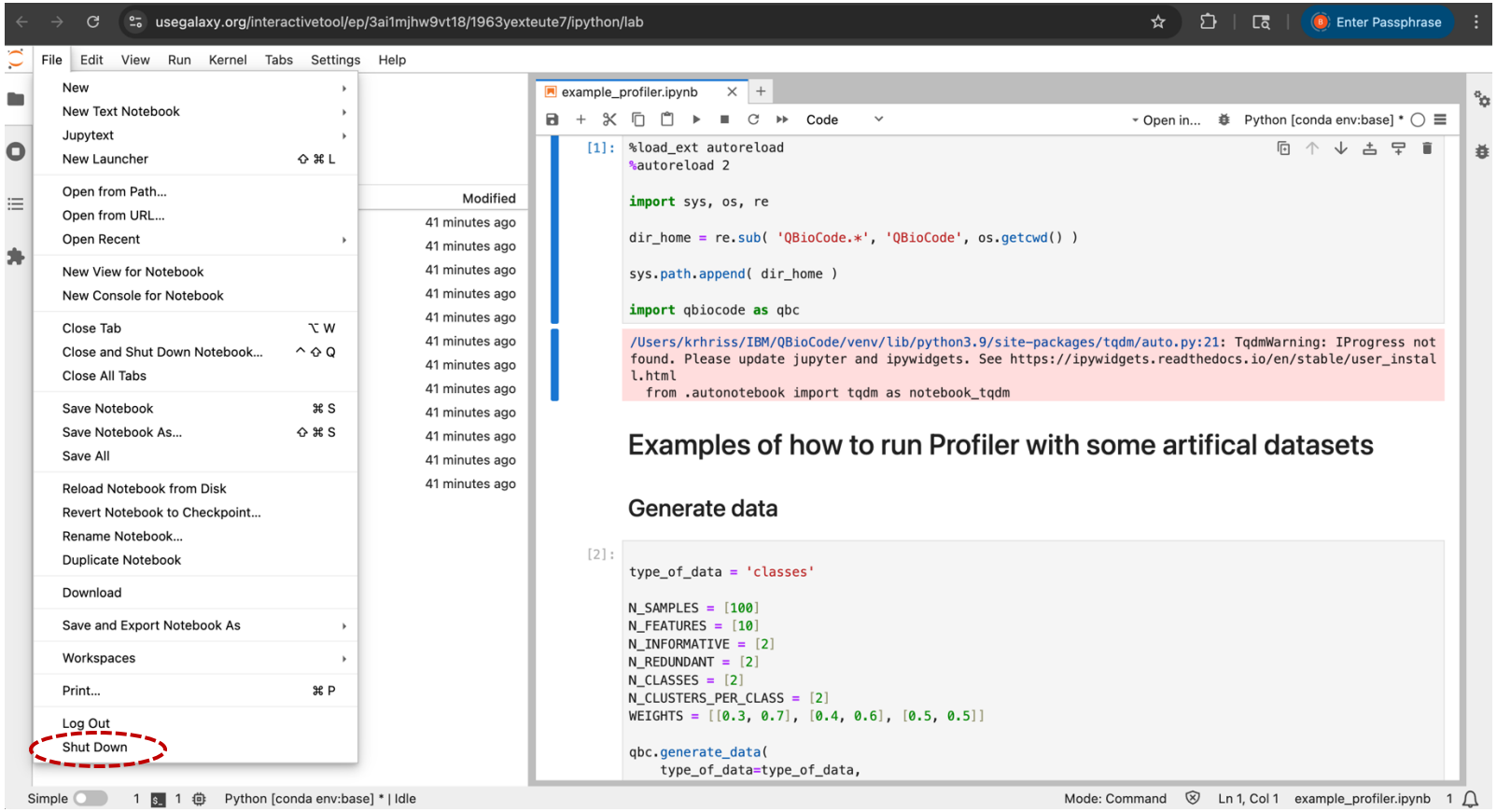
Saving your files

- Your saved file was now pushed back into your Galaxy history, where you can access again anytime.



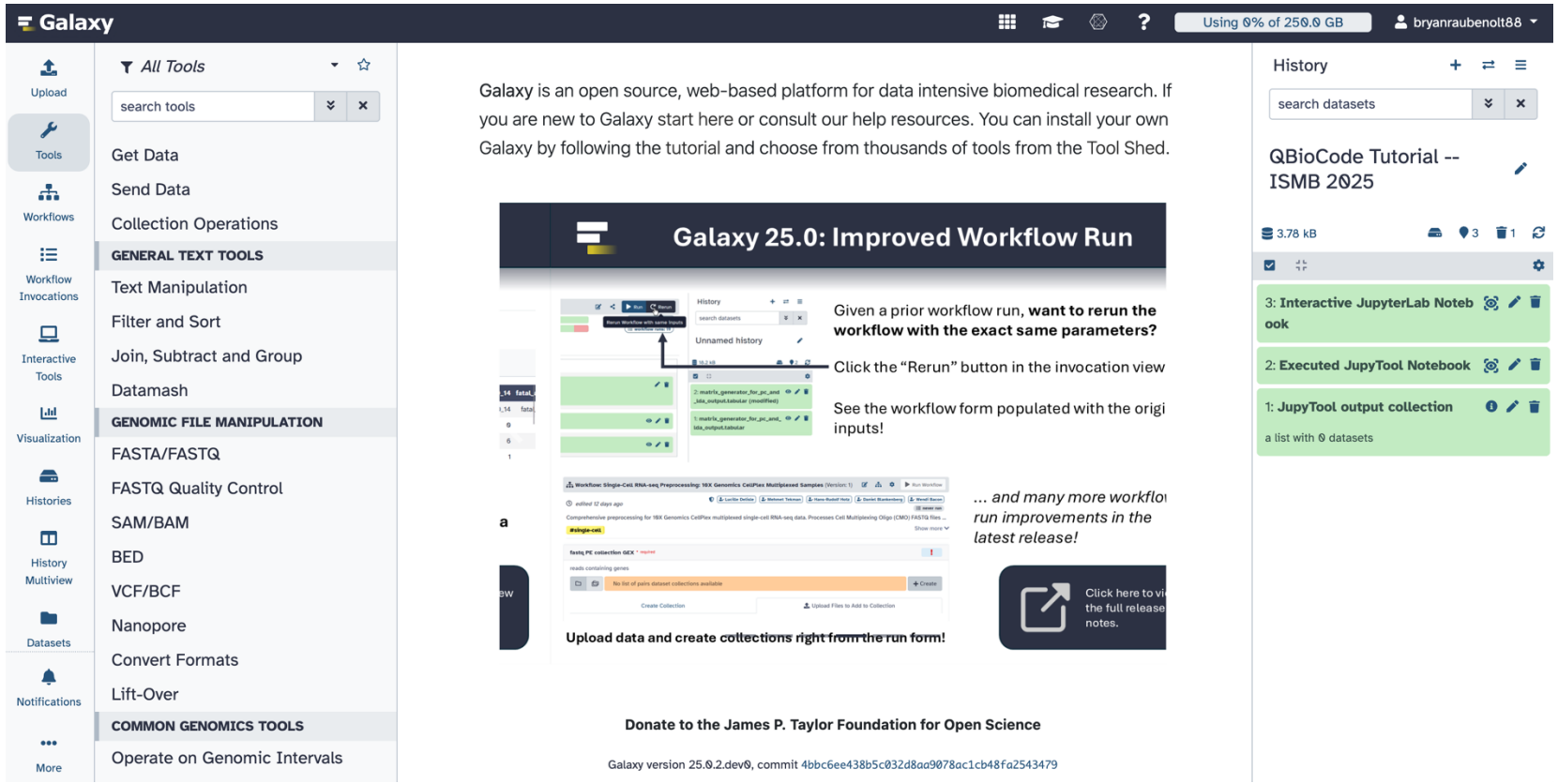
Shutting down your tool

- You will want to properly shutdown the Interactive JupyterLab Tool once the tutorial is done.



Shutting down your tool

- Your tool's history items will now light up in green, indicating a successful run and shutdown of the interactive tool!



Cleveland Clinic

IBM

Thanks for using Galaxy in this tutorial!

- For information on Galaxy, and other useful tutorials for biomedical research analysis:
  - https://training.galaxyproject.org/training-material/

- For more information on how to use this specific Interactive JupyterLab Tool:
  - https://training.galaxyproject.org/training-material/topics/galaxy-interface/tutorials/jupyterlab/tutorial.html

Qiskit

Galaxy