

QBioCode with JupyterLab *in* *Galaxy*

Create Account

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

The screenshot displays the Galaxy 25.0 web interface. The top navigation bar includes the Galaxy logo, a search bar, and a 'Login or Register' button, which is highlighted with a red dashed circle. The left sidebar contains a 'Tools' section with a search bar and a list of tool categories: 'All Tools', 'Get Data', 'Send Data', 'Collection Operations', 'GENERAL TEXT TOOLS', 'Text Manipulation', 'Filter and Sort', 'Join, Subtract and Group', 'Datamash', 'GENOMIC FILE MANIPULATION', 'FASTA/FASTQ', 'FASTQ Quality Control', 'SAM/BAM', 'BED', 'VCF/BCF', 'Nanopore', 'Convert Formats', 'Lift-Over', 'COMMON GENOMICS TOOLS', 'Operate on Genomic Intervals', and 'Fetch Sequences/Alignments'. The main content area features a banner for 'Galaxy 25.0: Improved Collection Creation' with a 'Next' button. Below the banner, there is a section titled 'Generalized collection creation for an expanded set of collection types.' which includes a progress bar and a table of collection types. The table has columns for 'Collection Type', 'New', 'Deleted', and 'Status'. The 'New' column shows a checkmark for 'FASTQ Quality Control' and a cross for 'Lift-Over'. The 'Deleted' column shows a cross for 'FASTQ Quality Control' and a checkmark for 'Lift-Over'. The 'Status' column shows a checkmark for 'FASTQ Quality Control' and a cross for 'Lift-Over'. The right sidebar contains a 'History' section with a search bar and a message stating 'This history is empty. You can load your own data or get data from an external source.'

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.

Galaxy 25.0: Improved Collection Creation

Choose a list builder to match your selected data and the kind of list you'd like to build.

- Flat List**
This option creates a single flat list of files. If your data isn't nested and does not contain paired datasets, this is the option to choose.
- List of Paired Datasets**
This option creates a collection list of paired datasets. Use this option if all of your data should be paired off.
- Rule Builder**
The rule builder allows building arbitrarily nested collections of data with reproducible metadata passing and other advanced features.
- Mixed List of Paired and Unpaired Datasets**
For datasets that have a mix of paired and unpaired data, this may be the right choice. Existing tools and workflows may have to be updated to allow this flexibility through.
- Nested List of Datasets**
A nested list of datasets. This type of collection is a list where each element is in turn a list of datasets. The user can specify which group samples together by condition, sample type, etc.
- Nested List of Dataset Pairs**
A nested list of datasets. This type of collection is a list where each element is in turn a list of pairs of datasets.

Try out the all-new Rule-Based Import activity.

Generalized collection creation for an expanded set of collection types.

And many more collection creation improvements in the latest release!

New wizards guide you step-by-step to create the exact structure you need.

Click here to view the full release notes.

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Galaxy version 25.0.2.dev0, commit 4bbc6ee438b5c032d8aa9078ac1cb48fa2543479

Create Account

Welcome to Galaxy, please log in

Public Name or Email Address

Password

or



Sign in with Google

Forgot password? [Click here to reset your password.](#)

Login

Don't have an account? [Register here.](#)

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.

Galaxy

Using 0 b

Login or Register

Please register only one account. The usegalaxy.org service is provided free of charge and has limited computational and data storage resources. **Registration and usage of multiple accounts is tracked and such accounts are subject to termination and data deletion.**

Create a Galaxy account

Email address

Password

Confirm password

Public name

Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes ('.', '_', '-').

☐ Stay in the loop and join the galaxy-announce mailing list.
This list is used for important Galaxy updates and newsletter access. We keep it streamlined, you should expect only 2-3 emails per month.

Create

Already have an account? [Log in here.](#)

Galaxy Service Terms of Service and Privacy Policy

Definitions

"**Galaxy Service**": any one of the Galaxy sites provided to you by the Galaxy Project, including but not limited to:

- <https://usegalaxy.org>
- <https://test.galaxyproject.org>

"**Data**": is any information stored in the Galaxy service, be it from form input, file uploaded to the service, fetched from an external site, or by any other means.

"**Operators**": Any personnel whose duties involve the administration, operation, and support of the Galaxy Service. This includes, but is not limited to: system administrators, software developers, and support personnel.

Use of Service

The Galaxy Service is a free, public, Internet accessible resource (the "Service"). Data transfer is encrypted. Data storage is not encrypted. The Operators of the Service use reasonable security measures to protect against the loss, misuse, and alteration of the information and Data under our control. However, no method of transmission over the Internet or method of electronic storage is 100% secure or reliable. If there are restrictions on the way your research data can be stored and used, please consult your local institutional review board or the project principal investigator before uploading it to any public site, including this Service. If you have protected data, large data storage requirements, or short deadlines you are encouraged to set up your own local Galaxy instance and not use this Service. Your access to the service may be revoked at any time for reasons deemed necessary by the Operators of the Service ("Operators").

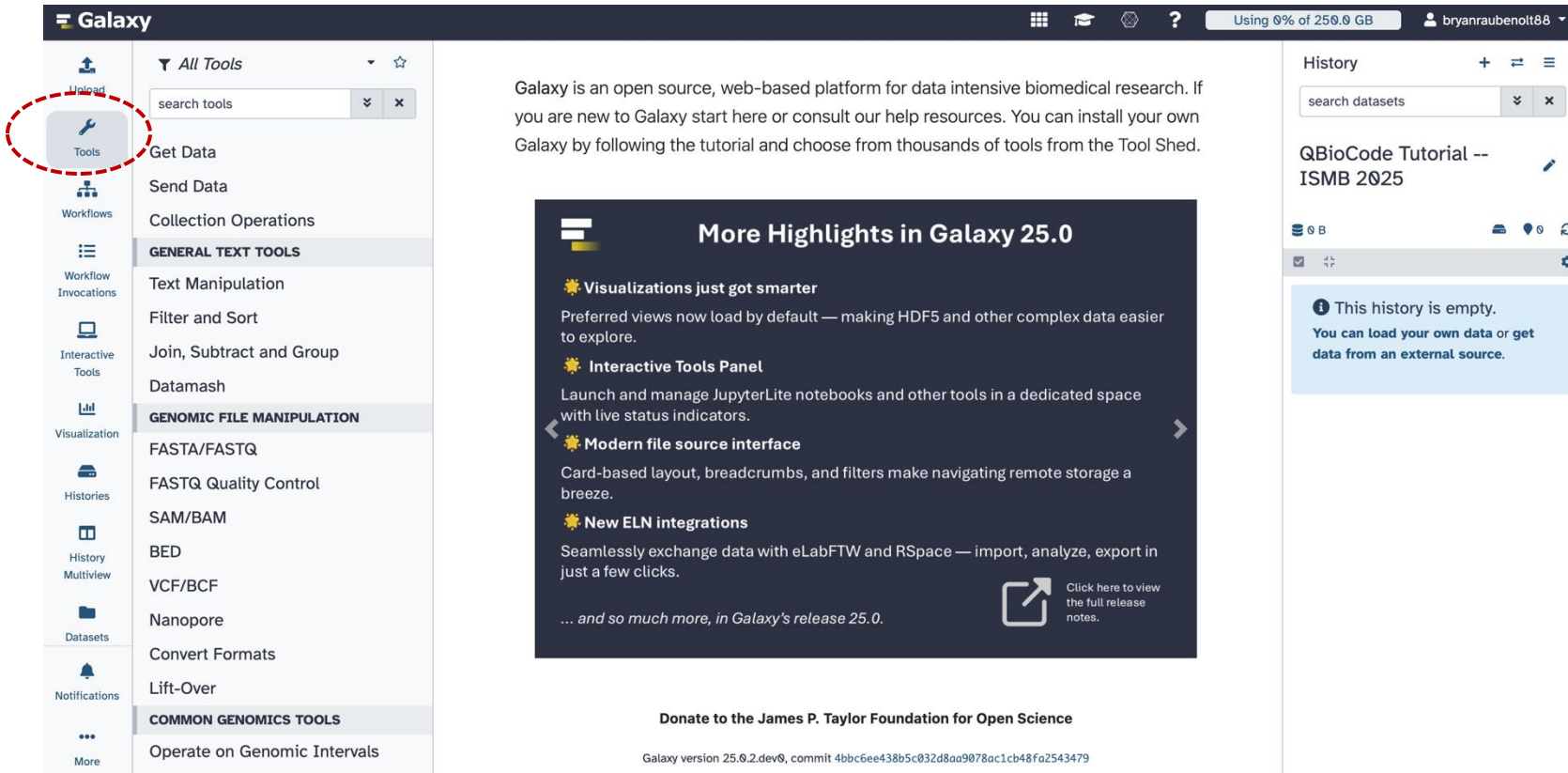
You are strictly prohibited from making use of the Galaxy Service for the storage or processing of any Data that can be used to identify personally identifiable information (PII) Data, Health Insurance Portability and Accountability Act (HIPAA) Data, or Federal

Access the Dedicated Training Allocation

- We have a dedicated allocation for this training session, providing more compute resources for you.
- Simply click the link below after you have logged into usegalaxy.org:
<https://usegalaxy.org/join-training/ismb2025-qbc/>
- Your jobs will now be run in the “ismb2025-qbc” allocation.

Find the Tool

- After you're logged in. Bring up the tool panel by clicking the “Tools” icon



The screenshot shows the Galaxy web interface. On the left sidebar, the 'Tools' icon (a wrench) is highlighted with a red dashed circle. The main content area displays a welcome message and a section titled 'More Highlights in Galaxy 25.0' with several bullet points. The right sidebar shows a 'History' section with a message that the history is empty.

Galaxy

Using 0% of 250.0 GB | bryanraubenolt88

Tools

search tools

Get Data

Send Data

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

Datamash

GENOMIC FILE MANIPULATION

FASTA/FASTQ

FASTQ Quality Control

SAM/BAM

BED

VCF/BCF

Nanopore

Convert Formats

Lift-Over

COMMON GENOMICS TOOLS

Operate on Genomic Intervals

Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed.

More Highlights in Galaxy 25.0

- Visualizations just got smarter**
Preferred views now load by default — making HDF5 and other complex data easier to explore.
- Interactive Tools Panel**
Launch and manage JupyterLite notebooks and other tools in a dedicated space with live status indicators.
- Modern file source interface**
Card-based layout, breadcrumbs, and filters make navigating remote storage a breeze.
- New ELN integrations**
Seamlessly exchange data with eLabFTW and RSpace — import, analyze, export in just a few clicks.

... and so much more, in Galaxy's release 25.0.

Click here to view the full release notes.

History

search datasets

QBioCode Tutorial -- ISMB 2025

This history is empty.
You can load your own data or get data from an external source.

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Galaxy version 25.0.2.dev0, commit 4bbcf6ee438b5c032d8aa9078ac1cb48fa2543479

Find the Tool

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

The screenshot displays the Galaxy web interface. On the left sidebar, the 'Tools' icon is highlighted. The main search bar, labeled 'All Tools', contains the text 'interactive jupyterLab' and is circled with a red dashed line. Below the search bar, the 'Interactive JupyterLab Notebook' is listed. The central panel features a dark blue banner titled 'More Highlights in Galaxy 25.0' with several bullet points: 'Visualizations just got smarter', 'Interactive Tools Panel', 'Modern file source interface', and 'New ELN integrations'. The right sidebar shows a 'History' section with a search bar and a message stating 'This history is empty. You can load your own data or get data from an external source.'

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More Highlights in Galaxy 25.0

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Galaxy version 25.0.2.dev0, commit 4bbc6ee438b5c032d8aa9078ac1cb48fa2543479

Run the Tool

- Click on “Run Tool”.

The screenshot displays the Galaxy web interface. The top navigation bar shows the Galaxy logo, a grid icon, a graduation cap icon, a gear icon, and a question mark icon. The user's profile 'bryanraubenolt88' and storage usage 'Using 0% of 250.0 GB' are visible on the right. The left sidebar contains icons for Upload, Tools, Workflows, Workflow Invocations, Interactive Tools, Visualization, Histories, History Multiview, Datasets, and Notifications. The main content area is titled 'Interactive JupyterLab Notebook (Galaxy Version 1.0.1)'. It includes a 'Tool Parameters' section with a dropdown menu set to 'Start with a fresh notebook'. Below this is the 'User inputs' section with a '+ Insert User inputs' button. The 'Additional Options' section contains two toggle switches: 'Email notification' (set to 'No') and 'Attempt to re-use jobs with identical parameters?' (set to 'No'). A red dashed circle highlights the 'Run Tool' button in the top right corner of the tool header. Another red dashed circle highlights the 'Run Tool' button at the bottom of the 'Additional Options' section. The right sidebar shows the 'History' section with a search bar and a message: 'This history is empty. You can load your own data or get data from an external source.'

Run the Tool

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

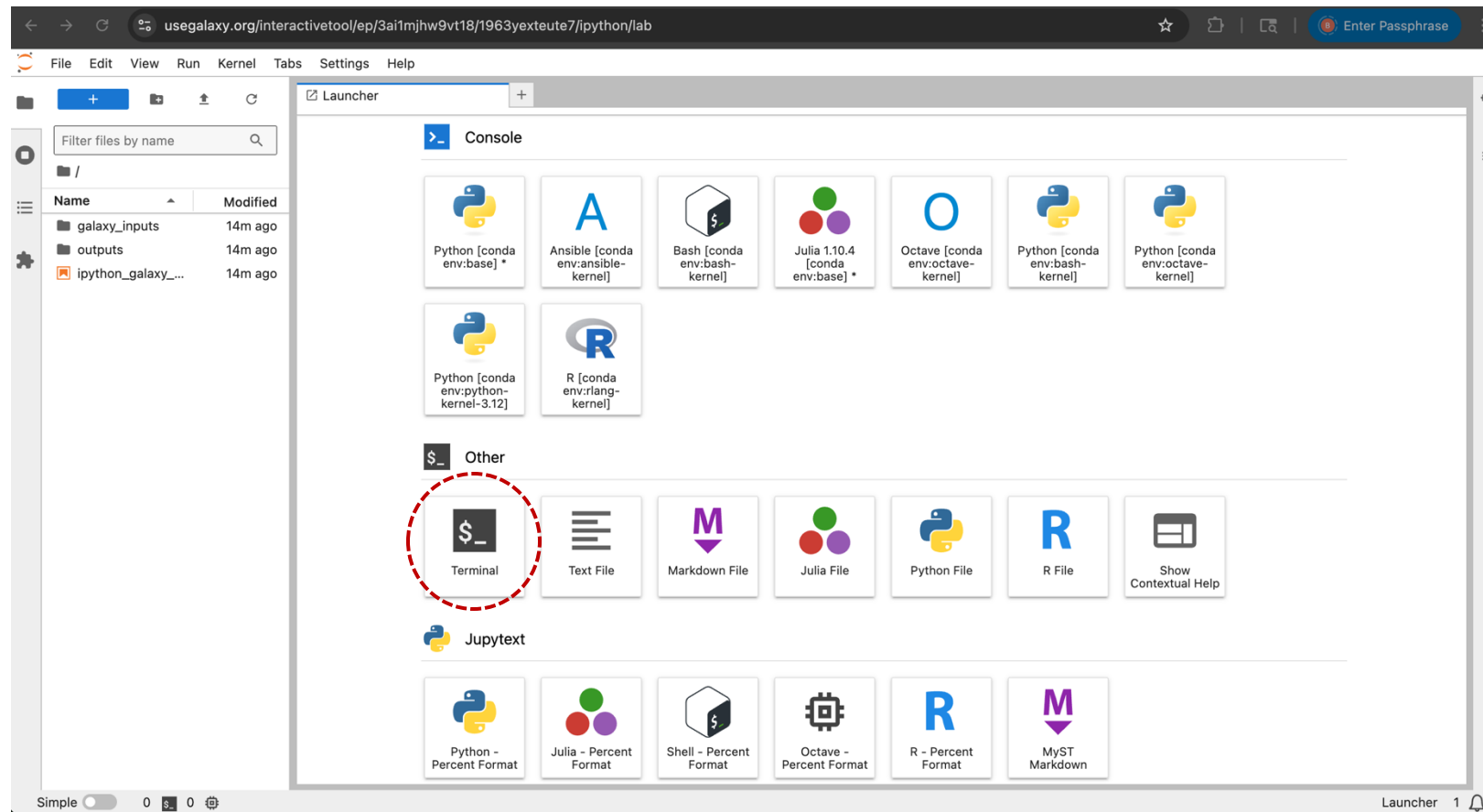
The screenshot displays the Galaxy web interface. On the left is a sidebar with navigation icons for Upload, Tools, Workflows, Workflow Invocations, Interactive Tools, Visualization, Histories, History Multiview, Datasets, and Notifications. The main panel is titled 'Interactive JupyterLab Notebook'. At the top of this panel, a blue notification bar states: 'There is an InteractiveTool result view available. [Open](#) [icon]'. Below this, a green success message reads: 'Started tool **Interactive JupyterLab Notebook** and successfully added 1 job to the queue. It produces 3 outputs:

- 2: Executed Jupyter Notebook
- 3: Interactive JupyterLab Notebook
- 1: Jupyter output collection

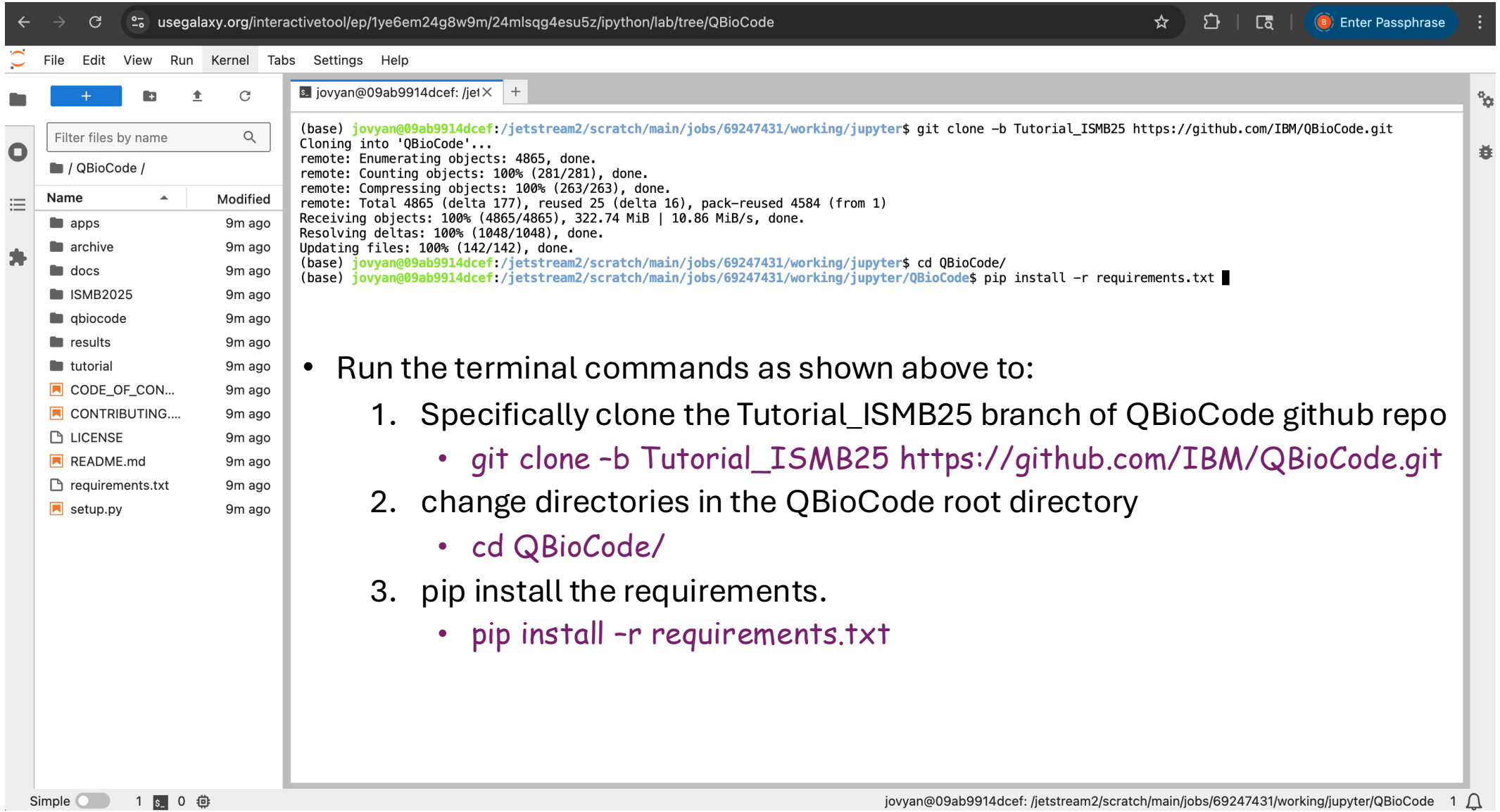
 You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered. Here is a link to the job: [bbd44e69cb8906b54d653ff160533355](#)'. On the right, the 'History' panel shows a search bar and a list of three items: '3: Interactive JupyterLab Notebook' (highlighted in orange), '2: Executed Jupyter Notebook' (highlighted in orange), and '1: Jupyter output collection' (highlighted in orange). The top of the interface shows the 'Galaxy' logo, user profile 'bryanraubenolt88', and storage usage 'Using 0% of 250.0 GB'.

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



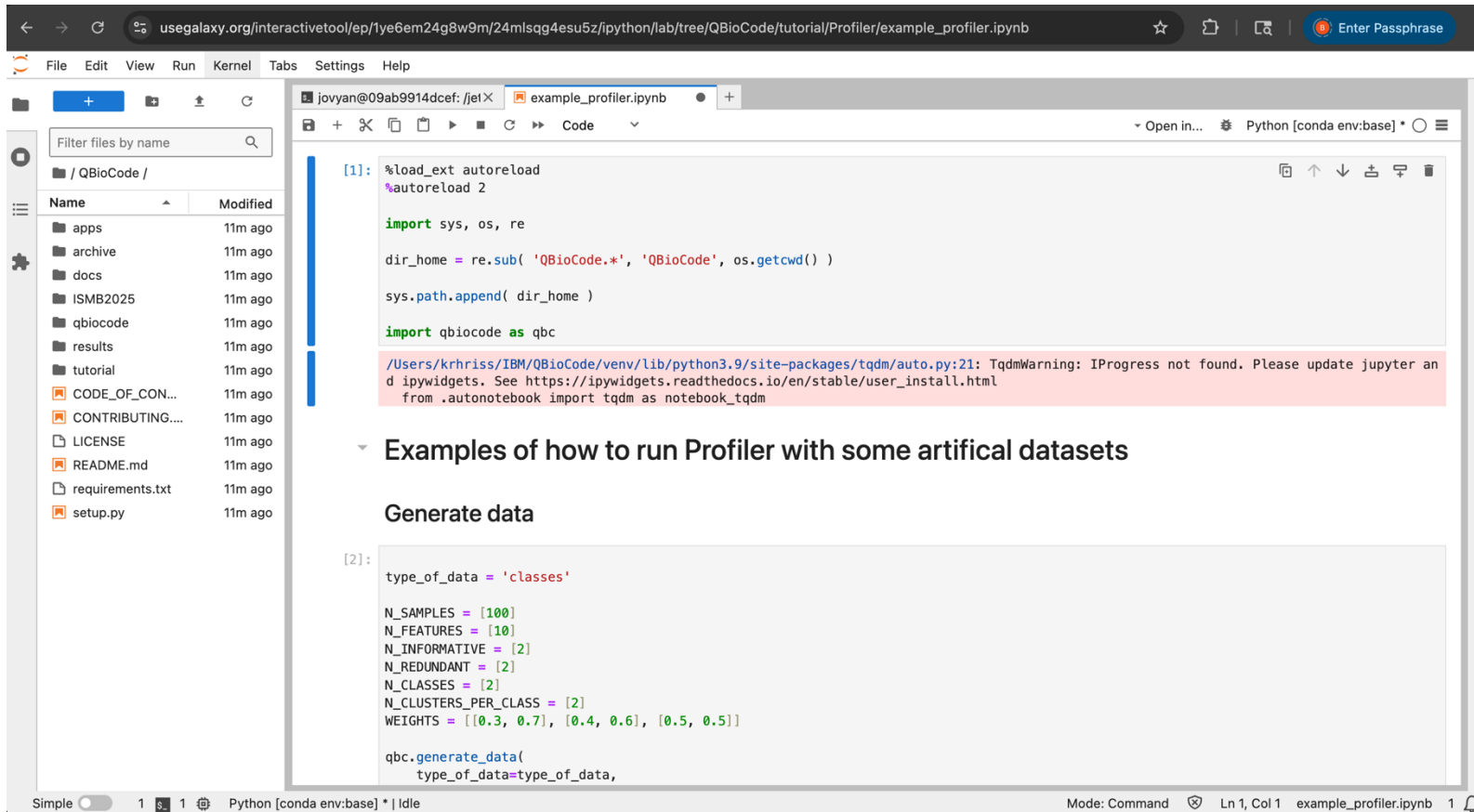
The screenshot displays the Galaxy web interface. On the left, a file browser shows a directory structure for 'QBioCode' with files like 'apps', 'archive', 'docs', 'ISMB2025', 'qbicode', 'results', 'tutorial', 'CODE_OF_CON...', 'CONTRIBUTING...', 'LICENSE', 'README.md', 'requirements.txt', and 'setup.py'. The main panel on the right is a terminal window with the following commands and output:

```
jovyan@09ab9914dcef: /jetX
(base) jovyan@09ab9914dcef:/jetstream2/scratch/main/jobs/69247431/working/jupyter$ git clone -b Tutorial_ISMB25 https://github.com/IBM/QBioCode.git
Cloning into 'QBioCode'...
remote: Enumerating objects: 4865, done.
remote: Counting objects: 100% (281/281), done.
remote: Compressing objects: 100% (263/263), done.
remote: Total 4865 (delta 177), reused 25 (delta 16), pack-reused 4584 (from 1)
Receiving objects: 100% (4865/4865), 322.74 MiB | 10.86 MiB/s, done.
Resolving deltas: 100% (1048/1048), done.
Updating files: 100% (142/142), done.
(base) jovyan@09ab9914dcef:/jetstream2/scratch/main/jobs/69247431/working/jupyter$ cd QBioCode/
(base) jovyan@09ab9914dcef:/jetstream2/scratch/main/jobs/69247431/working/jupyter/QBioCode$ pip install -r requirements.txt
```

- 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!



The screenshot displays the Galaxy web interface at `usegalaxy.org/interactivetool/ep/1ye6em24g8w9m/24mlsqg4esu5z/ipython/lab/tree/QBioCode/tutorial/Profiler/example_profiler.ipynb`. The interface includes a file explorer on the left showing the directory structure of the QBioCode tutorial, with files like `apps`, `archive`, `docs`, `ISMB2025`, `qbiocode`, `results`, `tutorial`, `CODE_OF_CON...`, `CONTRIBUTING...`, `LICENSE`, `README.md`, `requirements.txt`, and `setup.py`. The main area shows a Jupyter Notebook with the following code in the first cell:

```
[1]: %load_ext autoreload
      %autoreload 2

      import sys, os, re

      dir_home = re.sub( 'QBioCode.*', 'QBioCode', os.getcwd() )

      sys.path.append( dir_home )

      import qbiocode as qbc
```

A warning message is displayed below the code: `/Users/krhriss/IBM/QBioCode/venv/lib/python3.9/site-packages/tqdm/auto.py:21: TqdmWarning: IPProgress not found. Please update jupyter and ipywidgets. See https://ipywidgets.readthedocs.io/en/stable/user_install.html from .autonotebook import tqdm as notebook_tqdm`. The second cell contains the following code:

```
[2]: type_of_data = 'classes'

      N_SAMPLES = [100]
      N_FEATURES = [10]
      N_INFORMATIVE = [2]
      N_REDUNDANT = [2]
      N_CLASSES = [2]
      N_CLUSTERS_PER_CLASS = [2]
      WEIGHTS = [[0.3, 0.7], [0.4, 0.6], [0.5, 0.5]]

      qbc.generate_data(
          type_of_data=type_of_data,
```

The bottom status bar indicates the environment is `Python [conda env:base] * | Idle` and the mode is `Command`. The file `example_profiler.ipynb` is open at line 1, column 1.

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 usegalaxy.org and click on *Interactive Tools*.

The screenshot displays the Galaxy web interface. On the left sidebar, the 'Interactive Tools' icon is circled in red. The main panel shows the 'Interactive JupyterLab Notebook' tool interface. A notification banner at the top states: 'There is an InteractiveTool result view available, [Open](#). You may also access all active InteractiveTools from the **User menu**.' Below this, a green box with a checkmark indicates: 'Started tool **Interactive JupyterLab Notebook** and successfully added 1 job to the queue. It produces 3 outputs:

- 2: Executed Jupyter Notebook
- 3: Interactive JupyterLab Notebook
- 1: JupyterTool output collection

 You can check the status of queued jobs and view the resulting data by refreshing the History panel. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered. Here is a link to the job: [bbd44e69cb8906b54d653ff160533355](#)

 On the right, the 'History' panel shows a list of jobs: '3: Interactive JupyterLab Notebook', '2: Executed Jupyter Notebook', and '1: JupyterTool output collection'.

Reopening your session

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

The screenshot displays the Galaxy web interface. The top navigation bar shows the Galaxy logo, user profile (bryanraubenolt88), and storage usage (Using 0% of 250.0 GB). The left sidebar contains navigation icons for Upload, Tools, Workflows, Workflow Invocations, Interactive Tools (highlighted with a red circle), Visualization, Histories, History Multiview, Datasets, Notifications, and More.

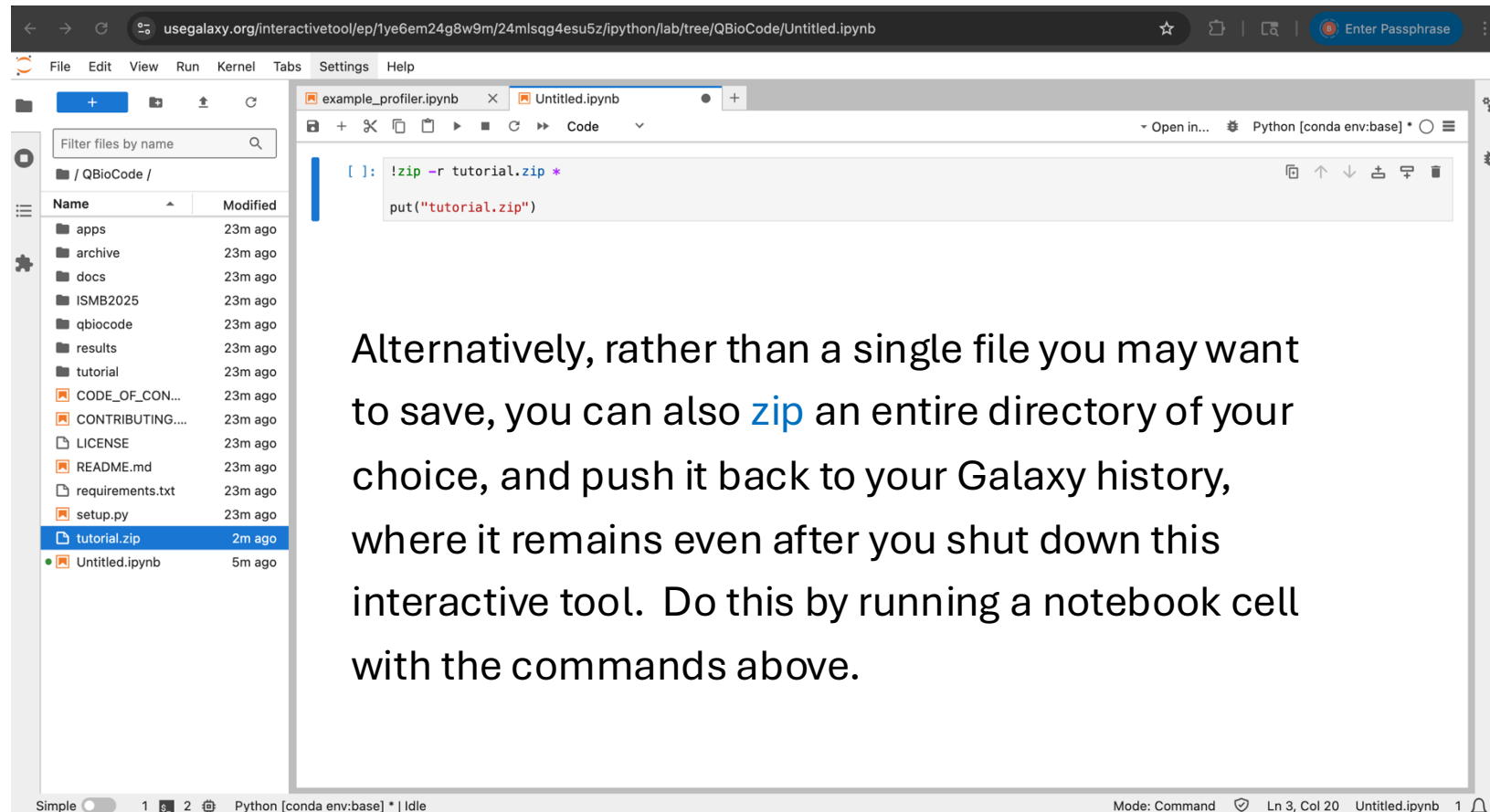
The main content area is divided into two panels. The left panel, titled 'Interactive Tools', lists various tools including 'Interactive JupyterLab Notebook', 'Panoply', 'Phinch Visualisation', 'Pavian', 'Qiskit Jupyter notebook', 'Interactive BlobToolKit', and 'Phylotree'. The right panel, titled 'Active Interactive Tools', displays a table of currently running tools.

Name	Job Info	Created	Last Updated
JupyTool interactive tool	Running	about 1 hour ago	about 1 hour ago

The right sidebar shows the 'History' section, listing previous sessions: '3: Interactive JupyterLab Notebook', '2: Executed JupyTool Notebook', and '1: JupyTool output collection'.

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")`



The screenshot displays the USeq Galaxy interactive tool interface. On the left, a file browser shows a directory structure under '/QBioCode/'. The files listed include 'apps', 'archive', 'docs', 'ISMB2025', 'qbiocode', 'results', 'tutorial', 'CODE_OF_CON...', 'CONTRIBUTING...', 'LICENSE', 'README.md', 'requirements.txt', 'setup.py', 'tutorial.zip' (highlighted), and 'Untitled.ipynb'. The 'tutorial.zip' file is highlighted in blue. On the right, a JupyterLab notebook is open, showing a code cell with the following commands:

```
[ ]: !zip -r tutorial.zip *  
put("tutorial.zip")
```

Below the code cell, the text "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." is displayed.

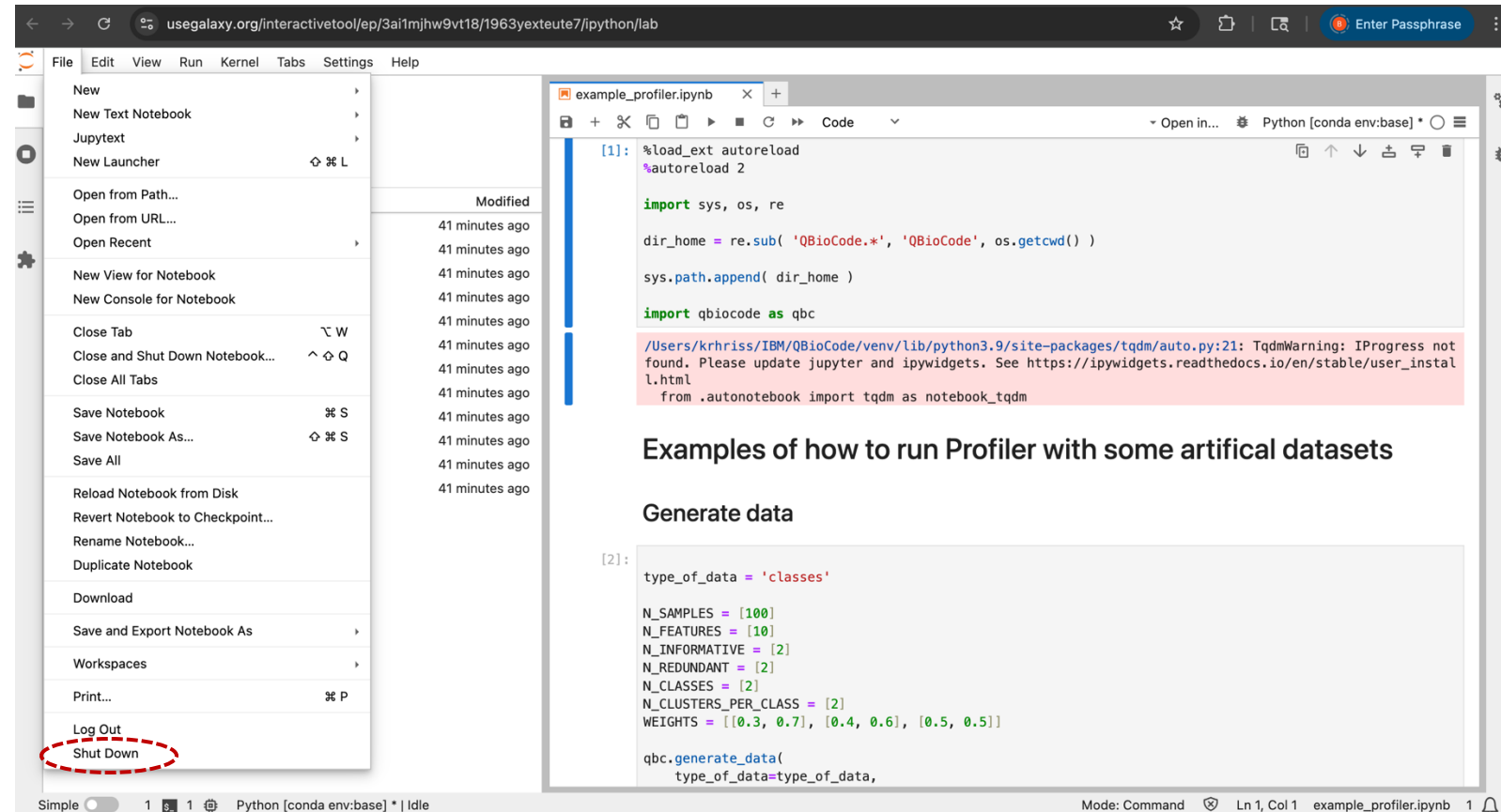
Saving your files

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

The screenshot displays the Galaxy web interface at `usegalaxy.org/jobs/submission/success`. The left sidebar contains navigation links for Upload, Tools, Workflows, Workflow Invocations, Interactive Tools, Visualization, Histories, History Multiview, Datasets, Notifications, and More. The main panel shows a success message: "Started tool **Interactive JupyterLab Notebook** and successfully added 1 job to the queue." It lists three outputs: "6: Executed Jupyter Notebook", "7: Interactive JupyterLab Notebook", and "8: Jupyter output collection". A job link is provided: `bbd44e69cb8906b5a584cb37fe744a87`. The right sidebar shows the History panel with a search bar and a list of datasets. The dataset "8: tutorial.zip" is highlighted with a red dashed circle, indicating it is the file saved to the history.

Shutting down your tool

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



The screenshot shows the JupyterLab interface in a web browser. The 'File' menu is open, and the 'Shut Down' option is highlighted with a red dashed circle. The notebook 'example_profiler.ipynb' is open, showing code for generating artificial datasets. The status bar at the bottom indicates 'Python [conda env:base] * | Idle'.

```
[1]: %load_ext autoreload
      %autoreload 2

      import sys, os, re

      dir_home = re.sub( 'QBioCode.*', 'QBioCode', os.getcwd() )

      sys.path.append( dir_home )

      import qbiocode as qbc

/Users/krhriiss/IBM/QBioCode/venv/lib/python3.9/site-packages/tqdm/auto.py:21: TqdmWarning: IPProgress not found. Please update jupyter and ipywidgets. See https://ipywidgets.readthedocs.io/en/stable/user_install.html
from .autonotebook import tqdm as notebook_tqdm

Examples of how to run Profiler with some artificial datasets

Generate data

[2]: type_of_data = 'classes'

      N_SAMPLES = [100]
      N_FEATURES = [10]
      N_INFORMATIVE = [2]
      N_REDUNDANT = [2]
      N_CLASSES = [2]
      N_CLUSTERS_PER_CLASS = [2]
      WEIGHTS = [[0.3, 0.7], [0.4, 0.6], [0.5, 0.5]]

      qbc.generate_data(
          type_of_data=type_of_data,
```

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!

The screenshot displays the Galaxy 25.0 web interface. On the left is a sidebar with navigation icons for Upload, Tools, Workflows, Workflow Invocations, Interactive Tools, Visualization, Histories, History Multiview, Datasets, Notifications, and More. The main panel shows a list of tools under the heading 'All Tools', with categories like 'GENERAL TEXT TOOLS' and 'GENOMIC FILE MANIPULATION'. A 'History' panel on the right shows a list of datasets, including '3: Interactive JupyterLab Notebook', '2: Executed Jupyter Notebook', and '1: JupyterTool output collection'. A large overlay window titled 'Galaxy 25.0: Improved Workflow Run' is centered on the screen. It contains text explaining that Galaxy is an open-source platform for data-intensive biomedical research and provides instructions on how to rerun a workflow. The overlay also features a 'History' section with a search bar and a list of datasets. At the bottom of the overlay, there is a 'Donate to the James P. Taylor Foundation for Open Science' link and the Galaxy version information: 'Galaxy version 25.0.2.dev0, commit 4bbc6ee438b5c032d8aa9078ac1cb48fa2543479'.

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Galaxy 25.0: Improved Workflow Run

Given a prior workflow run, want to rerun the workflow with the exact same parameters?

Click the "Rerun" button in the invocation view

See the workflow form populated with the original inputs!

... and many more workflow run improvements in the latest release!

Upload data and create collections right from the run form!

Donate to the James P. Taylor Foundation for Open Science

Galaxy version 25.0.2.dev0, commit 4bbc6ee438b5c032d8aa9078ac1cb48fa2543479

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>