Unlocking the Microbial Mysteries in Children with Special Needs: A High School Journey Through the Gut

Grades 9 – 12 Edition

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Background and Introduction.

Autism spectrum disorder is a developmental disability caused by differences in the brain. This causes people to have restricted behavior, problems with communication/paying attention or even physical learning challenges. There are a wide range of conditions that affect 1 in 44 children today. Autism symptoms, especially with more advanced cases, appear around the ages of 12-14 months or earlier.

Objectives.

- Identifying taxonomic differences between healthy patients and individuals with autism spectrum disorder using publicly available datasets and bioinformatics tools
- Understanding the implications of gut microbes in human health
- Developing education modules that can be disseminated into schools to promote STEM.

Student Background Knowledge.

Part I. Domains of life. The three domains of life are Archaea, Bacteria and Eukarya. Members of the domain Bacteria are unicellular and prokaryotic. This domain corresponds to the kingdom Eubacteria. Microbiome is a collection of all microbes, both commensal and pathogenic, that live in and on human bodies. A very well studied microbiome is the gut microbiome. Other examples are skin, oral, uro-genital, etc.

Part II. Gut microbiota- definition, function and autism.

These are the type of microbiota that live in the digestive tracts of vertebrates and invertebrates. It refers to microbes and bacterial species that live in your body- they help with digestion, destroy harmful bacteria and helps control the immune system. Microbes can be both helpful and potentially harmful. Most of them have symbiotic relationships with the human body where they both benefit while a few are pathogenic which spread/carry disease.

Benefits to having microbiota:

- Stimulate the immune system, meaning they aid in the breakdown of food compounds and synthesize certain vitamins and amino acids.
- Smaller compounds like table sugar and lactose can be absorbed quickly in the small intestine, microbiota help break down larger particles such as complex carbohydrates and starch with their digestive enzymes.

An imbalance of unhealthy and healthy gut microbiota can contribute to weight gain, high blood sugar, high cholesterol, and neuro-developmental conditions.

Many studies suggest gut microbes influence many neurological disorders, for example, autism. It has been found that patients with autism do not have a healthy gut. There is mounting evidence suggesting pathways between gut bacteria and the central nervous system, referred to as the gut–brain axis, which a profound effect on social behaviors.

Part III. DNA Sequencing.

Sequencing DNA means determining the order of the four chemical building blocks - called "bases" - that make up the DNA molecule. The sequence tells scientists the kind of genetic information that is carried in a particular DNA segment. For example, scientists can use sequence information to determine which stretches of DNA contain genes and which stretches carry regulatory instructions, turning genes on or off. In addition, and importantly, sequence data can highlight changes in a gene that may cause disease.

In the DNA double helix, the four chemical bases always bond with the same partner to form "base pairs." Adenine (A) always pairs with thymine (T); cytosine (C) always pairs with guanine (G). This pairing is the basis for the mechanism by which DNA molecules are copied when cells divide, and the pairing also underlies the methods by which most DNA sequencing experiments are done. The human genome contains about 3 billion base pairs that spell out the instructions for making and maintaining a human being.

Part IV. 16S rRNA Sequencing.

16S rRNA gene is used as a marker for identification and taxonomic classification of microbes. Since this gene is ubiquitous and highly conserved among bacteria as well as archaea, it is popularly used for phylogenetic studies.

The 16S rRNA gene consists of both conserved and variable regions. While the conserved region makes amplification possible through PCR, sequencing the variable regions allows distinction between different microorganisms such as bacteria and archaea.

Conserved- present in everything - not studied.
Hypervariable region- part that is studied.
Primers - enable you to read through hypervariable regions- present in both directions.

Part VI. Gut Microbiome and Autism Spectrum Disorder.

Research into the relationship between the gut microbiome and autism spectrum disorder (ASD) is an emerging and evolving field. While there is no conclusive evidence that links gut microbiota directly to the development of ASD, there is growing interest in understanding the potential connections between the two. Here are some key points and findings regarding the gut microbiome and ASD:

1. Gut-Brain Axis: The gut-brain axis is a bi-directional communication system between the gut and the brain. Emerging research suggests that the composition of the gut microbiota may influence brain function and behavior. Alterations in the gut microbiome could potentially impact neurological and behavioral development, which is relevant to ASD.

2. Microbiome Composition: Some studies have found differences in the gut microbiota of individuals with ASD compared to neurotypical individuals. These differences often involve changes in the relative abundance of certain bacterial species. However, these findings are not consistent across all studies, and there is a need for more research to establish clear patterns.

3. Potential Mechanisms: Several potential mechanisms have been proposed to explain how gut microbiota might influence ASD. These include the production of metabolites (such as shortchain fatty acids) that can affect the central nervous system, the modulation of the immune system, and the influence on the production of neurotransmitters.

4. Immune System: The gut microbiome plays a crucial role in the development and maintenance of the immune system. Dysregulation of the immune system has been observed in some individuals with ASD, and there is evidence to suggest that the gut microbiota can influence immune function.

5. Clinical Implications: While the link between gut microbiota and ASD is still not fully understood, some researchers and clinicians have explored potential dietary and probiotic interventions to modulate the gut microbiome as a complementary approach to managing certain symptoms of ASD. However, the effectiveness of these interventions remains a subject of ongoing investigation.

6. Limitations: It's essential to recognize that the research on the gut microbiome and ASD is in its early stages. Many studies are small and may have methodological limitations, making it challenging to draw definitive conclusions. In summary, there is growing interest in the potential role of the gut microbiome in ASD. While some research suggests there may be associations between gut microbiota composition and ASD, more extensive and rigorous studies are needed to establish the nature and mechanisms of this relationship.

Vocabulary

Microbiome: The collective term for all microorganisms, including bacteria, viruses, fungi, and archaea, that inhabit a particular environment.

Gut Microbiome: The gut microbiome refers to the community of microorganisms, including bacteria, viruses, fungi, and other microorganisms, that inhabit the human gastrointestinal tract.

ASD: Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition that affects an individual's social interaction, communication, behavior, and sensory processing. It is called a "spectrum disorder" because it encompasses a wide range of symptoms and severity levels, meaning that no two individuals with ASD are exactly alike. The term "spectrum" acknowledges that the condition can manifest differently in each person.

16S rRNA sequencing: A common technique used to analyze the microbial composition in a sample by targeting and sequencing a specific region of the 16S ribosomal RNA gene, which is highly conserved in bacteria and archaea. It helps identify and classify bacterial species.

Microbiome profiling: The process of characterizing and quantifying the composition of the microbiome in each sample.

Taxonomy: The classification of microorganisms into hierarchical categories, such as phylum, class, order, family, genus, and species.

Bioinformatics: Bioinformatics is an interdisciplinary field that merges computers and biology in order to analyze large datasets (such as DNA sequences) to discover new, biologically important knowledge.

Materials Checklist

Access to a laptop or desktop computer.
Access to datasets
Galaxy online server

Classroom Management

Overview.

Students are given the pdf document and required to read. Understand what gut microbiome is in the context of autism and why studying differences in microbial composition is important.

Pre-class preparation.

Ensure there is internet access for the activity along with limited storage on computer. If computers are limited, students can work in groups.

In-class activity

Go through activity step-by-step. Look at data and answer questions that follow post bioinformatics analysis.

References

Chiappori, Federica, Francesca Anna Cupaioli, Arianna Consiglio, Noemi Di Nanni, Ettore Mosca, Vito Flavio Licciulli, and Alessandra Mezzelani. "Analysis of Faecal Microbiota and Small ncRNAs in Autism: Detection of miRNAs and piRNAs with Possible Implications in Host–Gut Microbiota Cross-Talk." Nutrients 14, no. 7 (2022): 1340.

Xu, YuShuang, YiHua Wang, JinShuang Xu, Yu Song, BingQiang Liu, and ZhiFan Xiong. "Leveraging existing 16SrRNA microbial data to define a composite biomarker for autism spectrum disorder." Microbiology Spectrum 10, no. 4 (2022): e00331-22.

Questions

1) What do the different colors in the bar plots mean?

2) What are the differences (microbial composition) between healthy patients and compromised patient samples?

3) Describe what is on the x and y axis?

4) In addition to autism cvan you list other factor that influence gut microbiome?

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Tutorial Instructions created by Trisha Raichura, Dubai College, Dubai, UAE.

We will be using https://cancer.usegalaxy.org/ online web server to perform our analysis.

We will be using the following dataset.

CONTROL	AUTISM SPECTRUM DISORDER (ASD)
SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz	SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz
SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz	SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz
SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz	SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz
SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz	SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz
SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz	SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz
SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz	SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz

The files are approximately 2 MB in size. The data was part of the project published in the following study, Xu, Y., Wang, Y., Xu, J., Song, Y., Liu, B., & Xiong, Z. (2022). Leveraging existing 16SrRNA microbial data to define a composite biomarker for autism spectrum disorder. Microbiology Spectrum, 10(4), e00331-22. The authors made the data publicly in NCBI under Bioproject ID PRJNA813424.

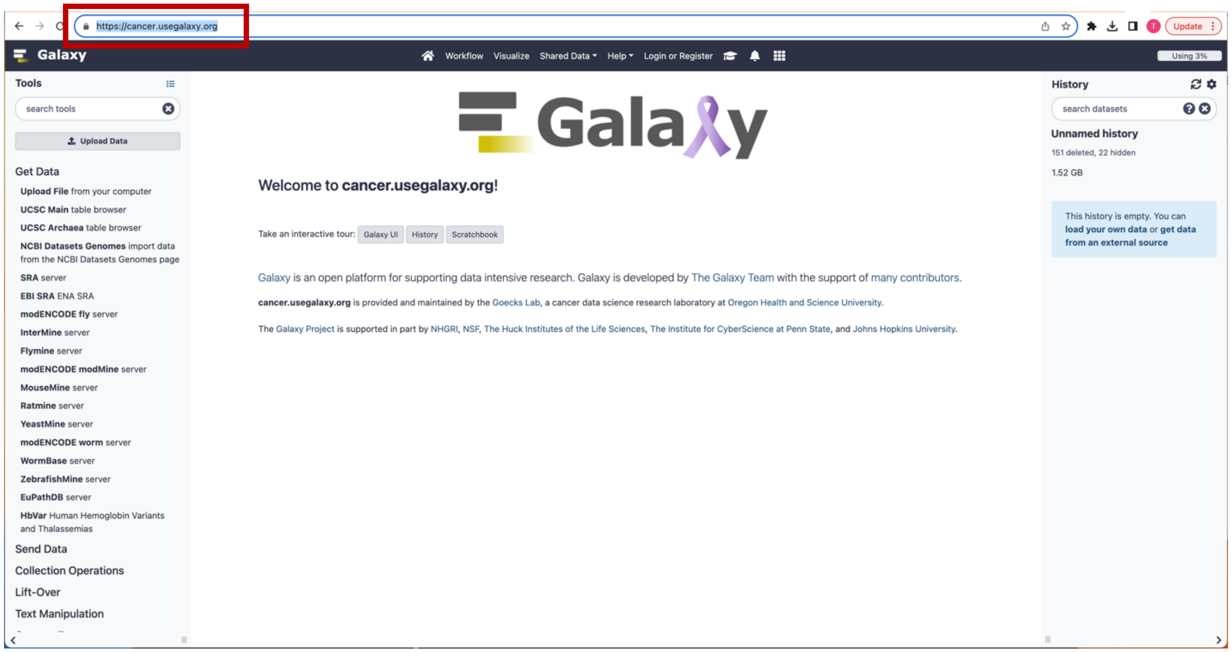
Data will be made available through google folder for students and teachers for downloading it onto their local machine before starting the analysis.

QIIME2 (https://qiime2.org/) will be used for exploring the bacterial diversity in the control versus ASD samples. QIIME2 is a collection several commands and we will using a subset of these commands, listed below for analysis.

QIIME2 Commands:

```
qiime2 tools import
qiime2 dada2 denoise-single
qiime2 feature-classifier classify-sklearn
qiime2 metadata tabulate
qiime2 feature-table tabulate-seqs
qiime2 feature-table filter-samples
qiime2 taxa bar-plot
```

STEP 1: Use a browser preferably latest version of google chrome to access https://cancer.usegalaxy.org/



Welcome to **cancer.usegalaxy.org!**

Take an interactive tour:

Galaxy is an open platform for supporting data intensive research. Galaxy is developed by The Galaxy Team with the support of many contributors.

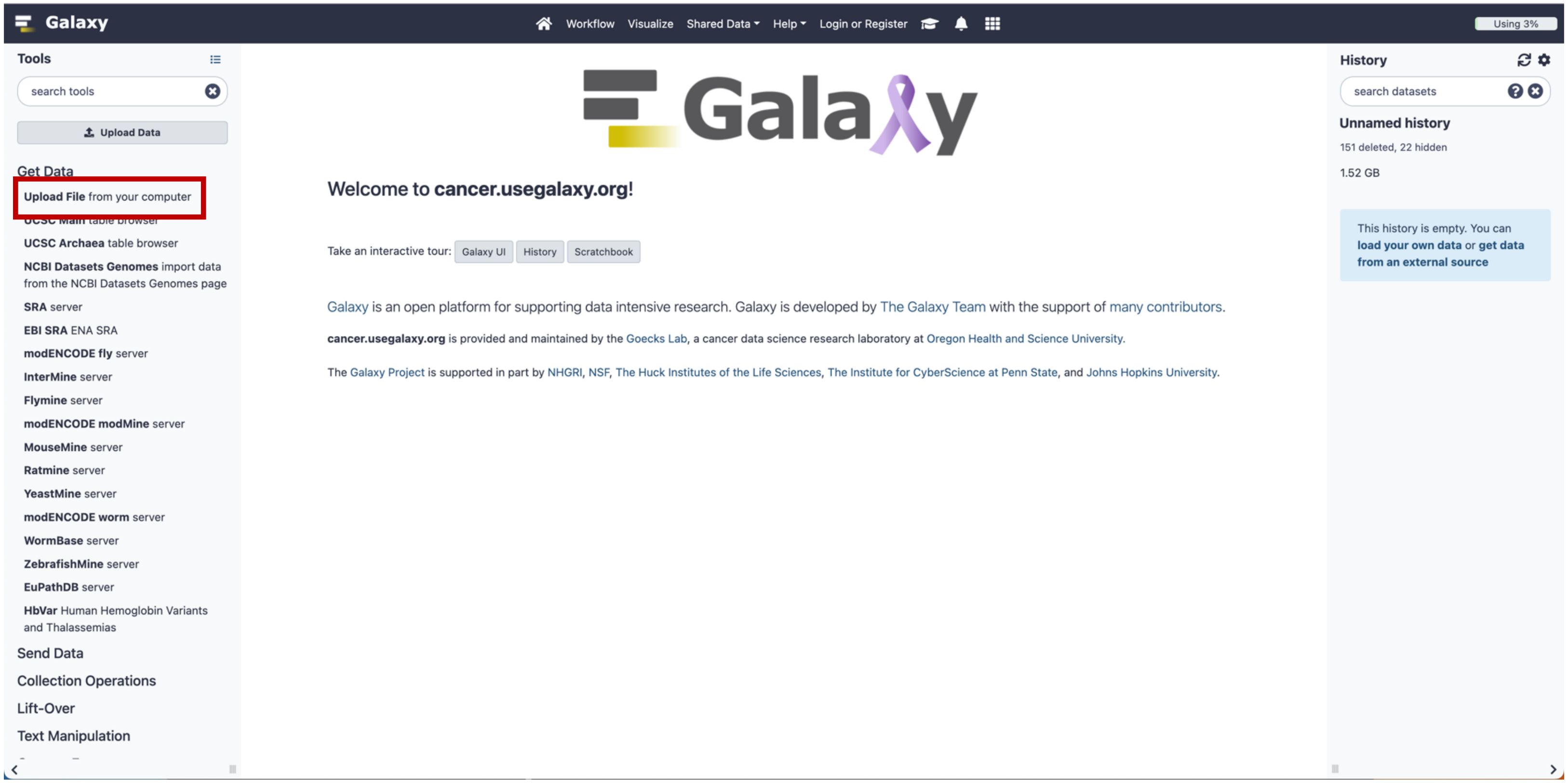
cancer.usegalaxy.org is provided and maintained by the Goecks Lab, a cancer data science research laboratory at Oregon Health and Science University.

The Galaxy Project is supported in part by NHGRI, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Johns Hopkins University.

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

Screenshot 1

STEP 2: Use “Upload File from your computer” option to load compressed FASTQ files of all the samples.



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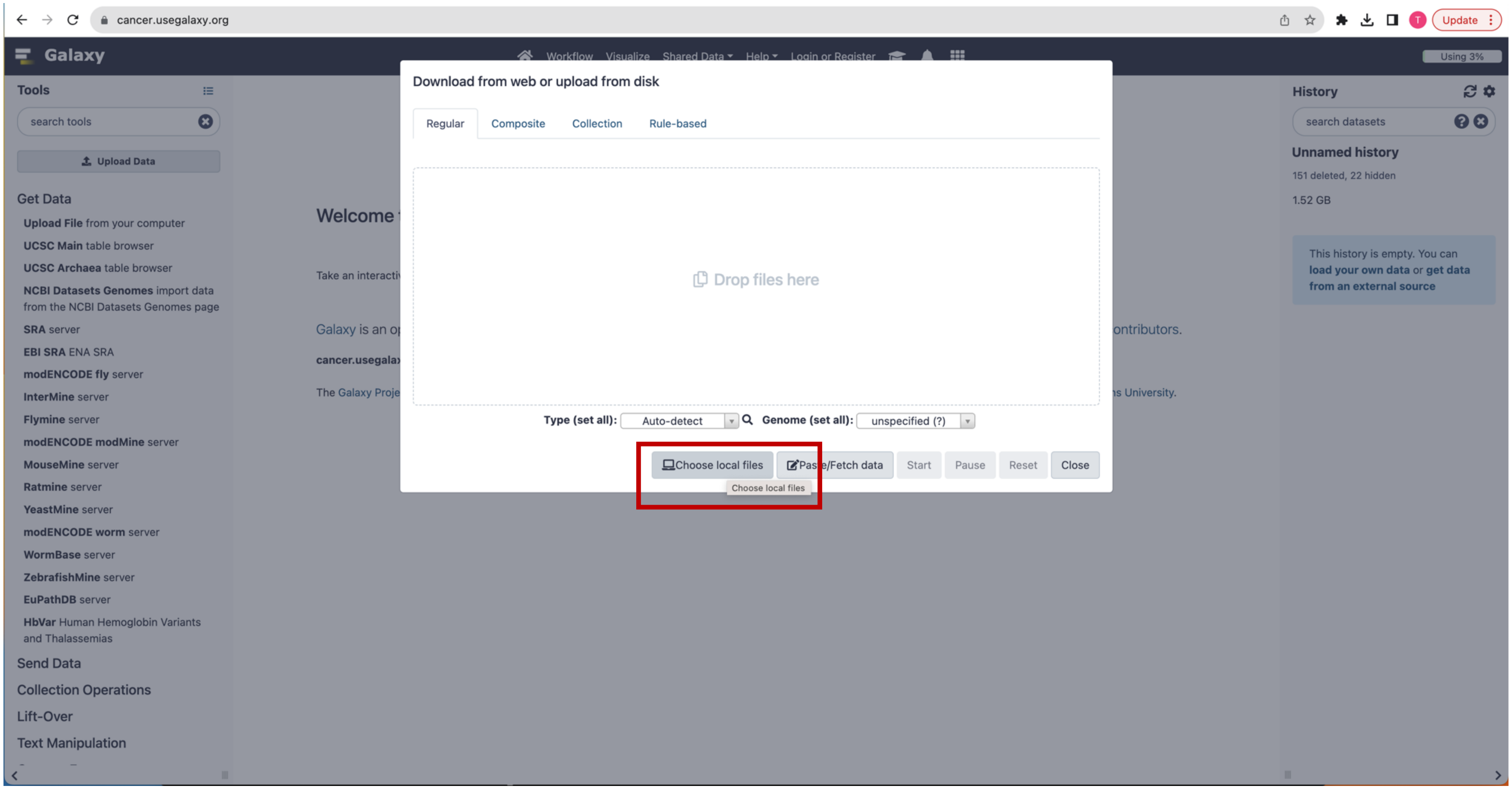
This history is empty. You can **load your own data** or **get data from an external source**

Screenshot 2

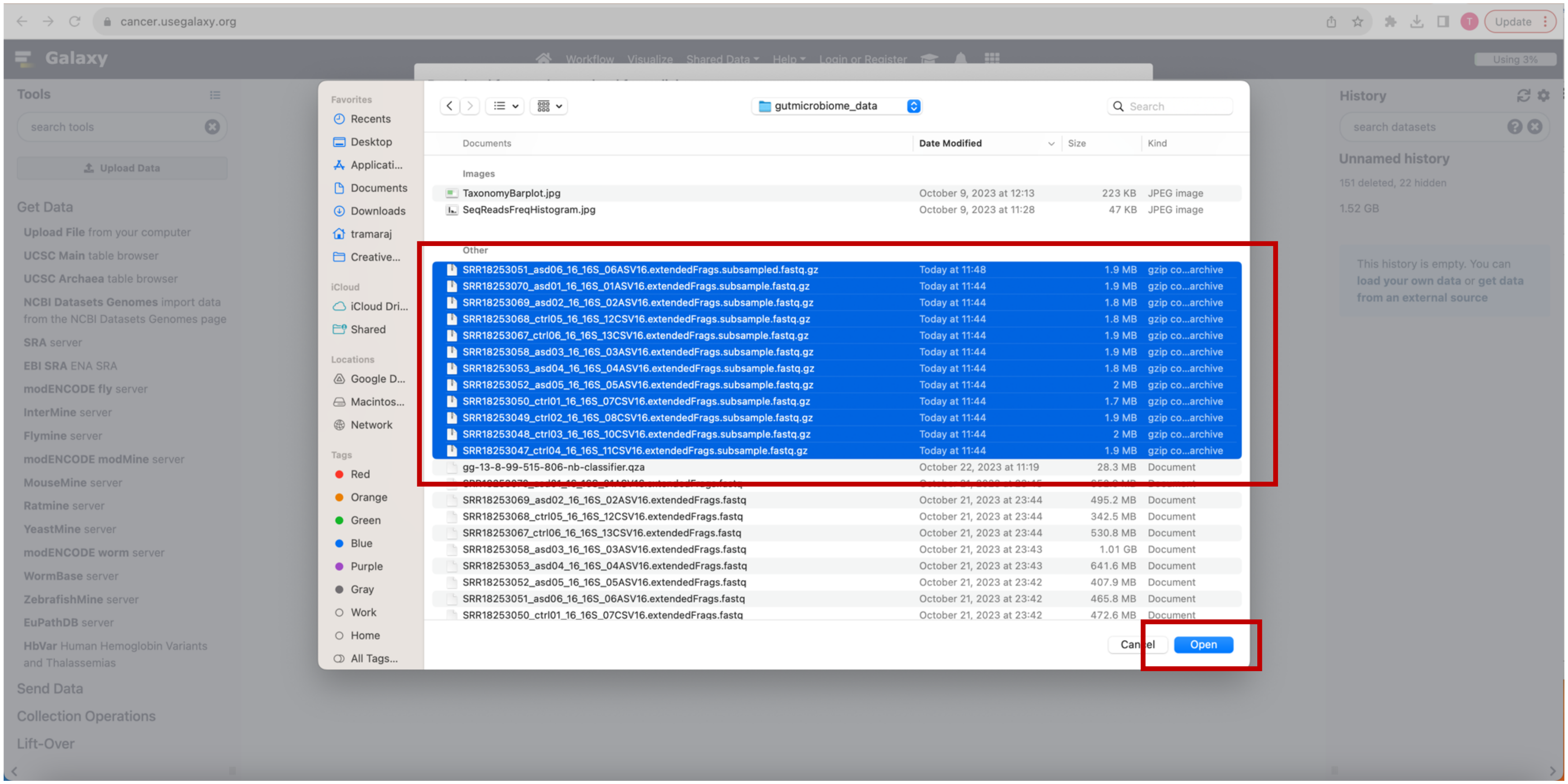
STEP3: Click “Choose local files” option to upload files from your computer.



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

Screenshot 3

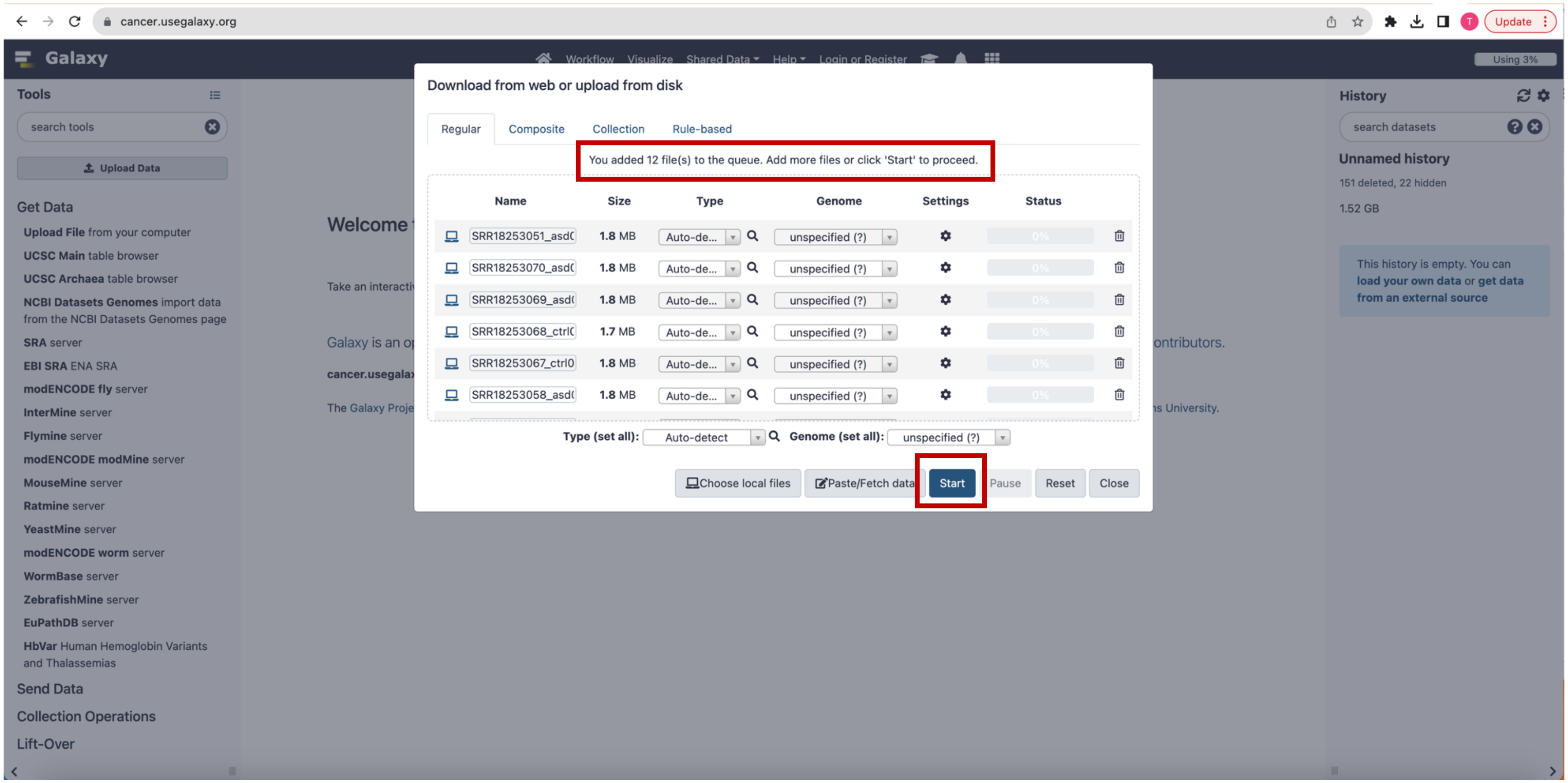
<u>STEP 4:</u> Go to appropriate folder and load required files for analysis by selecting all the files and clicking “Open”.



Documents	Date Modified	Size	Kind
Images			
TaxonomyBarplot.jpg	October 9, 2023 at 12:13	223 KB	JPEG image
SeqReadsFreqHistogram.jpg	October 9, 2023 at 11:28	47 KB	JPEG image
Other			
SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz	Today at 11:48	1.9 MB	gzip co...archive
SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.9 MB	gzip co...archive
SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.8 MB	gzip co...archive
SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.8 MB	gzip co...archive
SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.9 MB	gzip co...archive
SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.9 MB	gzip co...archive
SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.8 MB	gzip co...archive
SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz	Today at 11:44	2 MB	gzip co...archive
SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.7 MB	gzip co...archive
SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.9 MB	gzip co...archive
SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	2 MB	gzip co...archive
SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz	Today at 11:44	1.9 MB	gzip co...archive
gg-13-8-99-515-806-nb-classifier.qza	October 22, 2023 at 11:19	28.3 MB	Document
SRR18253070_asd01_16_16S_01ASV16.extendedFrags.fastq	October 21, 2023 at 23:45	[illegible]	Document
SRR18253069_asd02_16_16S_02ASV16.extendedFrags.fastq	October 21, 2023 at 23:44	495.2 MB	Document
SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.fastq	October 21, 2023 at 23:44	342.5 MB	Document
SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.fastq	October 21, 2023 at 23:44	530.8 MB	Document
SRR18253058_asd03_16_16S_03ASV16.extendedFrags.fastq	October 21, 2023 at 23:43	1.01 GB	Document
SRR18253053_asd04_16_16S_04ASV16.extendedFrags.fastq	October 21, 2023 at 23:43	641.6 MB	Document
SRR18253052_asd05_16_16S_05ASV16.extendedFrags.fastq	October 21, 2023 at 23:42	407.9 MB	Document
SRR18253051_asd06_16_16S_06ASV16.extendedFrags.fastq	October 21, 2023 at 23:42	465.8 MB	Document
SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.fastq	October 21, 2023 at 23:42	472.6 MB	Document

Screenshot 4

STEP 5: You should be able to see all the added files. Click “Start” to proceed with uploading the files onto the server.



Download from web or upload from disk

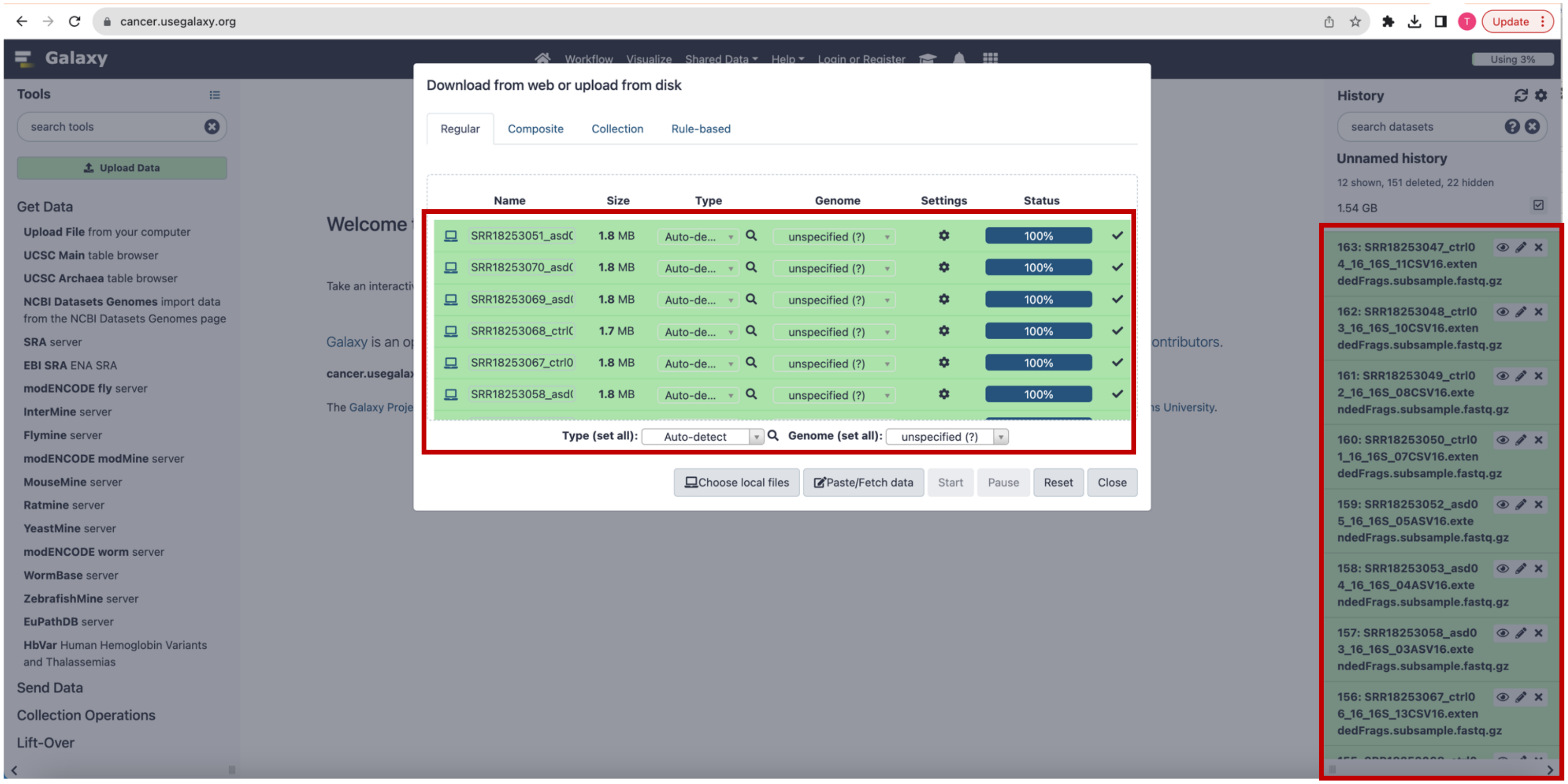
You added 12 file(s) to the queue. Add more files or click 'Start' to proceed.

Name	Size	Type	Genome	Settings	Status
SRR18253051_asd	1.8 MB	Auto-de...	unspecified (?)	⚙	0%
SRR18253070_asd	1.8 MB	Auto-de...	unspecified (?)	⚙	0%
SRR18253069_asd	1.8 MB	Auto-de...	unspecified (?)	⚙	0%
SRR18253068_ctrl	1.7 MB	Auto-de...	unspecified (?)	⚙	0%
SRR18253067_ctrl0	1.8 MB	Auto-de...	unspecified (?)	⚙	0%
SRR18253058_asd	1.8 MB	Auto-de...	unspecified (?)	⚙	0%

Type (set all): Auto-detect **Genome (set all):** unspecified (?)

Screenshot 5

STEP 6: We should see the status to be 100% for all the files and the files should be visible in the history (left hand side)



Download from web or upload from disk

Name	Size	Type	Genome	Settings	Status
SRR18253051_asd(	1.8 MB	Auto-de...	unspecified (?)	⚙	100% ✓
SRR18253070_asd(	1.8 MB	Auto-de...	unspecified (?)	⚙	100% ✓
SRR18253069_asd(	1.8 MB	Auto-de...	unspecified (?)	⚙	100% ✓
SRR18253068_ctrl(	1.7 MB	Auto-de...	unspecified (?)	⚙	100% ✓
SRR18253067_ctrl0	1.8 MB	Auto-de...	unspecified (?)	⚙	100% ✓
SRR18253058_asd(	1.8 MB	Auto-de...	unspecified (?)	⚙	100% ✓

Type (set all): Auto-detect Genome (set all): unspecified (?)

Unnamed history

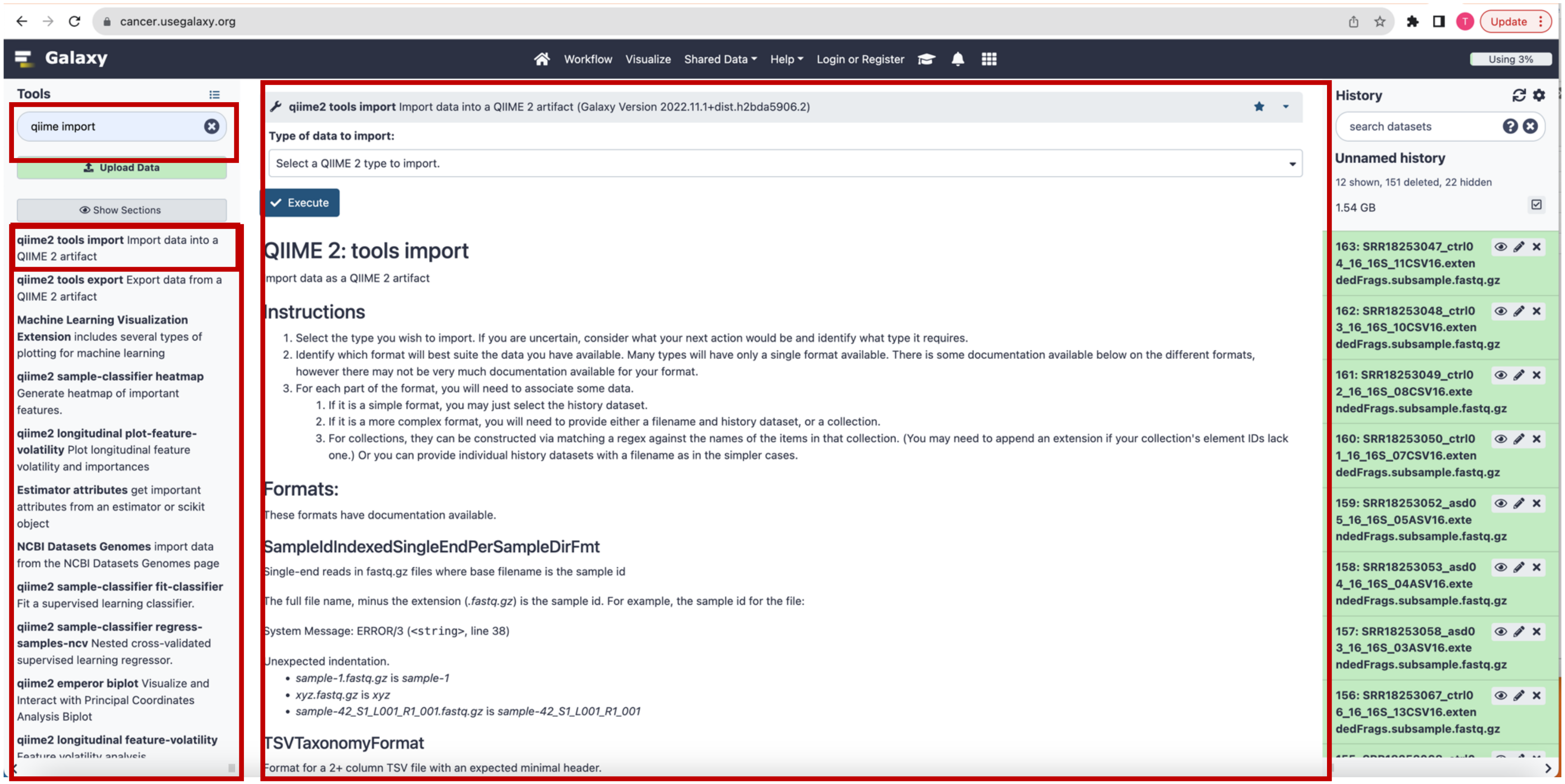
12 shown, 151 deleted, 22 hidden

1.54 GB

- 163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz
- 162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz
- 161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz
- 160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz
- 159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz
- 158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz
- 157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz
- 156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz

Screenshot 6

STEP 7: At this point we have all the files ready to be analyzed. Starting from this step we will be executing QIIME2 steps to investigate the gut microbiome community. To run QIIME2 the uploaded compressed FASTQ files should be imported as a QIIME2 artifact. To accomplish this, we will run the "qiime tools import" command. Using the search bar under "Tools" on the left-hand side type "qiime import" and hit "return" to complete search. You should be able to see the search results displayed on the left-hand side as well. From the search results select "qiime2 tools import Import data into a QIIME 2 artifact"



qiime2 tools import Import data into a QIIME 2 artifact

qiime2 tools export Export data from a QIIME 2 artifact

Machine Learning Visualization Extension includes several types of plotting for machine learning

qiime2 sample-classifier heatmap Generate heatmap of important features.

qiime2 longitudinal plot-feature-volatility Plot longitudinal feature volatility and importances

Estimator attributes get important attributes from an estimator or scikit object

NCBI Datasets Genomes import data from the NCBI Datasets Genomes page

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier regress-samples-ncv Nested cross-validated supervised learning regressor.

qiime2 emperor biplot Visualize and Interact with Principal Coordinates Analysis Biplot

qiime2 longitudinal feature-volatility Feature volatility analysis

qiime2 tools import Import data into a QIIME 2 artifact (Galaxy Version 2022.11.1+dist.h2bda5906.2)

Type of data to import: Select a QIIME 2 type to import.

QIIME 2: tools import

mport data as a QIIME 2 artifact

Instructions

1. Select the type you wish to import. If you are uncertain, consider what your next action would be and identify what type it requires.
2. Identify which format will best suite the data you have available. Many types will have only a single format available. There is some documentation available below on the different formats, however there may not be very much documentation available for your format.
3. For each part of the format, you will need to associate some data.
    1. If it is a simple format, you may just select the history dataset.
    2. If it is a more complex format, you will need to provide either a filename and history dataset, or a collection.
    3. For collections, they can be constructed via matching a regex against the names of the items in that collection. (You may need to append an extension if your collection's element IDs lack one.) Or you can provide individual history datasets with a filename as in the simpler cases.

Formats:

These formats have documentation available.

SampleIdIndexedSingleEndPerSampleDirFmt

Single-end reads in fastq.gz files where base filename is the sample id

The full file name, minus the extension (*.fastq.gz*) is the sample id. For example, the sample id for the file:

System Message: ERROR/3 (`<string>`, line 38)

Unexpected indentation.

- *sample-1.fastq.gz* is *sample-1*
- *xyz.fastq.gz* is *xyz*
- *sample-42_S1_L001_R1_001.fastq.gz* is *sample-42_S1_L001_R1_001*

TSVTaxonomyFormat

Format for a 2+ column TSV file with an expected minimal header.

Unnamed history

12 shown, 151 deleted, 22 hidden

1.54 GB

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz

160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz

159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz

158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz

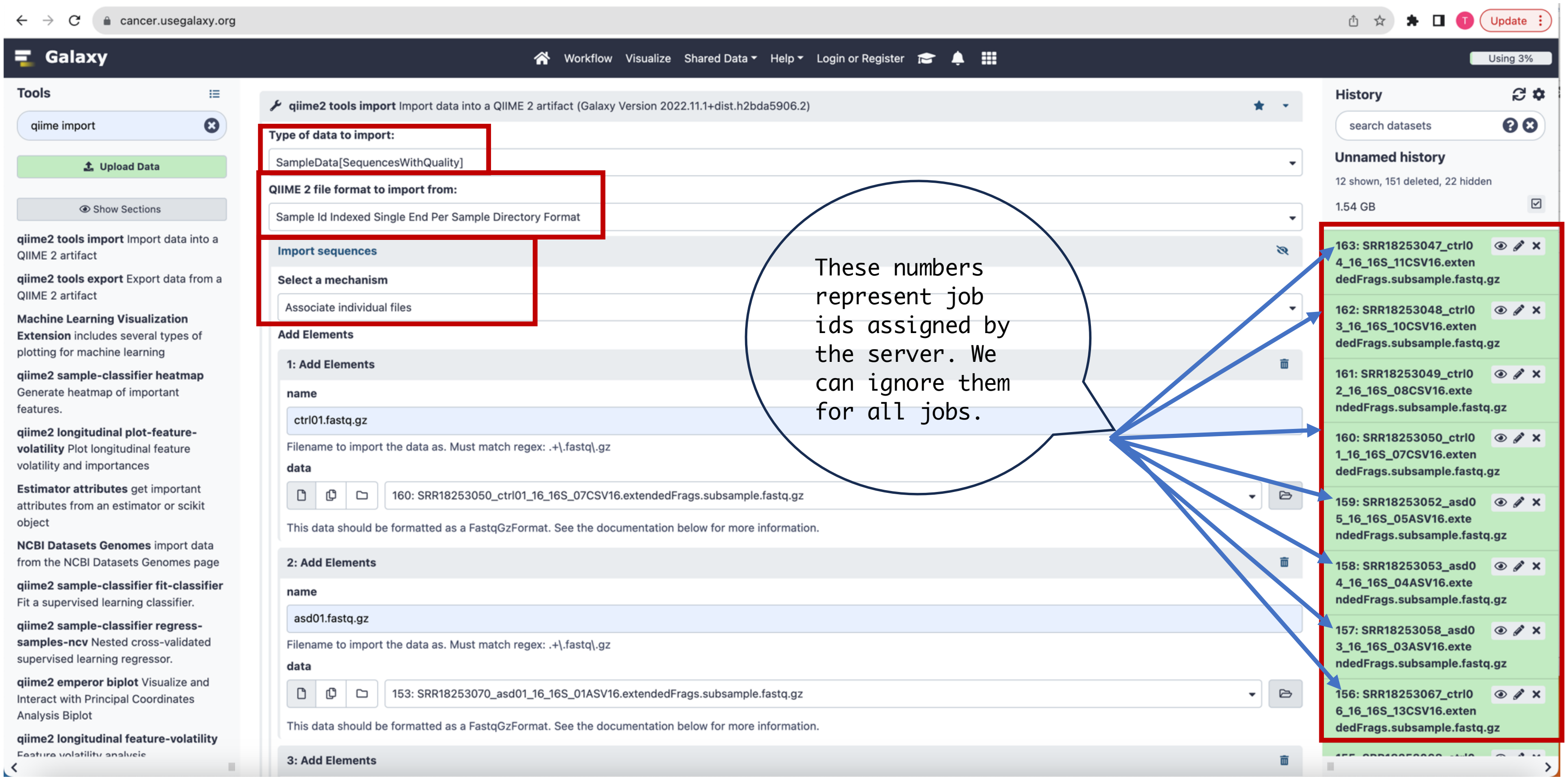
157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz

156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz

Screenshot 7

STEP 8: Here we will input required parameters for “qiime2 tools import”.

- FOR “Type of data to import:” SELECT “SampleData[SequencesWithQuality]
- FOR “QIIME 2 file format to import from:” SELECT “Sample Id Indexed Single End Per Sample Directory Format”.
- UNDER “Import sequences” FOR “Select a mechanism” SELECT “Associate Individual Files”.
- UNDER “Import sequences” FOR “Add Elements” you will add 12 elements for this analysis, 6 control (ctrl) samples and 6 autism spectrum disorder (asd) samples.
- For each element you will be providing a name for instance first element FOR “name” is assigned “ctrl01.fastq.gz” and SELECT “SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz” from the list.
- Screenshots 8 – 11 illustrates how to input all the parameters and hit “Execute”.
- Screenshot 12 - “qiime2 tools import” job has been submitted and is being executed. We can see that 12 files are being used as input and we will get file as output representing qiime2 artifact file which will be used for further downstream analysis.



qiime2 tools import Import data into a QIIME 2 artifact

qiime2 tools export Export data from a QIIME 2 artifact

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qiime2 emperor biplot Visualize and Interact with Principal Coordinates Analysis Biplot

qiime2 longitudinal feature-volatility Feature volatility analysis

qiime2 tools import Import data into a QIIME 2 artifact (Galaxy Version 2022.11.1+dist.h2bda5906.2)

Type of data to import: SampleData[SequencesWithQuality]

QIIME 2 file format to import from: Sample Id Indexed Single End Per Sample Directory Format

Import sequences

Select a mechanism: Associate individual files

Add Elements

1: Add Elements

name: ctrl01.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data: 160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

2: Add Elements

name: asd01.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data: 153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

3: Add Elements

Unnamed history

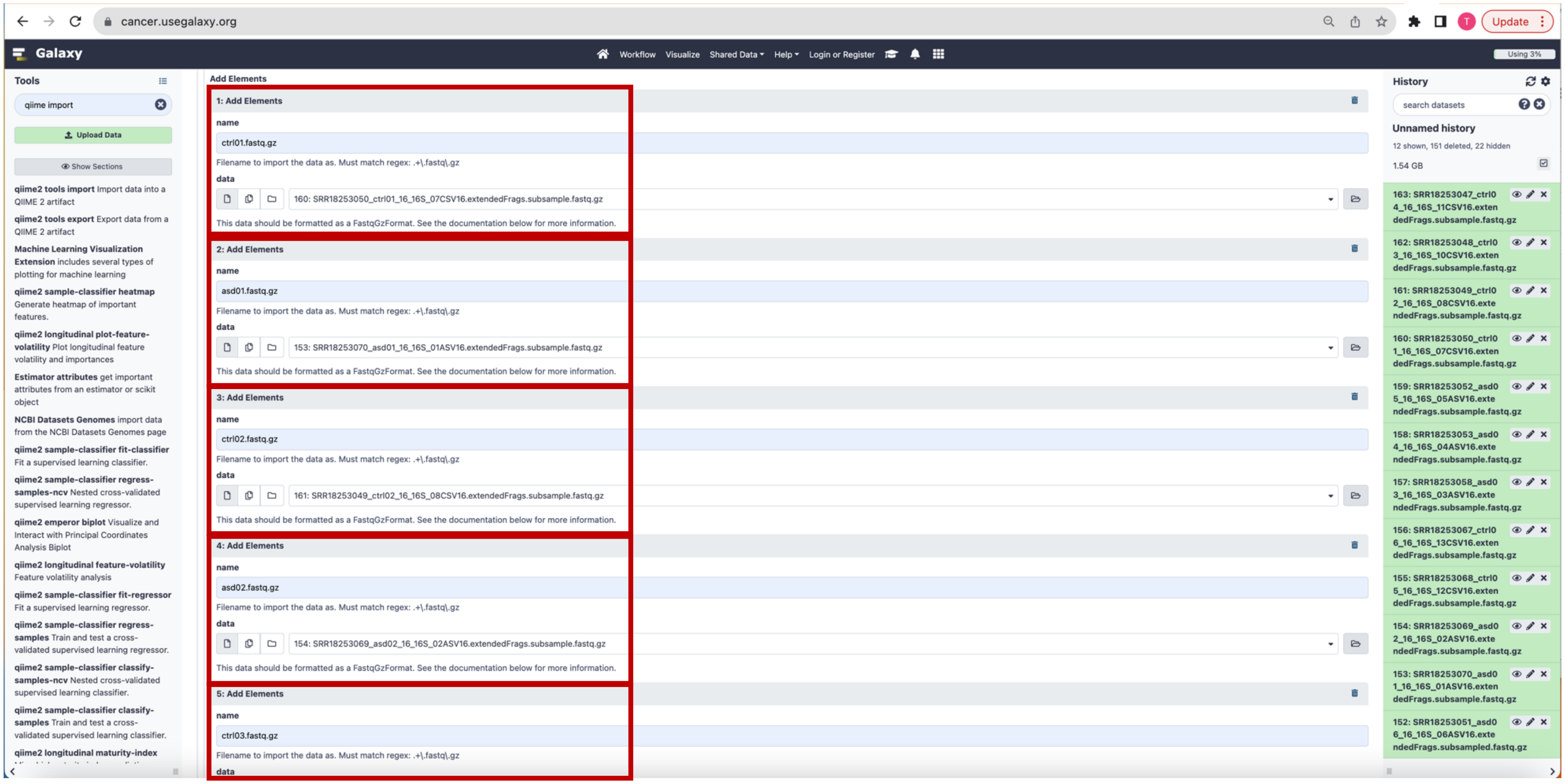
12 shown, 151 deleted, 22 hidden

1.54 GB

- 163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz
- 162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz
- 161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz
- 160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz
- 159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz
- 158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz
- 157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz
- 156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz

These numbers represent job ids assigned by the server. We can ignore them for all jobs.

Screenshot 8



Add Elements

1: Add Elements

name
ctrl01.fastq.gz
Filename to import the data as. Must match regex: .+\.fastq\.gz
data
160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz
This data should be formatted as a FastqGzFormat. See the documentation below for more information.

2: Add Elements

name
asd01.fastq.gz
Filename to import the data as. Must match regex: .+\.fastq\.gz
data
153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz
This data should be formatted as a FastqGzFormat. See the documentation below for more information.

3: Add Elements

name
ctrl02.fastq.gz
Filename to import the data as. Must match regex: .+\.fastq\.gz
data
161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz
This data should be formatted as a FastqGzFormat. See the documentation below for more information.

4: Add Elements

name
asd02.fastq.gz
Filename to import the data as. Must match regex: .+\.fastq\.gz
data
154: SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz
This data should be formatted as a FastqGzFormat. See the documentation below for more information.

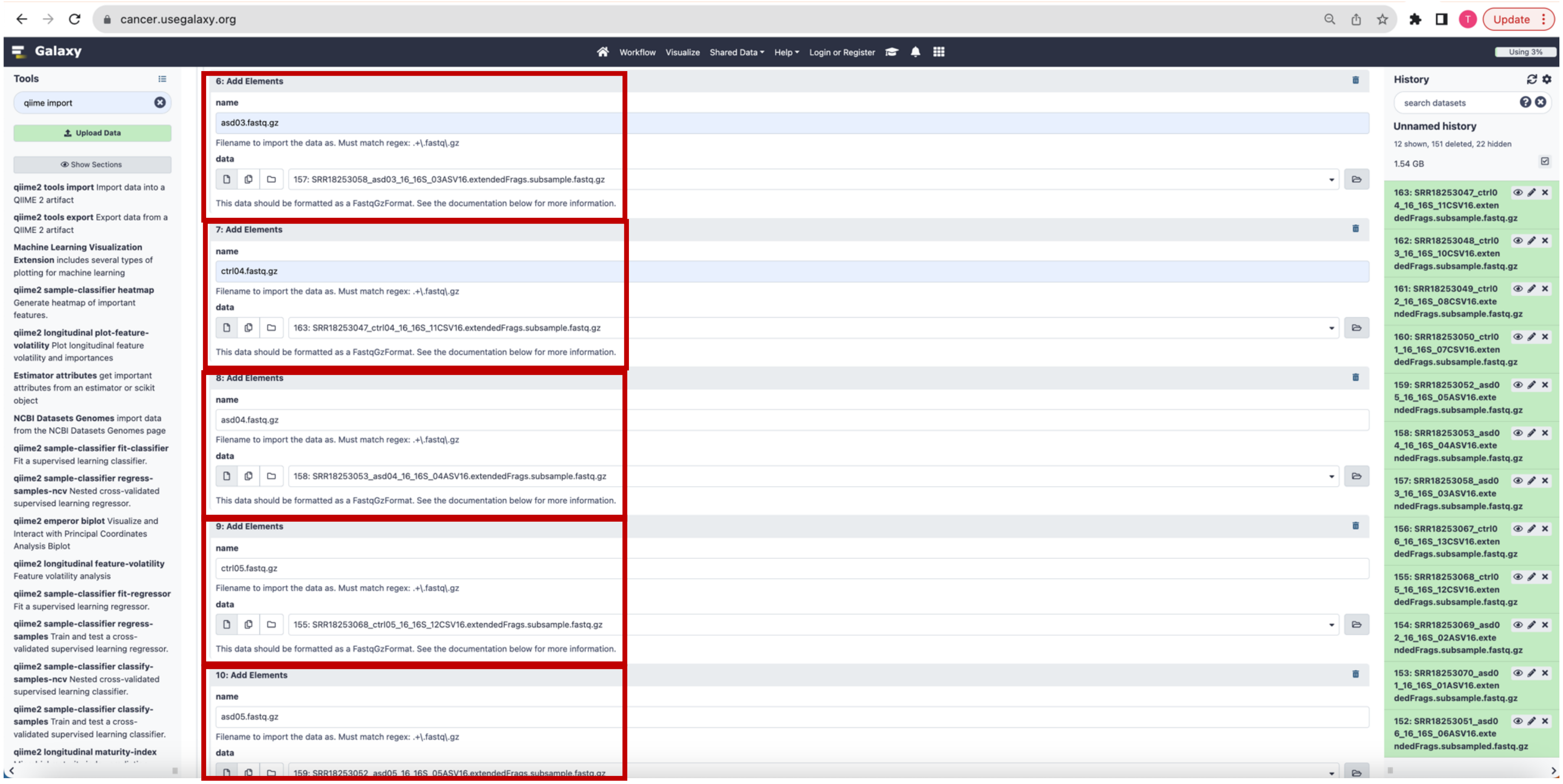
5: Add Elements

name
ctrl03.fastq.gz
Filename to import the data as. Must match regex: .+\.fastq\.gz
data

Unnamed history
12 shown, 151 deleted, 22 hidden
1.54 GB

- 163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz
- 162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz
- 161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz
- 160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz
- 159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz
- 158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz
- 157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz
- 156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz
- 155: SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz
- 154: SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz
- 153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz
- 152: SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz

Screenshot 9



qiime2 tools import Import data into a QIIME 2 artifact

qiime2 tools export Export data from a QIIME 2 artifact

Machine Learning Visualization Extension includes several types of plotting for machine learning

qiime2 sample-classifier heatmap Generate heatmap of important features.

qiime2 longitudinal plot-feature-volatility Plot longitudinal feature volatility and importances

Estimator attributes get important attributes from an estimator or scikit object

NCBI Datasets Genomes import data from the NCBI Datasets Genomes page

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier regress-samples-ncv Nested cross-validated supervised learning regressor.

qiime2 emperor biplot Visualize and Interact with Principal Coordinates Analysis Biplot

qiime2 longitudinal feature-volatility Feature volatility analysis

qiime2 sample-classifier fit-regressor Fit a supervised learning regressor.

qiime2 sample-classifier regress-samples Train and test a cross-validated supervised learning regressor.

qiime2 sample-classifier classify-samples-ncv Nested cross-validated supervised learning classifier.

qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 longitudinal maturity-index

6: Add Elements

name

asd03.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

7: Add Elements

name

ctrl04.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

8: Add Elements

name

asd04.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

9: Add Elements

name

ctrl05.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

155: SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

10: Add Elements

name

asd05.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz

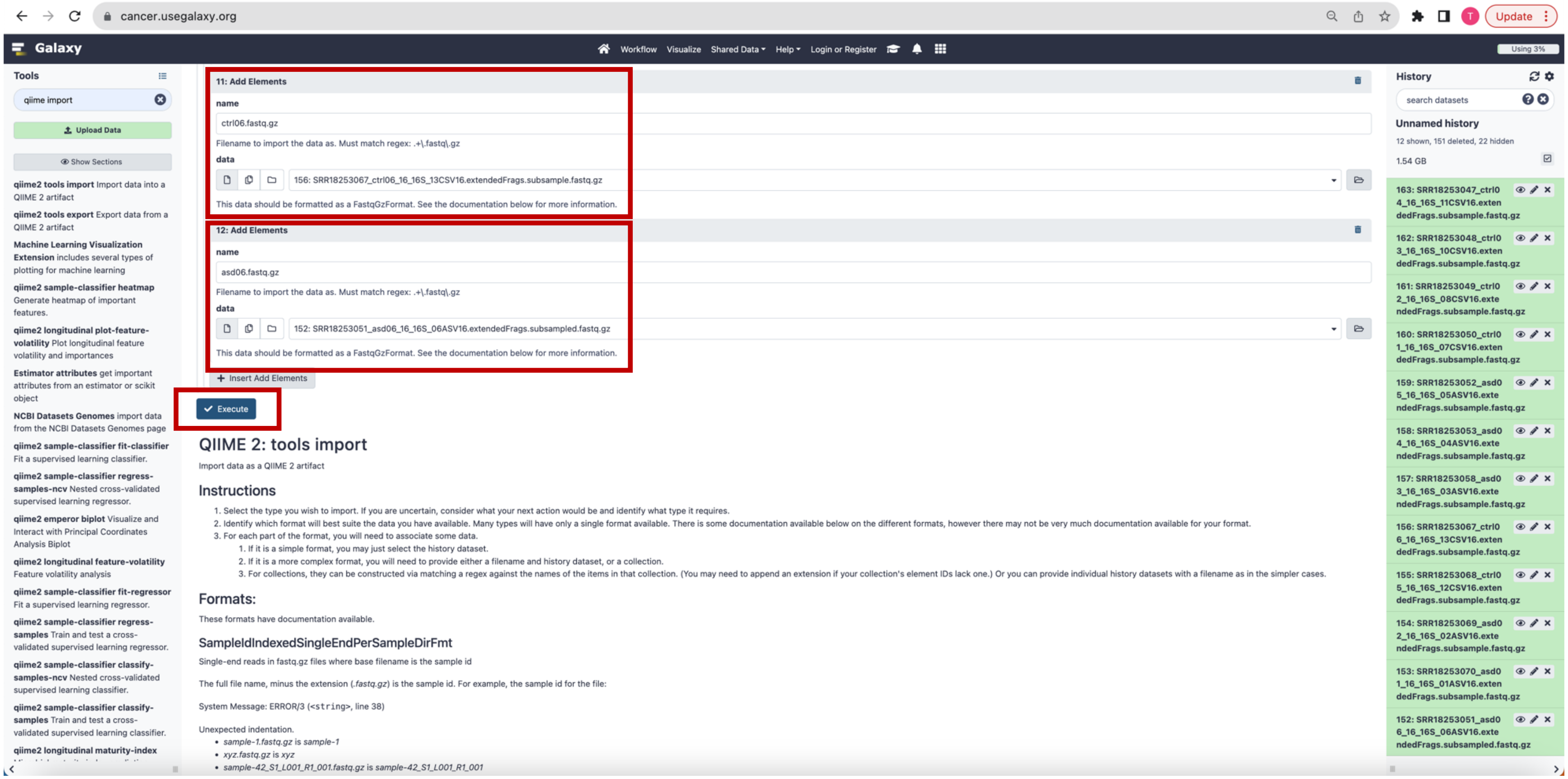
Unnamed history

12 shown, 151 deleted, 22 hidden

1.54 GB

- 163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz
- 162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz
- 161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz
- 160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz
- 159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz
- 158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz
- 157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz
- 156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz
- 155: SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz
- 154: SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz
- 153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz
- 152: SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz

Screenshot 10



11: Add Elements

name

ctrl06.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

12: Add Elements

name

asd06.fastq.gz

Filename to import the data as. Must match regex: .+\.fastq\.gz

data

152: SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz

This data should be formatted as a FastqGzFormat. See the documentation below for more information.

QIIME 2: tools import

Import data as a QIIME 2 artifact

Instructions

1. Select the type you wish to import. If you are uncertain, consider what your next action would be and identify what type it requires.
2. Identify which format will best suite the data you have available. Many types will have only a single format available. There is some documentation available below on the different formats, however there may not be very much documentation available for your format.
3. For each part of the format, you will need to associate some data.
    1. If it is a simple format, you may just select the history dataset.
    2. If it is a more complex format, you will need to provide either a filename and history dataset, or a collection.
    3. For collections, they can be constructed via matching a regex against the names of the items in that collection. (You may need to append an extension if your collection's element IDs lack one.) Or you can provide individual history datasets with a filename as in the simpler cases.

Formats:

These formats have documentation available.

SampleIdIndexedSingleEndPerSampleDirFmt

Single-end reads in fastq.gz files where base filename is the sample id

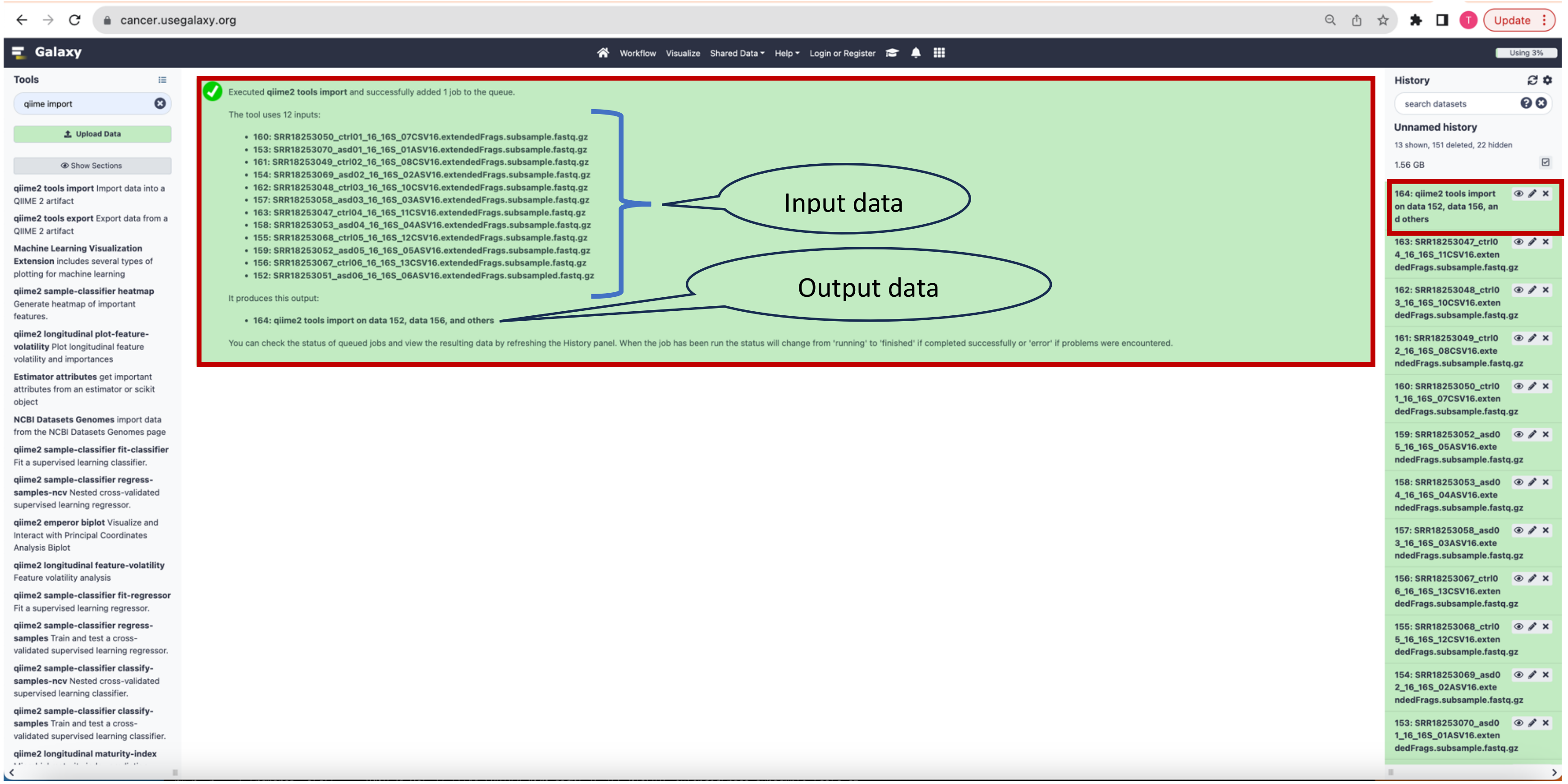
The full file name, minus the extension (*.fastq.gz*) is the sample id. For example, the sample id for the file:

System Message: ERROR/3 (`<string>`, line 38)

Unexpected indentation.

- *sample-1.fastq.gz* is *sample-1*
- *xyz.fastq.gz* is *xyz*
- *sample-42_S1_L001_R1_001.fastq.gz* is *sample-42_S1_L001_R1_001*

Screenshot 11



Executed **qiime2 tools import** and successfully added 1 job to the queue.

The tool uses 12 inputs:

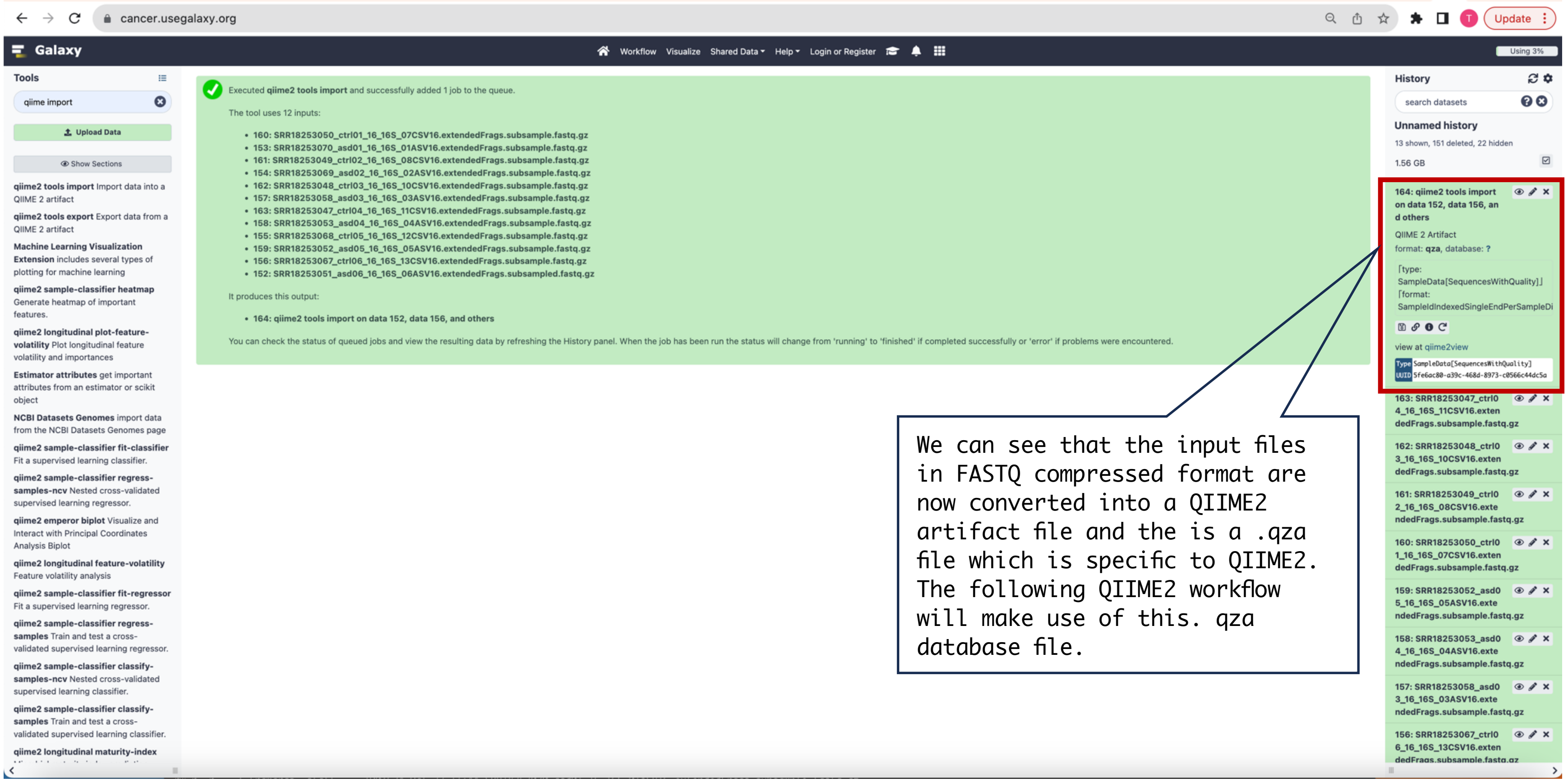
- **160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz**
- **153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz**
- **161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz**
- **154: SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz**
- **162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz**
- **157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz**
- **163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz**
- **158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz**
- **155: SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz**
- **159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz**
- **156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz**
- **152: SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz**

It produces this output:

- **164: qiime2 tools import on data 152, data 156, and others**

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.

Screenshot 12



Executed **qiime2 tools import** and successfully added 1 job to the queue.

The tool uses 12 inputs:

- **160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz**
- **153: SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz**
- **161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz**
- **154: SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz**
- **162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz**
- **157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz**
- **163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz**
- **158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz**
- **155: SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz**
- **159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz**
- **156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz**
- **152: SRR18253051_asd06_16_16S_06ASV16.extendedFrags.subsampled.fastq.gz**

It produces this output:

- **164: qiime2 tools import on data 152, data 156, and others**

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.

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: ?

⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz

160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz

159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz

158: SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz

157: SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz

156: SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz

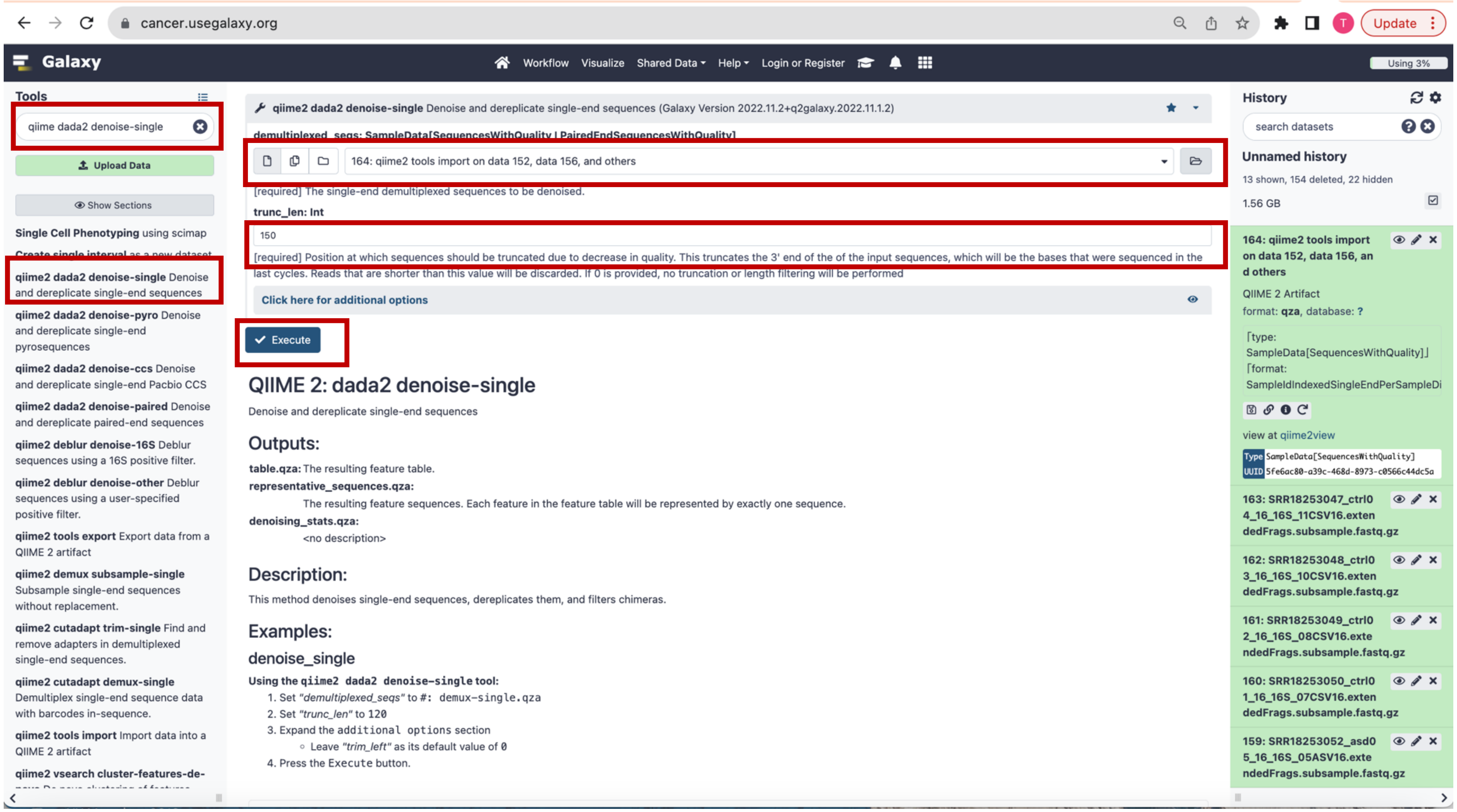
We can see that the input files in FASTQ compressed format are now converted into a QIIME2 artifact file and the is a .qza file which is specific to QIIME2. The following QIIME2 workflow will make use of this. qza database file.

Screenshot 13

<u>STEP 9:</u> Running “qiime2 dada2 denoise-single”.

FOR “demultiplexed_seqs:SampleData[SequencesWithQuality[PairedEndSequencesWithQuality] SELECT results from previous step as show in the screenshot below

For trunc_len:Int ENTER 150 and HIT “Execute”.



Single Cell Phenotyping using scimap

qiime2 dada2 denoise-single Denoise and dereplicate single-end sequences

qiime2 dada2 denoise-pyro Denoise and dereplicate single-end pyrosequences

qiime2 dada2 denoise-ccs Denoise and dereplicate single-end Pacbio CCS

qiime2 dada2 denoise-paired Denoise and dereplicate paired-end sequences

qiime2 deblur denoise-16S Deblur sequences using a 16S positive filter.

qiime2 deblur denoise-other Deblur sequences using a user-specified positive filter.

qiime2 tools export Export data from a QIIME 2 artifact

qiime2 demux subsample-single Subsample single-end sequences without replacement.

qiime2 cutadapt trim-single Find and remove adapters in demultiplexed single-end sequences.

qiime2 cutadapt demux-single Demultiplex single-end sequence data with barcodes in-sequence.

qiime2 tools import Import data into a QIIME 2 artifact

qiime2 vsearch cluster-features-de-

qiime2 dada2 denoise-single Denoise and dereplicate single-end sequences (Galaxy Version 2022.11.2+q2galaxy.2022.11.1.2)

demultiplexed_seqs: SampleData[SequencesWithQuality | PairedEndSequencesWithQuality]

164: qiime2 tools import on data 152, data 156, and others

[required] The single-end demultiplexed sequences to be denoised.

trunc_len: Int

150

[required] Position at which sequences should be truncated due to decrease in quality. This truncates the 3' end of the of the input sequences, which will be the bases that were sequenced in the last cycles. Reads that are shorter than this value will be discarded. If 0 is provided, no truncation or length filtering will be performed

QIIME 2: dada2 denoise-single

Denoise and dereplicate single-end sequences

Outputs:

table.qza: The resulting feature table.

representative_sequences.qza:

The resulting feature sequences. Each feature in the feature table will be represented by exactly one sequence.

denoising_stats.qza:

<no description>

Description:

This method denoises single-end sequences, dereplicates them, and filters chimeras.

Examples:

denoise_single

Using the `qiime2 dada2 denoise-single` tool:

1. Set *"demultiplexed_seqs"* to `#: demux-single.qza`
2. Set *"trunc_len"* to `120`
3. Expand the `additional options` section
   - Leave *"trim_left"* as its default value of `0`
4. Press the `Execute` button.

Unnamed history

13 shown, 154 deleted, 22 hidden

1.56 GB

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

⌈type: SampleData[SequencesWithQuality]⌋ ⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

Type SampleData[SequencesWithQuality]

UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

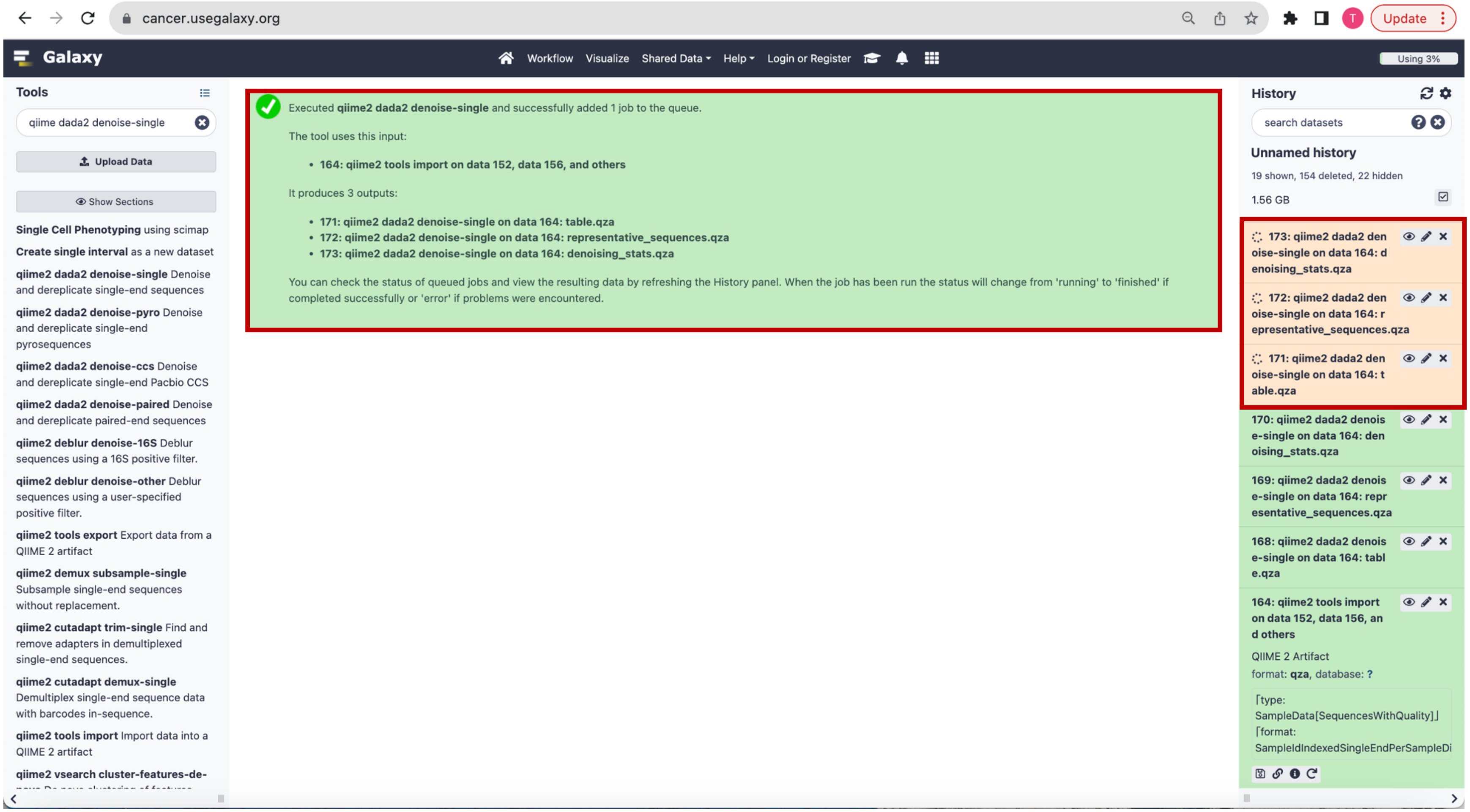
162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

161: SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz

160: SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz

159: SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz

Screenshot 14



Executed **qiime2 dada2 denoise-single** and successfully added 1 job to the queue.

The tool uses this input:

- **164: qiime2 tools import on data 152, data 156, and others**

It produces 3 outputs:

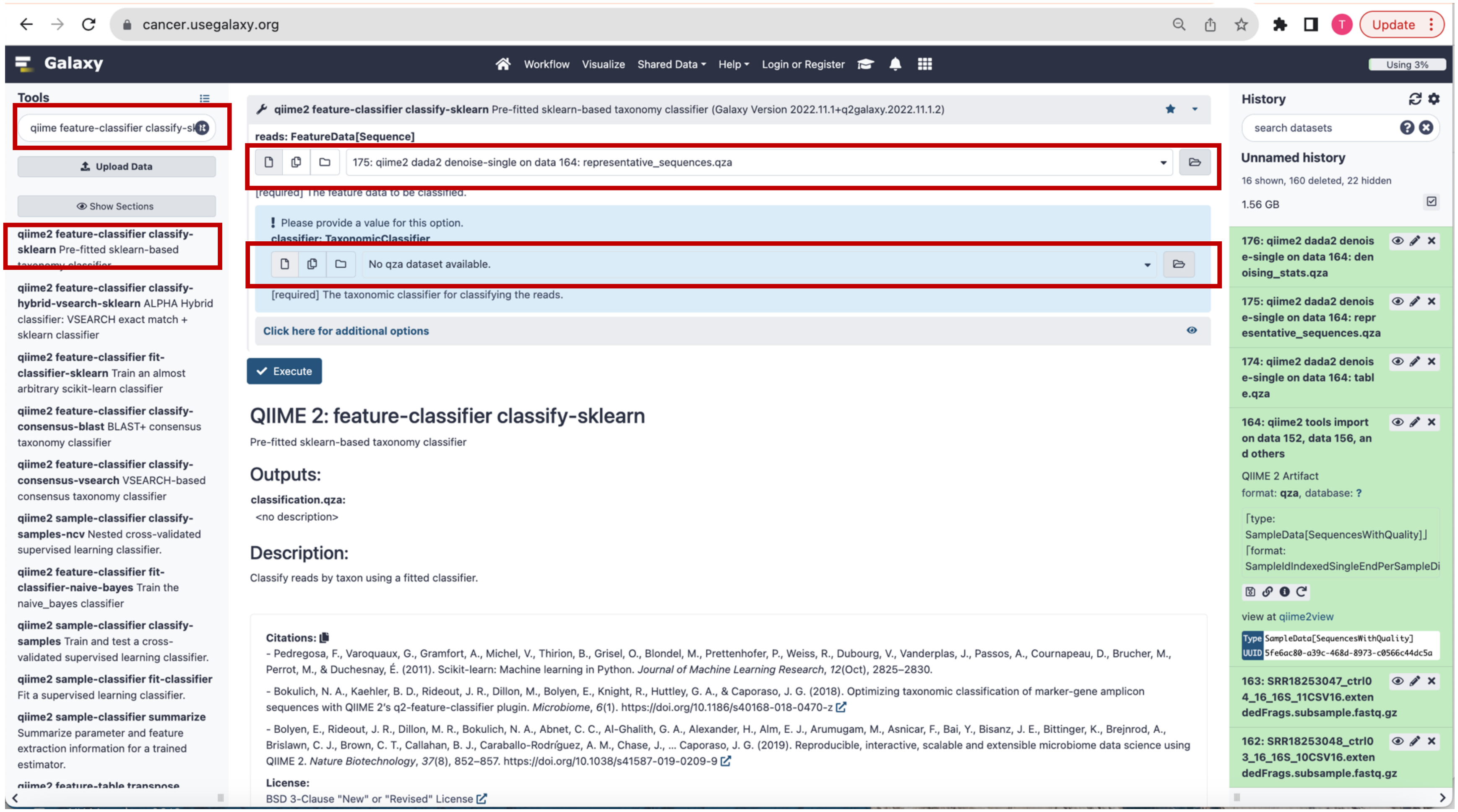
- **171: qiime2 dada2 denoise-single on data 164: table.qza**
- **172: qiime2 dada2 denoise-single on data 164: representative_sequences.qza**
- **173: qiime2 dada2 denoise-single on data 164: denoising_stats.qza**

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.

Screenshot 15

STEP 10: Run “qiime2 feature-classifier classify-sklearn”

FOR reads:FeatureData[Sequence] SELECT option highlighted in the box.
FOR classifier:taxonomicCLassifier follow instructions shown in screenshots 17 – 21
Screenshot 22: All required input values have been entered, hit “Execute”



qiime feature-classifier classify-sk

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

qiime2 feature-classifier fit-classifier-sklearn Train an almost arbitrary scikit-learn classifier

qiime2 feature-classifier classify-consensus-blast BLAST+ consensus taxonomy classifier

qiime2 feature-classifier classify-consensus-vsearch VSEARCH-based consensus taxonomy classifier

qiime2 sample-classifier classify-samples-ncv Nested cross-validated supervised learning classifier.

qiime2 feature-classifier fit-classifier-naive-bayes Train the naive_bayes classifier

qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

reads: FeatureData[Sequence]
175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza
[required] The feature data to be classified.

! Please provide a value for this option.
classifier: TaxonomicClassifier
No qza dataset available.
[required] The taxonomic classifier for classifying the reads.

QIIME 2: feature-classifier classify-sklearn

Pre-fitted sklearn-based taxonomy classifier

Outputs:

classification.qza:
<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:
- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.
- Bokulich, N. A., Kaehler, B. D., Rideout, J. R., Dillon, M., Bolyen, E., Knight, R., Huttley, G. A., & Caporaso, J. G. (2018). Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2’s q2-feature-classifier plugin. *Microbiome*, *6*(1). https://doi.org/10.1186/s40168-018-0470-z
- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., … Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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BSD 3-Clause "New" or "Revised" License

Unnamed history
16 shown, 160 deleted, 22 hidden
1.56 GB

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

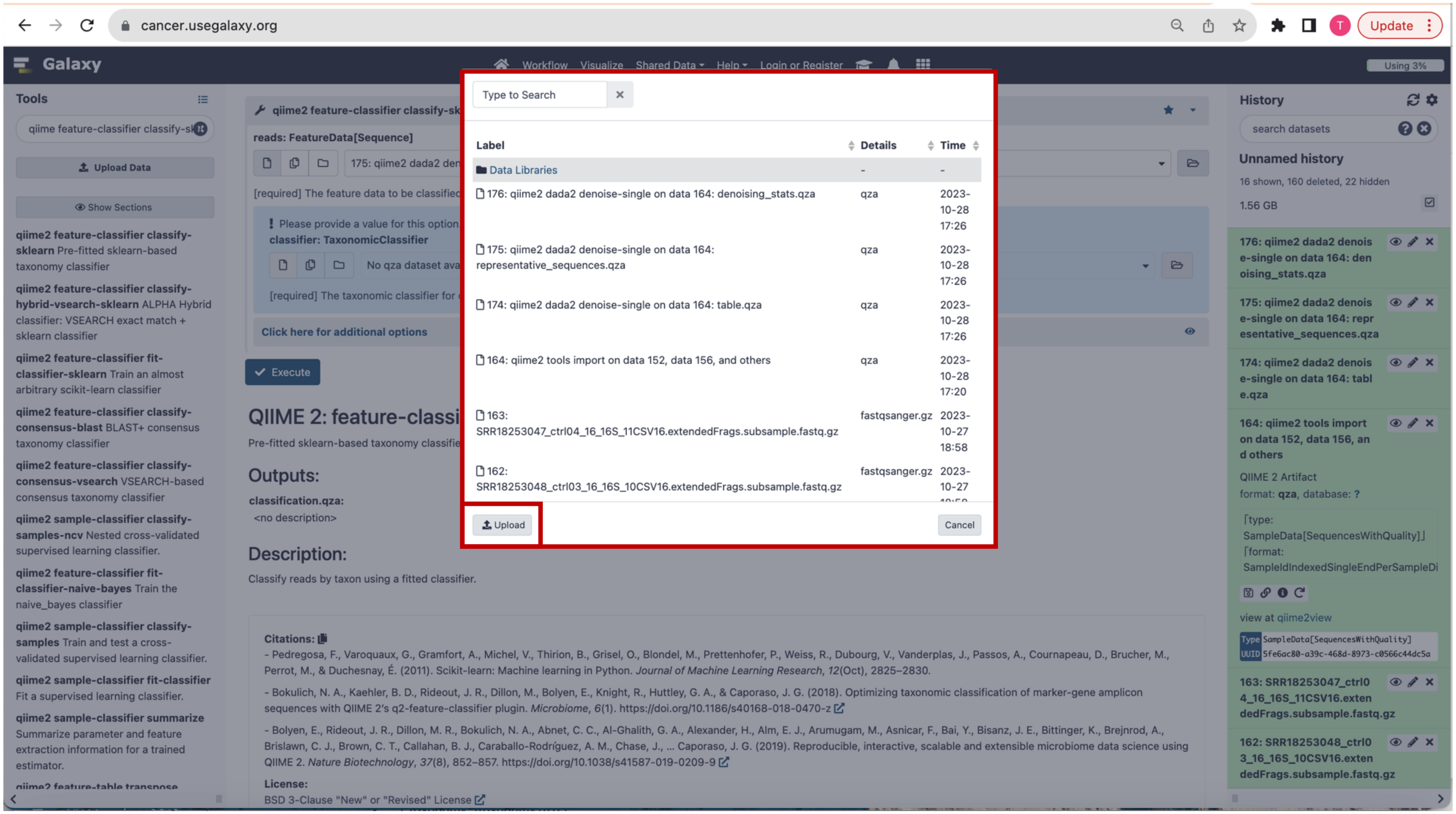
174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others
QIIME 2 Artifact
format: **qza**, database: **?**
[type: SampleData[SequencesWithQuality]]
[format: SampleIdIndexedSingleEndPerSampleDi
view at qiime2view
Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

Screenshot 16



qiime feature-classifier classify-sk

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

qiime2 feature-classifier fit-classifier-sklearn Train an almost arbitrary scikit-learn classifier

qiime2 feature-classifier classify-consensus-blast BLAST+ consensus taxonomy classifier

qiime2 feature-classifier classify-consensus-vsearch VSEARCH-based consensus taxonomy classifier

qiime2 sample-classifier classify-samples-ncv Nested cross-validated supervised learning classifier.

qiime2 feature-classifier fit-classifier-naive-bayes Train the naive_bayes classifier

qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

qiime2 feature-classifier classify-sk

reads: FeatureData[Sequence]

175: qiime2 dada2 den

[required] The feature data to be classified

! Please provide a value for this option
classifier: TaxonomicClassifier

No qza dataset ava

[required] The taxonomic classifier for

Click here for additional options

QIIME 2: feature-classi

Pre-fitted sklearn-based taxonomy classifie

Outputs:

classification.qza:
<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:

- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.

- Bokulich, N. A., Kaehler, B. D., Rideout, J. R., Dillon, M., Bolyen, E., Knight, R., Huttley, G. A., & Caporaso, J. G. (2018). Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. *Microbiome*, *6*(1). https://doi.org/10.1186/s40168-018-0470-z

- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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Label	Details	Time
Data Libraries	-	-
176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza	qza	2023-10-28 17:26
175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza	qza	2023-10-28 17:26
174: qiime2 dada2 denoise-single on data 164: table.qza	qza	2023-10-28 17:26
164: qiime2 tools import on data 152, data 156, and others	qza	2023-10-28 17:20
163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz	fastqsanger.gz	2023-10-27 18:58
162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz	fastqsanger.gz	2023-10-27

Unnamed history

16 shown, 160 deleted, 22 hidden

1.56 GB

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact
format: **qza**, database: **?**

[type: SampleData[SequencesWithQuality]] [format: SampleIdIndexedSingleEndPerSampleDi

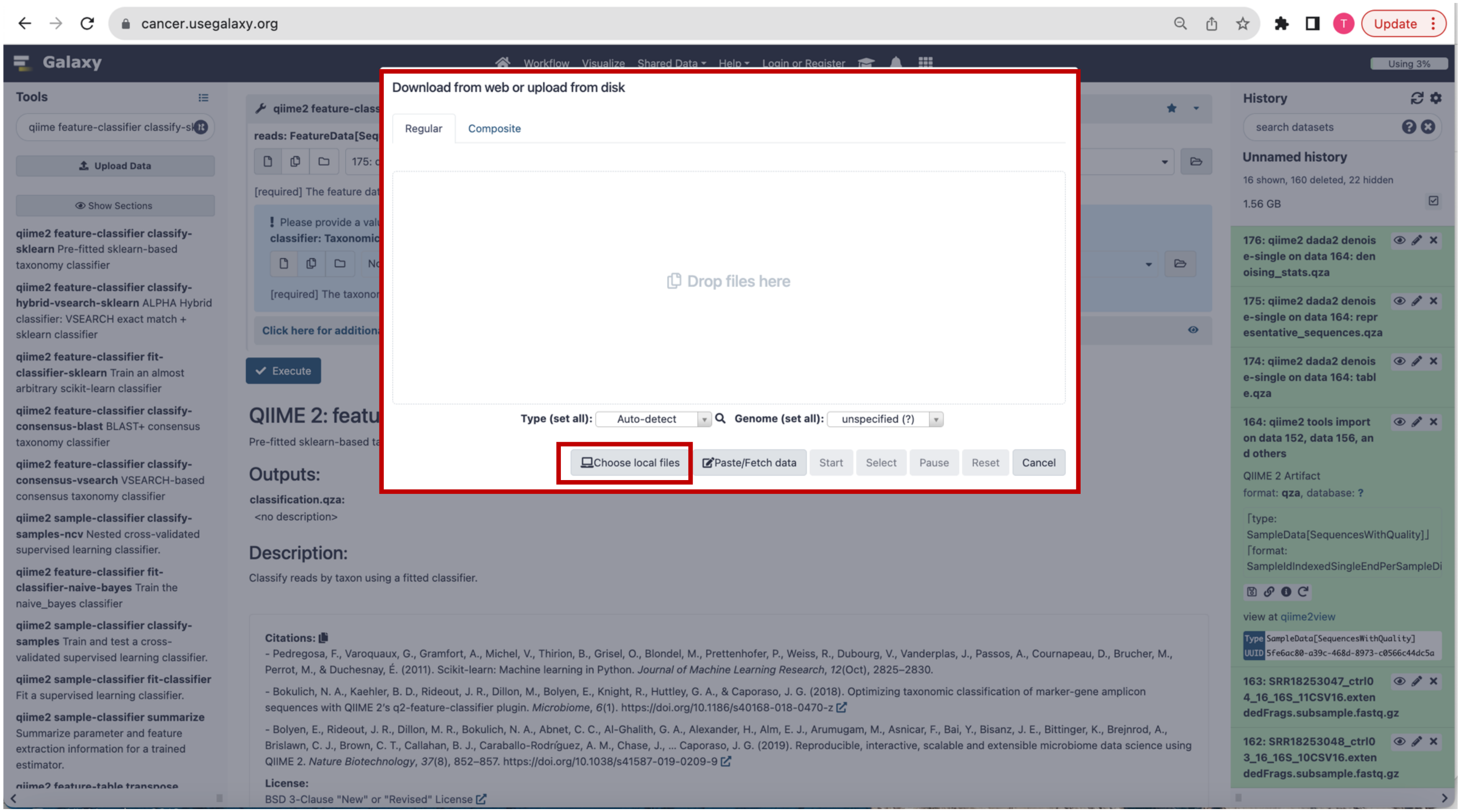
view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

Screenshot 17



Download from web or upload from disk

Type (set all): Auto-detect **Genome (set all):** unspecified (?)

qiime feature-classifier classify-sk

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

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qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

qiime2 feature-class

reads: FeatureData[Seq

175: c

[required] The feature dat

Please provide a val

classifier: Taxonomic

No

[required] The taxonon

Click here for addition

QIIME 2: featu

Pre-fitted sklearn-based ta

Outputs:

classification.qza:
<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:

- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.
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- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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Unnamed history

16 shown, 160 deleted, 22 hidden

1.56 GB

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact
format: **qza**, database: **?**

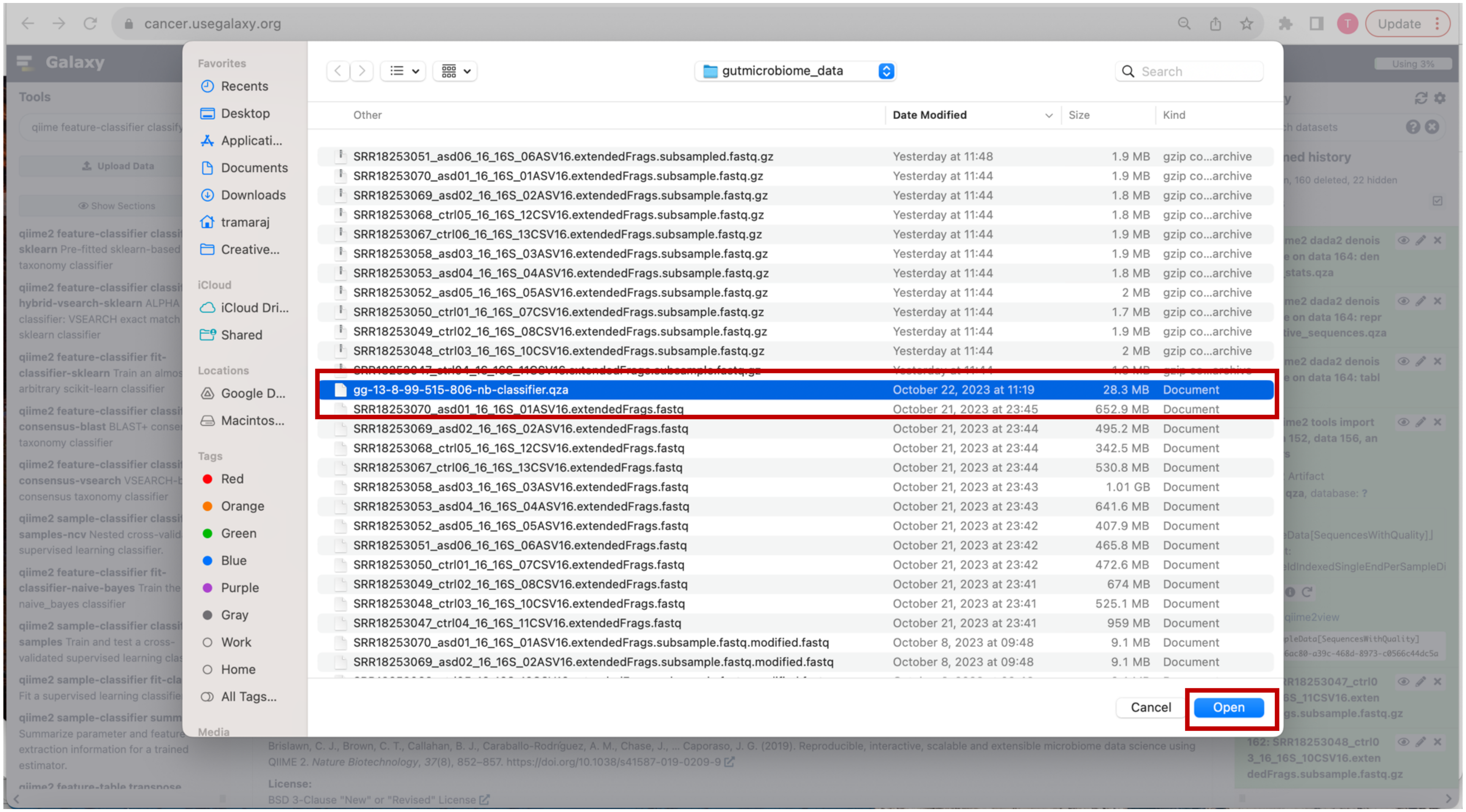
⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

Screenshot 18



Other	Date Modified	Size	Kind
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SRR18253070_asd01_16_16S_01ASV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.9 MB	gzip co...archive
SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.8 MB	gzip co...archive
SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.8 MB	gzip co...archive
SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.9 MB	gzip co...archive
SRR18253058_asd03_16_16S_03ASV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.9 MB	gzip co...archive
SRR18253053_asd04_16_16S_04ASV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.8 MB	gzip co...archive
SRR18253052_asd05_16_16S_05ASV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	2 MB	gzip co...archive
SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.7 MB	gzip co...archive
SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.9 MB	gzip co...archive
SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	2 MB	gzip co...archive
SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz	Yesterday at 11:44	1.9 MB	gzip co...archive
gg-13-8-99-515-806-nb-classifier.qza	October 22, 2023 at 11:19	28.3 MB	Document
SRR18253070_asd01_16_16S_01ASV16.extendedFrags.fastq	October 21, 2023 at 23:45	652.9 MB	Document
SRR18253069_asd02_16_16S_02ASV16.extendedFrags.fastq	October 21, 2023 at 23:44	495.2 MB	Document
SRR18253068_ctrl05_16_16S_12CSV16.extendedFrags.fastq	October 21, 2023 at 23:44	342.5 MB	Document
SRR18253067_ctrl06_16_16S_13CSV16.extendedFrags.fastq	October 21, 2023 at 23:44	530.8 MB	Document
SRR18253058_asd03_16_16S_03ASV16.extendedFrags.fastq	October 21, 2023 at 23:43	1.01 GB	Document
SRR18253053_asd04_16_16S_04ASV16.extendedFrags.fastq	October 21, 2023 at 23:43	641.6 MB	Document
SRR18253052_asd05_16_16S_05ASV16.extendedFrags.fastq	October 21, 2023 at 23:42	407.9 MB	Document
SRR18253051_asd06_16_16S_06ASV16.extendedFrags.fastq	October 21, 2023 at 23:42	465.8 MB	Document
SRR18253050_ctrl01_16_16S_07CSV16.extendedFrags.fastq	October 21, 2023 at 23:42	472.6 MB	Document
SRR18253049_ctrl02_16_16S_08CSV16.extendedFrags.fastq	October 21, 2023 at 23:41	674 MB	Document
SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.fastq	October 21, 2023 at 23:41	525.1 MB	Document
SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.fastq	October 21, 2023 at 23:41	959 MB	Document
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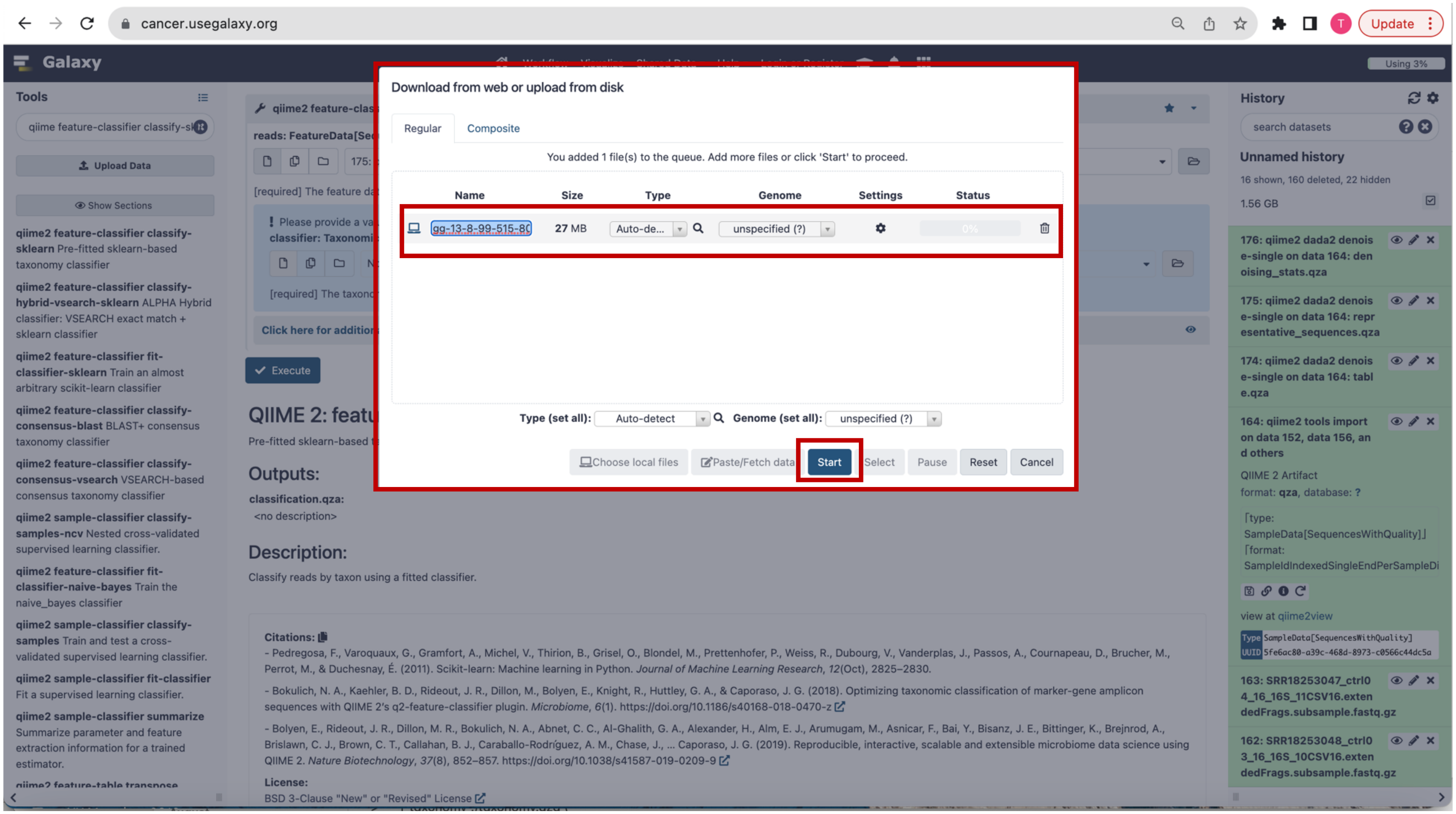
SRR18253069_asd02_16_16S_02ASV16.extendedFrags.subsample.fastq.modified.fastq	October 8, 2023 at 09:48	9.1 MB	Document

Screenshot 19



Download from web or upload from disk

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

Name	Size	Type	Genome	Settings	Status
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Type (set all): Auto-detect **Genome (set all):** unspecified (?)

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

qiime2 feature-classifier fit-classifier-sklearn Train an almost arbitrary scikit-learn classifier

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qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

qiime2 feature-clas

reads: FeatureData[Se

[required] The feature da

Please provide a va

classifier: Taxonomi

[required] The taxono

Click here for addition

QIIME 2: featu

Pre-fitted sklearn-based t

Outputs:

classification.qza:

<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:

- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.

- Bokulich, N. A., Kaehler, B. D., Rideout, J. R., Dillon, M., Bolyen, E., Knight, R., Huttley, G. A., & Caporaso, J. G. (2018). Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. *Microbiome*, *6*(1). https://doi.org/10.1186/s40168-018-0470-z

- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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Unnamed history

16 shown, 160 deleted, 22 hidden

1.56 GB

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

[type: SampleData[SequencesWithQuality]]

[format: SampleIdIndexedSingleEndPerSampleDi

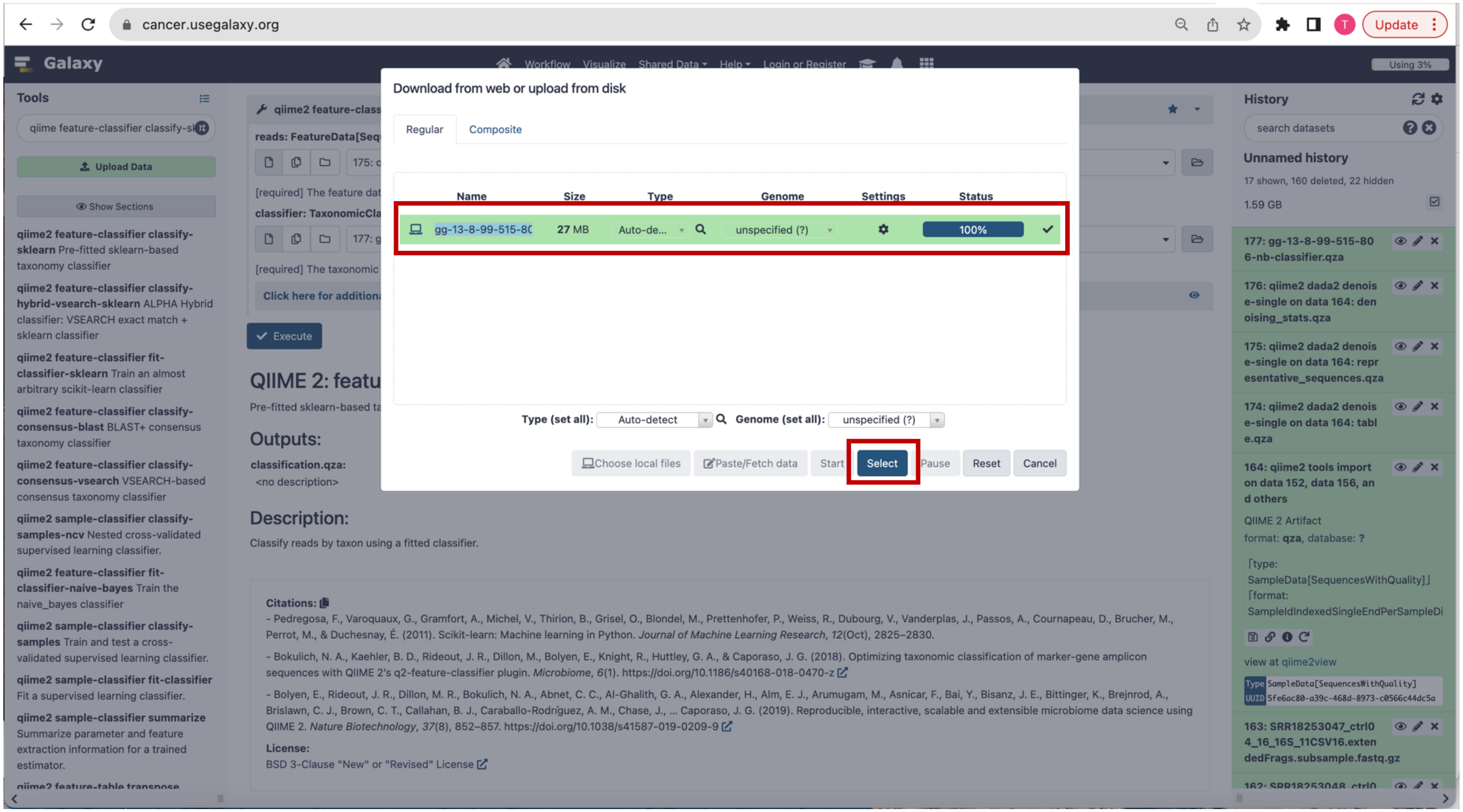
Type SampleData[SequencesWithQuality]

UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl03_16_16S_10CSV16.extendedFrags.subsample.fastq.gz

Screenshot 20



Download from web or upload from disk

Name	Size	Type	Genome	Settings	Status
gg-13-8-99-515-80	27 MB	Auto-de...	unspecified (?)		100% ✓

Type (set all): Auto-detect **Genome (set all):** unspecified (?)

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

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qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

reads: FeatureData[Seq

175: c

[required] The feature dat

classifier: TaxonomicCla

177: g

[required] The taxonomic

Click here for addition

QIIME 2: featu

Pre-fitted sklearn-based ta

Outputs:

classification.qza:
<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:

- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.

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- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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Unnamed history
17 shown, 160 deleted, 22 hidden
1.59 GB

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact
format: **qza**, database: **?**

[type: SampleData[SequencesWithQuality]]
[format: SampleIdIndexedSingleEndPerSampleDi

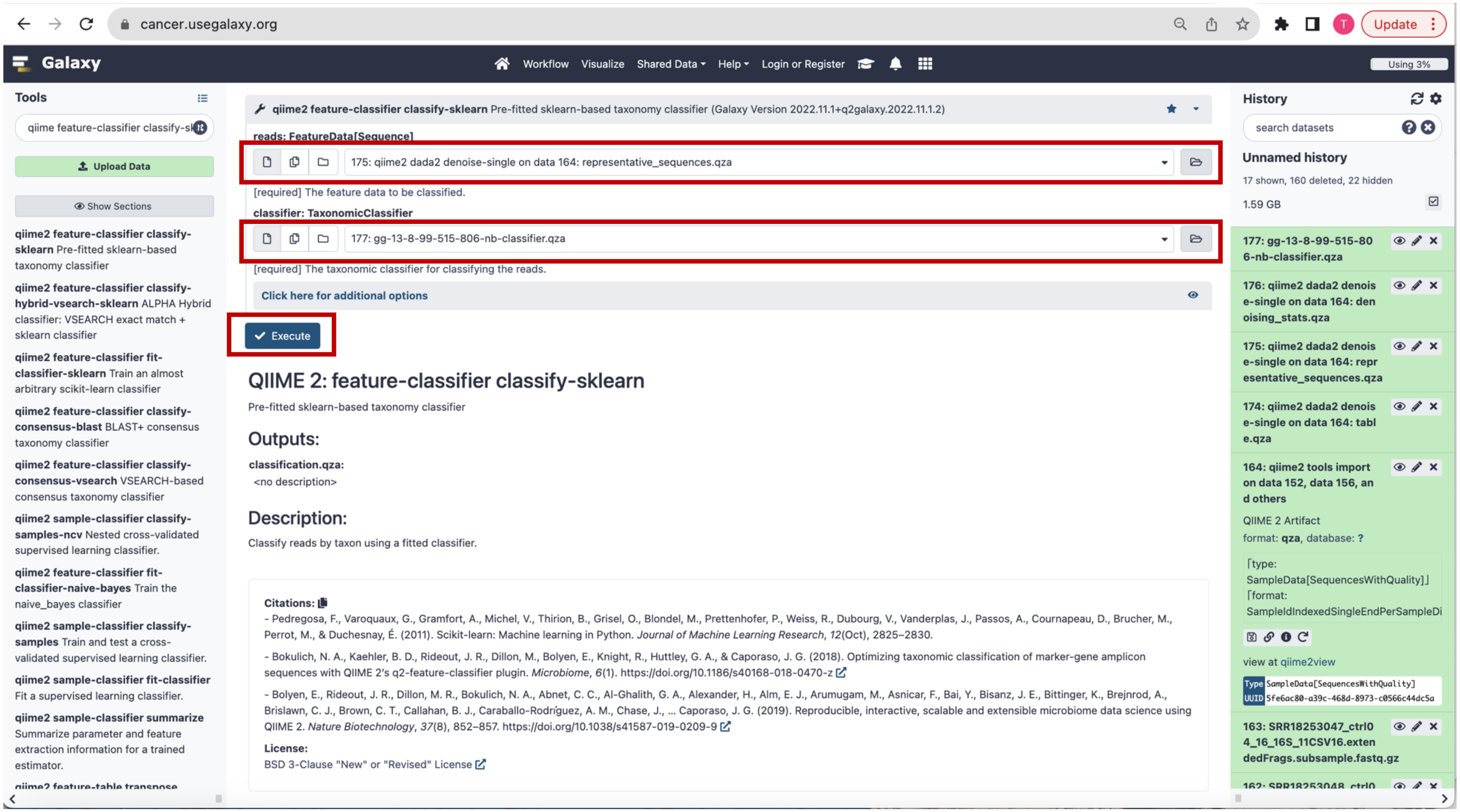
view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl0

Screenshot 21



qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

reads: FeatureData[Sequence]

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

[required] The feature data to be classified.

classifier: TaxonomicClassifier

177: gg-13-8-99-515-806-nb-classifier.qza

[required] The taxonomic classifier for classifying the reads.

QIIME 2: feature-classifier classify-sklearn

Pre-fitted sklearn-based taxonomy classifier

Outputs:

classification.qza:
<no description>

Description:

Classify reads by taxon using a fitted classifier.

Citations:

- Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V., Vanderplas, J., Passos, A., Cournapeau, D., Brucher, M., Perrot, M., & Duchesnay, É. (2011). Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, *12*(Oct), 2825–2830.

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- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, *37*(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

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qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact
format: **qza**, database: ?

[type: SampleData[SequencesWithQuality]]
[format: SampleIdIndexedSingleEndPerSampleDi

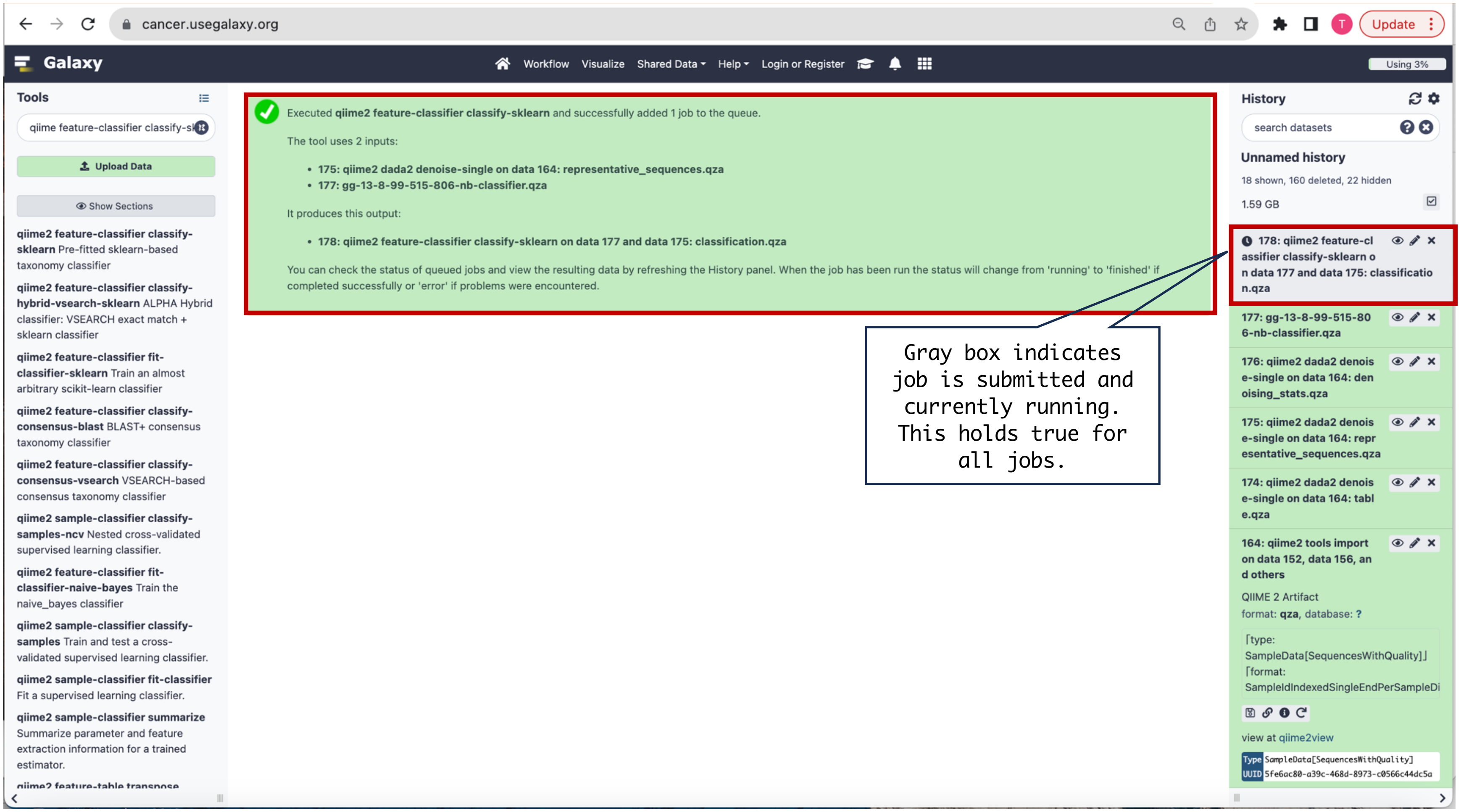
view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

163: SRR18253047_ctrl04_16_16S_11CSV16.extendedFrags.subsample.fastq.gz

162: SRR18253048_ctrl0

Screenshot 22



Executed **qiime2 feature-classifier classify-sklearn** and successfully added 1 job to the queue.

The tool uses 2 inputs:

- **175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza**
- **177: gg-13-8-99-515-806-nb-classifier.qza**

It produces this output:

- **178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza**

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.

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

qiime2 feature-classifier fit-classifier-sklearn Train an almost arbitrary scikit-learn classifier

qiime2 feature-classifier classify-consensus-blast BLAST+ consensus taxonomy classifier

qiime2 feature-classifier classify-consensus-vsearch VSEARCH-based consensus taxonomy classifier

qiime2 sample-classifier classify-samples-ncv Nested cross-validated supervised learning classifier.

qiime2 feature-classifier fit-classifier-naive-bayes Train the naive_bayes classifier

qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

Unnamed history

18 shown, 160 deleted, 22 hidden

1.59 GB

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

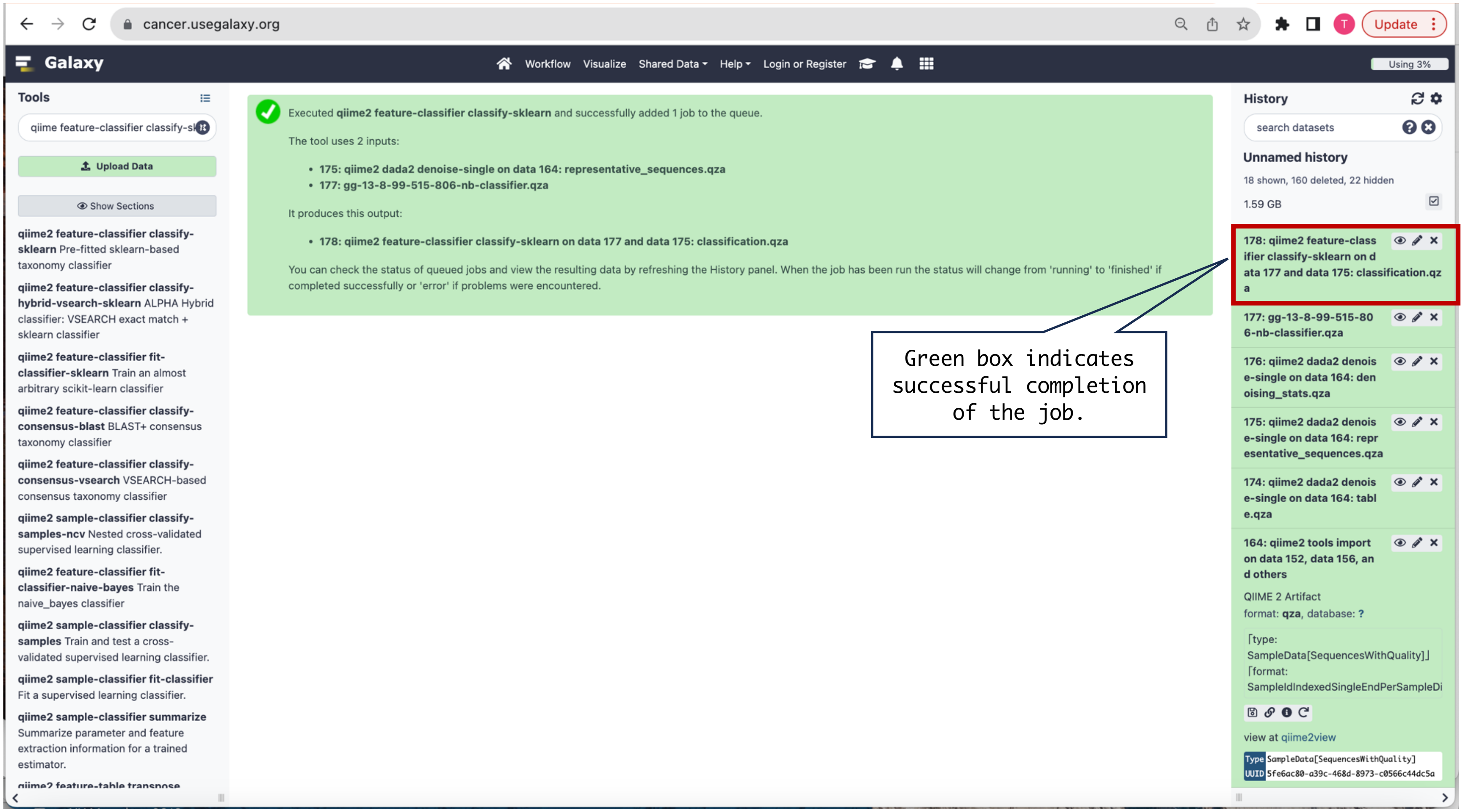
⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

Type	SampleData[SequencesWithQuality]
UUID	5fe6ac80-a39c-468d-8973-c0566c44dc5a

Gray box indicates job is submitted and currently running. This holds true for all jobs.

Screenshot 23



Executed **qiime2 feature-classifier classify-sklearn** and successfully added 1 job to the queue.

The tool uses 2 inputs:

- **175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza**
- **177: gg-13-8-99-515-806-nb-classifier.qza**

It produces this output:

- **178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza**

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.

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-classifier classify-hybrid-vsearch-sklearn ALPHA Hybrid classifier: VSEARCH exact match + sklearn classifier

qiime2 feature-classifier fit-classifier-sklearn Train an almost arbitrary scikit-learn classifier

qiime2 feature-classifier classify-consensus-blast BLAST+ consensus taxonomy classifier

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qiime2 sample-classifier classify-samples-ncv Nested cross-validated supervised learning classifier.

qiime2 feature-classifier fit-classifier-naive-bayes Train the naive_bayes classifier

qiime2 sample-classifier classify-samples Train and test a cross-validated supervised learning classifier.

qiime2 sample-classifier fit-classifier Fit a supervised learning classifier.

qiime2 sample-classifier summarize Summarize parameter and feature extraction information for a trained estimator.

qiime2 feature-table transpose

Unnamed history

18 shown, 160 deleted, 22 hidden

1.59 GB

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

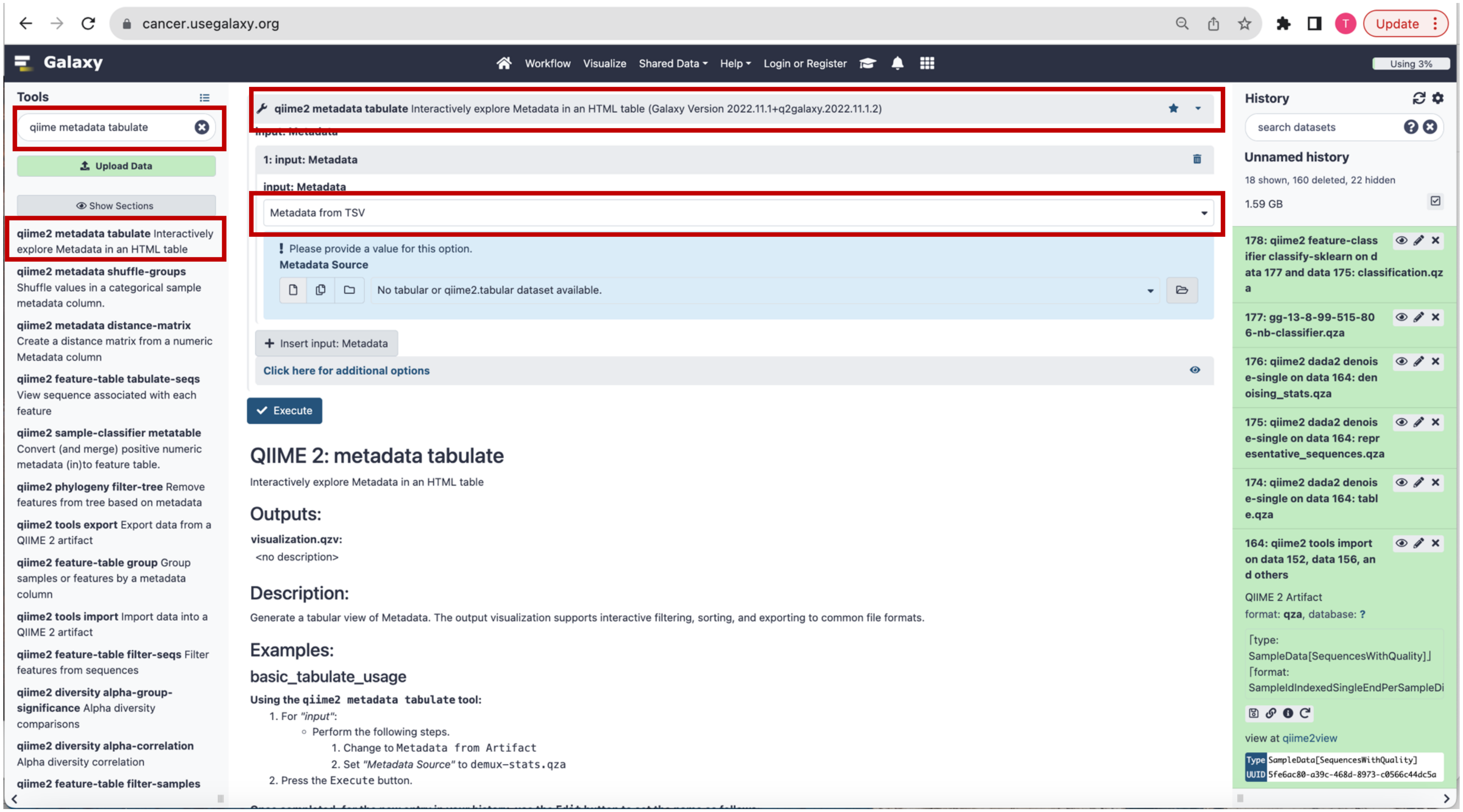
Type	SampleData[SequencesWithQuality]
UUID	5fe6ac80-a39c-468d-8973-c0566c44dc5a

Green box indicates successful completion of the job.

Screenshot 24

STEP 11: Run “qiime2 metadata tabulate”.

FOR input:Metadata SELECT “Metadata from Artifact” AND “Execute” as shown in screenshot 25 – 28.



qiime metadata tabulate

qiime2 metadata tabulate Interactively explore Metadata in an HTML table

qiime2 metadata shuffle-groups Shuffle values in a categorical sample metadata column.

qiime2 metadata distance-matrix Create a distance matrix from a numeric Metadata column

qiime2 feature-table tabulate-seqs View sequence associated with each feature

qiime2 sample-classifier metatable Convert (and merge) positive numeric metadata (in)to feature table.

qiime2 phylogeny filter-tree Remove features from tree based on metadata

qiime2 tools export Export data from a QIIME 2 artifact

qiime2 feature-table group Group samples or features by a metadata column

qiime2 tools import Import data into a QIIME 2 artifact

qiime2 feature-table filter-seqs Filter features from sequences

qiime2 diversity alpha-group-significance Alpha diversity comparisons

qiime2 diversity alpha-correlation Alpha diversity correlation

qiime2 feature-table filter-samples

qiime2 metadata tabulate Interactively explore Metadata in an HTML table (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

1: input: Metadata

input: Metadata

Metadata from TSV

Please provide a value for this option.

Metadata Source

No tabular or qiime2.tabular dataset available.

QIIME 2: metadata tabulate

Interactively explore Metadata in an HTML table

Outputs:

visualization.qzv:
<no description>

Description:

Generate a tabular view of Metadata. The output visualization supports interactive filtering, sorting, and exporting to common file formats.

Examples:

basic_tabulate_usage

Using the `qiime2 metadata tabulate` tool:

1. For *"input"*:
    - Perform the following steps.
        1. Change to `Metadata from Artifact`
        2. Set *"Metadata Source"* to `demux-stats.qza`
2. Press the Execute button.

Unnamed history

18 shown, 160 deleted, 22 hidden

1.59 GB

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

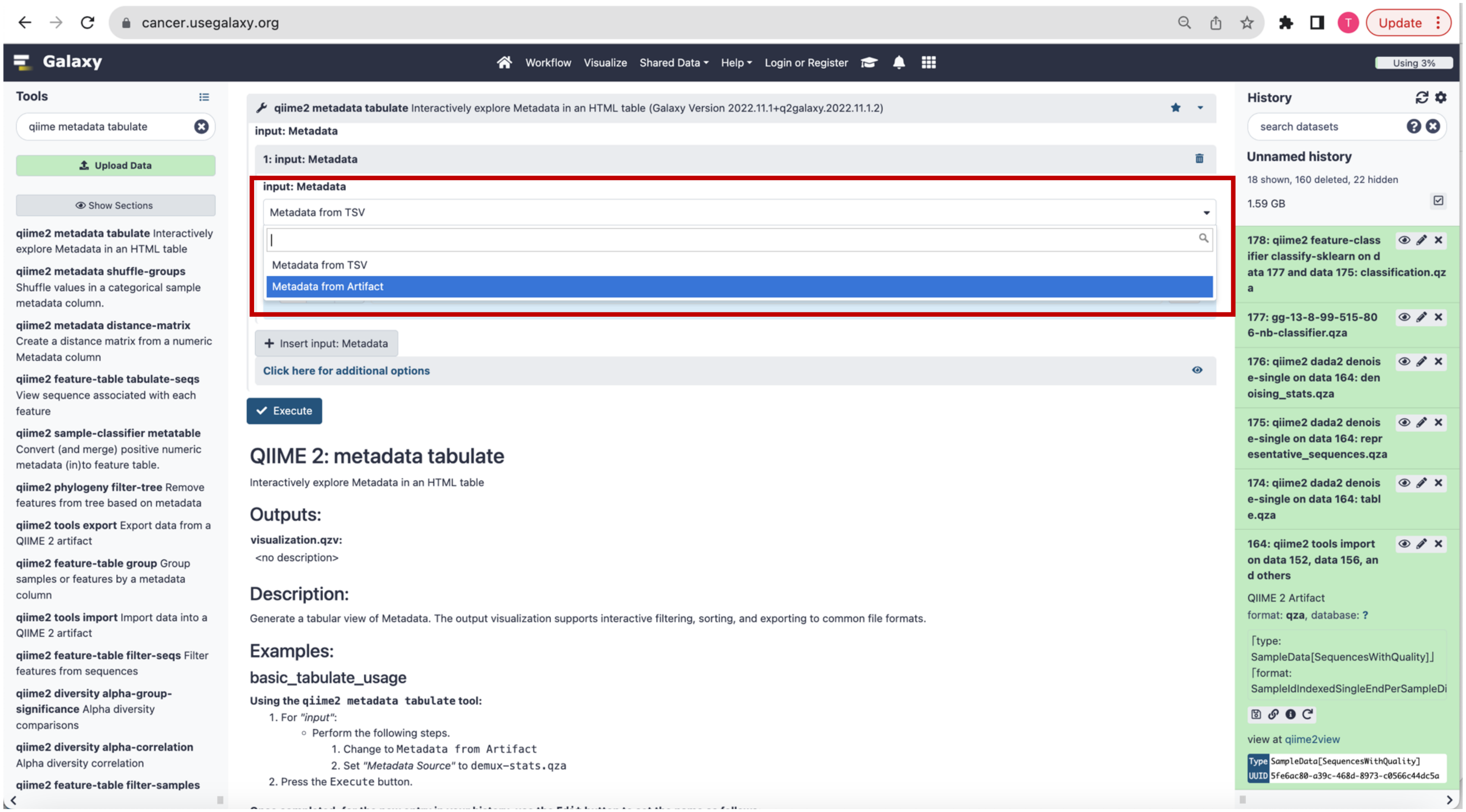
format: **qza**, database: ?

⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

Screenshot 25



qiime2 metadata tabulate Interactively explore Metadata in an HTML table (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

input: Metadata

1: input: Metadata

input: Metadata

Metadata from TSV

Metadata from TSV
Metadata from Artifact

QIIME 2: metadata tabulate

Interactively explore Metadata in an HTML table

Outputs:

visualization.qzv:
<no description>

Description:

Generate a tabular view of Metadata. The output visualization supports interactive filtering, sorting, and exporting to common file formats.

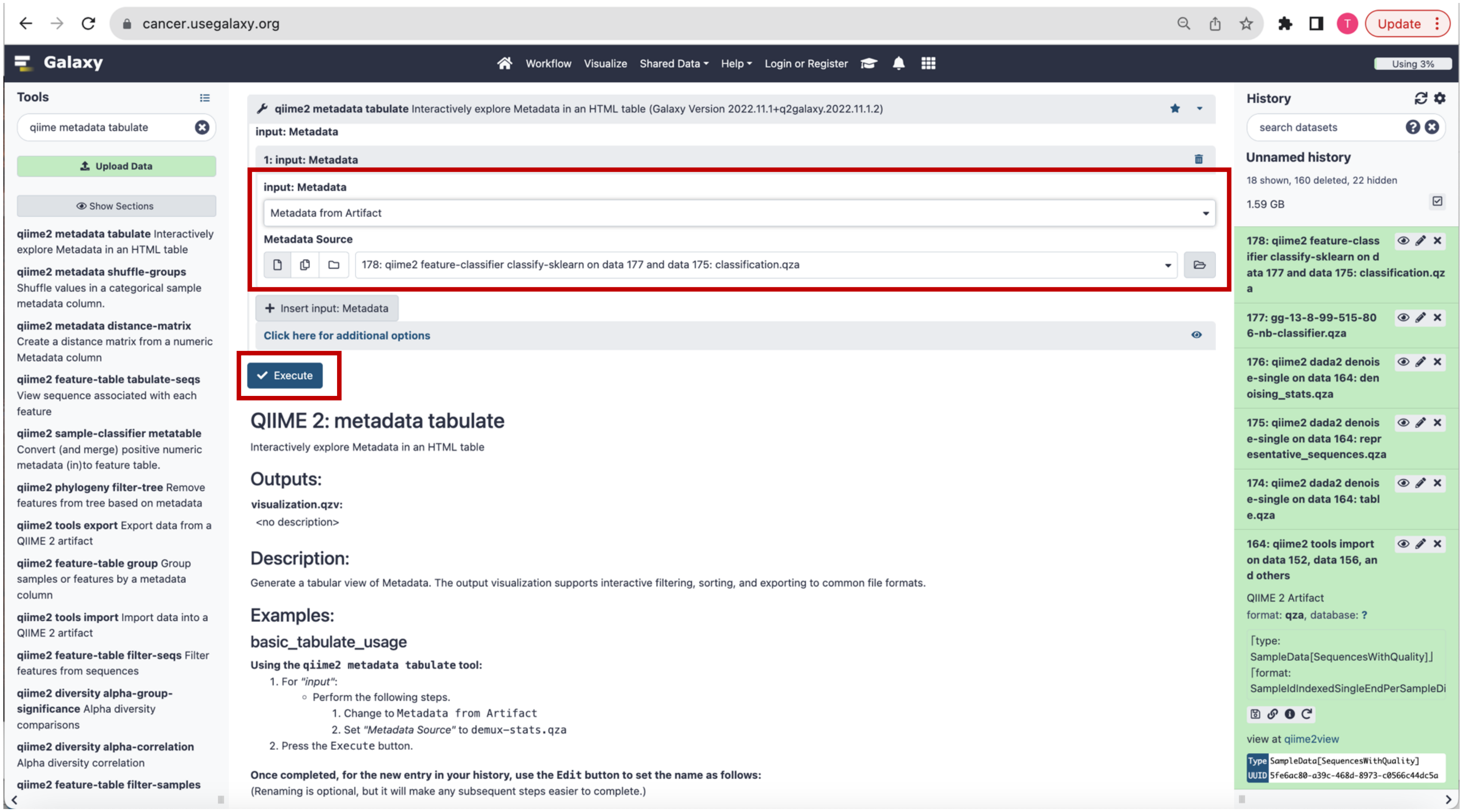
Examples:

basic_tabulate_usage

Using the `qiime2 metadata tabulate` tool:

1. For *"input"*:
   - Perform the following steps.
     1. Change to `Metadata from Artifact`
     2. Set *"Metadata Source"* to `demux-stats.qza`
2. Press the `Execute` button.

Screenshot 26



qiime metadata tabulate

qiime2 metadata tabulate Interactively explore Metadata in an HTML table

qiime2 metadata shuffle-groups Shuffle values in a categorical sample metadata column.

qiime2 metadata distance-matrix Create a distance matrix from a numeric Metadata column

qiime2 feature-table tabulate-seqs View sequence associated with each feature

qiime2 sample-classifier metatable Convert (and merge) positive numeric metadata (in)to feature table.

qiime2 phylogeny filter-tree Remove features from tree based on metadata

qiime2 tools export Export data from a QIIME 2 artifact

qiime2 feature-table group Group samples or features by a metadata column

qiime2 tools import Import data into a QIIME 2 artifact

qiime2 feature-table filter-seqs Filter features from sequences

qiime2 diversity alpha-group-significance Alpha diversity comparisons

qiime2 diversity alpha-correlation Alpha diversity correlation

qiime2 feature-table filter-samples

qiime2 metadata tabulate Interactively explore Metadata in an HTML table (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

input: Metadata

1: input: Metadata

input: Metadata

Metadata from Artifact

Metadata Source

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

QIIME 2: metadata tabulate

Interactively explore Metadata in an HTML table

Outputs:

visualization.qzv:
<no description>

Description:

Generate a tabular view of Metadata. The output visualization supports interactive filtering, sorting, and exporting to common file formats.

Examples:

basic_tabulate_usage

Using the `qiime2 metadata tabulate` tool:

1. For *"input"*:
   - Perform the following steps.
     1. Change to `Metadata from Artifact`
     2. Set *"Metadata Source"* to `demux-stats.qza`
2. Press the `Execute` button.

Once completed, for the new entry in your history, use the `Edit` button to set the name as follows:
(Renaming is optional, but it will make any subsequent steps easier to complete.)

Unnamed history

18 shown, 160 deleted, 22 hidden

1.59 GB

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

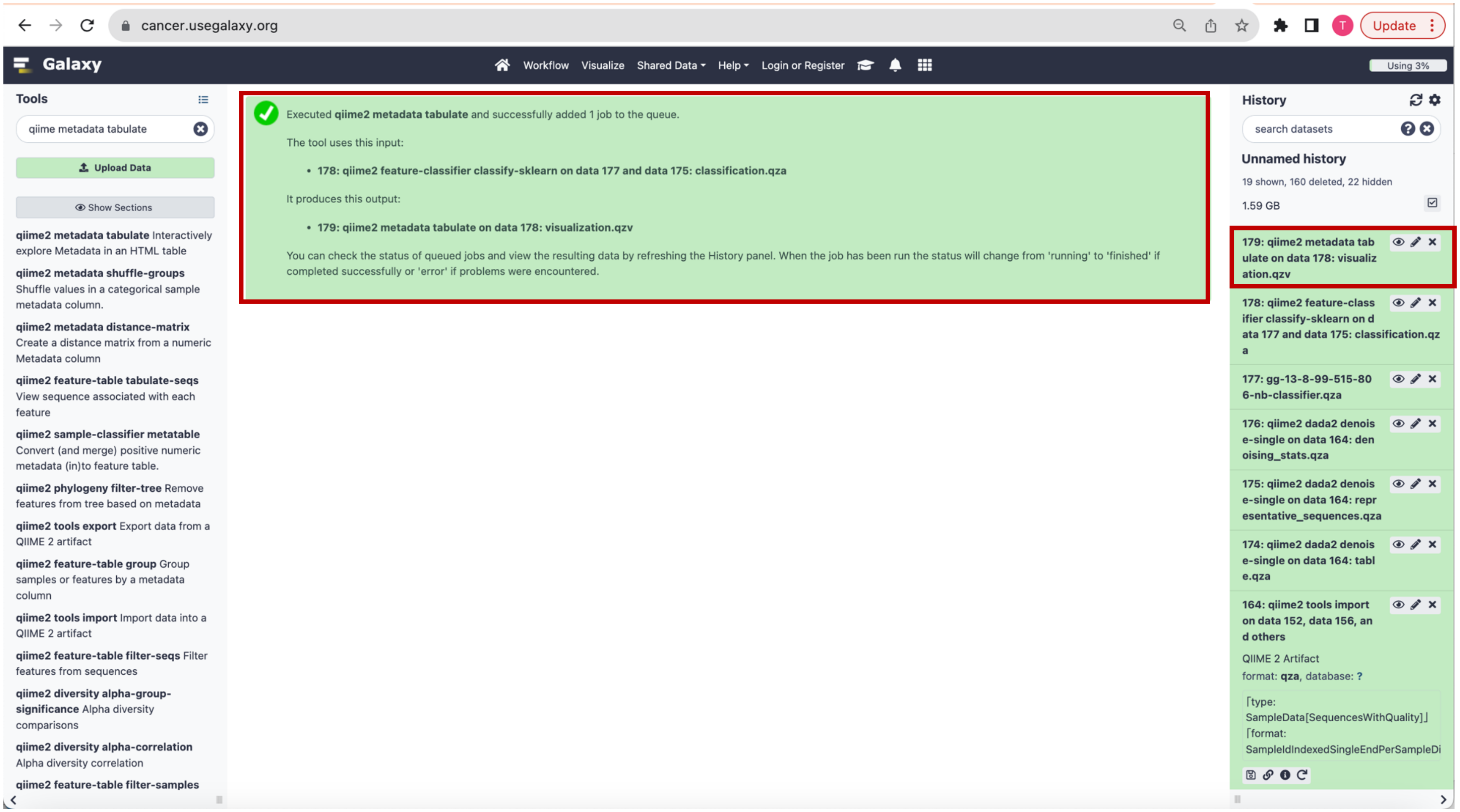
QIIME 2 Artifact
format: **qza**, database: **?**

⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

view at qiime2view

Type SampleData[SequencesWithQuality]
UUID 5fe6ac80-a39c-468d-8973-c0566c44dc5a

Screenshot 27



Executed **qiime2 metadata tabulate** and successfully added 1 job to the queue.

The tool uses this input:

- **178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza**

It produces this output:

- **179: qiime2 metadata tabulate on data 178: visualization.qzv**

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.

qiime2 metadata tabulate Interactively explore Metadata in an HTML table

qiime2 metadata shuffle-groups Shuffle values in a categorical sample metadata column.

qiime2 metadata distance-matrix Create a distance matrix from a numeric Metadata column

qiime2 feature-table tabulate-seqs View sequence associated with each feature

qiime2 sample-classifier metatable Convert (and merge) positive numeric metadata (in)to feature table.

qiime2 phylogeny filter-tree Remove features from tree based on metadata

qiime2 tools export Export data from a QIIME 2 artifact

qiime2 feature-table group Group samples or features by a metadata column

qiime2 tools import Import data into a QIIME 2 artifact

qiime2 feature-table filter-seqs Filter features from sequences

qiime2 diversity alpha-group-significance Alpha diversity comparisons

qiime2 diversity alpha-correlation Alpha diversity correlation

qiime2 feature-table filter-samples

Unnamed history

19 shown, 160 deleted, 22 hidden

1.59 GB

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

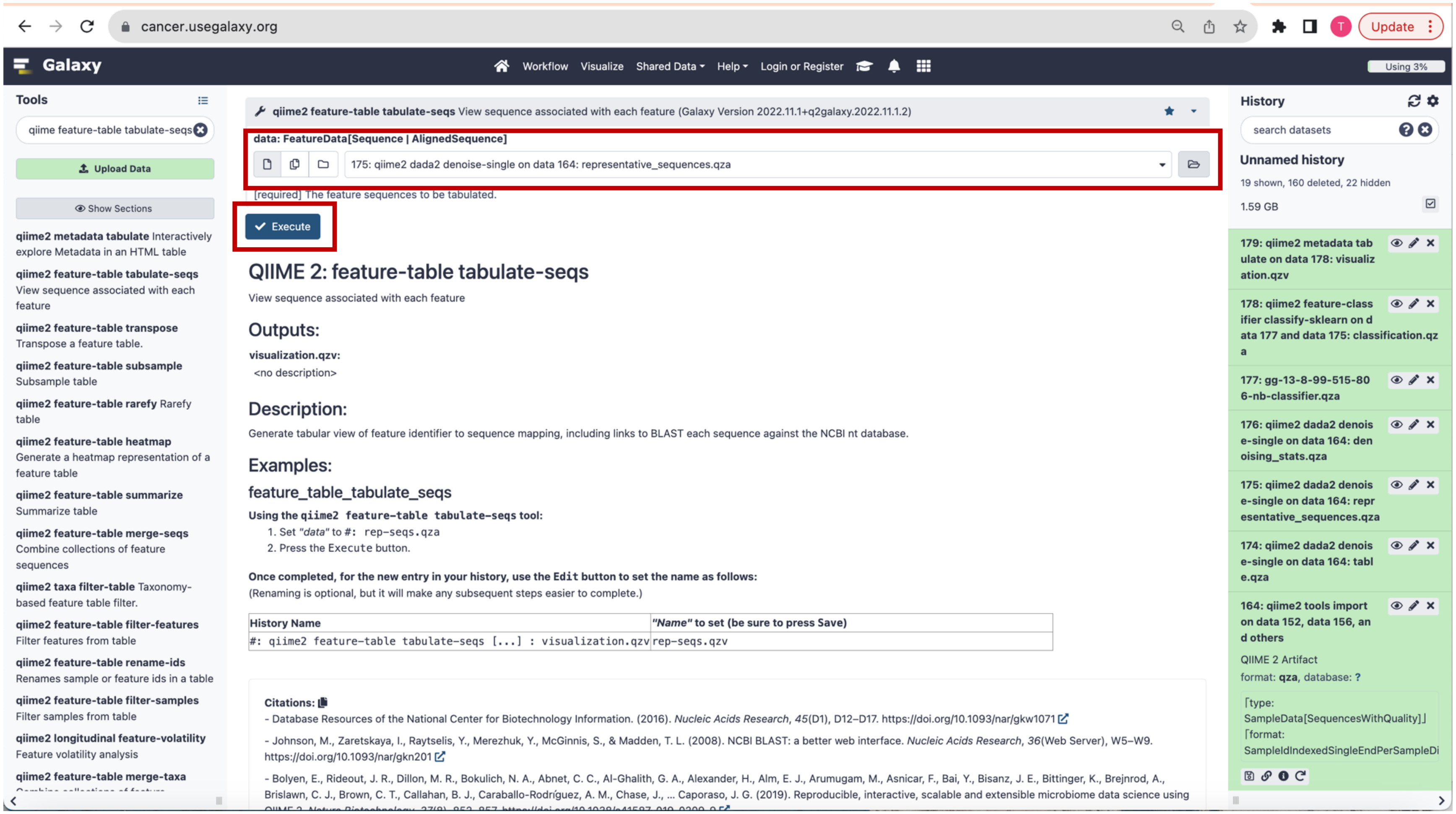
format: **qza**, database: **?**

[type: SampleData[SequencesWithQuality]]
[format: SampleIdIndexedSingleEndPerSampleDi

Screenshot 28

STEP 12: Run “qiime2 feature-table tabulate-seqs”.

FOR data:FeatureData[Sequence|AlignedSequence] SELECT option highlighted in the box AND “Execute” as illustrated in screenshot 29 – 30.



qiime2 metadata tabulate Interactively explore Metadata in an HTML table

qiime2 feature-table tabulate-seqs View sequence associated with each feature

qiime2 feature-table transpose Transpose a feature table.

qiime2 feature-table subsample Subsample table

qiime2 feature-table rarefy Rarefy table

qiime2 feature-table heatmap Generate a heatmap representation of a feature table

qiime2 feature-table summarize Summarize table

qiime2 feature-table merge-seqs Combine collections of feature sequences

qiime2 taxa filter-table Taxonomy-based feature table filter.

qiime2 feature-table filter-features Filter features from table

qiime2 feature-table rename-ids Renames sample or feature ids in a table

qiime2 feature-table filter-samples Filter samples from table

qiime2 longitudinal feature-volatility Feature volatility analysis

qiime2 feature-table merge-taxa

qiime2 feature-table tabulate-seqs View sequence associated with each feature (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

data: FeatureData[Sequence | AlignedSequence]

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

[required] The feature sequences to be tabulated.

QIIME 2: feature-table tabulate-seqs

View sequence associated with each feature

Outputs:

visualization.qzv:
<no description>

Description:

Generate tabular view of feature identifier to sequence mapping, including links to BLAST each sequence against the NCBI nt database.

Examples:

feature_table_tabulate_seqs

Using the `qiime2 feature-table tabulate-seqs` tool:

1. Set *"data"* to `#: rep-seqs.qza`
2. Press the `Execute` button.

Once completed, for the new entry in your history, use the `Edit` button to set the name as follows:
(Renaming is optional, but it will make any subsequent steps easier to complete.)

History Name	*"Name"* to set (be sure to press Save)
`#: qiime2 feature-table tabulate-seqs [...] : visualization.qzv`	`rep-seqs.qzv`

Citations:

- Database Resources of the National Center for Biotechnology Information. (2016). *Nucleic Acids Research*, *45*(D1), D12–D17. https://doi.org/10.1093/nar/gkw1071

- Johnson, M., Zaretskaya, I., Raytselis, Y., Merezhuk, Y., McGinnis, S., & Madden, T. L. (2008). NCBI BLAST: a better web interface. *Nucleic Acids Research*, *36*(Web Server), W5–W9. https://doi.org/10.1093/nar/gkn201

- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., … Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using

History

Unnamed history

19 shown, 160 deleted, 22 hidden

1.59 GB

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

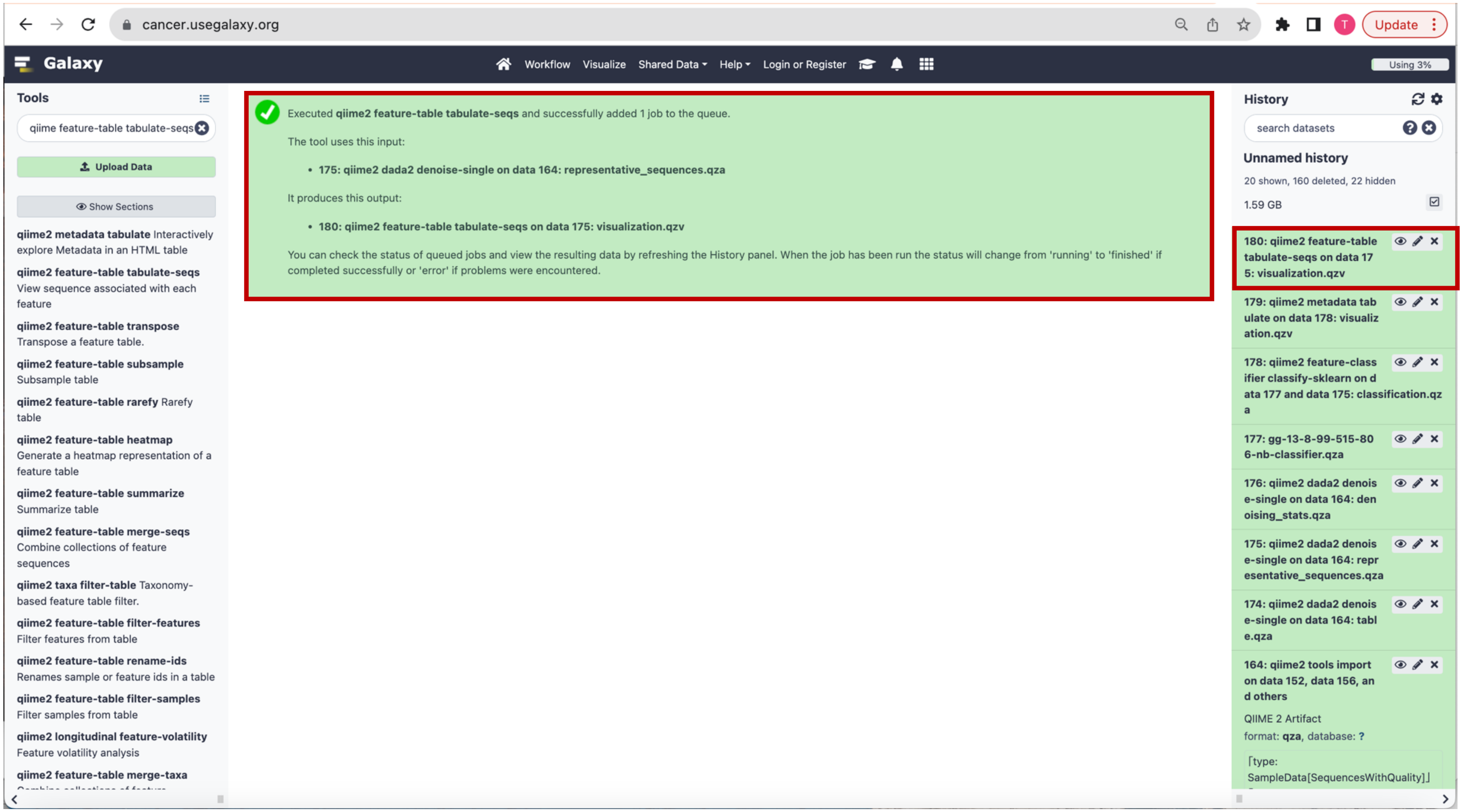
164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: ?

⌈type: SampleData[SequencesWithQuality]⌋
⌈format: SampleIdIndexedSingleEndPerSampleDi

Screenshot 29



Executed **qiime2 feature-table tabulate-seqs** and successfully added 1 job to the queue.

The tool uses this input:

- **175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza**

It produces this output:

- **180: qiime2 feature-table tabulate-seqs on data 175: visualization.qzv**

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.

qiime2 metadata tabulate Interactively explore Metadata in an HTML table

qiime2 feature-table tabulate-seqs View sequence associated with each feature

qiime2 feature-table transpose Transpose a feature table.

qiime2 feature-table subsample Subsample table

qiime2 feature-table rarefy Rarefy table

qiime2 feature-table heatmap Generate a heatmap representation of a feature table

qiime2 feature-table summarize Summarize table

qiime2 feature-table merge-seqs Combine collections of feature sequences

qiime2 taxa filter-table Taxonomy-based feature table filter.

qiime2 feature-table filter-features Filter features from table

qiime2 feature-table rename-ids Renames sample or feature ids in a table

qiime2 feature-table filter-samples Filter samples from table

qiime2 longitudinal feature-volatility Feature volatility analysis

qiime2 feature-table merge-taxa

Unnamed history

20 shown, 160 deleted, 22 hidden

1.59 GB

180: qiime2 feature-table tabulate-seqs on data 175: visualization.qzv

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

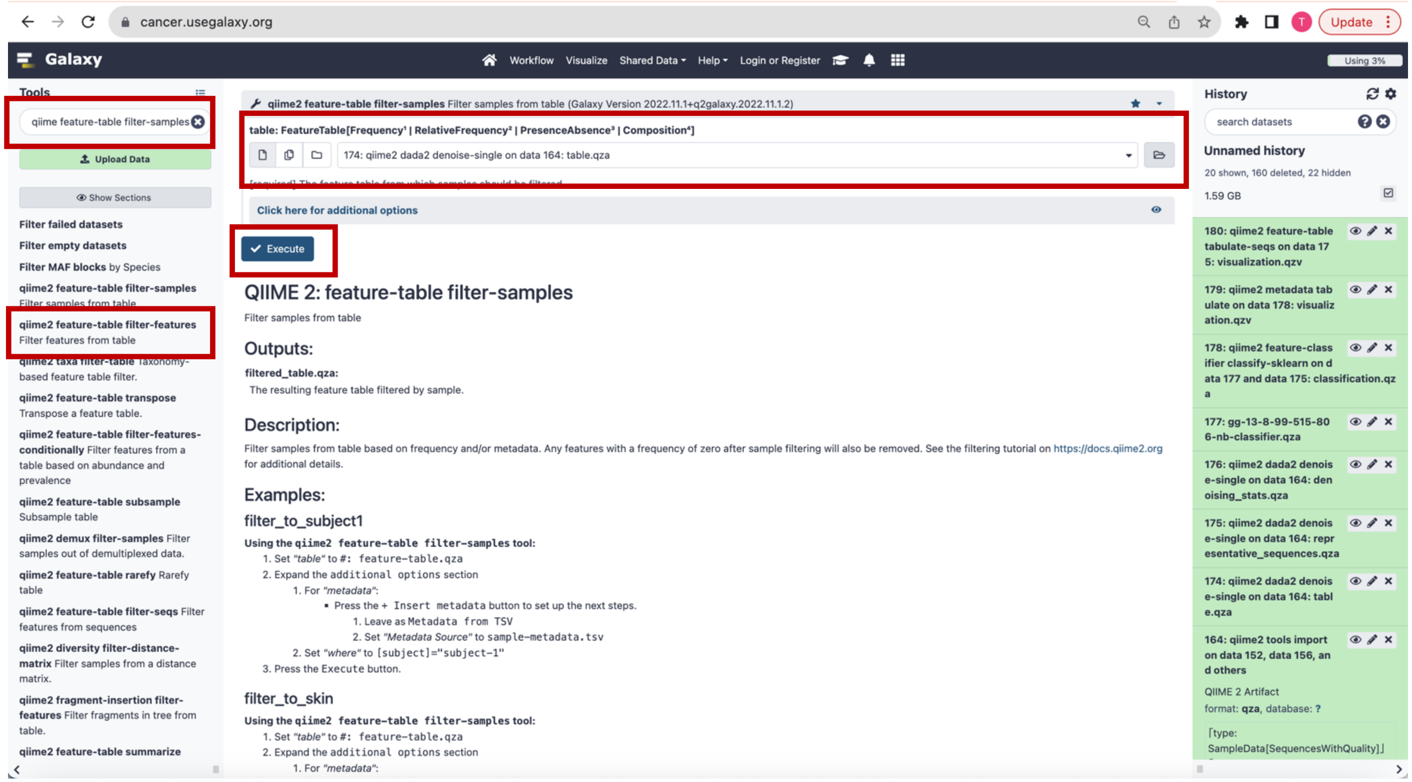
[type: SampleData[SequencesWithQuality]]

Screenshot 30

<u>STEP 13:</u> Run “qiime feature-table filter-samples”.

FOR table:FeatureTable[Frequency^{1}|RelativeFrequency^{2}|PresenceAbsence^{3}|Composition^{4}] SELECT option highlighted in the box.

For this command we must input an additional parameter listed under “Click here for additional options”. Follow screenshots 31 – 33 to fulfill this requirement.



qiime2 feature-table filter-samples Filter samples from table (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

table: FeatureTable[Frequency^{1} | RelativeFrequency^{2} | PresenceAbsence^{3} | Composition^{4}]

174: qiime2 dada2 denoise-single on data 164: table.qza

[required] The feature table from which samples should be filtered.

QIIME 2: feature-table filter-samples

Filter samples from table

Outputs:

filtered_table.qza:
The resulting feature table filtered by sample.

Description:

Filter samples from table based on frequency and/or metadata. Any features with a frequency of zero after sample filtering will also be removed. See the filtering tutorial on https://docs.qiime2.org for additional details.

Examples:

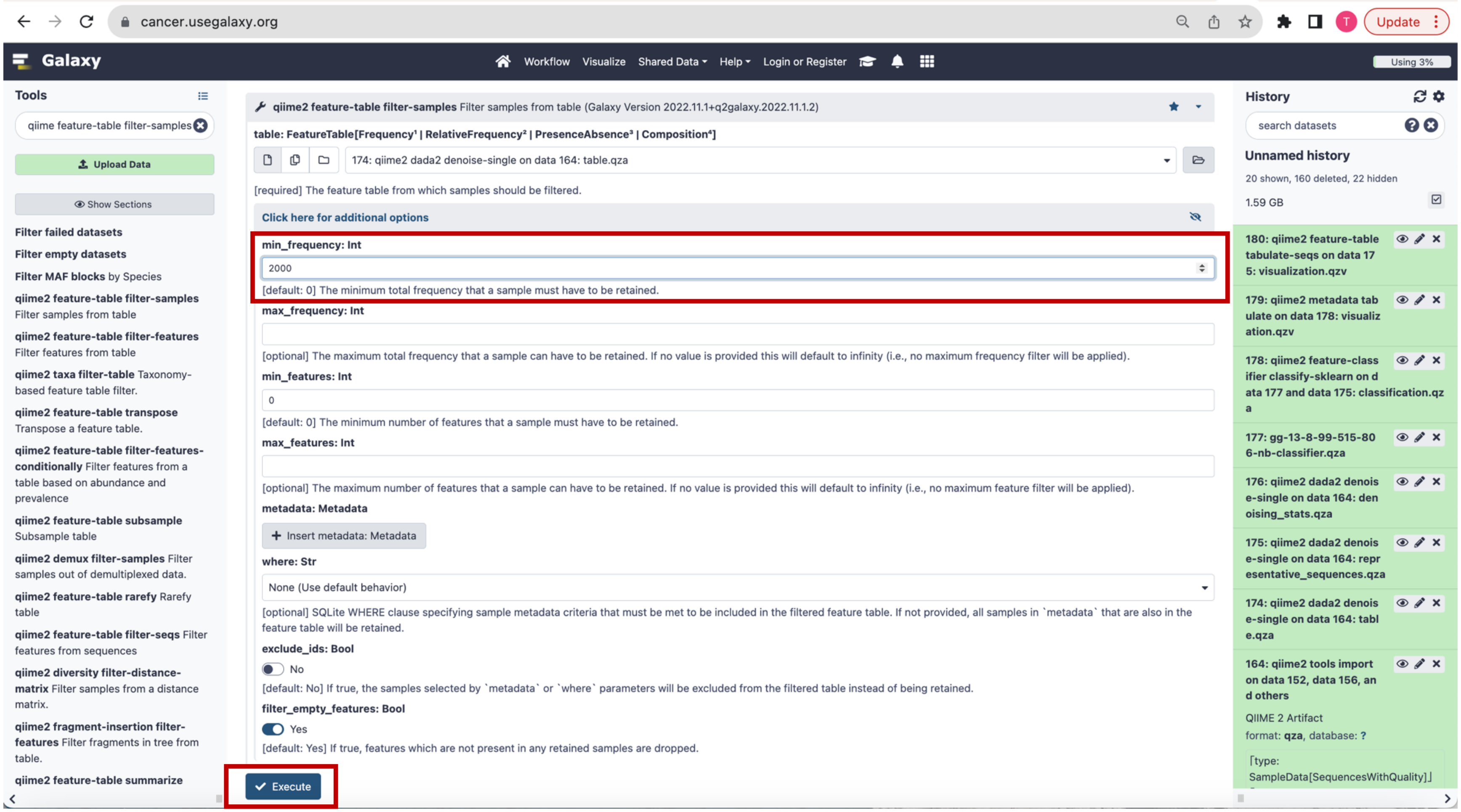
filter_to_subject1

Using the `qiime2 feature-table filter-samples` tool:
1. Set *"table"* to `#: feature-table.qza`
2. Expand the `additional options` section
    1. For *"metadata"*:
        - Press the `+ Insert metadata` button to set up the next steps.
            1. Leave as `Metadata from TSV`
            2. Set *"Metadata Source"* to `sample-metadata.tsv`
    2. Set *"where"* to `[subject]="subject-1"`
3. Press the `Execute` button.

filter_to_skin

Using the `qiime2 feature-table filter-samples` tool:
1. Set *"table"* to `#: feature-table.qza`
2. Expand the `additional options` section
    1. For *"metadata"*:

Screenshot 31



qiime feature-table filter-samples

Filter failed datasets

Filter empty datasets

Filter MAF blocks by Species

qiime2 feature-table filter-samples Filter samples from table

qiime2 feature-table filter-features Filter features from table

qiime2 taxa filter-table Taxonomy-based feature table filter.

qiime2 feature-table transpose Transpose a feature table.

qiime2 feature-table filter-features-conditionally Filter features from a table based on abundance and prevalence

qiime2 feature-table subsample Subsample table

qiime2 demux filter-samples Filter samples out of demultiplexed data.

qiime2 feature-table rarefy Rarefy table

qiime2 feature-table filter-seqs Filter features from sequences

qiime2 diversity filter-distance-matrix Filter samples from a distance matrix.

qiime2 fragment-insertion filter-features Filter fragments in tree from table.

qiime2 feature-table summarize

qiime2 feature-table filter-samples Filter samples from table (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

table: FeatureTable[Frequency¹ | RelativeFrequency² | PresenceAbsence³ | Composition⁴]

174: qiime2 dada2 denoise-single on data 164: table.qza

[required] The feature table from which samples should be filtered.

Click here for additional options

min_frequency: Int

2000

[default: 0] The minimum total frequency that a sample must have to be retained.

max_frequency: Int

[optional] The maximum total frequency that a sample can have to be retained. If no value is provided this will default to infinity (i.e., no maximum frequency filter will be applied).

min_features: Int

0

[default: 0] The minimum number of features that a sample must have to be retained.

max_features: Int

[optional] The maximum number of features that a sample can have to be retained. If no value is provided this will default to infinity (i.e., no maximum feature filter will be applied).

metadata: Metadata

+ Insert metadata: Metadata

where: Str

None (Use default behavior)

[optional] SQLite WHERE clause specifying sample metadata criteria that must be met to be included in the filtered feature table. If not provided, all samples in `metadata` that are also in the feature table will be retained.

exclude_ids: Bool

No

[default: No] If true, the samples selected by `metadata` or `where` parameters will be excluded from the filtered table instead of being retained.

filter_empty_features: Bool

Yes

[default: Yes] If true, features which are not present in any retained samples are dropped.

Unnamed history

20 shown, 160 deleted, 22 hidden

1.59 GB

180: qiime2 feature-table tabulate-seqs on data 175: visualization.qzv

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

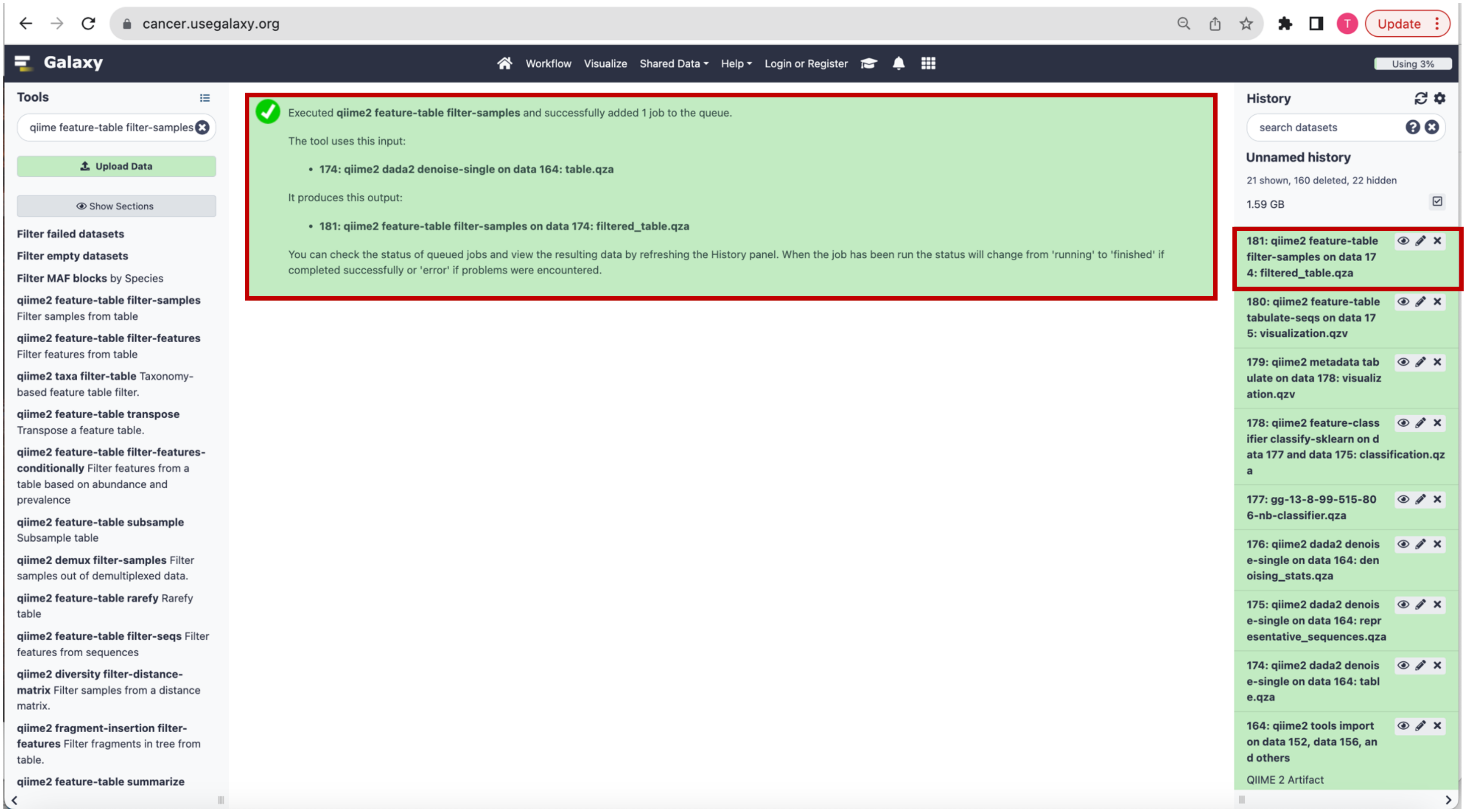
164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

format: **qza**, database: **?**

[type: SampleData[SequencesWithQuality]]

Screenshot 32



Executed **qiime2 feature-table filter-samples** and successfully added 1 job to the queue.

The tool uses this input:

- **174: qiime2 dada2 denoise-single on data 164: table.qza**

It produces this output:

- **181: qiime2 feature-table filter-samples on data 174: filtered_table.qza**

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.

Filter failed datasets

Filter empty datasets

Filter MAF blocks by Species

qiime2 feature-table filter-samples Filter samples from table

qiime2 feature-table filter-features Filter features from table

qiime2 taxa filter-table Taxonomy-based feature table filter.

qiime2 feature-table transpose Transpose a feature table.

qiime2 feature-table filter-features-conditionally Filter features from a table based on abundance and prevalence

qiime2 feature-table subsample Subsample table

qiime2 demux filter-samples Filter samples out of demultiplexed data.

qiime2 feature-table rarefy Rarefy table

qiime2 feature-table filter-seqs Filter features from sequences

qiime2 diversity filter-distance-matrix Filter samples from a distance matrix.

qiime2 fragment-insertion filter-features Filter fragments in tree from table.

qiime2 feature-table summarize

Unnamed history

21 shown, 160 deleted, 22 hidden

1.59 GB

181: qiime2 feature-table filter-samples on data 174: filtered_table.qza

180: qiime2 feature-table tabulate-seqs on data 175: visualization.qzv

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-806-nb-classifier.qza

176: qiime2 dada2 denoise-single on data 164: denoising_stats.qza

175: qiime2 dada2 denoise-single on data 164: representative_sequences.qza

174: qiime2 dada2 denoise-single on data 164: table.qza

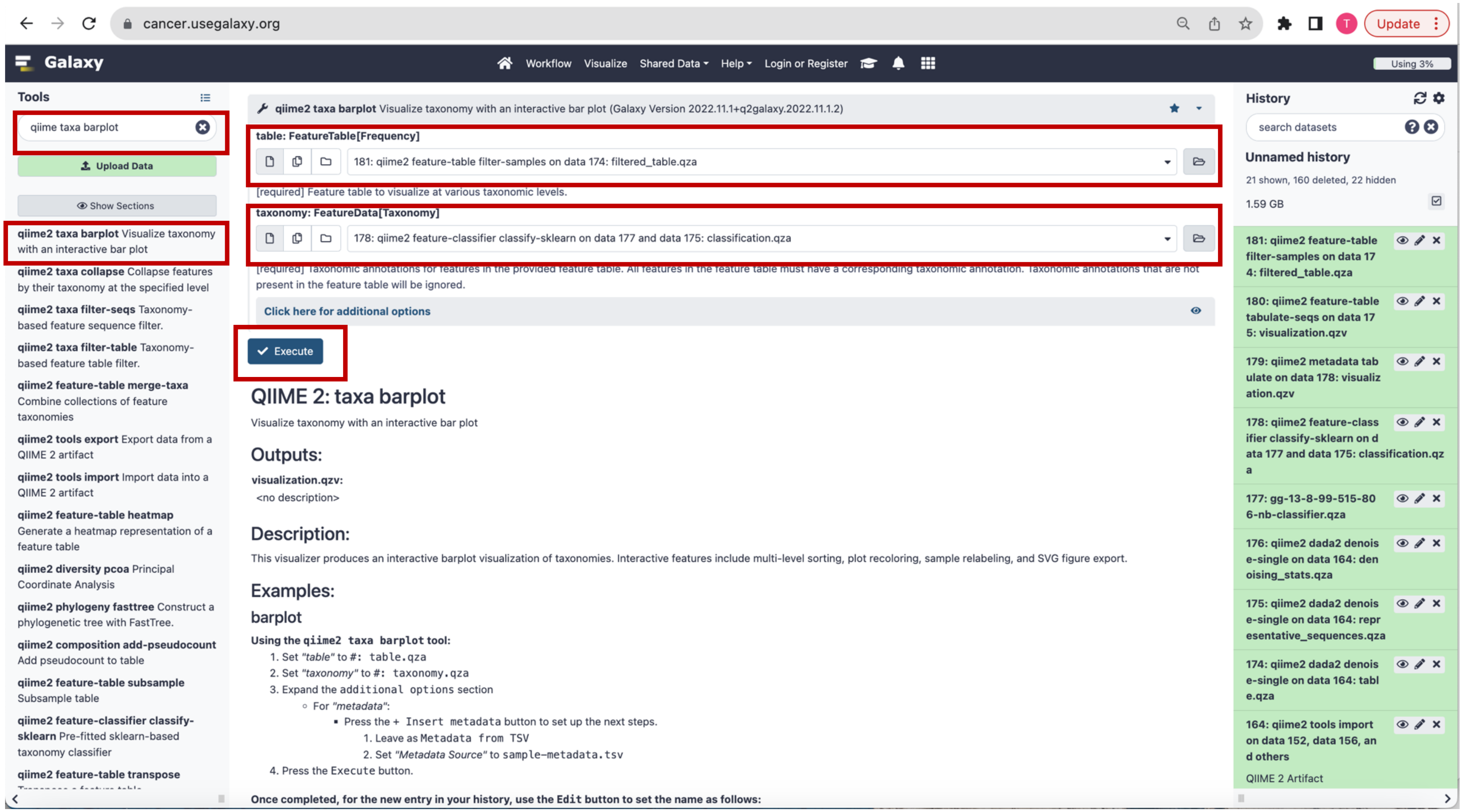
164: qiime2 tools import on data 152, data 156, and others

QIIME 2 Artifact

Screenshot 33

STEP 13: Run “qiime2 taxa barplot”.

FOR table:FeatureTable[Frequency] AND taxonomy:FeatureData[Taxonomy] SELECT options highlighted in the box AND “Execute” as shown in screenshot 34 – 36.



qiime2 taxa barplot Visualize taxonomy with an interactive bar plot (Galaxy Version 2022.11.1+q2galaxy.2022.11.1.2)

table: FeatureTable[Frequency]

181: qiime2 feature-table filter-samples on data 174: filtered_table.qza

[required] Feature table to visualize at various taxonomic levels.

taxonomy: FeatureData[Taxonomy]

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

[required] Taxonomic annotations for features in the provided feature table. All features in the feature table must have a corresponding taxonomic annotation. Taxonomic annotations that are not present in the feature table will be ignored.

Click here for additional options

Execute

QIIME 2: taxa barplot

Visualize taxonomy with an interactive bar plot

Outputs:

visualization.qzv:

<no description>

Description:

This visualizer produces an interactive barplot visualization of taxonomies. Interactive features include multi-level sorting, plot recoloring, sample relabeling, and SVG figure export.

Examples:

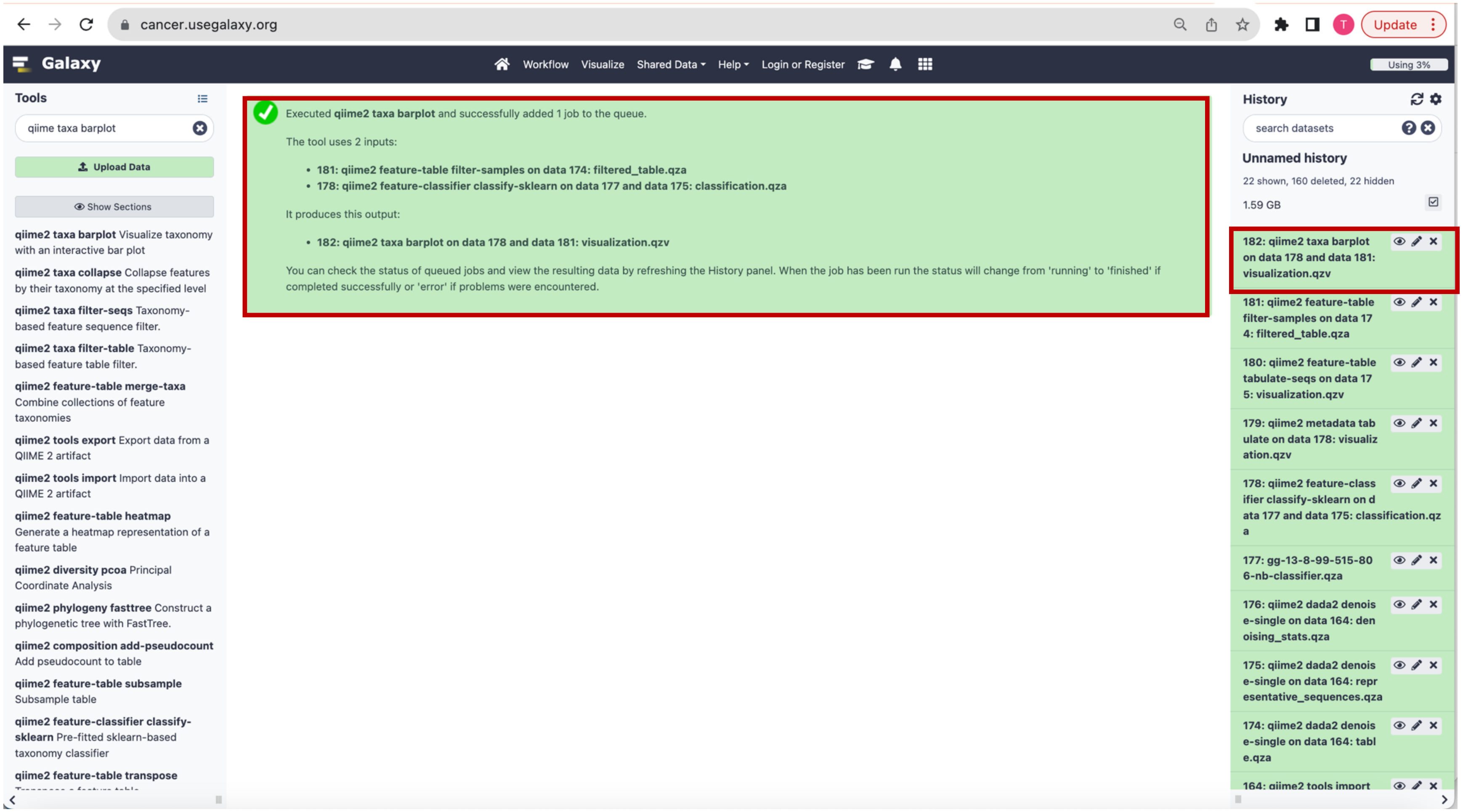
barplot

Using the `qiime2 taxa barplot` tool:

1. Set *"table"* to `#: table.qza`
2. Set *"taxonomy"* to `#: taxonomy.qza`
3. Expand the `additional options` section
   - For *"metadata"*:
     - Press the `+ Insert metadata` button to set up the next steps.
       1. Leave as `Metadata from TSV`
       2. Set *"Metadata Source"* to `sample-metadata.tsv`
4. Press the `Execute` button.

Once completed, for the new entry in your history, use the `Edit` button to set the name as follows:

Screenshot 34



Executed **qiime2 taxa barplot** and successfully added 1 job to the queue.

The tool uses 2 inputs:

- **181: qiime2 feature-table filter-samples on data 174: filtered_table.qza**
- **178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza**

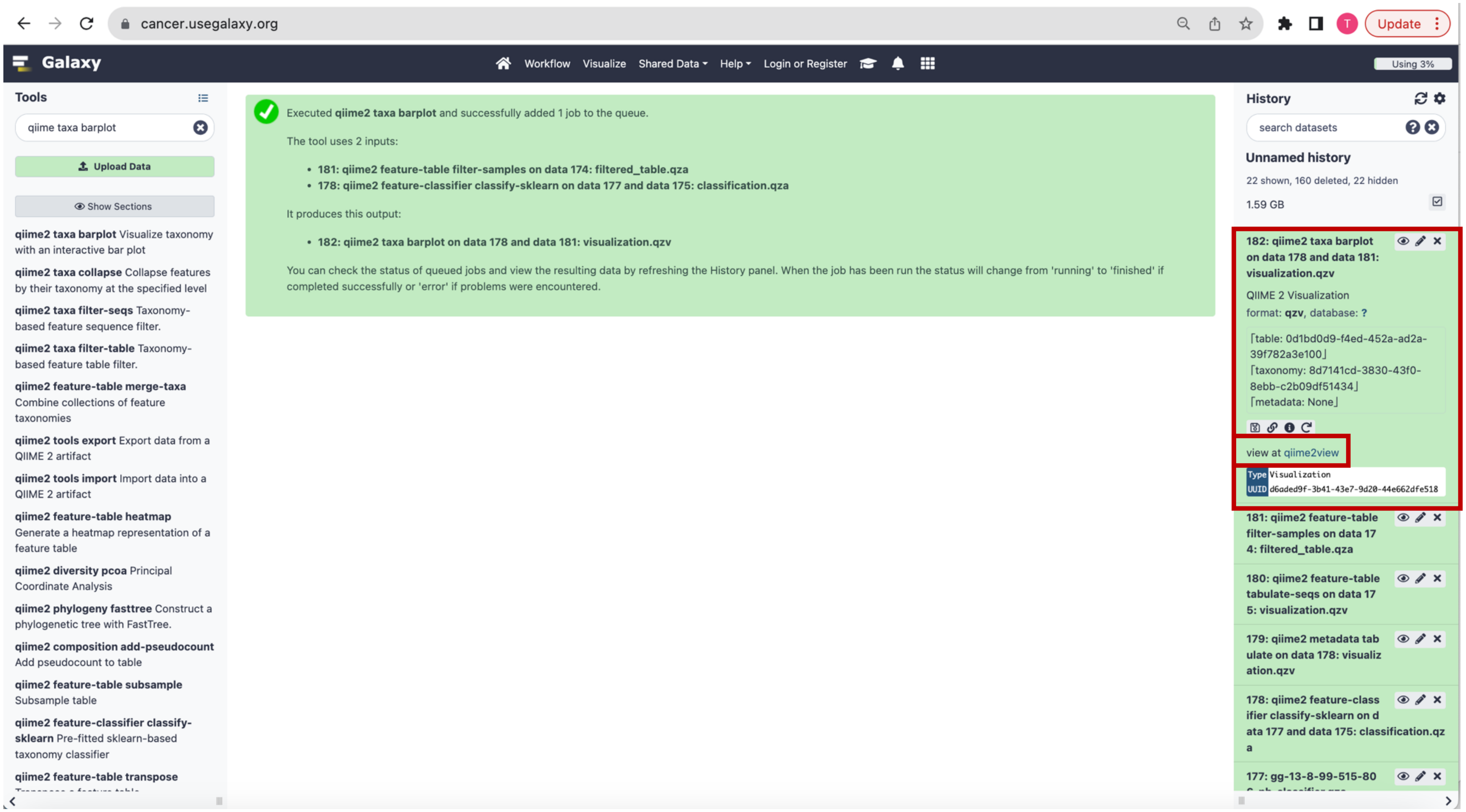
It produces this output:

- **182: qiime2 taxa barplot on data 178 and data 181: visualization.qzv**

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.

Screenshot 35

To visualize the taxonomies, click “view at qiime2view” option listed in the right-hand box. This will open a new page in the browser. It will be an interactive page which will let user interactively explore the taxonomies in different samples. An example screenshot of the webpage is shown in screenshot 37.



Executed **qiime2 taxa barplot** and successfully added 1 job to the queue.

The tool uses 2 inputs:

- **181: qiime2 feature-table filter-samples on data 174: filtered_table.qza**
- **178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza**

It produces this output:

- **182: qiime2 taxa barplot on data 178 and data 181: visualization.qzv**

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.

qiime2 taxa barplot Visualize taxonomy with an interactive bar plot

qiime2 taxa collapse Collapse features by their taxonomy at the specified level

qiime2 taxa filter-seqs Taxonomy-based feature sequence filter.

qiime2 taxa filter-table Taxonomy-based feature table filter.

qiime2 feature-table merge-taxa Combine collections of feature taxonomies

qiime2 tools export Export data from a QIIME 2 artifact

qiime2 tools import Import data into a QIIME 2 artifact

qiime2 feature-table heatmap Generate a heatmap representation of a feature table

qiime2 diversity pcoa Principal Coordinate Analysis

qiime2 phylogeny fasttree Construct a phylogenetic tree with FastTree.

qiime2 composition add-pseudocount Add pseudocount to table

qiime2 feature-table subsample Subsample table

qiime2 feature-classifier classify-sklearn Pre-fitted sklearn-based taxonomy classifier

qiime2 feature-table transpose

Unnamed history

22 shown, 160 deleted, 22 hidden

1.59 GB

182: qiime2 taxa barplot on data 178 and data 181: visualization.qzv

QIIME 2 Visualization

format: **qzv**, database: **?**

⌈table: 0d1bd0d9-f4ed-452a-ad2a-39f782a3e100⌋
⌈taxonomy: 8d7141cd-3830-43f0-8ebb-c2b09df51434⌋
⌈metadata: None⌋

view at qiime2view

Type	Visualization
UUID	d6aded9f-3b41-43e7-9d20-44e662dfe518

181: qiime2 feature-table filter-samples on data 174: filtered_table.qza

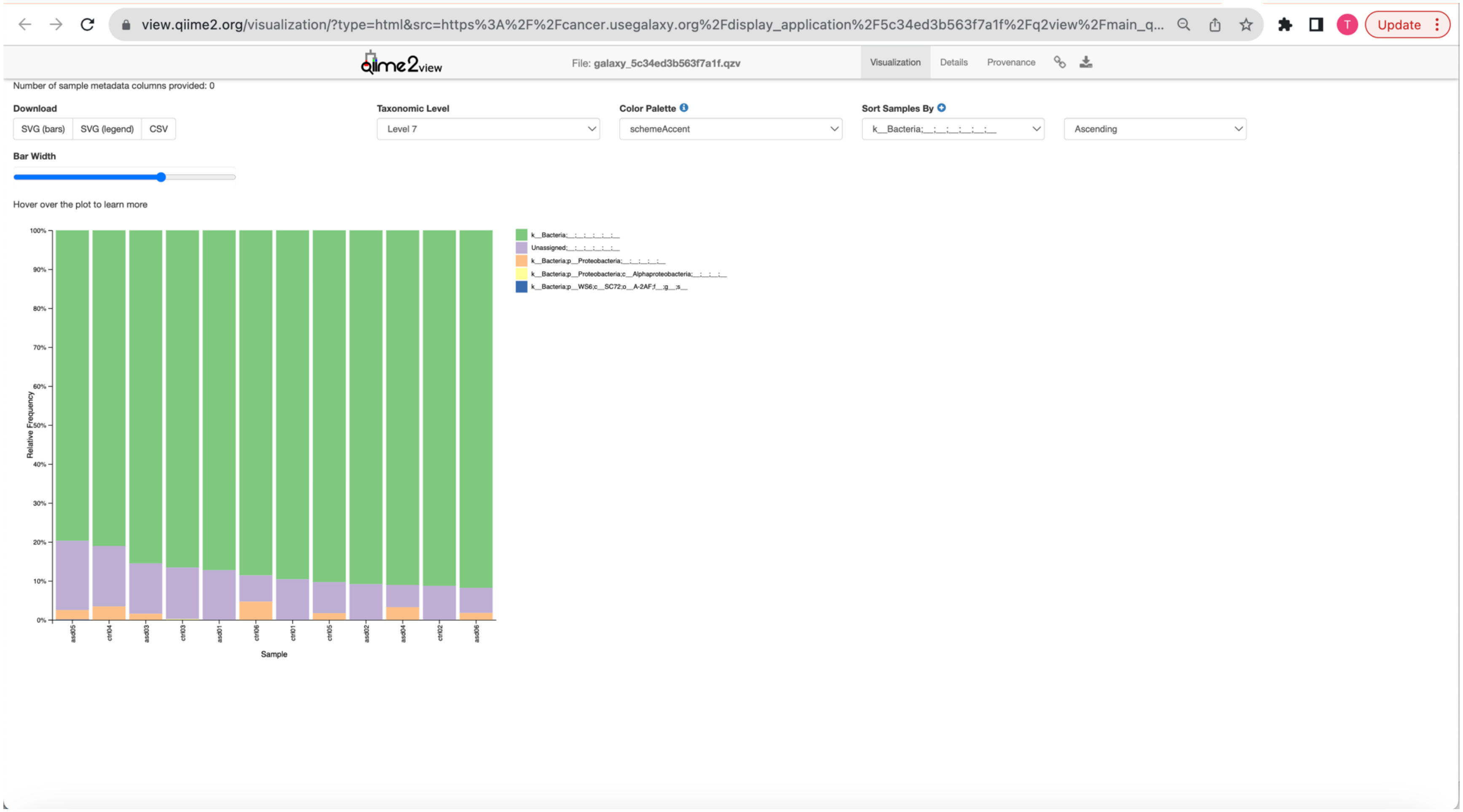
180: qiime2 feature-table tabulate-seqs on data 175: visualization.qzv

179: qiime2 metadata tabulate on data 178: visualization.qzv

178: qiime2 feature-classifier classify-sklearn on data 177 and data 175: classification.qza

177: gg-13-8-99-515-80

Screenshot 36



File: galaxy_5c34ed3b563f7a1f.qzv

Number of sample metadata columns provided: 0

Download

Taxonomic Level: Level 7

Color Palette: schemeAccent

Sort Samples By: k__Bacteria;__;__;__;__;__;__ — Ascending

Bar Width

Hover over the plot to learn more

- 🟩 k__Bacteria;__;__;__;__;__;__
- 🟪 Unassigned;__;__;__;__;__;__
- 🟧 k__Bacteria;p__Proteobacteria;__;__;__;__;__
- 🟨 k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;__;__;__;__
- 🟦 k__Bacteria;p__WS6;c__SC72;o__A-2AF;f__;g__;s__

Screenshot 37

Preliminary results from this analysis represents similar results described in the published article.

Reference: Chiappori, F., Cupaioli, F.A., Consiglio, A., Di Nanni, N., Mosca, E., Licciulli, V.F. and Mezzelani, A., 2022. Analysis of Faecal Microbiota and Small ncRNAs in Autism: Detection of miRNAs and piRNAs with Possible Implications in Host–Gut Microbiota Cross-Talk. Nutrients, 14(7), p.1340.